Deletion of Cardiomyocyte GSK-3β Improves Systemic Glucose Tolerance with Maintained Heart Function in Established Obesity

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RNA Extraction and Quantitative PCR Analysis

Total RNA was extracted from heart tissue using the RNeasy Mini Kit (74104, Qiagen, Hilden, Germany) according to manufacturer's protocol. cDNA was synthesized using the iScript cDNA synthesis kit (170-8891, Bio-Rad Laboratories, Hercules, CA, USA) following manufacturer's instructions. Gene expression was analyzed by quantitative PCR (qPCR) using the TaqMan Gene Expression Master Mix (4369016, Applied Biosystems, Foster City, CA, USA) and TaqMan gene expression assays as specified in the table immediately below. The assay was performed with a Bio-Rad CFX96 Real-Time PCR Detection machine (Bio-Rad Laboratories, Hercules, CA, USA) . Relative gene expression was determined by using the comparative CT method ($2^{-\Delta\Delta C}$ T) and was represented as fold change. Briefly, the first ΔCT is the difference in threshold cycle between the target and reference genes: $\Delta CT = CT$ (a target gene X) – CT (18SrRNA) while $\Delta\Delta CT$ is the difference in ΔCT as described in the above formula between the CTL and KO group, which is = ΔCT (KO target gene X) – ΔCT (CTL target gene X). Fold change is calculated using $2^{-\Delta\Delta CT}$ equation.

| Gene | Assay ID | Cat. No. | |
|--------------------|-----------------------|----------|--|
| Nppa (ANP) | Mm01255747_g1 | 4331182 | |
| Nppb (BNP) | Mm01255770_g1 | 4331182 | |
| Eukarvotic 18S rRN | NA Endogenous Control | 4319413E | |

Table S1. TaqMan gene expression assays used for the quantification of fetal gene program.

| Table S2. Detailed list of different antibodies used and application | ations. |
|--|---------|
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| S. No. | Antibody | Vendor | Catalog No | Dilution | Application |
|--------|---------------------------|----------------|------------|----------|------------------|
| 1 | Beta-Catenin | Cell Signaling | 9562 | 1:1000 | Western Blotting |
| 2 | phospho-GSK-3α/β(Ser21/9) | Cell Signaling | 9331 | 1:1000 | Western Blotting |
| 3 | GAPDH | Fitzgerald | 10R-G109a | 1:10,000 | Western Blotting |
| 4 | GSK-3α/β | Cell Signaling | 5676 | 1:1000 | Western Blotting |
| 5 | p-ERK | Cell Signaling | 4370 | 1:1000 | Western Blotting |
| 6 | T-ERK | Santacruz | 93 | 1:1000 | Western Blotting |
| 7 | p-JNK | Cell Signaling | 9255 | 1:1000 | Western Blotting |
| 8 | t-JNK | Cell Signaling | 9252 | 1:1000 | Western Blotting |
| 9 | p-p38 | Cell Signaling | 9211 | 1:1000 | Western Blotting |
| 10 | P38 | Santacruz | 535 | 1:1000 | Western Blotting |
| 11 | p-AKT | Cell Signaling | 4060 | 1:1000 | Western Blotting |
| 12 | t-AKT | Cell Signaling | 4691 | 1:1000 | Western Blotting |



Figure S1. Comparable expression of GSK-3 α / β in the skeleton muscle of controls and CM-GSK-3 β KOs.



Figure S2. A strong trend of fetal gene program activation in high fat fed CM-GSK-3β KOs. CD–WT, N = 3; CD–KO, N = 5; HFD–WT, N = 6; HFD–KO, N = 5.