DeZwaan-McCabe et al., Fig. S1

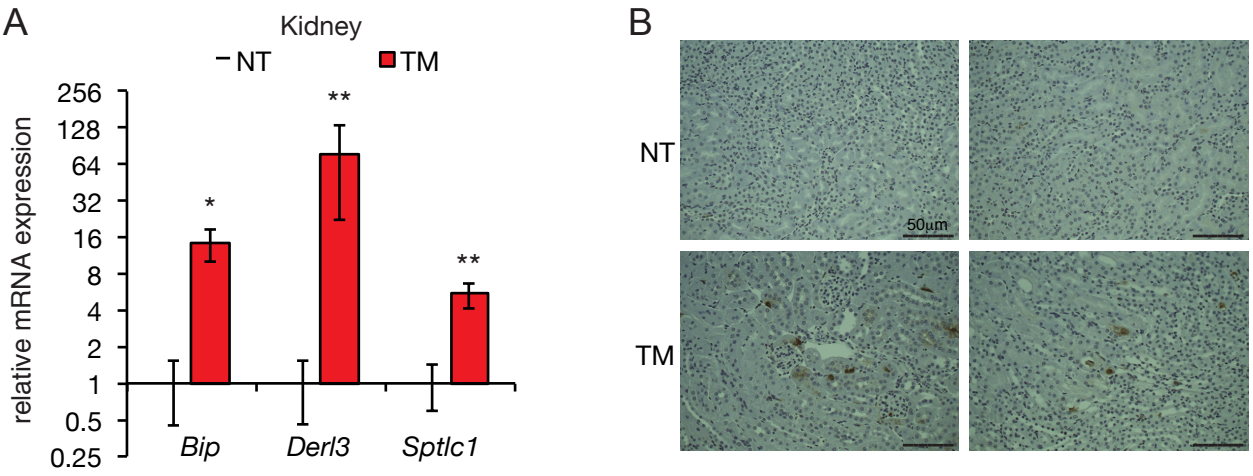

Figure S1, related to Figure 5 and Table 1

(A) *Atf6*α-/- mice were treated with vehicle or TM for 48h, and expression of the UPR target genes *Bip* and *Derl3* and the gene encoding the de novo ceramide synthesis enzyme SPTLC1 were analyzed by qRT-PCR. (B) TUNEL staining was carried out in kidney sections from *Atf6*α-/- mice treated with vehicle or TM for 48h. Representative data are shown from two separate mice in each group.

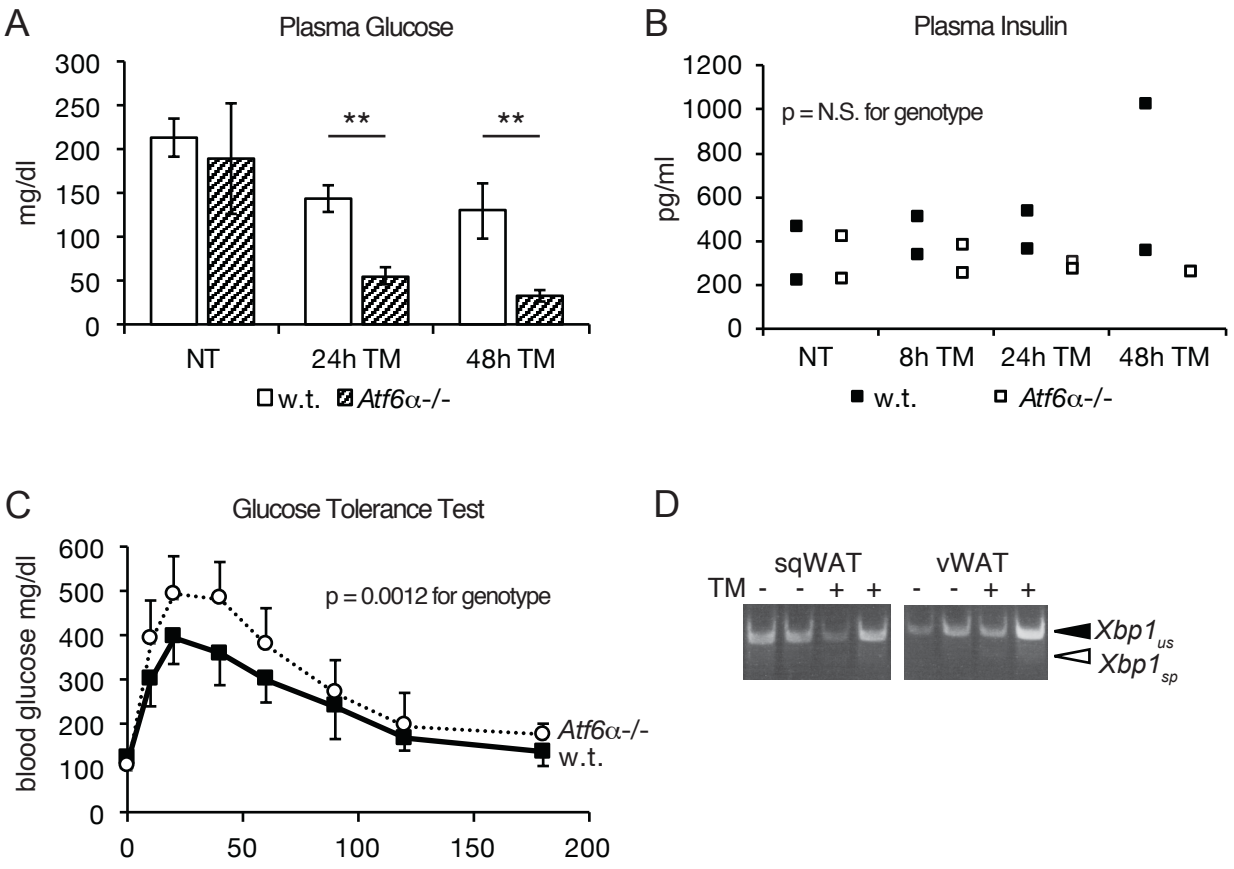

Figure S2, related to Figure 6

(A) Wild-type or *Atf6*α-/- mice were treated with vehicle or TM for 24 or 48h, and plasma glucose levels were quantified. n=3 animals per group. (B) Wild-type or *Atf6*α-/- mice were treated with vehicle or TM for 8, 24 or 48h, and plasma insulin levels were quantified. Each point represents a separate animal (i.e., each time point used separate animals). (C) Male wild-type or *Atf6*α-/- mice were subjected to a glucose tolerance test (injected with 2g/kg b.w. intraperiotneally following 20h fast). n=4-5 animals per group. For (A), significance was calculated by t-test; for (B) and (C), significance was calculated by two-way ANOVA (for time and genotype). (D) *Xbp1* mRNA was amplified by RT-PCR from subcutaneous white adipose (sqWAT; inguinal depot) or visceral white adipose (vWAT; gonadal depot) as in Figure 1A.