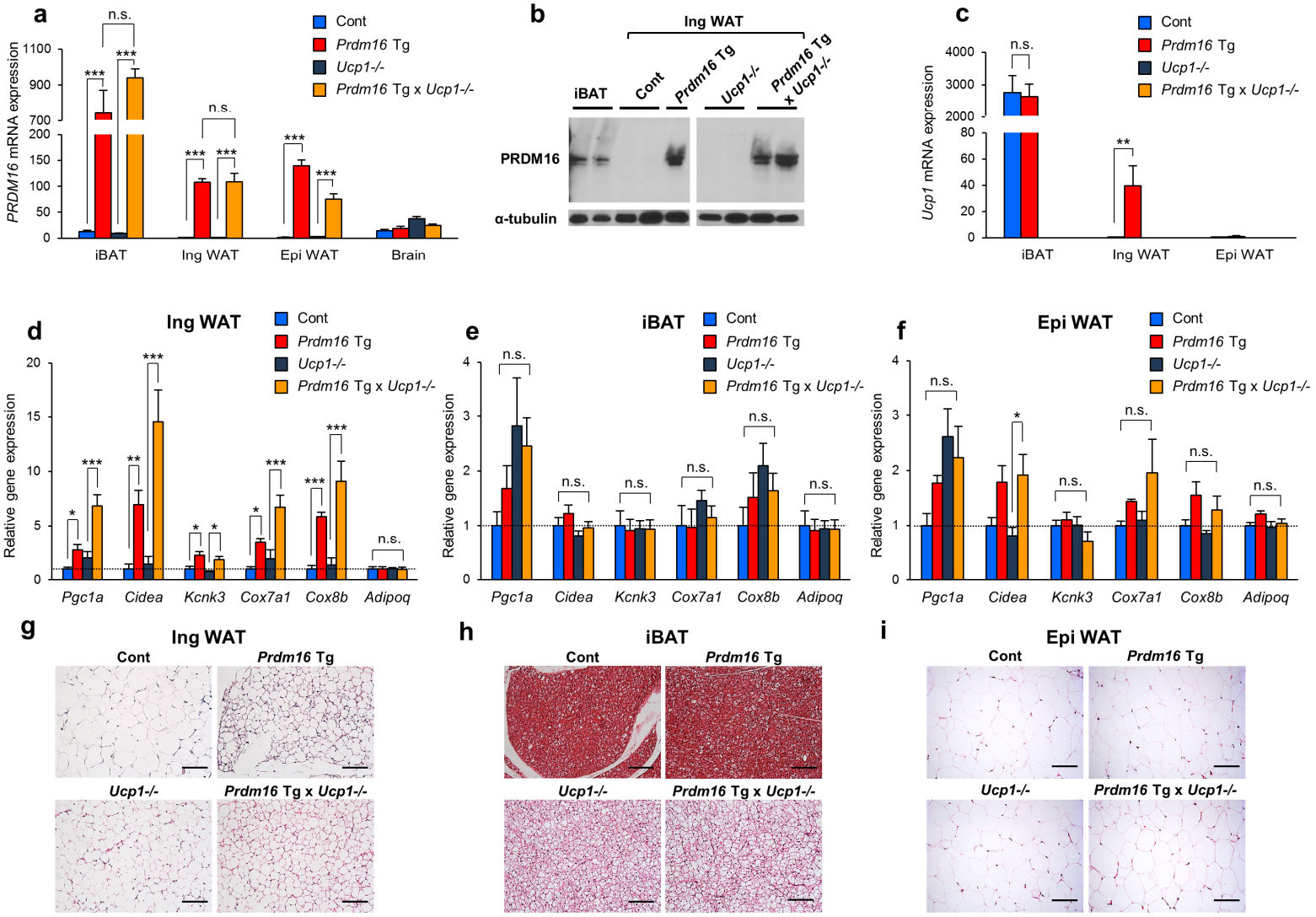
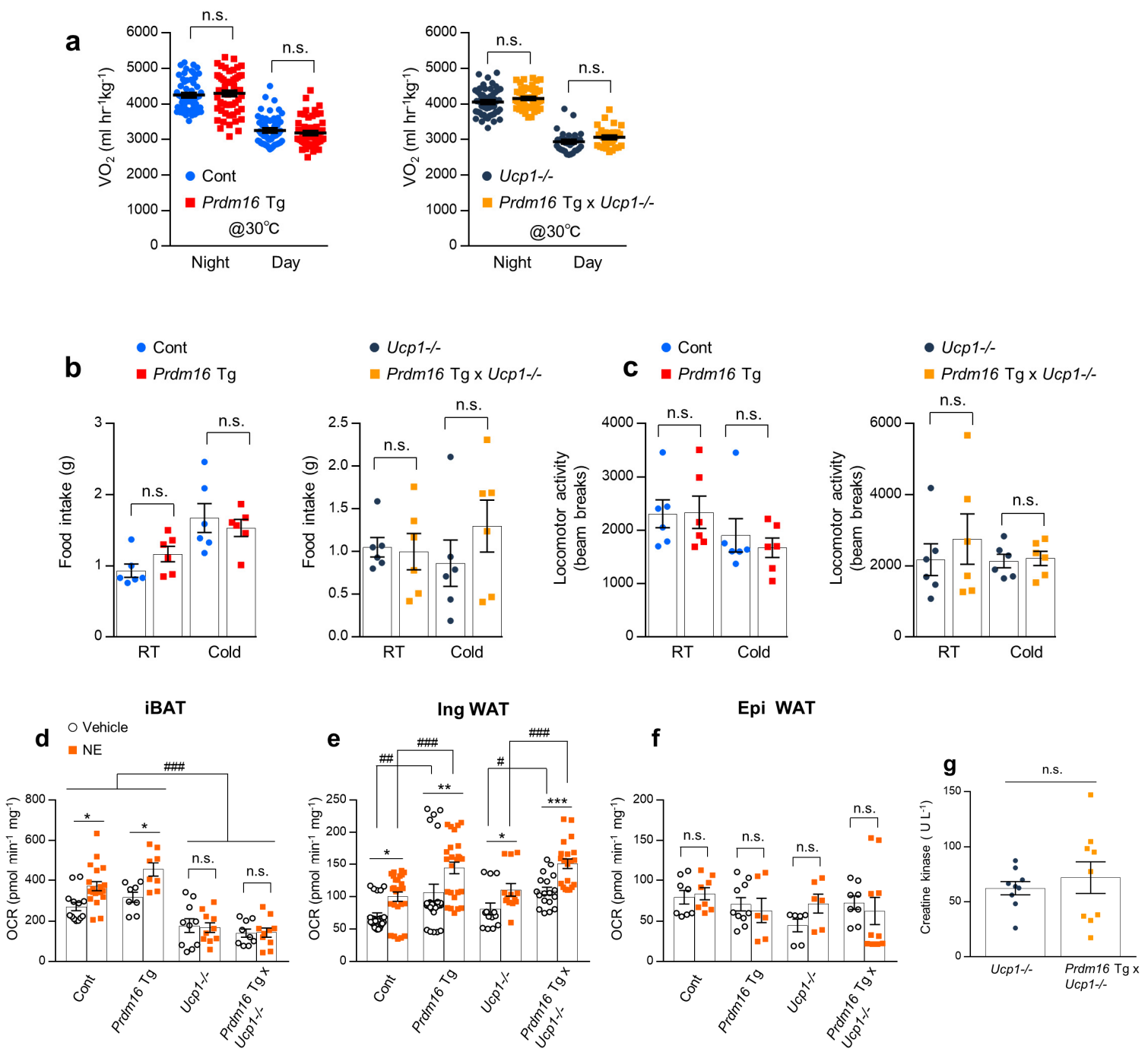
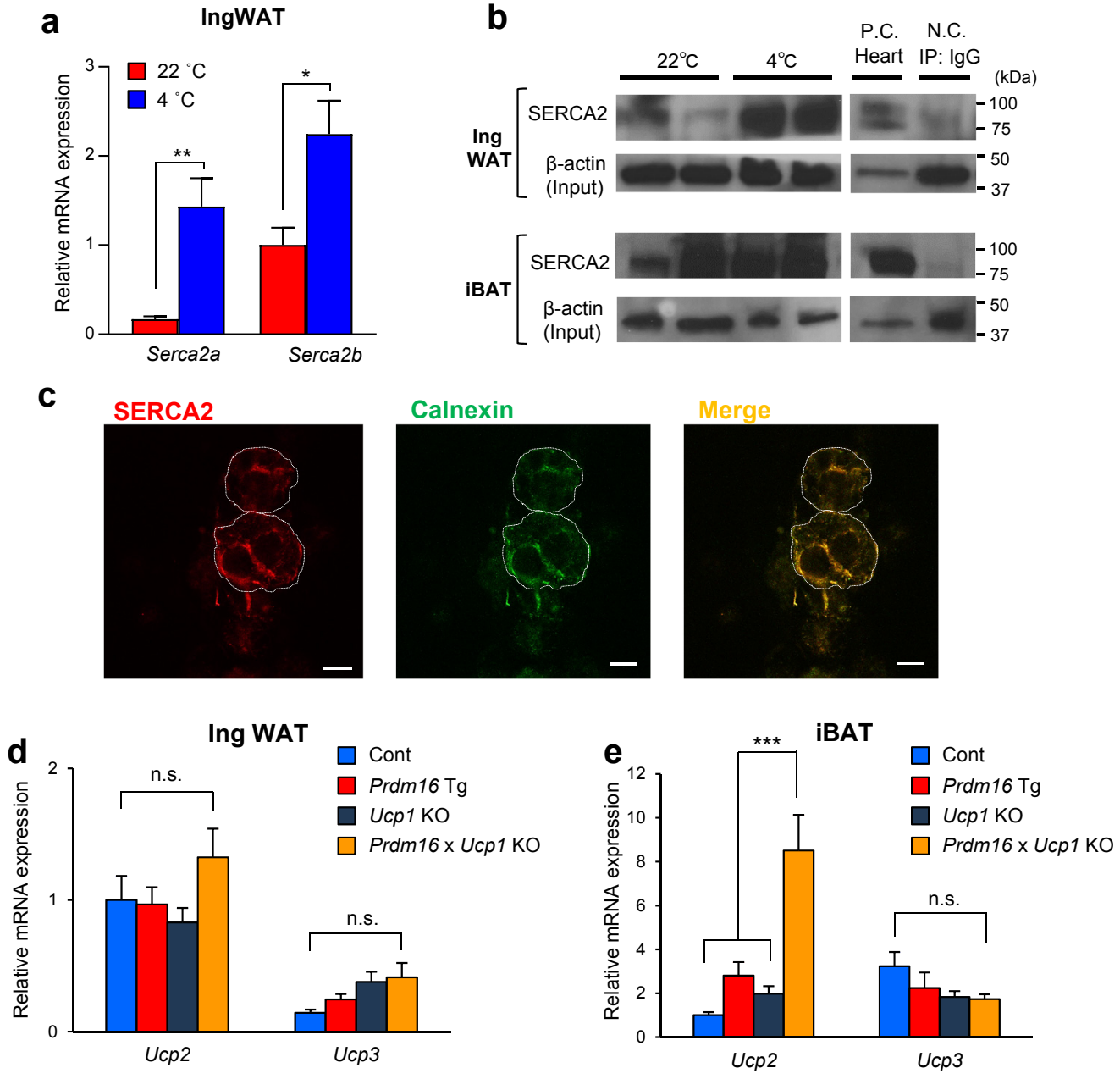


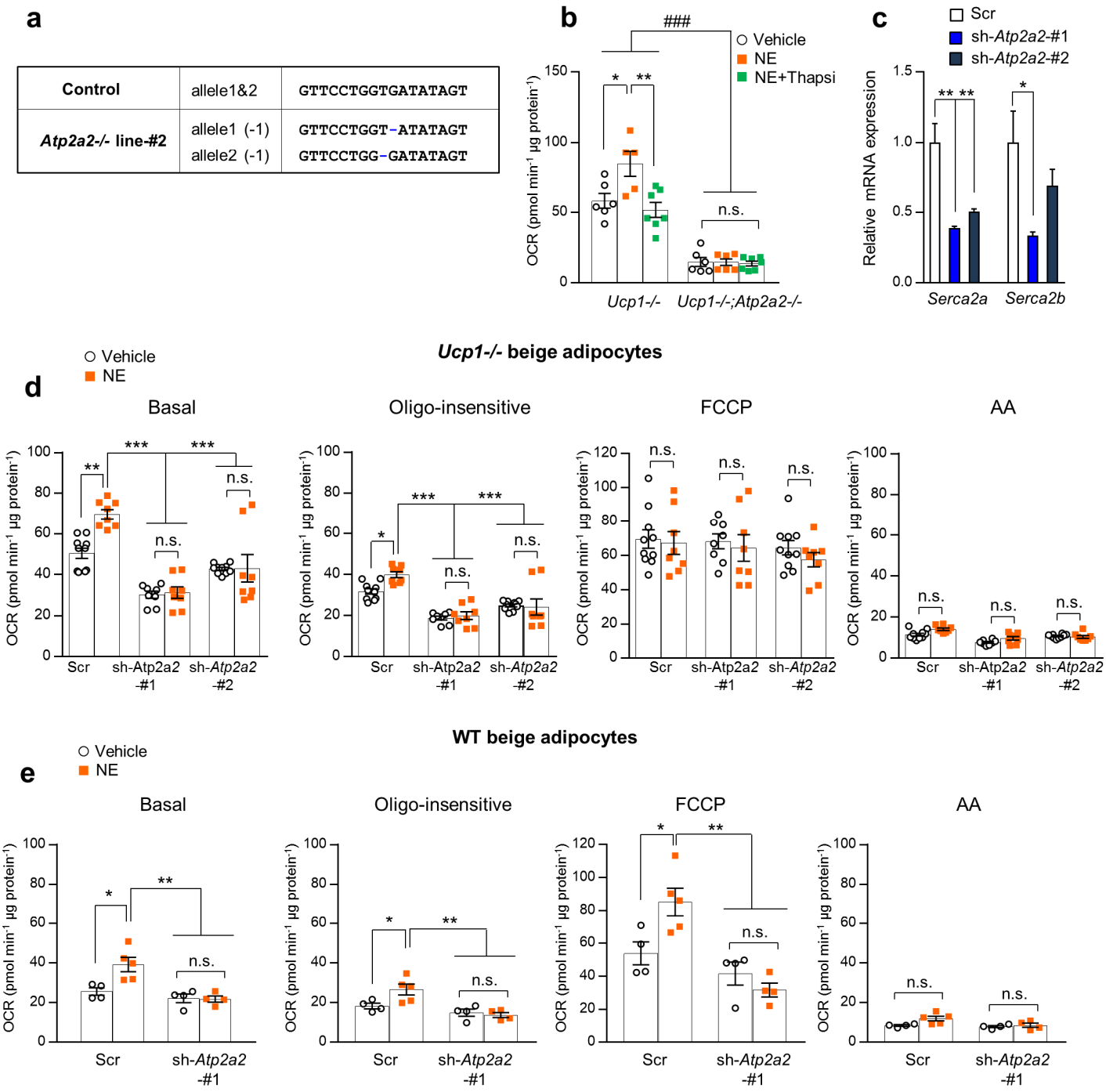
Supplementary Figure 1 Characterization of *Prdm16* Tg x *Ucp1-/-* mice. (**a**) mRNA expression of *Prdm16* in the indicated tissues of control, *Prdm16* Tg, *Ucp1-/-*, and *Prdm16* Tg x *Ucp1-/-* mice. Male mice at 14 weeks of age were used for the analysis. iBAT of control, *n* = 7; *Prdm16* Tg, *n* = 8; *Ucp1-/-, n* = 6; *Prdm16* Tg x *Ucp1-/-, n* = 6; Ing WAT of control, *n* = 4; *Prdm16* Tg, *n* = 4; *Ucp1-/-, n* = 7; *Prdm16* Tg x *Ucp1-/-, n* = 5; Epi WAT and Brain of control, *n* = 4; *Prdm16* Tg, *n* = 4; *Ucp1-/-, n* = 5; *Prdm16* Tg x *Ucp1-/-, n* = 6. (**b**) PRDM16 protein in the inguinal WAT of mice in **a**. using the PRDM16 antibody. (**c**) mRNA expression of *Ucp1* in the interscapular BAT (iBAT), inguinal WAT (Ing WAT), and epididymal WAT (epi WAT) of mice in **a**. (**d-f**) mRNA expression of brown/beige fat-selective genes (*Pgc1a*, *Cidea, Kcnk3*), mitochondrial genes (*Cox7a*, *Cox8b*) and a general adipogenic gene (*Adipoq*) in the inguinal WAT (Ing WAT) (**d**), iBAT (**e**), and epi WAT(**f**) of mice in **a**. (**g-i**) Histology by Hematoxylin & eosin (H&E) staining in Ing WAT (**g**), iBAT (**h**), and epi WAT (**i**) of mice in **a**. Scale bar = 100 um. Data are expressed as means ± s.e.m. Data analyzed by one-way ANOVA followed by Tukey's test (**a**,**d-f**) and by unpaired two-tailed Student's *t*-test (**c**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001. n.s., not significant.



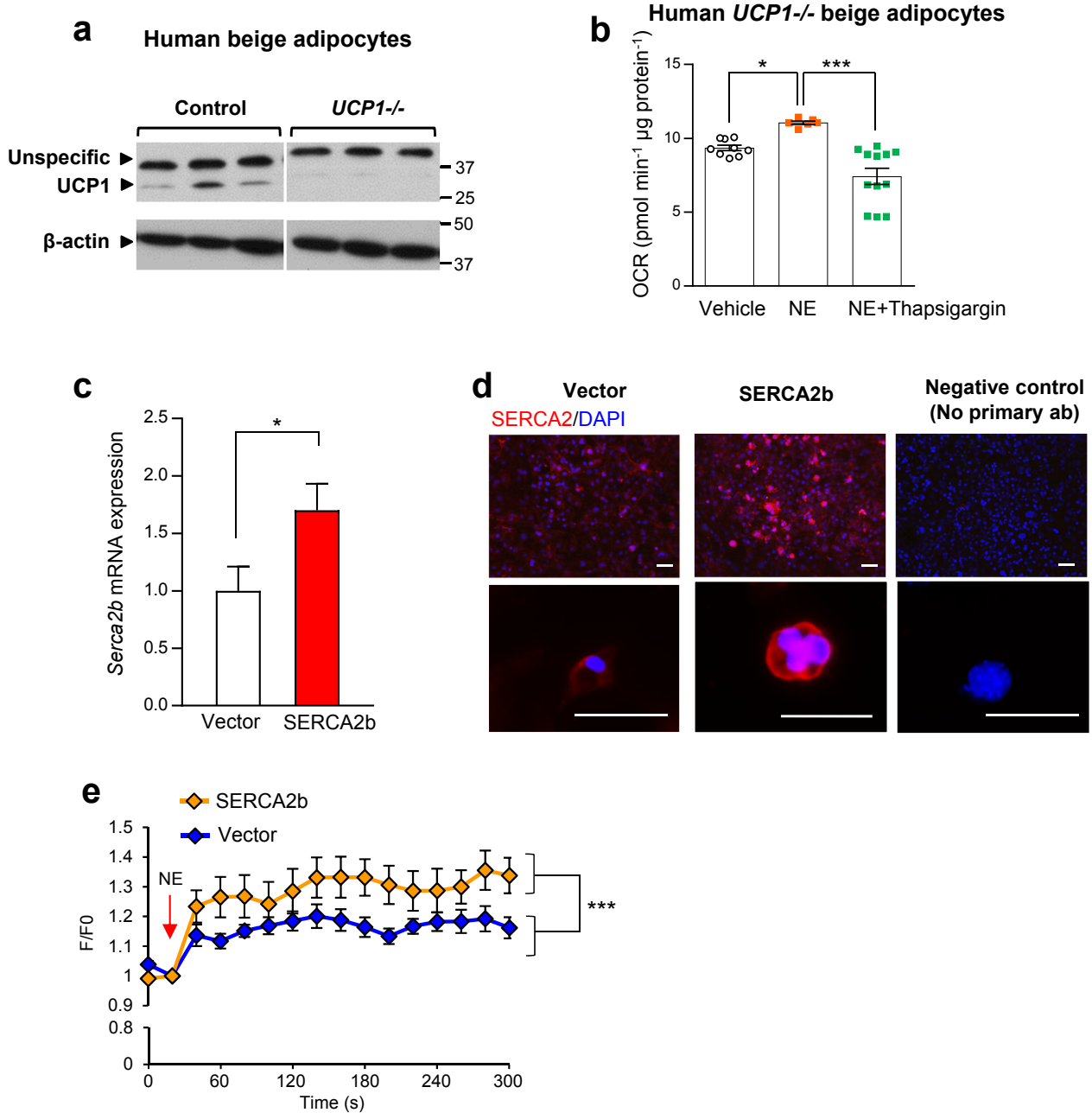
Supplementary Figure 2 Metabolic characterization of *Prdm16* Tg x *Ucp1-/-* mice. (**a**) Whole-body oxygen consumption rate (VO_2) of *Prdm16* Tg and the littermate controls (left) and *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1-/-* mice (right) under thermoneutrality (30℃). *n* = 6 for all genotypes. (**b**) Food intake of the mice during cold exposure (6℃). Food intake was measured by CLAMS. *n* = 6 for all genotypes. (**c**) Locomotor activity of the mice in **b**. (**d**) OCR in the iBAT of *Prdm16* Tg, *Ucp1-/-*, and *Prdm16* Tg x *Ucp1-/-* mice. OCR is shown per 1 mg of tissue. Control with vehicle, *n* = 13; Control with NE, *n* = 20, *Prdm16* Tg with vehicle and NE, *n* = 8 for both groups; *Ucp1-/-* with vehicle and NE, *n* = 10 for both groups; *Prdm16* Tg x *Ucp1-/-* with vehicle, *n* = 9; *Prdm16* Tg x *Ucp1-/-* with NE, *n* = 10. (**e**) OCR in the inguinal WAT of control, *Prdm16* Tg, *Ucp1-/-*, and *Prdm16* Tg x *Ucp1-/-* mice. Control with vehicle and NE, *n* = 25 for both groups; *Prdm16* Tg with vehicle and NE, *n* = 25 for both groups; *Ucp1-/-* with vehicle and NE, *n* = 13; *Prdm16* Tg x *Ucp1-/-* with vehicle, *n* = 18; *Prdm16* Tg x *Ucp1-/-* with NE, *n* = 20. (**f**) OCR in the epididymal WAT of control, *Prdm16* Tg, *Ucp1-/-*, and *Prdm16* Tg x *Ucp1-/-* mice. Control with vehicle and NE, *n* = 8 for both groups; *Prdm16* Tg with vehicle, *n* = 10; *Prdm16* Tg with NE, *n* = 6; *Ucp1-/-* with vehicle and NE, *n* = 6 for both groups; *Prdm16* Tg x *Ucp1-/-* with vehicle, *n* = 8; *Prdm16* Tg x *Ucp1-/-* with NE, *n* = 10. (**g**) Serum creatine kinase levels in *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1-/-* mice after cold exposure. *n* = 9 for both groups. Data are expressed as means ± s.e.m. Data analyzed by unpaired two-tailed Student's *t*-test (**a-c**,**g**) and one-way ANOVA followed by Tukey's test (**d-f**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001, #*P* < 0.05, ##*P* < 0.01, ###*P* < 0.001. n.s., not significant.



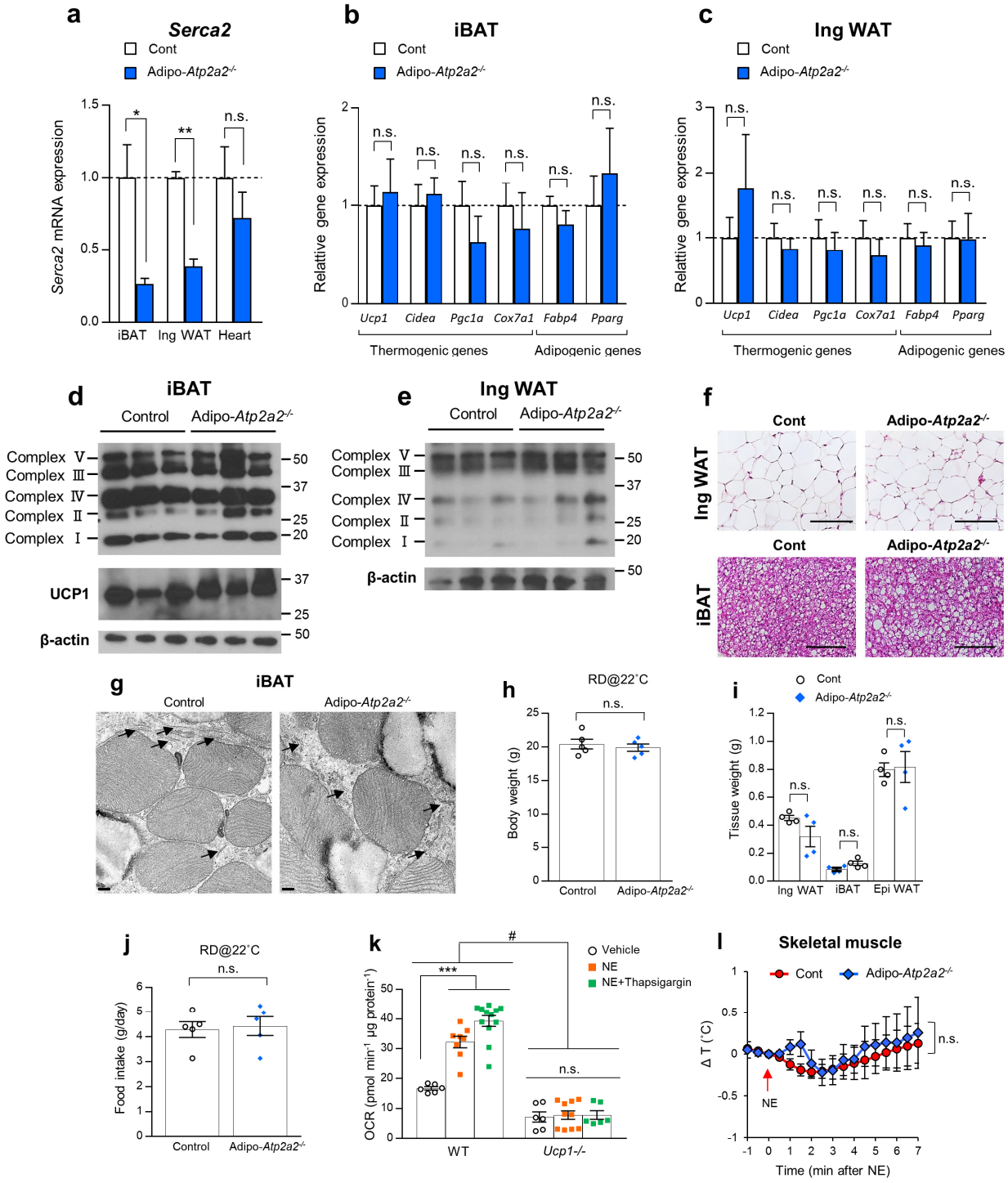
Supplementary Figure 3 Expression profiles of SERCA2 and UCP1 in beige fat. (**a**) mRNA expression of *Serca2a* and *Searca2b* in the inguinal WAT of wild-type male mice under the ambient temperature at 22°C and cold at 4°C for 7 days. *n* = 8 for all groups. (**b**) SERCA2 protein detected by immunoprecipitation followed by immunoblot using the SERCA2 antibody in the inguinal WAT and in the iBAT of wild-type mice housed at 22°C and cold at 4°C. Immunoprecipitants using mouse IgG was used as a negative control (N.C.). Tissue lysates from the heart were used as a positive control (P.C.) for immunoblot. Immunoblot using the ß-actin antibody was shown as a loading control for each sample (input). Molecular weight (kDa) is shown on the right. The data represent the results from 3 replicates. (**c**) Cellular localization of SERCA2 in differentiated beige adipocytes. SERCA2 (red) was co-localized with a ER/SR marker Calnexin (green). The merged image is shown on the right. Scale bar = 10μm. (**d**-**e**) mRNA expression of *Ucp2* and *Ucp3* in the inguinal WAT (**d**) and iBAT (**e**). Control, *n* = 5; *Prdm16* Tg, *n* = 8; *Ucp1-/-*, *n* = 6; *Prdm16* Tg x *Ucp1-/-, n* = 6. Data are expressed as means ± s.e.m. Data analyzed by unpaired two-tailed Student's *t*-test (**a**) and one-way ANOVA followed by Tukey's test (**d**,**e**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001. n.s., not significant.



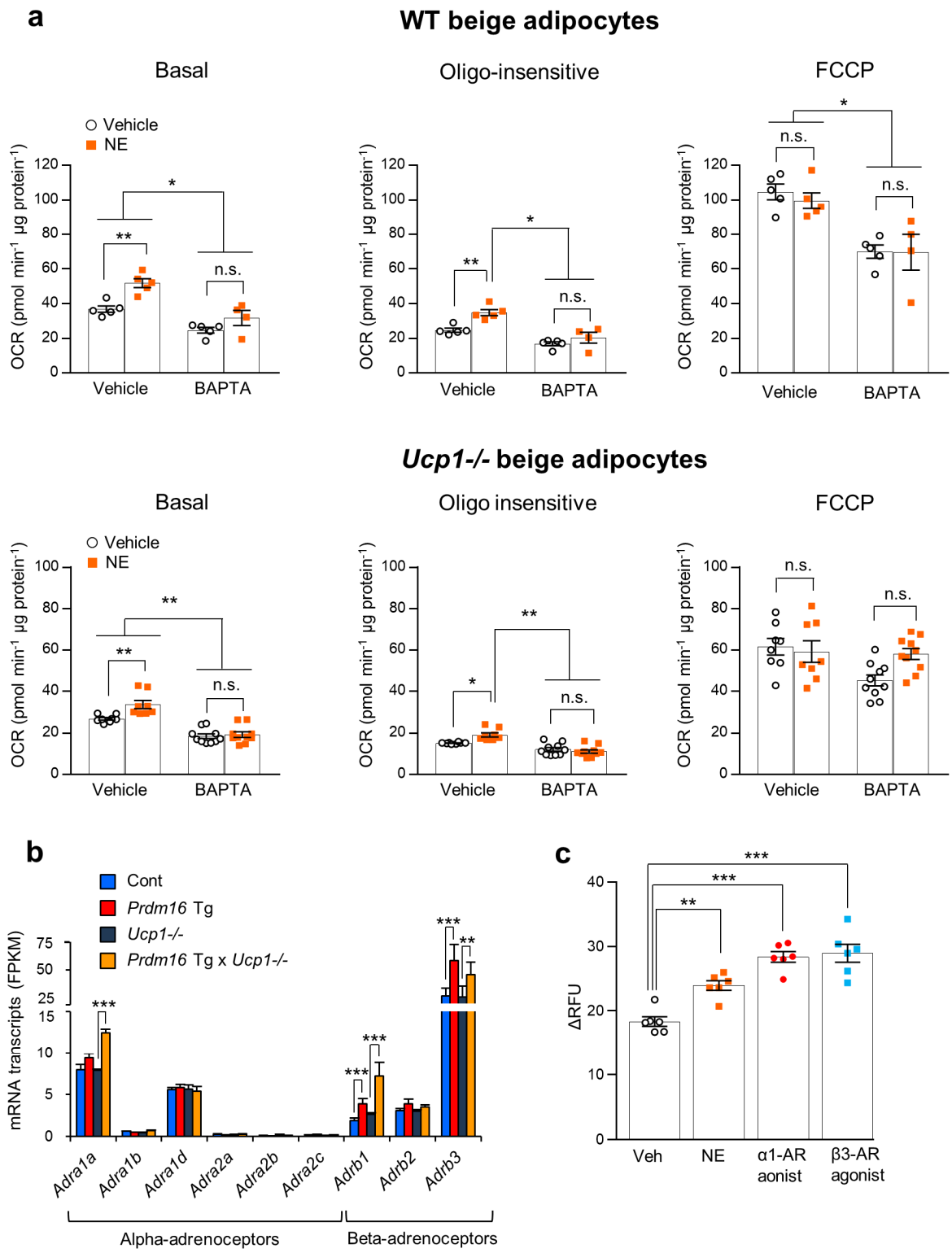
Supplementary Figure 4 Requirement of *Atp2a2* for beige fat thermogenesis. (**a**) Genomic sequences of a clonal *Ucp1*-/- beige adipocyte line (line #2) carrying the homozygous mutation in *Atp2a2* by the CRISPR-Cas9 system. Mutations (-, deletion) and wild-type allele sequences are shown. (**b**) Basal OCR in *Ucp1*-/- beige adipocytes expressing a control guide RNA (*Ucp1*-/-) and *Ucp1*-/-;*Atp2a2*-/- beige adipocytes (*Ucp1*-/-;*Atp2a2*-/-#2). Differentiated cells were treated with vehicle, NE, and thapsigargin for one hour. *Ucp1*-/- with vehicle, *n* = 6; *Ucp1*-/- with NE *n* = 5; *Ucp1*-/- with NE+Thapsigargin, *n* = 7; *Ucp1*-/-;*Atp2a2*-/- with vehicle or NE *n* = 6 for both groups; *Ucp1*-/-;*Atp2a2*-/- with NE+Thapsigargin, *n* = 7. (**c**) mRNA expression of *Serca2a* and *Serca2b* in differentiated *Ucp1*-/- beige adipocytes expressing a scrambled control RNA (Scr) or two independent shRNAs targeting *Atp2a2* (sh-#1 and sh-#2). *n* = 4 for all groups. (**d**) Basal OCR (left), oligomycin-insensitive OCR (middle), and FCCP-stimulated OCR (right) in *Ucp1*-/- beige adipocytes expressing a scrambled control RNA (Scr) or shRNAs targeting *Atp2a2* (sh-*Atp2a2*-#1 and sh-*Atp2a2*-#1). Scr with vehicle, *n* = 10: scr with NE, *n* = 8; sh-*Atp2a2*-#1 with vehicle or NE, *n* = 8 for both groups; sh-*Atp2a2*-#2 with vehicle, *n* = 10, sh-*Atp2a2*-#2 with NE, *n* = 8. (**e**) Basal OCR (left), oligomycin-insensitive OCR (middle), and FCCP-stimulated OCR (right) in beige adipocytes from the wild-type mice. Scr with vehicle, *n* = 4; Scr with NE, *n* = 5; sh-*Atp2a2*-#1 with vehicle or NE, *n* = 4 for both groups. Data are expressed as means ± s.e.m. Data analyzed by one-way ANOVA followed by Tukey's test (**b-e**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001, ###*P* < 0.001. n.s., not significant.



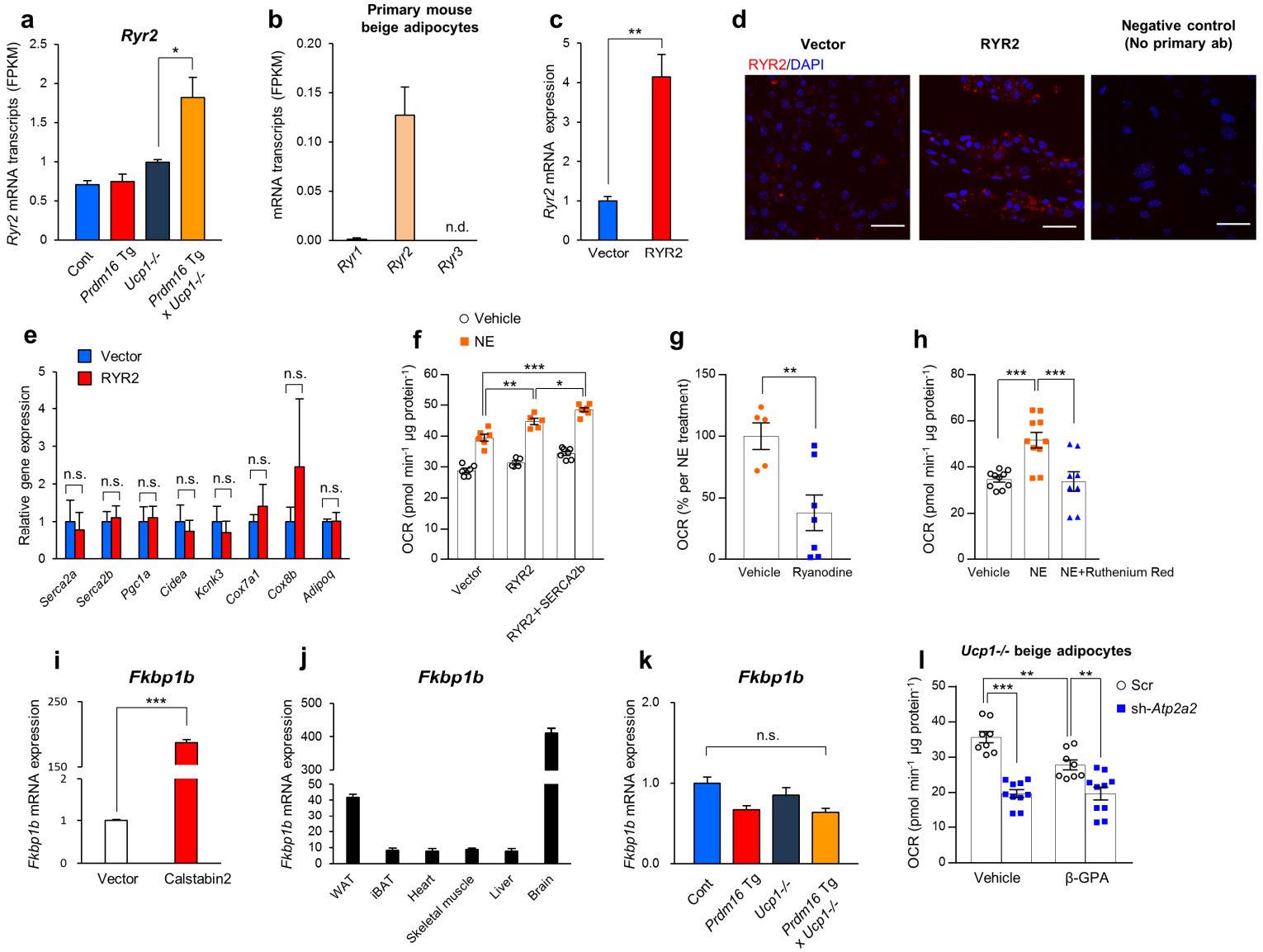
Supplementary Figure 5 SERCA2 controls UCP1-independent thermogenesis in mice and humans. (**a**) Western blot of UCP1 proteins in differentiated WT and *UCP1*-/- human beige adipocytes. Control cells expressed a scrambled guide RNA. β-actin was used as a loading control. Molecular weight (kDa) is shown on the right. (**b**) Basal OCR in human *UCP1*-/- beige adipocytes treated with NE and thapsigargin. Vehicle, n = 9; NE, n = 6; NE+thapsigargin, n = 12. (**c**) mRNA expression of *Serca2b* in *Ucp1*-/- beige adipocytes expressing SERCA2b or an empty vector. Vector, n = 3; SERCA2b, n = 4. (**d**) Protein expression of SERCA2 in *Ucp1*-/- beige adipocytes expressing SERCA2b or an empty vector. Immunohistochemistry was used antibody against SERCA2. Negative control contained no primary antibody in the staining. Upper panel is shown low magnification and lower panel is shown high magnification scale bar = 50 µm. (**e**) NE-induced Ca^{2+} release from the ER by the Fura-8 Ca^{2+} indicator in *Ucp1*-/- beige adipocytes expressing SERCA2b or an empty vector in a Ca^{2+} depleted medium. Vector, n = 7; SERCA2b, n = 5. Data are expressed as means ± s.e.m. Data analyzed by one-way ANOVA followed by Tukey's test (**b**) and unpaired two-tailed Student's t-test (**c**,**e**). *P < 0.05, ***P < 0.001. n.s., not significant.



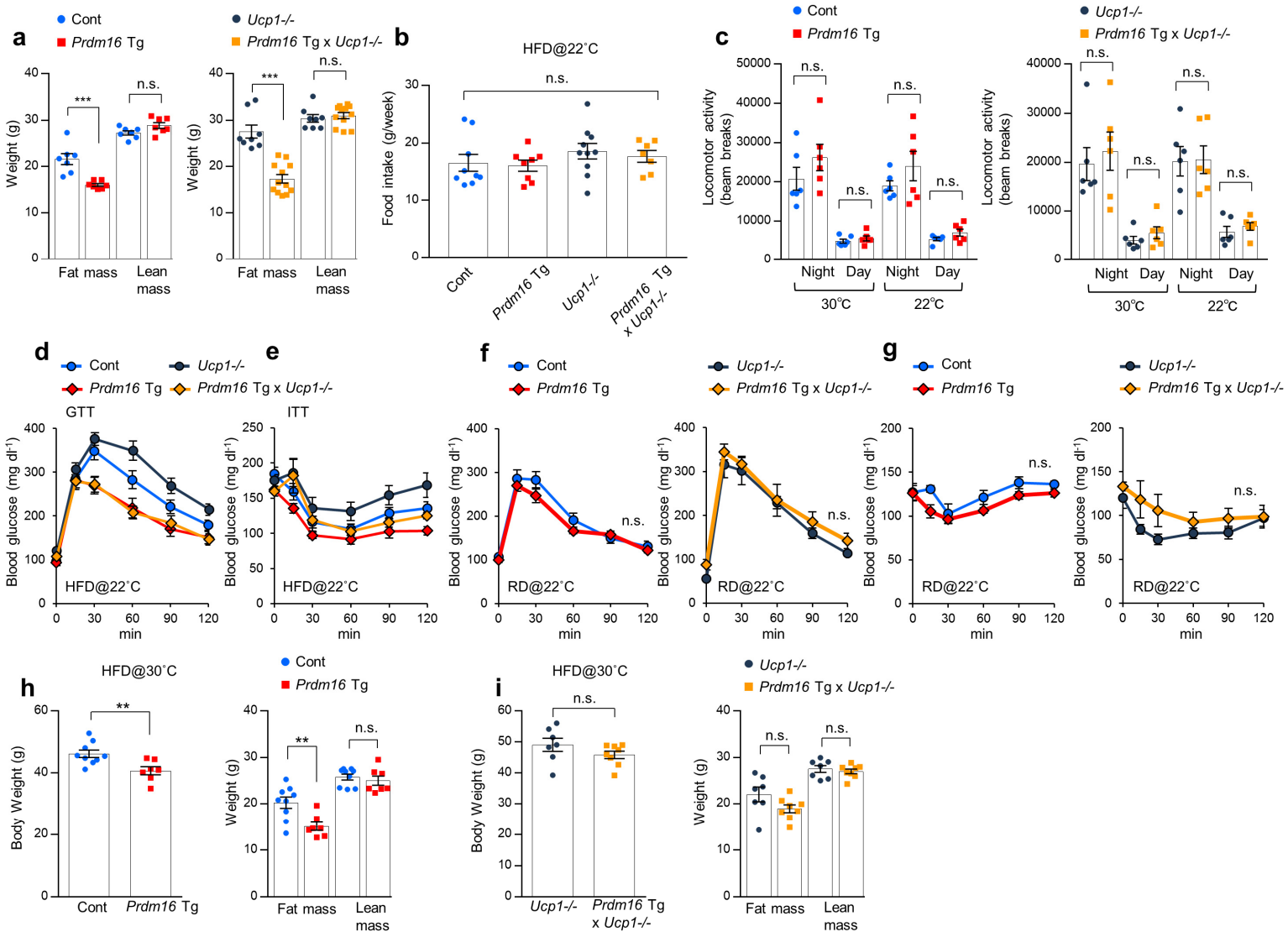
Supplementary Figure 6 Characterization of fat-specific *Atp2a2*-/- mice. (**a**) mRNA expression of *Serca2* in the iBAT, the inguinal WAT (adipocytes), and the heart of Adipo-*Atp2a2*-/- mice (*Adiponection*-Cre; *Atp2a2*$^{flox/flox}$) and the littermate control mice (*Atp2a2*$^{flox/flox}$). Ing WAT(adipocytes) of control, *n* = 3; iBAT and Heart of control, *n* = 5; Adipo-*Atp2a2*-/-, *n* = 4. (**b-c**) mRNA expression of thermogenic genes and general adipogenic genes (as indicated) in the iBAT (**b**) and inguinal WAT (**c**) of mice. Control, *n* = 5; Adipo-*Atp2a2*-/-, *n* = 4. (**d-e**) Immunoblotting for UCP1 and the indicated mitochondrial complex components in the iBAT (**d**) and inguinal WAT (**e**) of Adipo-*Atp2a2*-/- and the control mice. Molecular weight is shown on the right.(**f**) Histology of iBAT and inguinal WAT of Adipo-*Atp2a2*-/- mice and the control mice by H&E staining. Scale bar = 100 μm.(**g**) Electron microscopy images of brown adipocytes in the iBAT of Adipo-*Serca2*-/- and the control mice. Arrow shows endoplasmic reticulum. (**h**) Body weight of Adipo-*Atp2a2*-/- and the littermate control mice under a regular diet for 10 weeks at 22 ˚C. *n* = 5 for both groups. (**i**) Adipose tissue weight of Adipo-*Atp2a2*-/- and the littermate control mice under a regular diet up for 10 weeks at 22 ˚C. *n* = 4 for both groups. (**j**) Food intake was monitored for 5 days (gram per day). Control, Adipo-*Atp2a2*-/-, *n* = 5 for both groups. (**k**) Basal OCR in wild-type and *Ucp1*-/- brown adipocytes treated with vehicle, NE, and thapsigargin. WT with vehicle, *n* = 6; WT with NE, *n* = 8; WT with NE+Thapsigargin, *n* = 12; *Ucp1*-/- with vehicle, *n* = 6; *Ucp1*-/- with NE, *n* = 10; *Ucp1* -/- with NE+Thapsigargin, *n* = 6. (**l**) Changes in tissue temperature (Δ*T*) in the skeletal muscle following NE treatment. *n* = 5 for both groups. Data are expressed as means ± s.e.m. Data analyzed by unpaired two-tailed Student's *t*-test (**a-c**,**h-j**,**l**) and one-way ANOVA followed by Tukey's test (**k**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001, #*P* < 0.05. n.s., not significant.



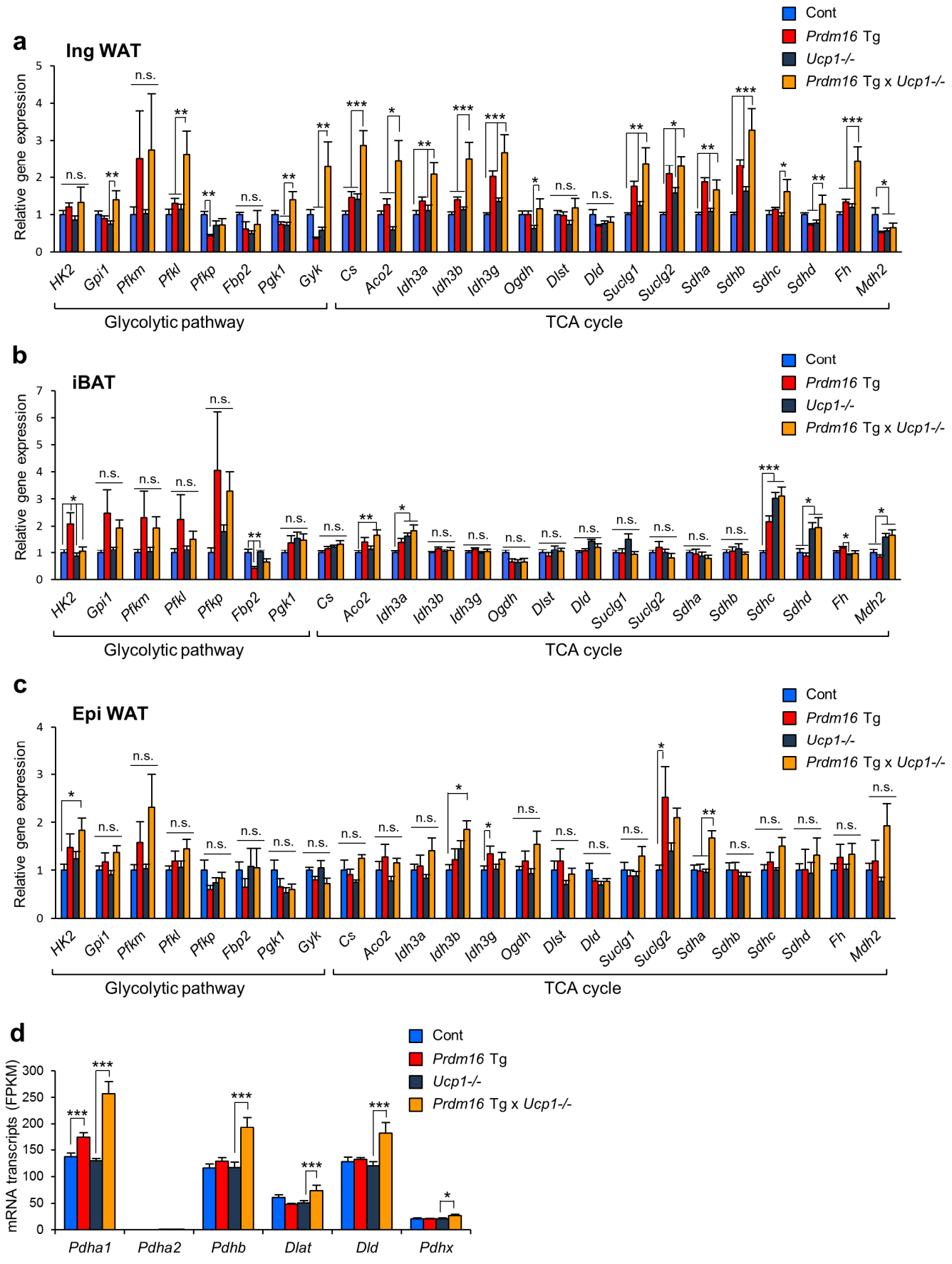
Supplementary Figure 7 The role of intracellular Ca^{2+} cycling in beige fat thermogenesis. (**a**) Basal OCR (left), oligomycin-insensitive OCR (middle), and FCCP-stimulated OCR (right) in WT and *Ucp1*-/- beige adipocytes incubated in a medium containing a cell permeant calcium chelator, BAPTA at 10 µM, or vehicle. WT with vehicle or NE, *n* = 5 for both groups; BAPTA-WT with vehicle, *n* = 5; WT-BAPTA with NE, *n* = 4. *Ucp1*-/- with vehicle or NE, *n* = 8 for both groups; BAPTA-*Ucp1*-/- with vehicle or NE, *n* = 10 for both groups. (**b**) mRNA transcripts (FPKM) of α and β adrenergic receptors by RNA-sequencing in the inguinal WAT. *n* = 3 for all groups. (**c**) Intracellular Ca^{2+} levels in *Ucp1*-/- beige adipocytes by the Fura-8 Ca^{2+} indicator following the treatment with NE or agonists for α1-AR (phenylephrine) and ß3-AR (CL316,243). *n* = 6 for all groups. Data are expressed as means ± s.e.m. Data analyzed by unpaired two-tailed Student's *t*-test (**b**) and one-way ANOVA followed by Tukey's test (**a**,**c**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001. n.s., not significant.



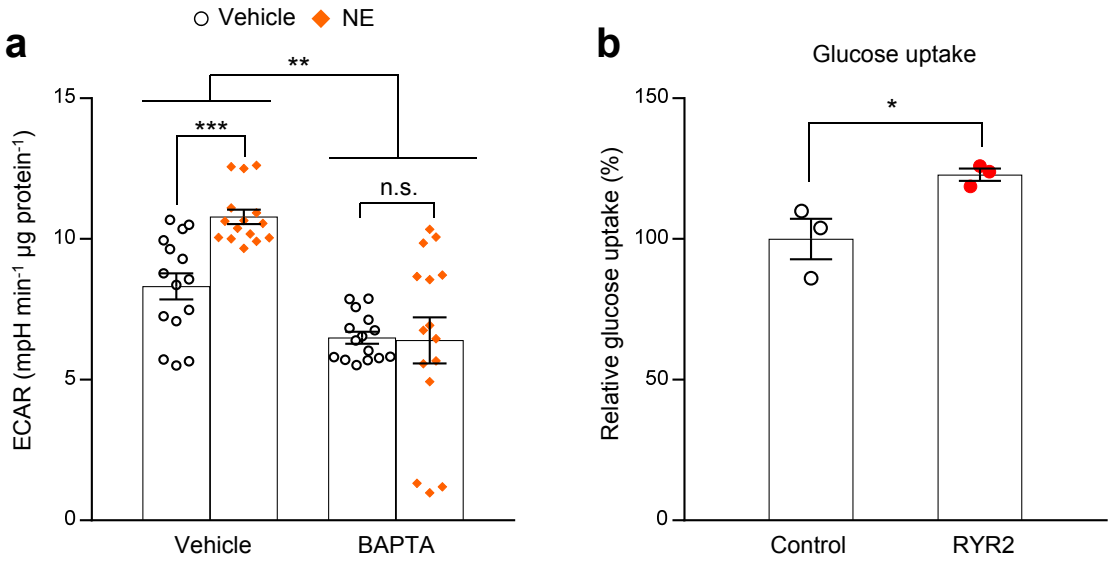
Supplementary Figure 8 Regulation of UCP1-independent thermogenesis by the SERCA2-RyR2 pathway and creatine-drivensubstrate cycling. (**a**) mRNA transcripts (FPKM) of *Ryr2* by RNA-sequencing in the inguinal WAT. *n* = 3 for all groups. (**b**) mRNA transcripts (FPKM) of the ryanodine receptor family members in differentiated mouse beige adipocytes by RNA-sequencing. *n* = 2 for all groups. n.d., not detected. (**c**) mRNA expression of *Ryr2* in beige adipocytes expressing RYR2 or an empty vector. Control, *n* = 3; RYR2, *n* = 4. (**d**) Protein expression of RYR2 in beige adipocytes expressing RYR2 or an empty vector by immunohistochemistry using an antibody against RYR2. Negative control contained no primary antibody in the staining. Scale bar = 50 µm. (**e**) mRNA expression of the beige adipocyte-enriched genes (as indicated) in **c**. (**f**) Basal OCR in mouse *Ucp1*-/- beige adipocytes expressing an empty vector or RYR2 and/or SERCA2b. Vector with vehicle or NE, *n* = 6 for both groups; RYR2 with vehicle or NE, *n* = 5 for both groups; RyR2+SERCA2b with vehicle or NE, *n* = 7 for both groups. (**g**) Basal OCR in mouse *Ucp1*-/- beige adipocytes treated with ryanodine at 100 µM or vehicle for one hour. Cells were subsequently treated with NE. Vehicle, *n* = 5; ryanodine, *n* = 7. The values were shown as changes per NE treatment.(**h**) Basal OCR in mouse *Ucp1*-/- beige adipocytes treated with ruthenium red at 10 µM or vehicle for one hour. Cells were subsequently treated with NE. Vehicle, *n* = 10; NE, *n* = 10, Ruthenium red, *n* = 8. (**i**) mRNA expression of *Fkbp1b* in *Ucp1*-/- beige adipocytes expressing Calstabin2 or an empty vector. *n* = 3 for all groups. (**j**) Tissue distribution of *Fkbp1b* expression in mice. The data are obtained from the BioGPS (http://biogps.org). (**k**) mRNA expression of *Fkbp1b* in the inguinal WAT of mice. Control, *n* = 6; *Prdm16* Tg, *n* = 7; *Ucp1*-/-, *n* = 10; *Prdm16* Tg x *Ucp1*-/-, *n* = 5. (**l**) Basal OCR in mouse *Ucp1*-/- beige adipocytes expressing a scrambled control RNA (Scr) or shRNA targeting *Atp2a2* (sh-*Atp2a2*). Differentiated cells were treated with ß-GPA or vehicle. Scr with vehicle, *n* = 8; sh-*Atp2a2* with vehicle, *n* = 10; Scr with ß-GPA, *n* = 8; sh-*Atp2a2* with ß-GPA, *n* = 10. Data are expressed as means ± s.e.m. Data analyzed by unpaired two-tailed Student's *t*-test (**a**,**c**,**e**,**g**,**i**) and one-way ANOVA followed by Tukey's test (**f**,**h**,**k**,**l**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001. n.s., not significant.



Supplementary Figure 9 Whole-body metabolic phenotypes of *Prdm16* Tg x *Ucp1-/-* mice. (**a**) Body composition of *Prdm16* Tg and the littermate controls (left) and *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1-/-* mice (right) at 18 weeks of HFD. Control, *Prdm16* Tg, *n* = 7 for both groups; *Ucp1 -/-*, *n* = 8; *Prdm16* Tg x *Ucp1-/-*, *n* = 12. (**b**) Food intake of *Prdm16* Tg and the littermate controls (left) and *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1-/-* mice (right). Food intake was monitored throughout the HFD experiment and showed as gram per week. Control, *n* = 9; *Prdm16* Tg, *n* = 8; *Ucp1 -/-*, *n* = 10; *Prdm16* Tg x *Ucp1-/-*, *n* = 7. (**c**) Locomotor activity (beam break account) of *Prdm16* Tg and the littermate controls (left) and *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1-/-* mice (right) at 12 weeks of HFD were measured by CLAMS. *n* = 6 for all groups. (**d**) GTT at 10 weeks of HFD at 22˚C. The values were normalized by the respective controls. Control, *n* = 9; *Prdm16* Tg, *n* = 8; *Ucp1-/-*, *n* = 10; *Prdm16* Tg x *Ucp1-/-*, *n* = 7. (**e**) ITT was performed in mice in **d**. at 11 weeks of HFD. (**f**) GTT in *Prdm16* Tg and the littermate controls (left) and in *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1 -/-* mice (right) at 10 weeks of RD at 22˚C. Control, *n* = 7; *Prdm16* Tg, *n* = 7; *Ucp1-/-*, *n* = 5; *Prdm16* Tg x *Ucp1-/-*, *n* = 7. (**g**) ITT in mice in at 11 weeks of RD. Control, *n* = 4; *Prdm16* Tg, *n* = 5; *Ucp1-/-*, *n* = 5; *Prdm16* Tg x *Ucp1-/-*, *n* = 5. (**h-i**) Body weight (left) and body composition (right) of *Prdm16* Tg and the littermate controls at 13 weeks of HFD at 30˚C (**h**) and *Prdm16* Tg x *Ucp1-/-* and the littermate *Ucp1-/-* mice at 14 weeks of HFD at 30˚C (**i**). Control, *n* = 9; *Prdm16* Tg, *n* = 7; *Ucp1-/-*, *n* = 7; *Prdm16* Tg x *Ucp1-/-*, *n* = 8. Data are expressed as means ± s.e.m. Data analyzed by unpaired two-tailed Student's *t*-test (**a**,**c**,**h**,**i**), one-way ANOVA followed by Tukey's test (**b**), and two-way ANOVA followed by Fisher's LSD test (**f**,**g**). ***P* < 0.01, ****P* < 0.001. n.s., not significant.

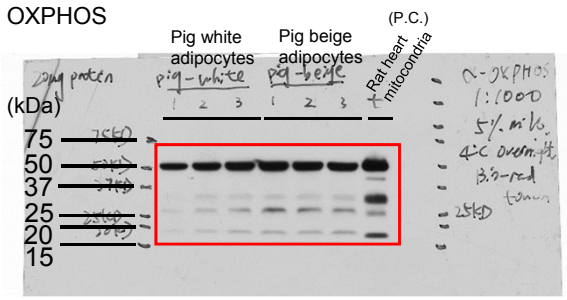


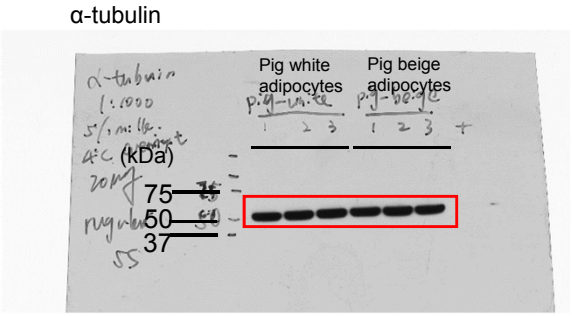
Supplementary Figure 10 Metabolic gene expression in *Prdm16* Tg x *Ucp1*-/- mice. (**a-c**) mRNA expression of the indicated genes in glycolysis and TCA metabolism in the inguinal WAT (**a**), iBAT (**b**), and epididymal WAT (**c**). Control, *n* = 9; *Prdm16* Tg, *n* = 8; *Ucp1*-/-, *n* = 10; *Prdm16* Tg x *Ucp1*-/-, *n* = 7. (**d**) mRNA transcripts (FPKM) of the PDH complex genes by RNA-sequencing in the inguinal WAT. *n* = 3 for all groups. Data are expressed as means ± s.e.m. Data analyzed by one-way ANOVA followed by Tukey's test (**a-c**) and unpaired two-tailed Student's *t*-test (**d**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001. n.s., not significant.



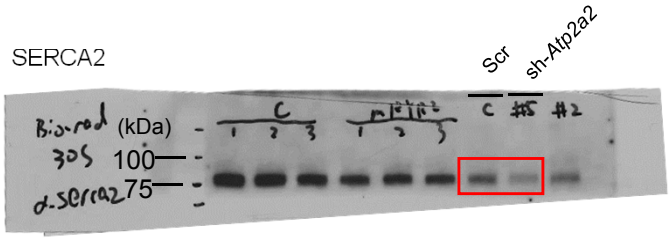
Supplementary Figure 11 Calcium cycling controls glucose oxidation in beige fat. (**a**) ECAR in differentiated *Ucp1-/-* beige adipocytes in the culture medium with BAPTA at 10 µM or vehicle for two hours. NE or vehicle was added for one hour prior to the analysis. *n* = 15 for all groups. (**b**) Glucose uptake in *Ucp1-/-* beige adipocytes expressing RYR2 or an empty vector (control). Differentiated adipocytes were incubated with [^{3}H] labelled glucose for 5 min. *n* = 3 for both groups. Data are expressed as means ± s.e.m. Data analyzed by one-way ANOVA followed by Tukey's test (**a**) and unpaired two-tailed Student's *t*-test (**b**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001. n.s., not significant.

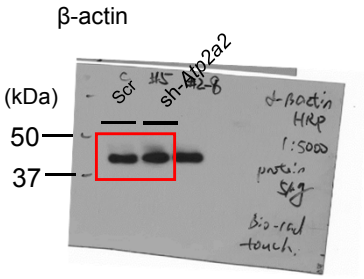
Full-sized Western blot images for Figure 6j





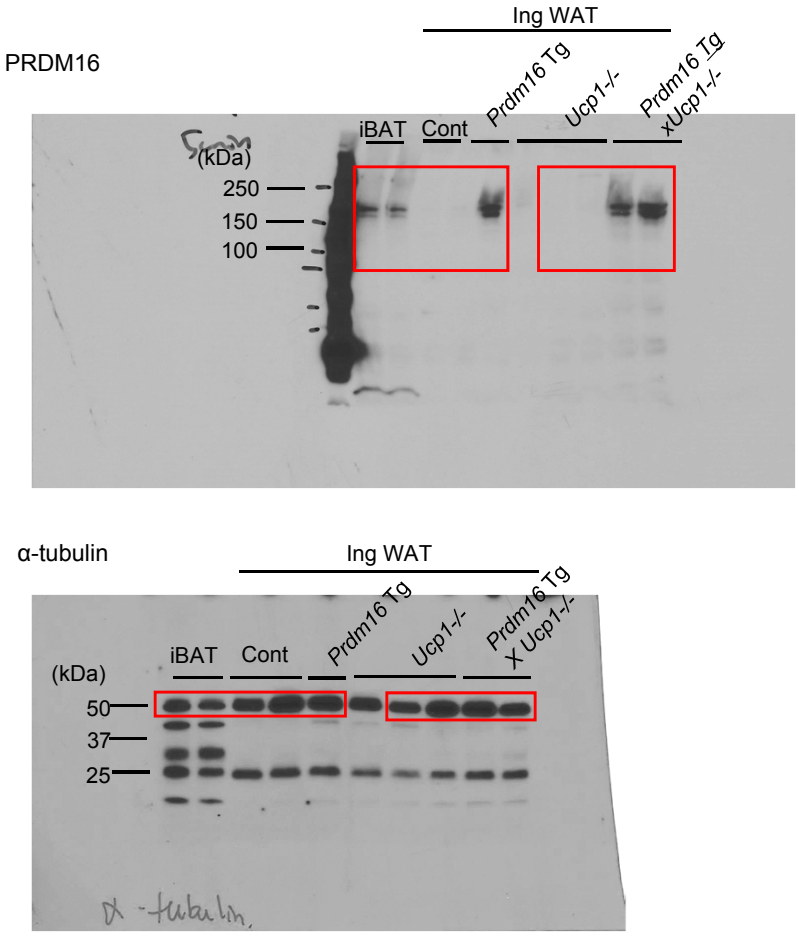
Full-sized Western blot images for Figure 6k





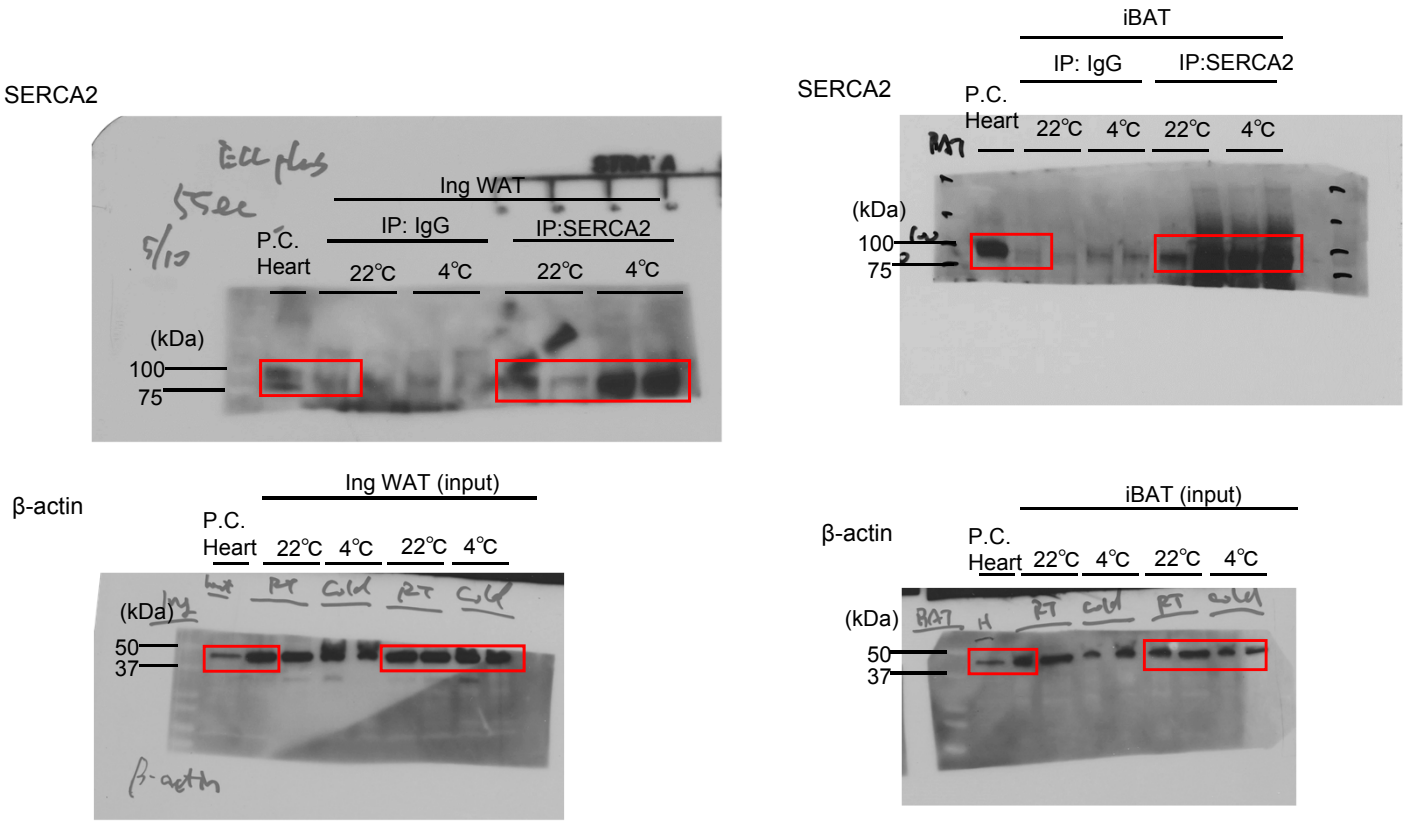
Supplementary Figure 12 Full-scans of Western blots. Full-sized image of Western blot from Figure 6j and 6k. Red box indicates area that was cropped and displayed in the indicated figure.

Full-sized Western blot images for Supplementary figure 1b

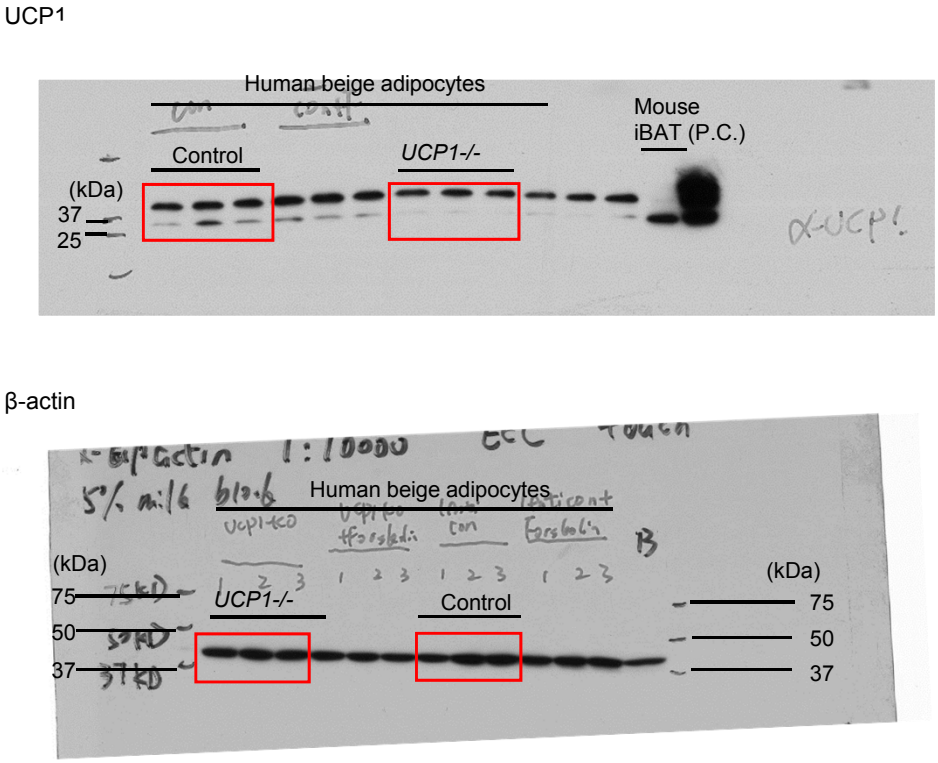


Supplementary Figure 12 Full-scans of Western blots. Full-sized image of Western blot from Supplementary figure 1b. Red box indicates area that was cropped and displayed in the indicated figure.

Full-sized Western blot images for Supplementary figure 3b



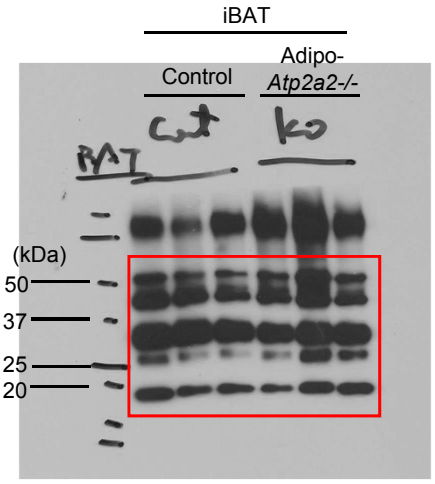
Full-sized Western blot images for Supplementary figure5a



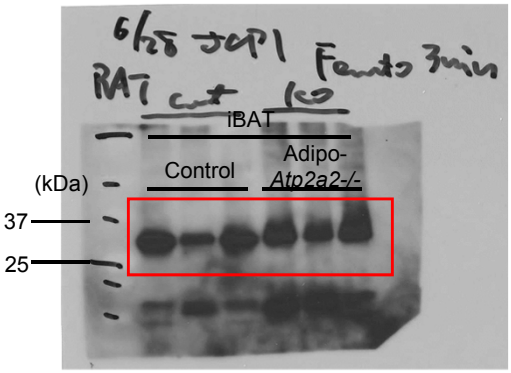
Supplementary Figure 12 Full-scans of Western blots. Full-sized image of Western blot from Supplementary figure 3b and 5a. Red box indicates area that was cropped and displayed in the indicated figure.

Full-sized Western blot images for Supplementary figure 6d

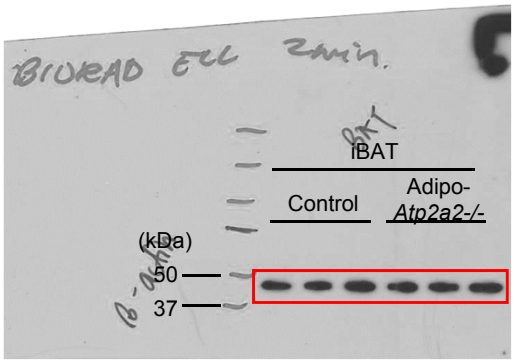
OXPHOS



UCP1



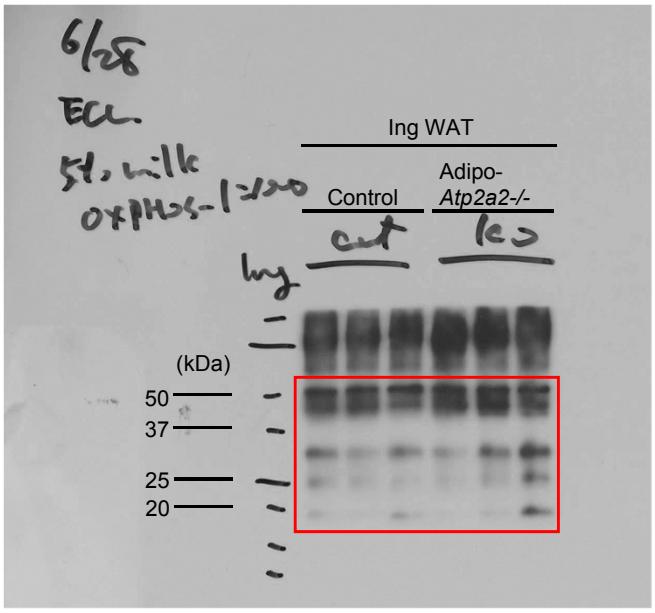
β-actin



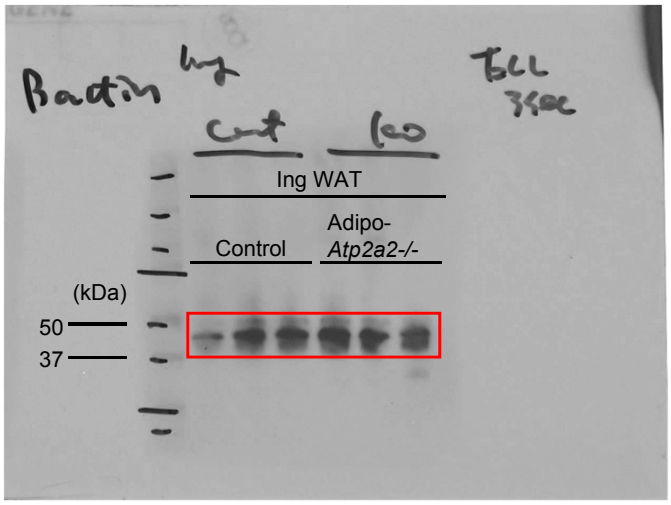
Supplementary Figure 12 Full-scans of Western blots. Full-sized image of Western blot from Supplementary figure 6d. Red box indicates area that was cropped and displayed in the indicated figure.

Full-sized Western blot images for Supplementary figure 6e

OXPHOS



β-actin



Supplementary Figure 12 Full-scans of Western blots. Full-sized image of Western blot from Supplementary figure 6e. Red box indicates area that was cropped and displayed in the indicated figure.

Supplementary Table 2 Primer sequences.

	Gene	Forward Primer	Reverse Primer
Human	***SERCA1***	CTCCTGGTGCGGATTCTCC	GATGGCGTTCTCTGCGTT
	SERCA2a	TGAGACGCTCAAGTTTGTGG	TCATGCACAGGGTTGGTAGA
	SERCA2b	AGTGGGGCAAGATTTTCCTT	GACAATGTCTGCTGGCTCAA
	SERCA3	CTGGTCATCATGCTGATCCTC	CAGCGTGGTGGACTTGATCT
	TBP	CACGAACCACGGCACTGATT	TTTTCTTGCTGCCAGTCTGGA
Pig	***Cidea***	TTCATGGTCCTGGAGAAAGG	GTACATGGTGGCCTTGACG
	Dio2	AGGAAGCAACAACCATGGAC	CAGGTACTGCCCAACCATCT
	Elovl3	CACTGGTACCACCACAGCAC	GGTGATGAACATGGGAAACC
	Tmem26	CCTGGTCTACGCCATCCTTA	CAGGAAGGGACCGTCTTGTA
	Tbp	AACAGTTCAGTAGTTATGAGCCAGA	AGATGTTCTCAAACGCTTCG
Mouse	***Aco2***	ATCGAGCGGGGAAAGACATAC	TGATGGTACAGCCACCTTAGG
	Adipoq	GCACTGGCAAGTTCTACTGCAA	GTAGGTGAAGAGAACGGCCTTGT
	Cidea	ATCACAACTGGCCTGGTTACG	TACTACCCGGTGTCCATTTCT
	Cox7a1	CAGCGTCATGGTCAGTCTGT	AGAAAACCGTGTGGCAGAGA
	Cox8b	GAACCATGAAGCCAACGACT	GCGAAGTTCACAGTGGTTCC
	Cs	GGACAATTTTCCAACCAATCTGC	TCGGTTCATTCCCTCTGCATA
	Dld	GAGCTGGAGTCGTGTGTACC	CCTATCACTGTCACGTCAGCC
	Fabp4	ACACCGAGATTTCCTTCAAACTG	CCATCTAGGGTTATGATGCTCTTCA
	Dlst	GGAACTGCCCTCTAGGGAGA	GACGCTACCACTGTTAATGACC
	Fbp2	ACCCTGACCCGTTACGTTATG	ACATTCACGCTCCCCGAAATC
	Fh	GGTCATCAAAATTGGGCGAAC	CTTGCTGAACGTAACCACTGAA
	Fkbp1b	TGATGTGGCCTATGGAGCTA	CCTTCACTCTAAGCTGAGCA
	Gpi1	TCAAGCTGCGCGAACTTTTTG	GGTTCTTGGAGTAGTCCACCAG
	Gyk	TGAAGAAAGCGAAATCCGTTACT	CCCAAAGGCAGACTACAGAAG
	Hk2	TGATCGCCTGCTTATTCACGG	AACCGCCTAGAAATCTCCAGA
	Idh3a	TGGGTGTCCAAGGTCTCTC	CTCCCACTGAATAGGTGCTTTG
	Idh3b	GGATTTGTTTGCCAACGTAGTC	GCTCTCGAATGATAACCAGGTCT
	Idh3g	GCTGCAAAGGCAATGCTCAAG	TATGCCGCCCACCATACTTAG
	Kcnk3	ACGGAGGCAAGGTGTTCTG	ACGACACGAAACCGATGAGC
	Mdh2	TTGGGCAACCCCTTTCACTC	GCCTTTCACATTTGCTCTGGTC
	Ogdh	ACTTGTGCTGCTAAGTTAAGGC	TGAAACGTCCTAATTGCTGCTG
	Pfkl	GGAGGCGAGAACATCAAGCC	CGGCCTTCCCTCGTAGTGA
	Pfkm	TGTGGTCCGAGTTGGTATCTT	GCACTTCCAATCACTGTGCC
	Pfkp	TGGTGCCATCATGCTATCTGA	GGTCGCACGTCTCGACAAT
	Pgc1α	AGCCGTGACCACTGACAACGA	GCTGCATGGTTCTGAGTGCT
	Pgk1	ATGTCGCTTTCCAACAAGCTG	GCTCCATTGTCCAAGCAGAAT
	Pparg	TGAAAGAAGCGGTGAACCACTG	TGGCATCTCTGTGTCAACCATG
	Prdm16	CAGCACGGTGAAGCCATTC	GCGTGCATCCGCTTGTG
	Rn18s	AGTCCCTGCCCTTTGTACACA	CGATCCGAGGGCCTCACT
	Rplp0	GGCCCTGCACTCTCGCTTTC	TGCCAGGACGCGCTTGT
	Ryr2	ATGGCTTTAAGGCACAGCG	CAGAGCCCGAATCATCCAGC
	Sdha	GAACACTCCAAAAACAGACCTGC	TCCACCACTGGGTATTGAGTAG
	Sdhb	ATTTACCGATGGGACCCAGAC	GTCCGCACTTATTCAGATCCAC
	Sdhc	TTCAAACCGTCCTCTGTCTCC	CCTCCACTCAAGGCTATTCCA
	Sdhd	TGGTCAGACCCGCTTATGTG	GGTCCAGTGGAGAGATGCAG
	Serca1	TGTTTGTCCTATTTCGGGGTG	AATCCGCACAAGCAGGTCTTC
	Serca2(all forms)	TCGACAGGACAGAAAGAGTGTG	AAACTGAATTCAACTCACCAGC
	Serca2a	GCTCATTTTCCAGATCACACCG	GTTACTCCAGTATTGCGGGTTG
	Serca2b	ACCTTTGCCGCTCATTTTCCAG	AGGCTGCACACACTCTTTACC
	Serca3	GGAGCAGTTTGAGGACCTCTT	GGCCACGAGAATTAGCATGATG
	Suclg1	GGATACGACACGGGTCTTACA	GTGGTTCCTCCCACGAGTTTG
	Suclg2	CCCCGAAGATGGCTGAACC	ACCTCCTTTCAAACCGCTATTG
	Tbp	ACCCTTCACCAATGACTCCTATG	TGACTGCAGCAAATCGCTTGG
	Ucp1	CACCTTCCCGCTGGACACT	CCCTAGGACACCTTTATACCTAATGG
	Ucp2	TTAAGTGTTTCGTCTCCCAGCC	ACTCTGCCGGAGTTCTGGA
	Ucp3	CCGATTTCAAGCCATGATACGC	CCTGGCGATGGTTCTGTAGG