SUPPLEMENTARY DATA

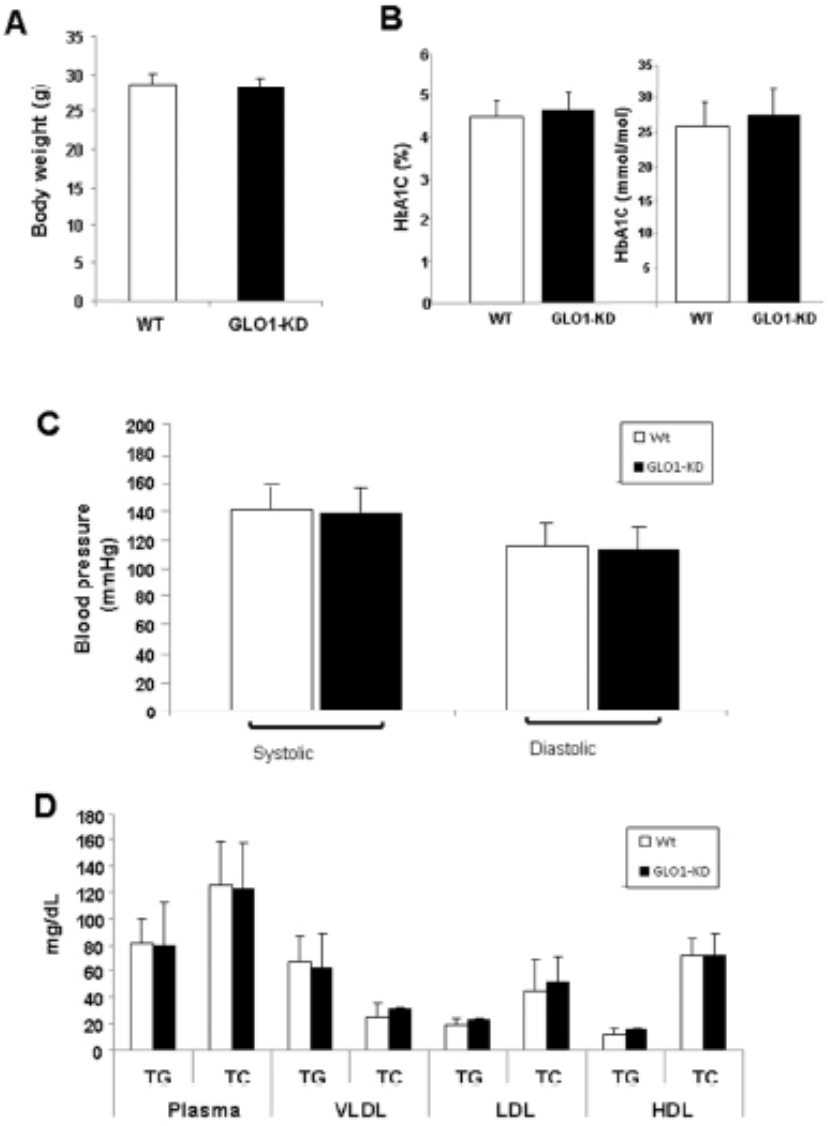
Metabolic characterization:
Body weight was measured using the Scout pro system (Chaus, NJ). HbA1c values were determined using the A1C Now kit (Bayer,CA). Systolic and diastolic blood pressures were analyzed using the Coda6 v6.2 system (EMKA TECHNOLOGIES S.A, Paris, FRANCE). Complete lipid profiles was evaluated in the laboratory of Dr Ira Goldberg (Columbia University). Briefly, serum was collected from overnight-fasted animals and triglycerides, total cholesterol and lipoprotein fractions (VLDL, LDL, HDL) were measured as previous described [1].

Proteasome activity:
Kidneys were lysed and processed as previous described [2]. Proteasome activity was calculated as described by Lima et al. [3].

Chromatin Immunoprecipitation: Chromatin immunoprecipitation experiments were performed as previous described [4-6]. Antibodies to unmodified histone H3 (catalog# ab1791) and to histone H3 mono methyl K4 (catalog# ab8895) were from Abcam. Results were quantified comparing input vs. IP signal, and histone H3 mono methyl K4 levels were normalized using unmodified H3 levels as previous described [5, 7].

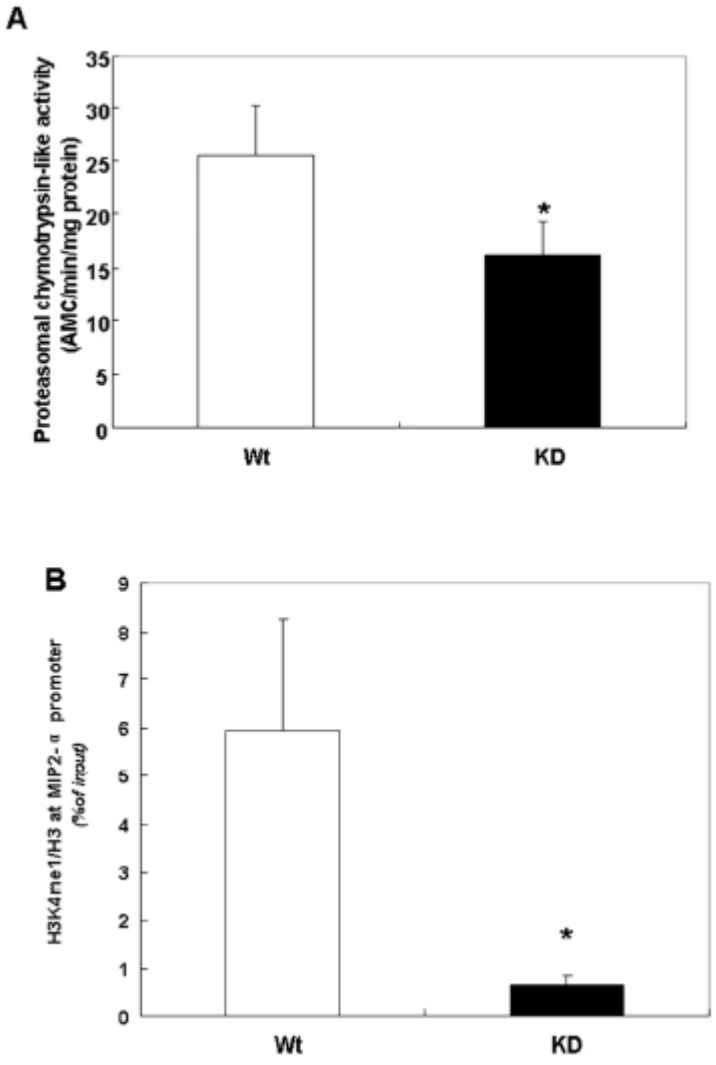
SUPPLEMENTARY DATA

Supplementary Figure 1. Metabolic characterization of Wt and GLO1-KD mice (n=5). (A) Body weight; (B) HbA1c. (C) Blood pressure. (D) Blood lipids. TG=triglycerides, TC=total cholesterol. Data are expressed as mean ± SD.



SUPPLEMENTARY DATA

Supplementary Figure 2. Proteasomal activity and epigenetic changes in kidney of Wt and GLO1-KD mice (n=5). (A) Proteasomal chemotrypsin-like activity; (B) H3K4me1 at the MIP2-alpha promoter. Data are expressed as mean ± SD (*, $P \leq 0.05$ vs Wt).



Reference

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