#### **Supplementary information file**

Concerning the manuscript with the title 'Reduced fatty acid uptake aggravates cardiac contractile dysfunction in streptozotocin-induced diabetic cardiomyopathy'

#### **Authors**

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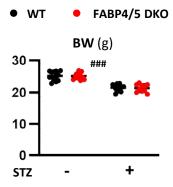
#### **Supplemental Methods**

#### **Cross sectional area**

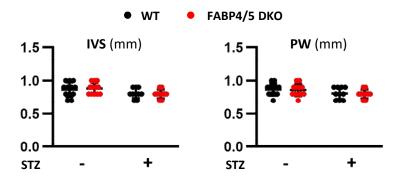
Hearts were fixed with 10% formalin, embedded in paraffin and sectioned into 8 μm slices. To assess cardiomyocyte cross-sectional area, tissue was stained with wheat germ agglutinin (WGA; plasma membrane staining, Alexa Fluor 488 conjugated).

#### RNA isolation and real time PCR

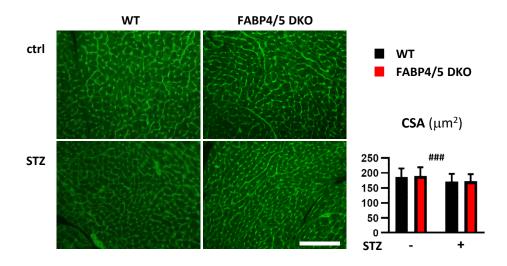
Total RNA was isolated from hearts using the TRIzol Reagent (Invitrogen). Quantitative real-time PCR was performed with SYBR Green PCR Master Mix (Applied Biosystems), according to the manufacturer's instructions. The expression level of the target gene was normalized to the GAPDH (glyceraldehyde-3-phosphate dehydrogenase) mRNA level. The ready-to-use gene-specific primers for cDNA (Perfect Real Time Primer) were purchased from Takara Bio Inc. (Shiga, Japan).



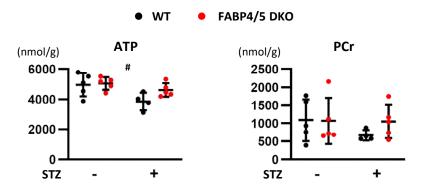
**Figure S1**. Body weight (BW) was significantly reduced by STZ treatment (n=10-12). STZ  $^{\#\#\#}$ p<0.001.



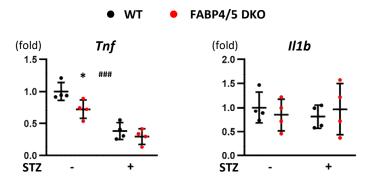
**Figure S2.** Wall thickness of left ventricles estimated by echocardiography (n=10-12). IVS; interventricular septum, PW; posterior wall.



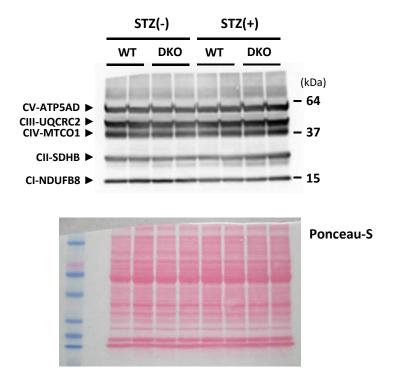
**Figure S3.** Cross sectional area (CSA) was reduced by STZ treatment in both mice (n=6). Scale bar = 100 mm. STZ ###p<0.001.



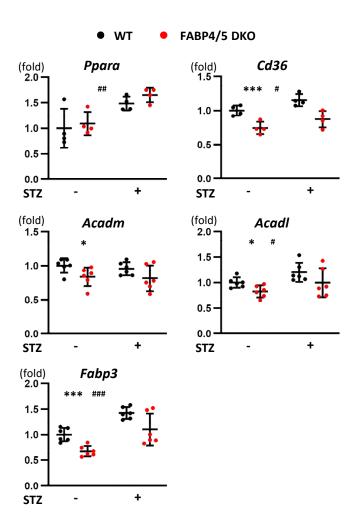
**Figure S4.** ATP and PCr levels measured by metabolome analysis (n=4-5). ATP; adenosine triphosphate, PCr; creatinine phosphate. STZ \*p<0.05.



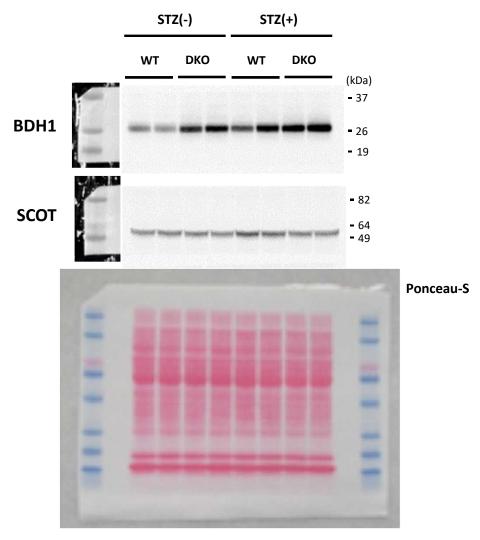
**Figure S5.** Expression levels of mRNA for *Tnf* and *Il1b* (n=4). Tnf: tumor necrosis factor  $\alpha$ , Il1b; interleukin-1 $\beta$ . DKO \*p<0.05, STZ ###p<0.001.



**Figure S6.** Full length western blots of representative proteins in mitochondrial electron transport chain complex. Equal amount of loaded protein was confirmed by ponceau-S staining. The 1<sup>st</sup> antibody used was total OXPHOS rodent western blot antibody cocktail (Abcam110413, MA). CV-ATP5A; complex V-ATP synthase subunit alpha, CIII-UQCRC2; complex III-cytochrome b-c1 complex subunit 2, CIV-MTCO1; complex IV-cytochrome c oxidase subunit 1, CII-SDHB; complex II-succinate dehydrogenase subunit B, CI-NDUFB8; complex I- NADH dehydrogenase (ubiquinpone) 1 beta subunit 8.



**Figure S7.** Expression levels of mRNA for *Ppara, Cd36, Acadm, Acadl* and *Fabp3* (n=6). Ppara: peroxisome proliferator activated receptor  $\alpha$ , Acadm; acyl-CoA dehydrogenase medium chain, Acadl; acyl-CoA dehydrogenase long chain, Fabp3; fatty acid binding protein 3. DKO \*p<0.05, \*\*\* p<0.001, STZ \*p<0.05, \*\*\* p<0.01.



**Figure S8.** Full length western blots of figure 3B. Membranes were cut after ponceau-S staining to save 1<sup>st</sup> antibodies.

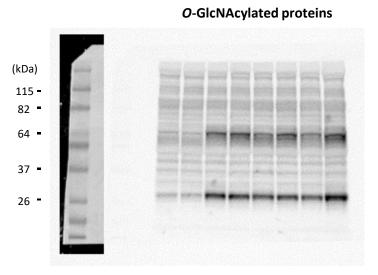


Figure S9. Full length western blot of figure 5B.