Supplementary Information

Loss of progesterone receptor membrane component 1 promotes hepatic steatosis via the induced *de novo* lipogenesis

Sang R. Lee¹, Sun Woo Kwon¹, Pelin Kaya¹, Young Ho Lee¹, Jong Geol Lee², Globinna Kim², In-Jeoung Baek^{2*}, and Eui-Ju Hong^{1*}

¹Laboratory of Biochemistry, College of Veterinary Medicine, Chungnam National University, Daejeon 34134, Republic of Korea
²Department of Convergence Medicine, University of Ulsan College of Medicine, Asan Medical Center, Seoul 05505, Republic of Korea.

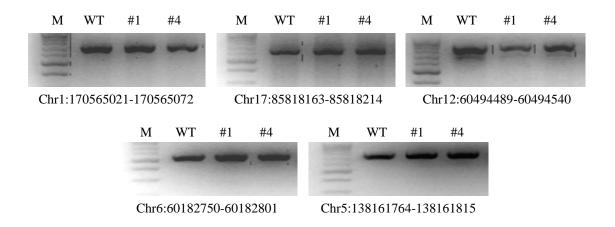


Fig. S1. Analysis of off-target effects of TALEN targeting the *Pgrmc1* gene. T7E1 assays examining the putative off-target effects of *Pgrmc1*-TALEN. The integrity of potential off-target sites as listed in Table 1 was examined in founder mice.

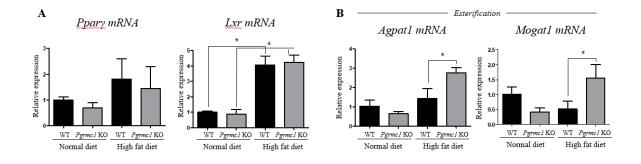


Fig. S2. Transcriptional regulators and TG esterification enzymes related to *Srebp1* gene. Major fatty acid synthesis transcriptional regulator genes which are on the crosstalk with SREBP-1 (A). Genes regulates TG esterification in liver (B). After fed a high fat diet for 1 month, mRNA levels were determined by quantitative RT-PCR. *Rplp0* mRNA was used as an internal control. Values represent means \pm SD at least 3 experiments. *, P<0.05. Number of mice used in experiment for normal diet group is at least 3 and for high fat diet groups is at least 4 for each group.

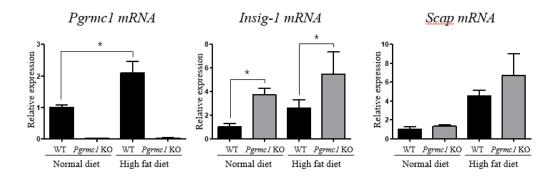


Fig. S3. Structural components related to *Srebp-1* gene. Genes forming complex with *Srebp-1* in endoplasmic reticulum. After fed a high fat diet for 1 month, mRNA levels were determined by quantitative RT-PCR. *Rplp0* mRNA was used as an internal control. Values represent means \pm SD at least 3 experiments. *, P<0.05. Number of mice used in experiment for normal diet group is at least 3 and for high fat diet groups is at least 4 for each group.

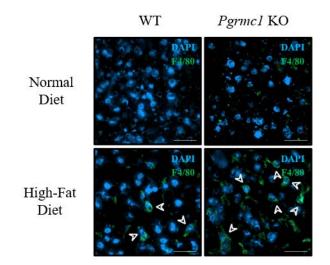


Fig. S4. Immunofluorescence staining of mouse macrophage marker, F4/80. Cytoplasm stained with green represents positive for F4/80. Nucleus stained with blue representing DAPI was used as an internal control. Number of mice used in experiment for normal diet group is at least 3 and for high fat diet groups is at least 4 for each group.

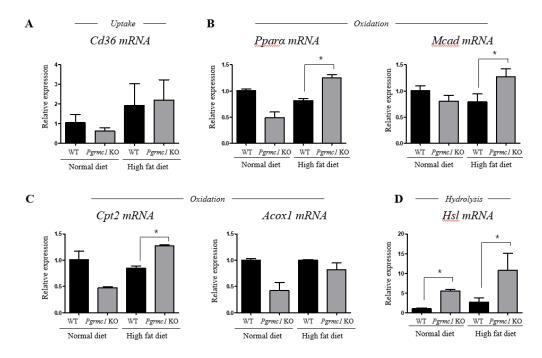


Fig. S5. Levels of fatty acid metabolic genes increased with TG accumulation. Genes related to fatty acid uptake, oxidation, and hydrolysis (A - D). After fed a high fat diet for 1 month, mRNA levels were determined by quantitative RT-PCR. *Rplp0* mRNA was used as an internal control. Values represent means \pm SD at least 3 experiments. *, P<0.05. Number of mice used in experiment for normal diet group is at least 3 and for high fat diet groups is at least 4 for each group.

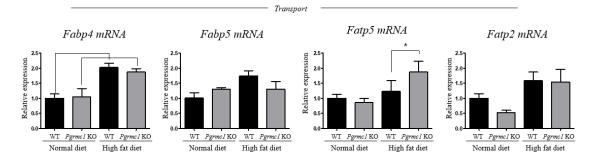


Fig. S6. Levels of fatty acid transport related genes. After fed a high fat diet for 1 month, mRNA levels were determined by quantitative RT-PCR. *Rplp0* mRNA was used as an internal control. Values represent means \pm SD at least 3 experiments. *, P<0.05. Number of mice used in experiment for normal diet group is at least 3 and for high fat diet groups is at least 4 for each group.

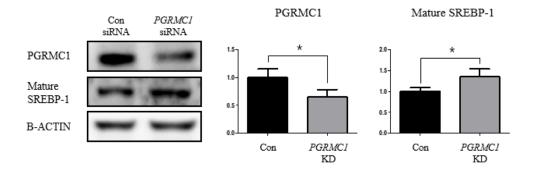


Fig. S7. Level of mature SREBP-1 protein in *PGRMC1* siRNA transfection. After transfected with siRNA, cells were treated with fatty acids (Palmitic acid; 330 μ M, Oleic acid; 660 μ M) for 24 hrs. Beta actin was used as an internal control. Values represent means \pm SD at least 3 experiments. *, P<0.05. All experiments were repeated at least 3 times.

|

Fig. 1B

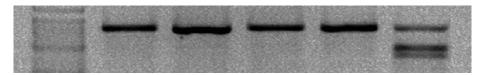
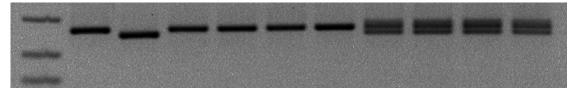
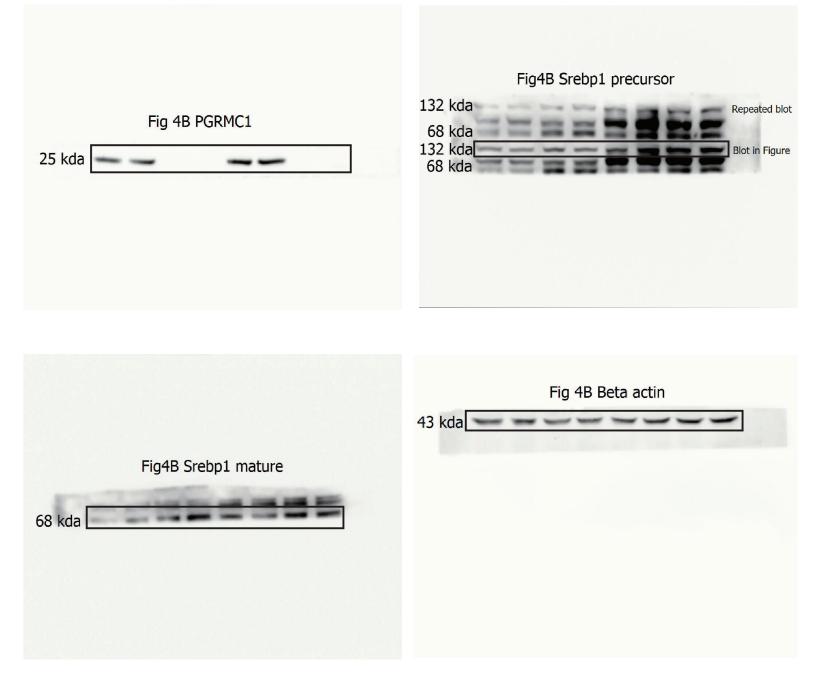
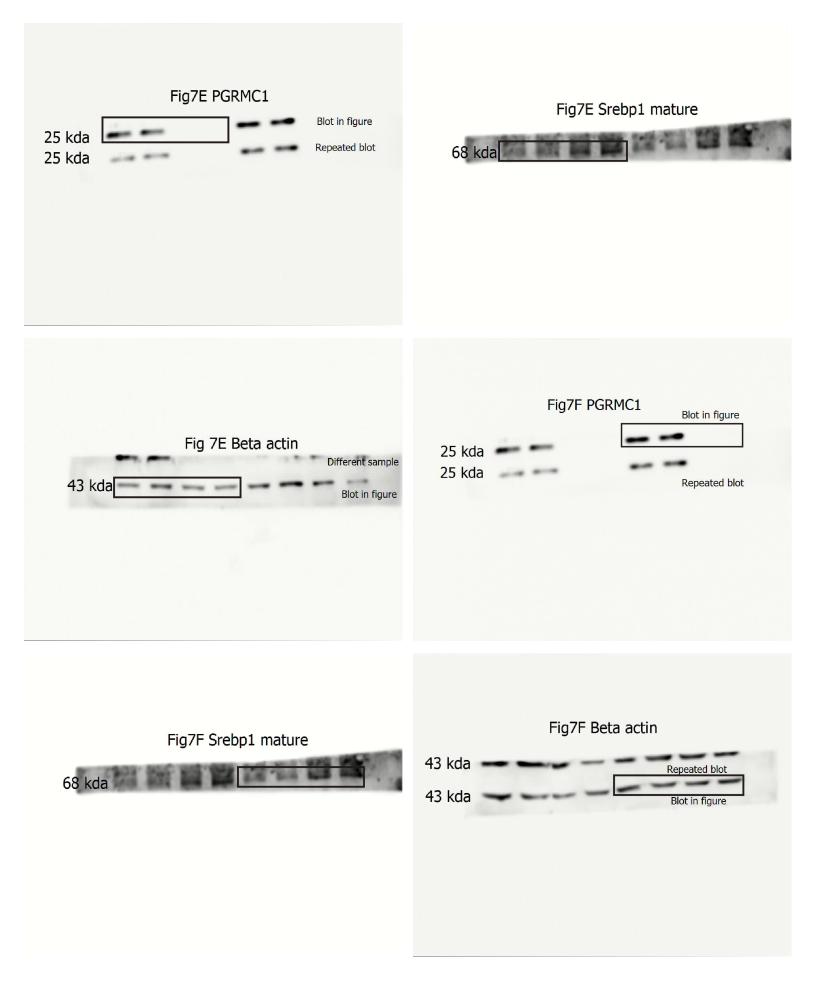
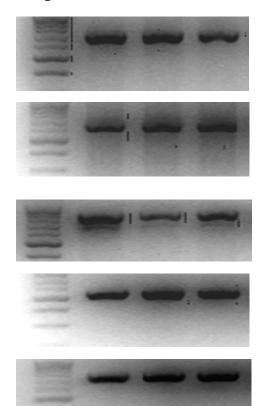


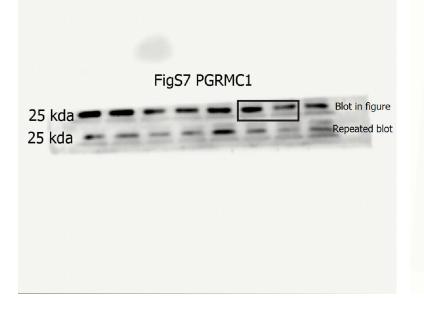
Fig. 1C











FigS7 Srebp1 mature

