Supplemental Information

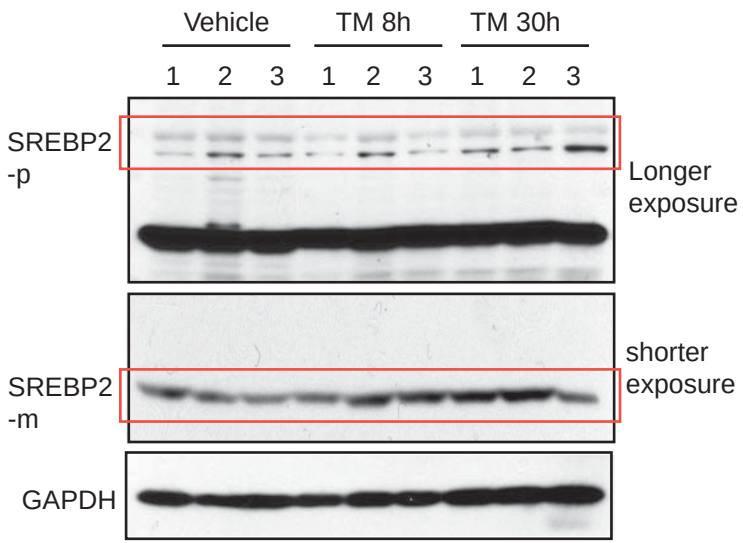
Supplemental figure 1. Cleavage of SREBP2 in the liver of mice challenged with TM**.** Western blot analysis of protein levels of SREBP in the liver tissues from the mice challenged with TM (2 μg/gram body weight) or vehicle control. Levels of GAPDH were included as internal controls. The SREBP2 precursor signals in the liver tissue samples can only be visible after relatively long time exposure of the film to the membrane. A protein signal image from a relatively short time exposure of the film, which only showed the mature SREBP2, was also included. The graph beside the images showed the ratios of mature/cleaved SREBP2 to precursor SREBP in the liver of mice challenged with TM or vehicle. The protein signal intensities shown by Western blot analysis were quantified by NIH imageJ software. Each bar represents the mean ± SEM (n=3 mice per group); ** $p<0.01$. SREBP-p, SREBP precursor; SREBP-m, mature/cleaved SREBP.

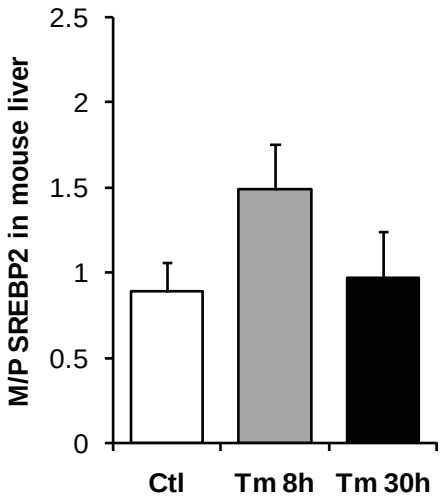
Supplemental figure 2. Quantitative real-time RT-PCR analysis of levels of mRNAs encoding DGAT1, DGAT2, FSP27, PGC1α, ApoC2, LSR, and PPARα in the liver of mice challenged with TM (2 μg/gram body weight) or vehicle control for 8 or 30 hours. The analysis was performed by using two internal controls, Gapdh and Hprt1, which is reported to provide accurate measurements of gene expression {Vandesompele, 2002 #6553}. Normalization factors were calculated as previously described {Walker, 2009 #6554}. The normalization factors were derived from the geometric mean of the C_T values of the two controls. RQ values were calculated by the comparative C_T method. Fold changes of mRNA are shown by comparing to one of the control mice. Each bar denotes the mean ± SEM (n=4 mice per group); * $P<0.05$; ** $P<0.01$.

Supplemental figure 3. Quantitative real-time RT-PCR analysis of the mRNAs encoding FASN (A), ADRP (B), SCD1 (C), and ACC1 (D) in Huh7 cells. Total RNAs were isolated from Huh-7 cells treated with TM (5, 10, and 20 μg/ml) for 6, 12 and 24 hours. Fold changes of mRNA are shown by comparing to the vehicle-treated control (defined as 1). Normalization was calculated by using β-actin mRNA levels as an internal control .Each bar denotes mean ± SEM (n= 3). * $p<0.05$; ** $p<0.01$.

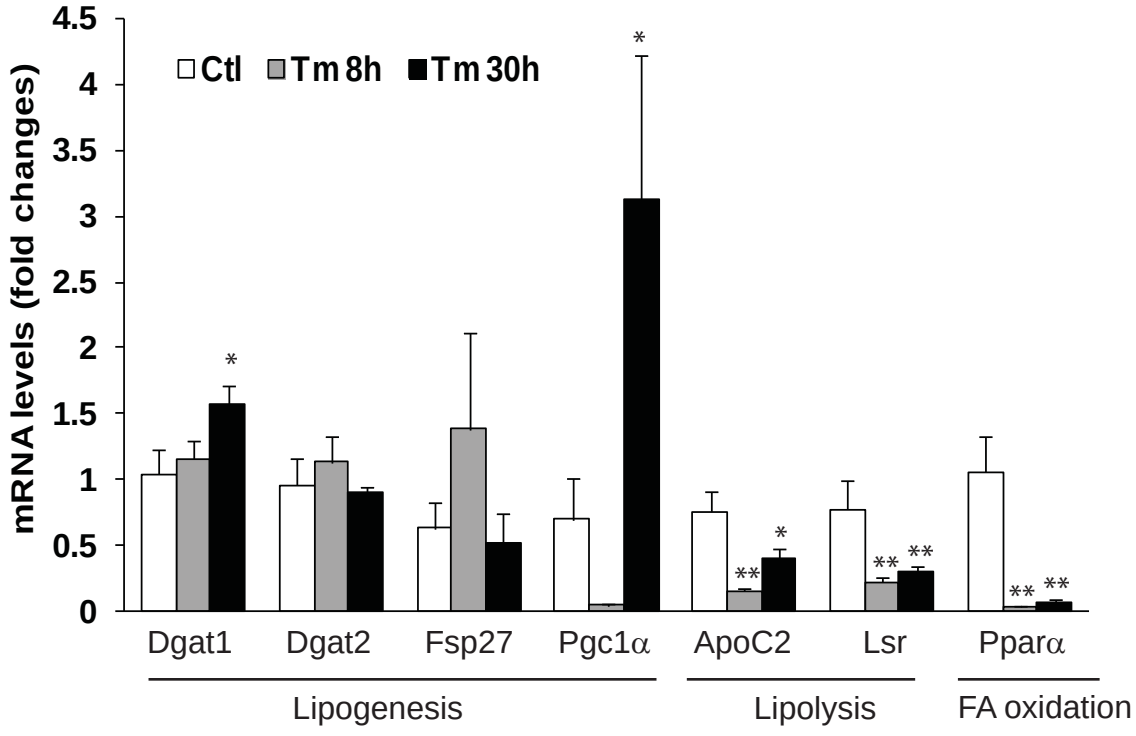
Supplemental figure 4. A working model by which TM-induced ER stress causes hepatic steatosis and inflammation in the liver.

Supplemental information 5. Sequence information for the real-time PCR analysis in this study.



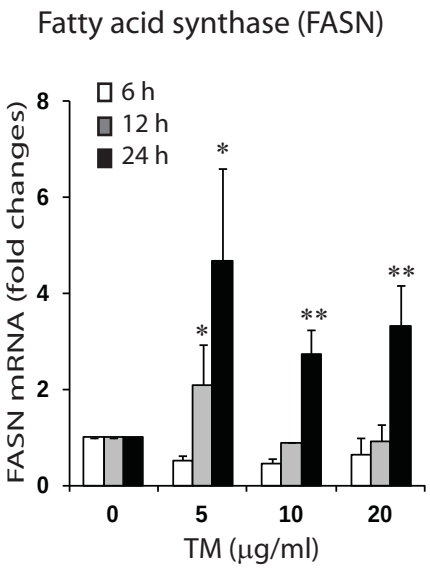


Supplemental figure 1



Supplemental figure 2

A



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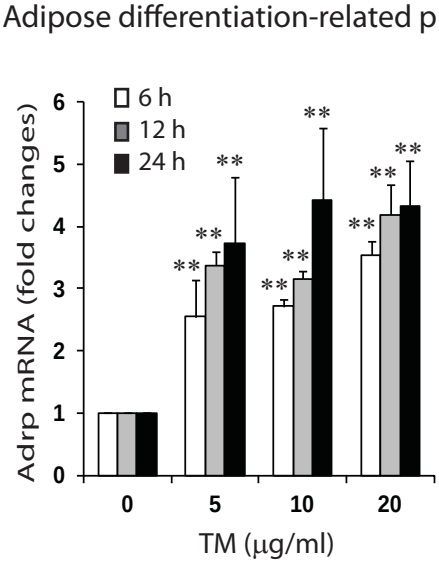

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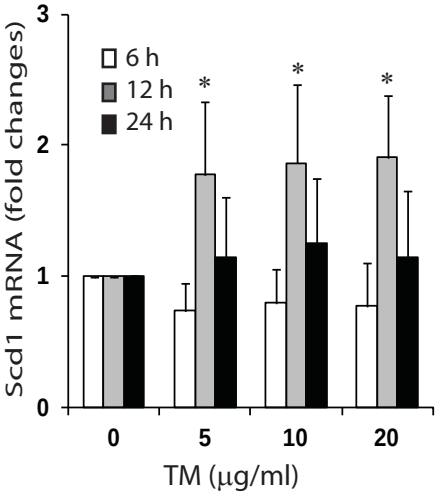

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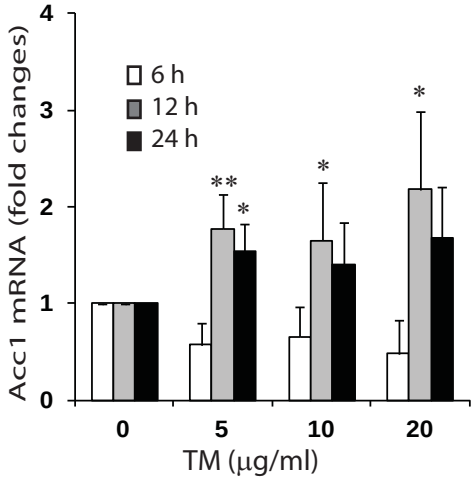
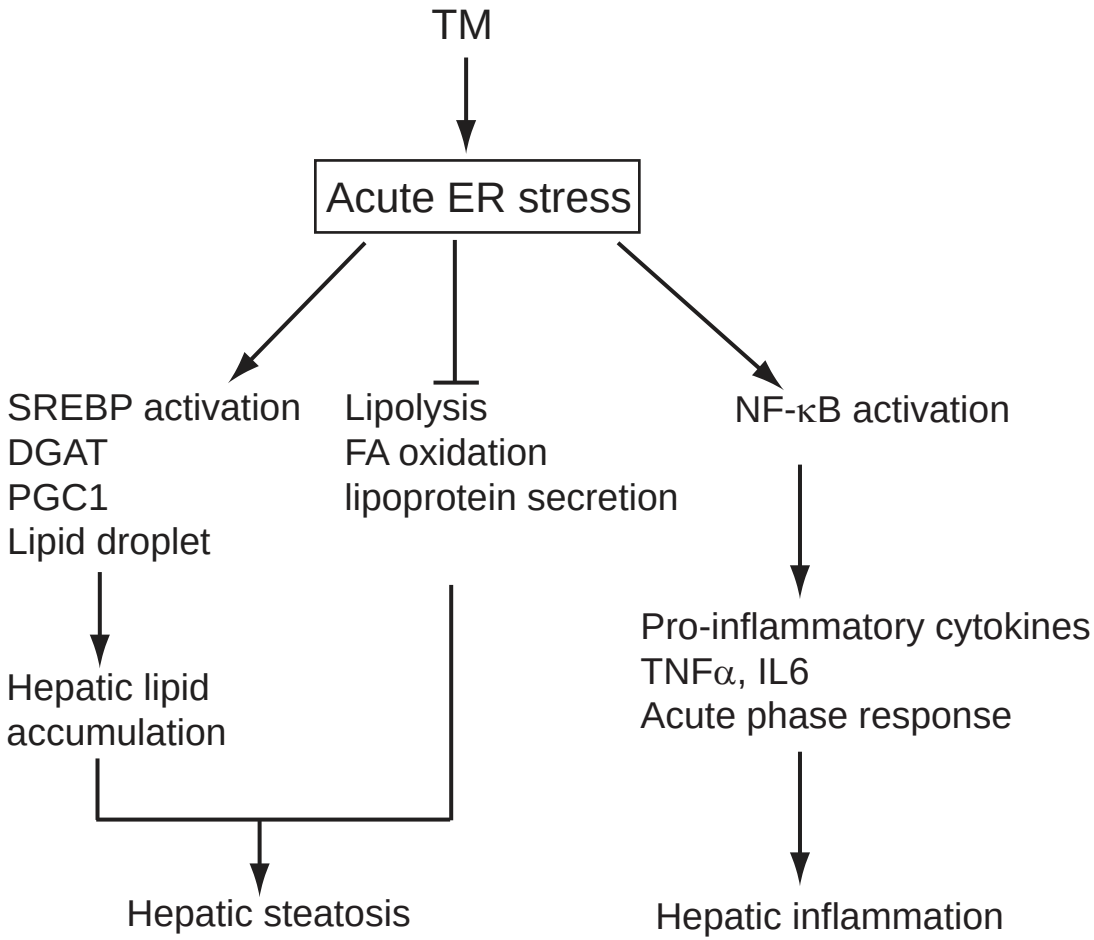


Supplemental figure 3



Supplemental figure 4

Supplemental information 5. Sequence information for the real-time PCR analysis in this study

Gene name	Forward primer	Reverse primer
Pgc1α	TATGGAGTGACATAGAGTGTGCT	CCACTTCAATCCACCCAGAAAG
Pgc1β	TCCTGTAAAAGCCCGGAGTAT	GCTCTGGTAGGGGCAGTGA
PPARα	GAAGGGCACACGCGTGCGAGTTTTCAG	CTGTGATGACAACGTCTTGTTCCCGAACT
Fsp27	AGCTAGCCCTTTCCCAGAAG	CCTTGTAGCAGTGCAGGTCA
Acox1	GGGAGTGCTACGGGTTACATG	CCGATATCCCCAACAGTGATG
Dgat1	CTGATCCTGAGTAATGCAAGGTT	TGGATGCAATAATCACGCATGG
Dgat2	TTCCTGGCATAAGGCCCTATT	AGTCTATGGTGTCTCGGTTGAC
Adrp	TCTCAGGGGTGGTGGATAAG	TCTACCAGCAGCTCCGACTT
Xbp1(s)	GAGTCCGCAGCAGGTG	GTGTCAGAGTCCATGGGA
Chop	CTGCCTTTCACCTTGGAGAC	CGTTTCCTGGGGATGAGATA
Edem1	TGGAATTTGGGATTCTGAGC	CTGCAGTCCAGGGAAGAAAG
Fit2	GCCTCAAGGACACTCTCTGG	AACAACCATCCAGGCACTTC
Sap	TGTCTGGGATTGAGATCTTACAACA	CTGCCGCCTTGACCTCTTAC
Saa3	CGGGACATGGAGCAGAGG	TTGCCACTCCGGCCC
TNFα	CCA ACG CCC TCC TGG CCA AC	GAG CAC GTA GTC GGG GCA GC
Lsr	CAA CCG GCC TGG CTC CAC TG	AGG TCA TCC CGG CTG CGA CT
Apoc2	CTC TGC TGG GCA CGG TGC A	GCC GCC GAG CTT TTG CTG TAC
β-actin	GATCTGGCACCACACCTTCT	GGGGTGTTGAAGGTCTCAAA