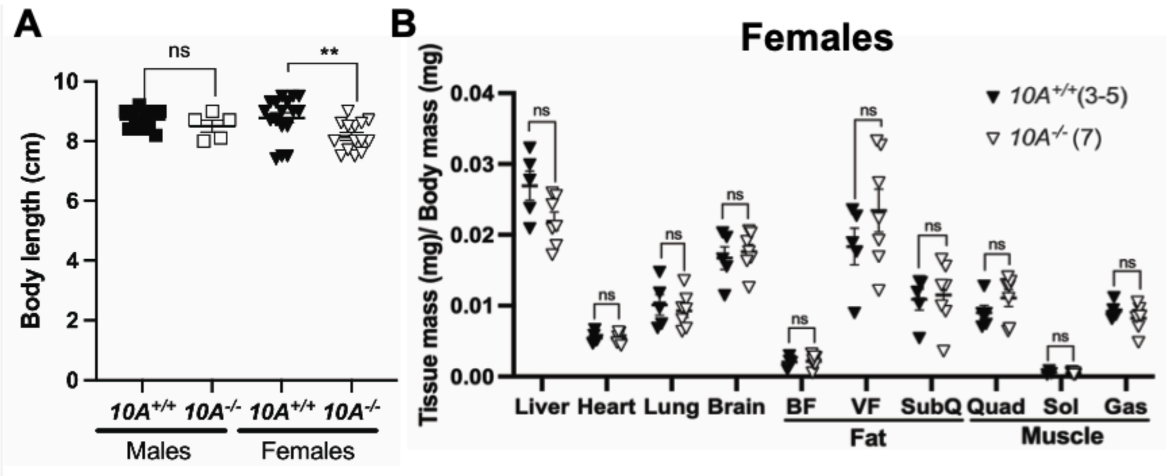
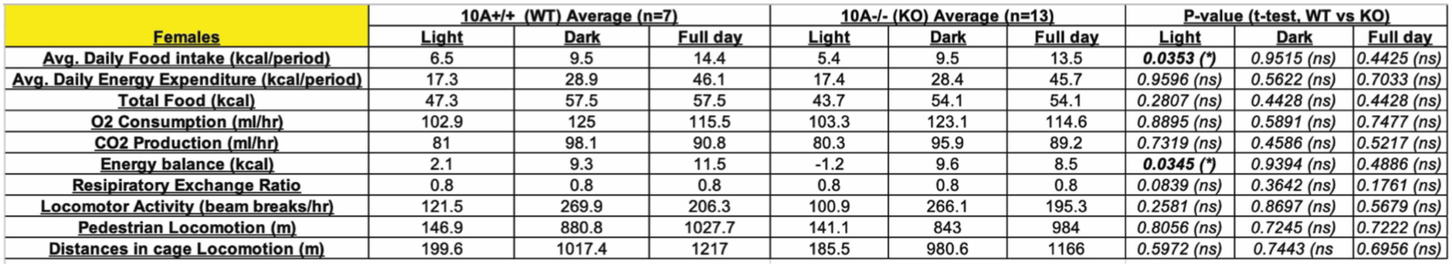
Appendix A: Supplemental Figures for Chapter 2

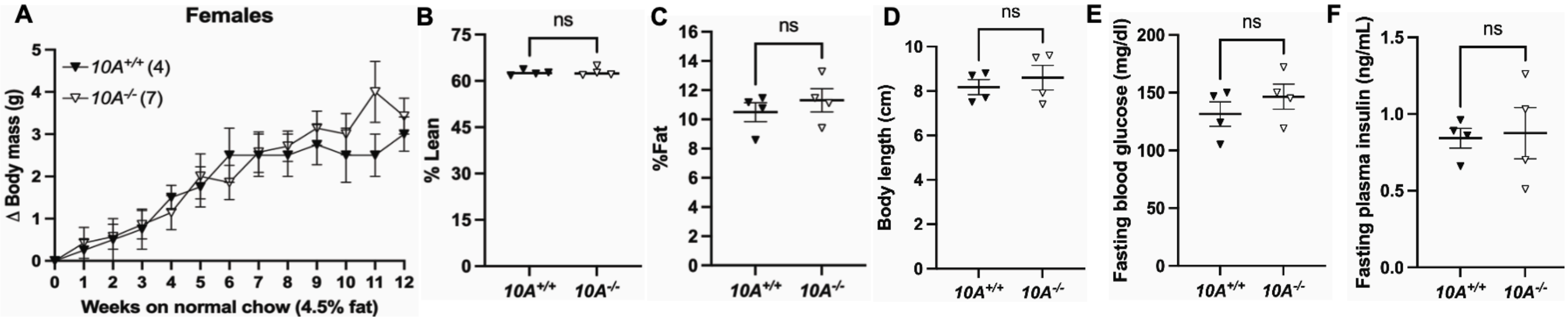


Supplemental Figure 1. *Atp10A* KO female mice have smaller bodies on the 12th week of the HFD. (A) Body length of mice was measured after CO_2 sacrifice. P value by unpaired t-test, **P=0.0094. (**Male:** *10A*$^{+/+}$ n=11, *10A*$^{-/-}$ n=5; **Female**: *10A*$^{+/+}$ n=17, *10A*$^{-/-}$ n=14). (B)The wet mass of tissue was measured after removal from female mice on the 12th week on the HFD. Tissue mass is normalized to body mass. P value by unpaired t-tests. (*10A*$^{+/+}$ n=3-5,*10A*$^{-/-}$ n=7).

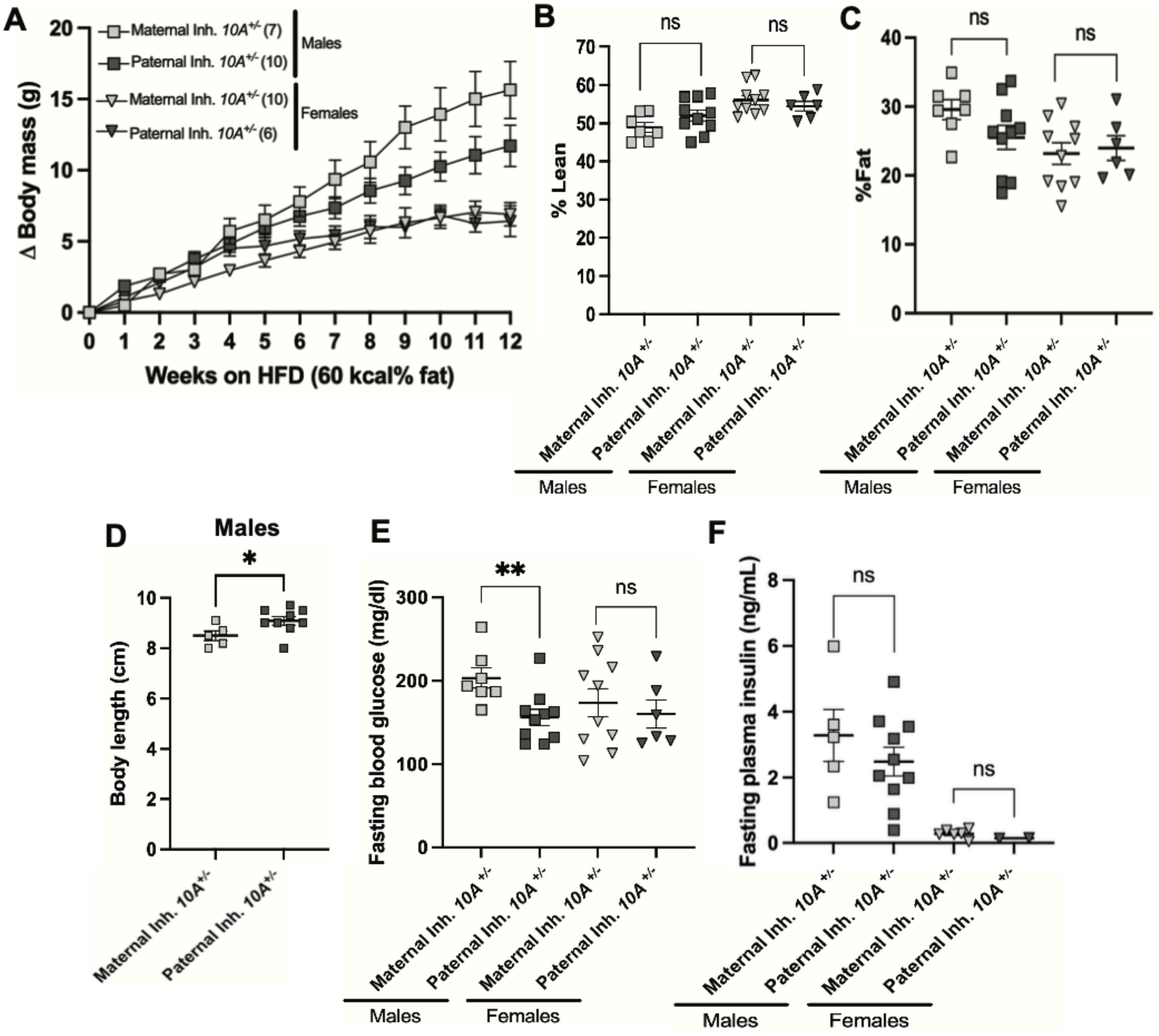


Females	10A+/+ (WT) Average (n=7)			10A-/- (KO) Average (n=13)			P-value (t-test, WT vs KO)		
	Light	Dark	Full day	Light	Dark	Full day	Light	Dark	Full day
Avg. Daily Food intake (kcal/period)	6.5	9.5	14.4	5.4	9.5	13.5	***0.0353 (*)***	*0.9515 (ns)*	*0.4425 (ns)*
Avg. Daily Energy Expenditure (kcal/period)	17.3	28.9	46.1	17.4	28.4	45.7	*0.9596 (ns)*	*0.5622 (ns)*	*0.7033 (ns)*
Total Food (kcal)	47.3	57.5	57.5	43.7	54.1	54.1	*0.2807 (ns)*	*0.4428 (ns)*	*0.4428 (ns)*
O2 Consumption (ml/hr)	102.9	125	115.5	103.3	123.1	114.6	*0.8895 (ns)*	*0.5891 (ns)*	*0.7477 (ns)*
CO2 Production (ml/hr)	81	98.1	90.8	80.3	95.9	89.2	*0.7319 (ns)*	*0.4586 (ns)*	*0.5217 (ns)*
Energy balance (kcal)	2.1	9.3	11.5	-1.2	9.6	8.5	***0.0345 (*)***	*0.9394 (ns)*	*0.4886 (ns)*
Resipiratory Exchange Ratio	0.8	0.8	0.8	0.8	0.8	0.8	*0.0839 (ns)*	*0.3642 (ns)*	*0.1761 (ns)*
Locomotor Activity (beam breaks/hr)	121.5	269.9	206.3	100.9	266.1	195.3	*0.2581 (ns)*	*0.8697 (ns)*	*0.5679 (ns)*
Pedestrian Locomotion (m)	146.9	880.8	1027.7	141.1	843	984	*0.8056 (ns)*	*0.7245 (ns)*	*0.7222 (ns)*
Distances in cage Locomotion (m)	199.6	1017.4	1217	185.5	980.6	1166	*0.5972 (ns)*	*0.7443 (ns*	*0.6956 (ns)*

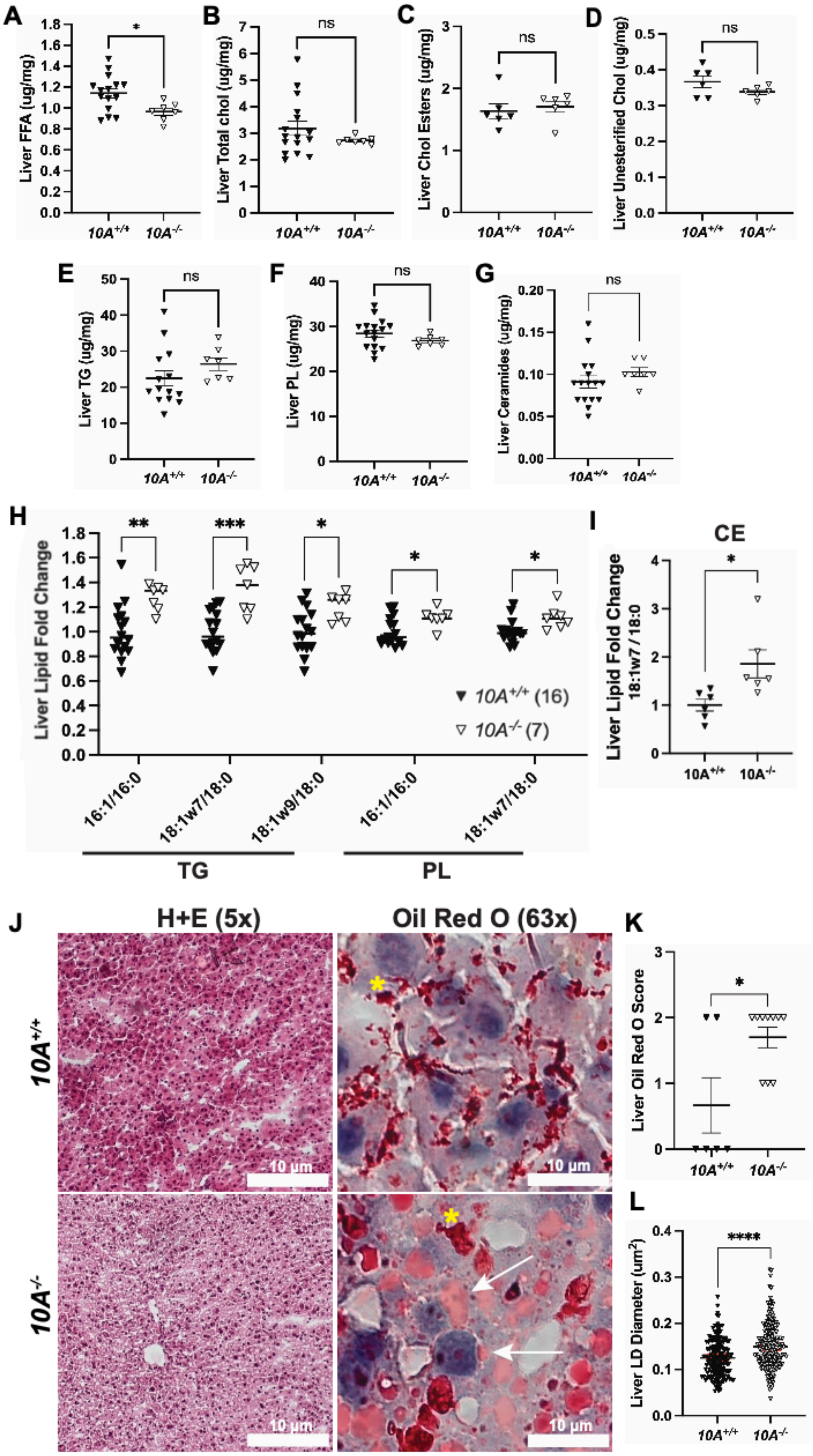
Supplemental Figure 2. *Atp10A* deletion causes alterations to average daily food intake and energy balance during the light hours in female mice fed a HFD for 13 weeks. The table indicates the parameters measured in the Sable System's Promethion Indirect Calorimetry System where the mice were single-housed. The values are an average measurement from 5 days in the system with ad libitum feeding. P value by unpaired t-test (*10A*$^{+/+}$ n=7, *10A*$^{-/-}$ n=13).



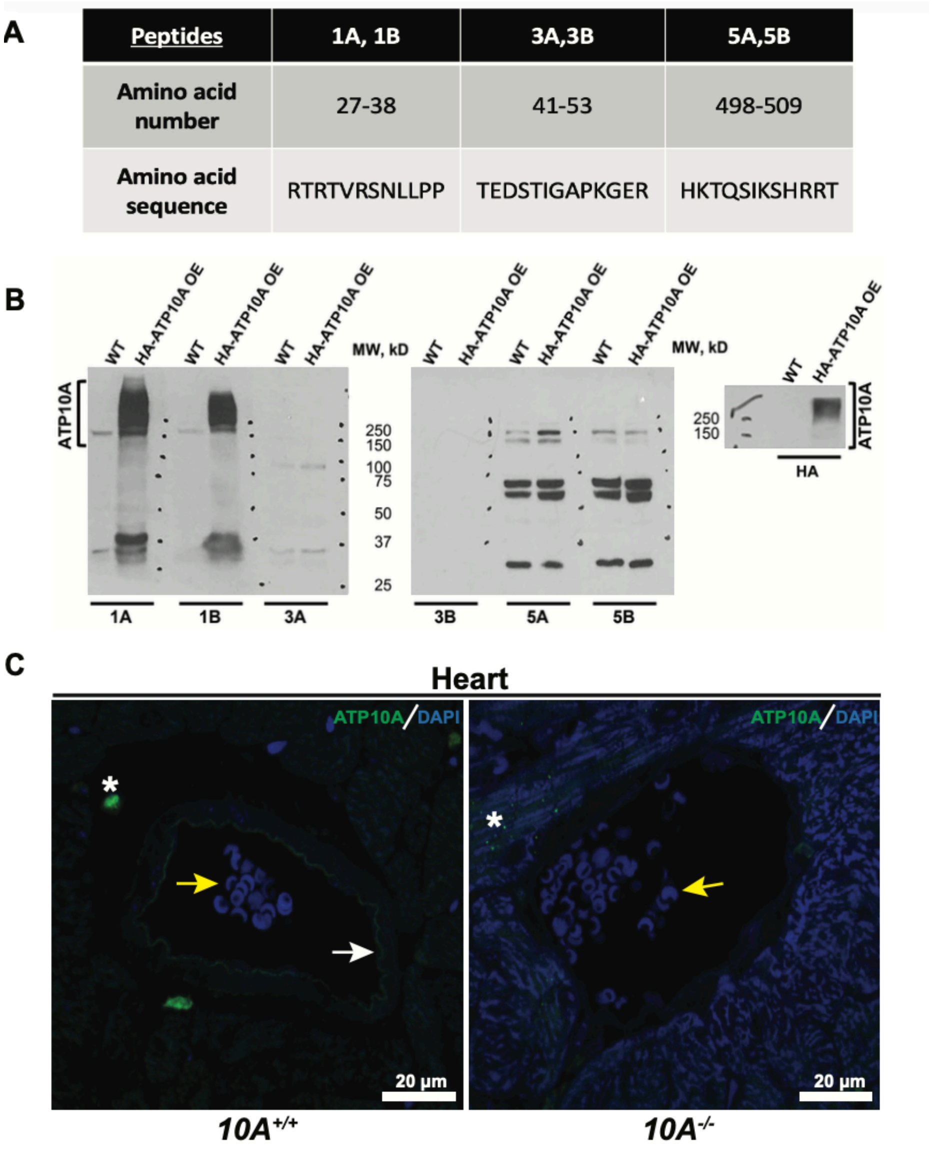
Supplemental Figure 3. *Atp10A* deletion does not affect weight gain, body composition, or glucose homeostasis in female mice after 12 weeks on normal chow. (A) Weight gain of *10A*$^{+/+}$ and *10A*$^{-/-}$ female mice over the course of 12 weeks on normal chow (4.5 kcal% fat, Ad lib feeding), P value by 2-way ANOVA with Sidak's multiple comparison. (*10A*$^{+/+}$ n=4,*10A*$^{-/-}$ n=7). (B) Lean and (C) fat body mass was normalized to total body mass to calculate % Lean and % Fat mass. P value by unpaired t-test (*10A*$^{+/+}$ n=4, *10A*$^{-/-}$ n=4). (D) Body length of mice was measured after CO_2 sacrifice. P value by unpaired t-test (*10A*$^{+/+}$ n=4,*10A*$^{-/-}$ n=4). (E) Fasting blood glucose was measured a 5 hour fast, via a glucometer. P value by unpaired t-test (*10A*$^{+/+}$ n=4,*10A*$^{-/-}$ n=4). (F) Fasting plasma insulin was measured aftr a 5 hour fast. P-value by unpaired t test (*10A*$^{+/+}$ n=4,*10A*$^{-/-}$ n=4).



Supplemental Figure 4. Maternally inherited *Atp10A* deletion leads to smaller bodies and elevated fasting blood glucose in male mice on the 12th week on the HFD. (A) Weight gain of heterozygous males and females inheriting the KO allele maternally (Maternal Inheritance (Inh.), *10A*$^{+/-}$ dam X *10A*$^{+/+}$ sire) or paternally (Paternal Inh, *10A*$^{+/+}$ dam x *10A*$^{+/-}$ sire) over the course of 12 weeks on a HFD (60 kcal% fat, Ad lib feeding). P value by 2-way ANOVA with Sidak's multiple comparison. (**Males**: Maternal Inh.*10A*$^{+/-}$ n=7, Paternal Inh.*10A*$^{+/-}$ n=10; **Females**: Maternal Inh.*10A*$^{+/-}$ n=10, Paternal Inh.*10A*$^{+/-}$ n=6). (B) Lean and (C) fat body mass were normalized to body mass to calculate % Lean and % Fat mass. P value by unpaired t-test (**Male**: Maternal Inh.*10A*$^{+/-}$ n=7, Paternal Inh.*10A*$^{+/-}$ n=10; **Female**: Maternal Inh.*10A*$^{+/-}$ n=10, Paternal Inh.*10A*$^{+/-}$ n=6). (D) Body length of male mice was measured after CO_2 sacrifice. P value by unpaired t-test, *P=0.0490. (Maternal Inh.*10A*$^{+/-}$ n=4, Paternal Inh.*10A*$^{+/-}$ n=9). (E) Fasting blood glucose was measured after a 5 hour fast, via a glucometer. P value by unpaired t-test, **P=0.0081. (**Male**: Maternal Inh.*10A*$^{+/-}$ n=7, Paternal Inh.*10A*$^{+/-}$ n=10; **Female**: Maternal Inh.*10A*$^{+/-}$ n=10, Paternal Inh.*10A*$^{+/-}$ n=6). (F) Fasting plasma insulin was measured after a 5 hour fast, P value by unpaired t-test. (**Male**: Maternal Inh.*10A*$^{+/-}$ n=6, Paternal Inh.*10A*$^{+/-}$ n=10; **Female**: Maternal Inh.*10A*$^{+/-}$ n=5, Paternal Inh.*10A*$^{+/-}$ n=2).

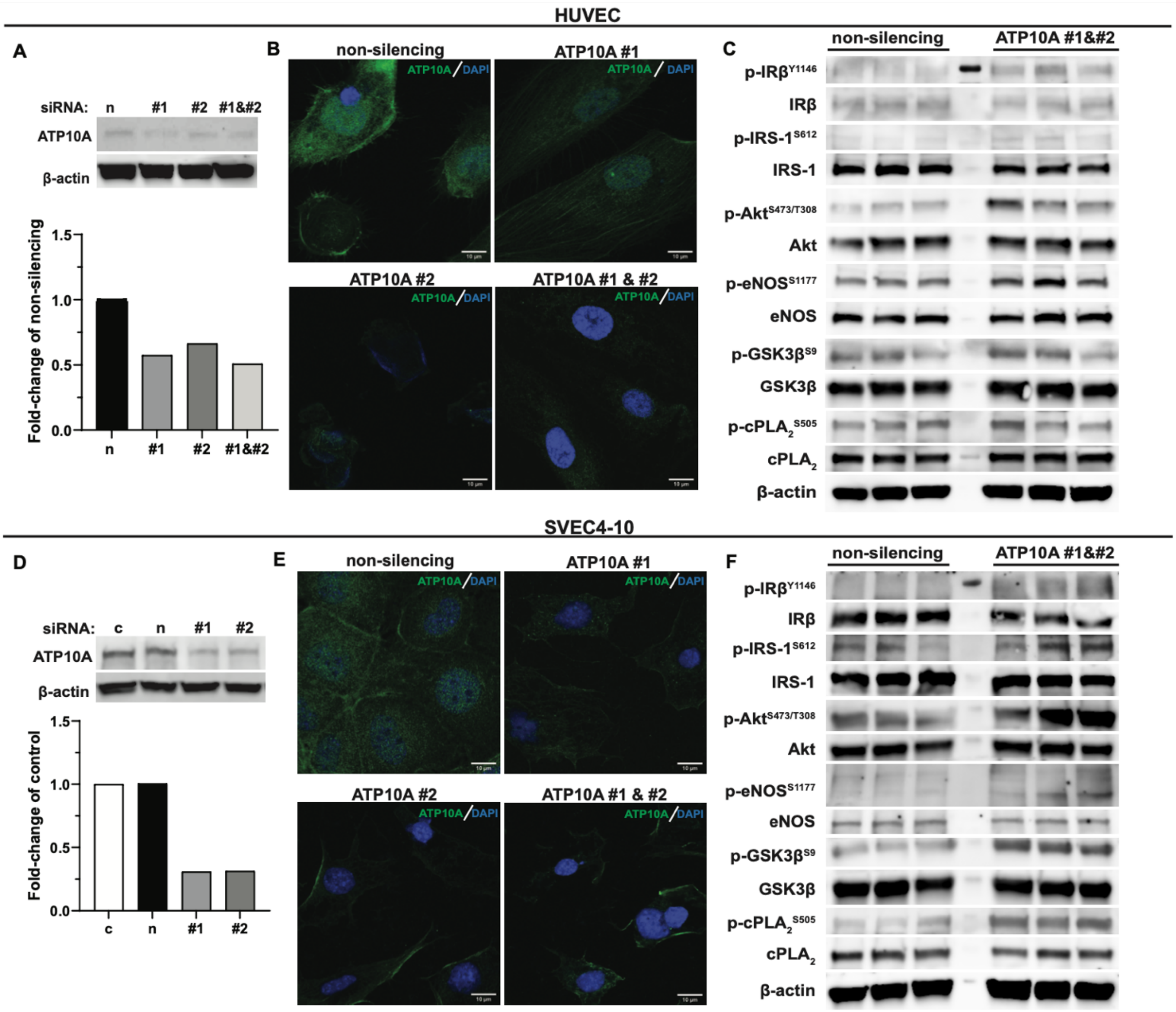


Supplemental Figure 5. *Atp10A* deletion causes changes to liver lipid metabolism in female mice after 12 weeks on a HFD. (A-G) FFAs, Total cholesterol, cholesterol esters, unesterifed cholesterol, TGs, PLs, and ceramides were measured from flash frozen livers via gas chromatography. Livers were collected after a 5 hour fast or after a 5 hour fast followed by an OGTT. P value by unpaired t-test (FFA: *10A*$^{+/+}$ n=15,*10A*$^{-/-}$ n=7, *P=0.0201; Total cholesterol: *10A*$^{+/+}$ n=16, *10A*$^{-/-}$ n=7; Cholesterol esters: *10A*$^{+/+}$ n=6,*10A*$^{-/-}$ n=6; Unesterified cholesterol: *10A*$^{+/+}$ n=6,*10A*$^{-/-}$ n=6; TG: *10A*$^{+/+}$ n=14, *10A*$^{-/-}$ n=7; PLs: *10A*$^{+/+}$ n=16, *10A*$^{-/-}$ n=7; Ceramides: *10A*$^{+/+}$ n=16, *10A*$^{-/-}$ n=7). The saturation of liver (H) TG, PL, and (I) CE species was determined by gas chromatography. The fold change of unsaturated vs saturated TG, PL, CE is shown. P value by 2-way ANOVA with Sidak's multiple comparison, **TG**: **P=0.0025, ***P=0.0001, *P=0.0443, **PL**: *P=0.0297, *P=0.0281 (*10A*$^{+/+}$ n=16, *10A*$^{-/-}$ n=7). **CE:** P value by unpaired t-test, *P=0.0223 (*10A*$^{+/+}$ n=6, *10A*$^{-/-}$ n=6). (J) Representative images of livers stained with H+E (5x) or Oil Red O (63x). The coalescence of the Oil Red O stain is indicated by yellow asterisks (artifact) and the arrows point to neutral lipids stained by Oil Red O. Scale bars = 10 μM. (K) Liver sections were scored using the Oil Red O Score described in the Materials and Methods. P value by nonparametric t-test (Mann-Whitney U), *P=0.0327 (*10A*$^{+/+}$ n=6, *10A*$^{-/-}$ n=10). (L) The diameters of Oil Red O positive lipid droplets (LD) in the liver sections with a score of 2 were measured using ImageJ. The red line in the graph represents the SEM. P value by unpaired t-test, ****P=<0.0001 (*10A*$^{+/+}$,120 LDs measured, n=2, *10A*$^{-/-}$, 203 LDs measured, n=3).

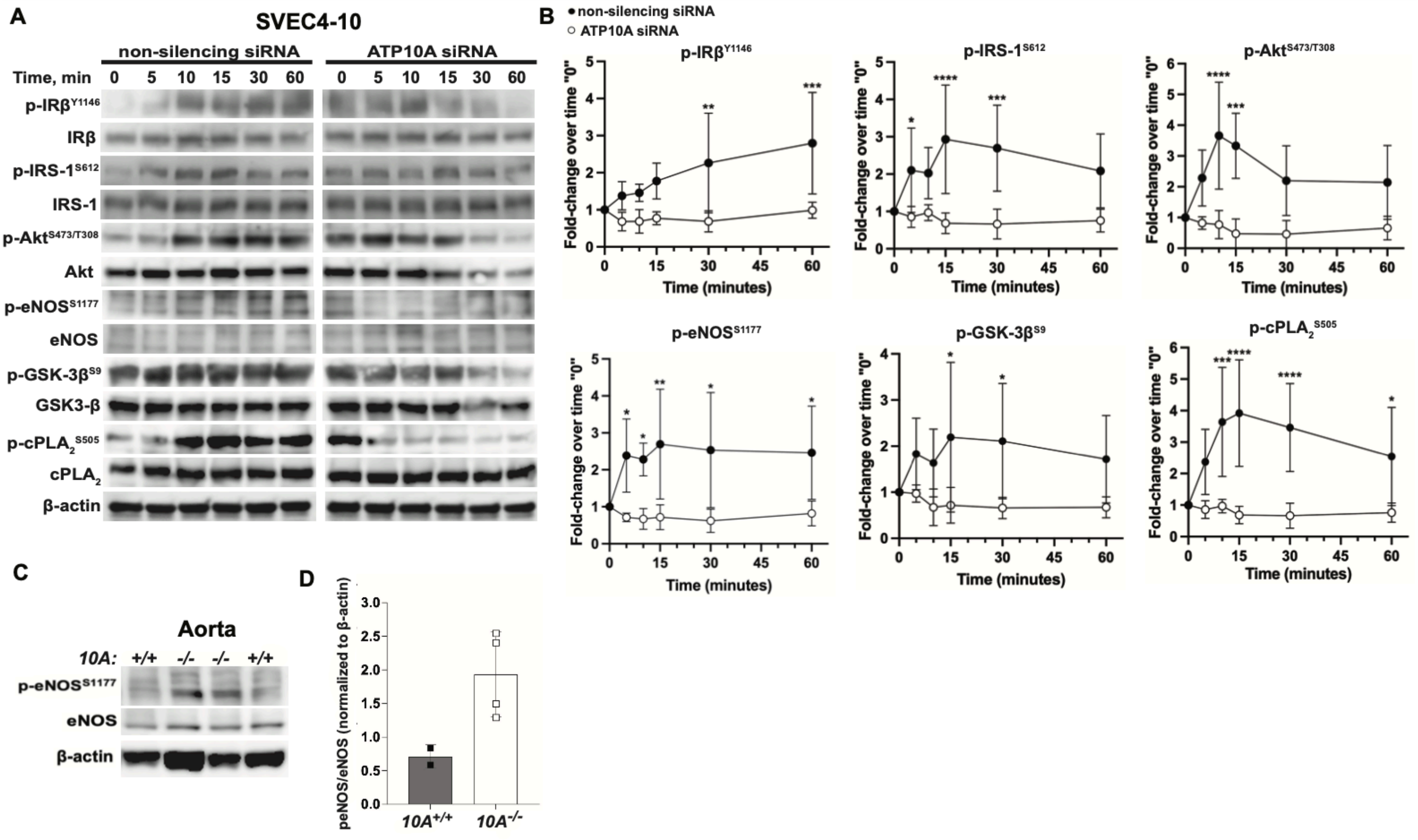


Peptides	1A, 1B	3A,3B	5A,5B
Amino acid number	27-38	41-53	498-509
Amino acid sequence	RTRTVRSNLLPP	TEDSTIGAPKGER	HKTQSIKSHRRT

Supplemental Figure 6. Validation of anti-ATP10A antibody: expression of ATP10A in HeLa cells with over-expressed HA-ATP10A and in mouse heart. (A) Table indicating the sequences of the ATP10A peptides that were injected into rabbits to produce antibodies. (B) Representative images of total cell lysates from HeLa cells with over-expressed HA-ATP10A (40 µg total protein) that were subjected to Western immunoblot analyses for expression of ATP10A using antibody produced against ATP10A peptides (left and central panels) and HA (right panel). (C) Representative immunofluorescent images of hearts from female mice showing expression of ATP10A (green) and DAPI (blue). Scale bar = 20 µm. The white asterisk indicates background staining, the white arrow indicates ATP10A positive staining, the yellow arrow indicates auto fluorescent red blood cells (*10A*$^{+/+}$ n=1, *10A*$^{-/-}$ n=1).



Supplemental Figure 7. ATP10A expression level regulates basal activity of insulin signaling pathways in endothelial cells. (A,D) Representative images and quantitative analysis of ATP10A from immunoblots of HUVEC (A) and SVEC4-10 (D) untreated (c), transfected with non-silencing siRNA or ATP10A siRNA constructs (#1, #2, #1&#2). (B, E) Representative immunofluorescent images showing expression of ATP10A and DAPI in HUVEC (B) and SVEC4-10 (E) transfected with non-silencing siRNA (n) or ATP10A siRNA constructs (ATP10A#1, ATP10A#2, ATP10A#1&#2). Scale bar=10 µm. (C, F) Representative images of basal phosphorylated and total IRβ, IRS-1, Akt, eNOS, GSK-3β, and cPLA2 from immunoblots of HUVEC (C) and SVEC4-10 (F) transfected with non-silencing siRNA or ATP10A#1&#2 siRNA constructs. Note th the lane between the non-silencing and ATP10A#1&#2 treated lanes contains the molecular weight marker.



Supplemental Figure 8. ATP10A expression regulates insulin signaling pathway in SVEC4-10 cells and mouse aorta. (A) Representative images and (B) quantitative analysis from immunoblots of phosphorylated and total IRβ, IRS-1, Akt, eNOS, GSK-3β, and $cPLA_2$ from SVEC4-10 cells transfected with non-silencing siRNA or ATP10A siRNA constructs and then treated with insulin for 0-60 mins. Mean measurements of 3-6 independent experiments are shown. *$p \le 0.05$; **$p \le 0.005$; ***$p \le 0.0005$; ***$p \le 0.0001$ between cells transfected with non-silencing or ATP10A siRNA by 2-way ANOVA with Sidak's multiple comparison test. (C) Representative blots and (D) quantitative analysis from immunoblots of phosphorylated and total eNOS from total aorta lysates from male mice (*10A*$^{+/+}$ n=2, *10A*$^{-/-}$ n=4, statistics were not done due to low n). Mean measurements of 3-6 independent experiments are shown.

Appendix B. Supplemental Tables for Chapter 2

Supplemental Table 1

Figure 2	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(B) Weight gain	Males		Females		
n	17	15	34	31	
Avg. body mass on 12th week of HFD (g)	34	33.9	23.6	25.1	
t-test (p-value) from body mass at 12th week on HFD	0.7672 (ns)		0.0498 (*)		
Avg. Age on 12th week of HFD (weeks)	18	19.4	17.8	19.2	
Outliers removed by ROUT analysis	0	0	0	0	
(C,D) Body comp.	Males		Females		
n	11	13	13	14	
Avg. body mass on 12th week of HFD (g)	35.6	33.8	24.2	26.5	
t-test (p-value) from body mass at 12th week on HFD	0.3636 (ns)		0.0799 (ns)		
Avg. Age on 12th week of HFD (weeks)	17.4	19.5	16.5	19.2	
Outliers removed by ROUT analysis	0	0	0	0	
(E) Fasting blood glucose	Males		Females		
n	10	11	19	14	
Avg. body mass on 12th week of HFD (g)	36.3	34.2	23.1	26.5	
t-test (p-value) from body mass at 12th week on HFD	0.3418 (ns)		0.0049 (**)		
Avg. Age on 12th week of HFD (weeks)	17.2	19.5	16.7	19.2	
Outliers removed by ROUT analysis	0	0	0	0	
(F) Fasting plasma insulin	Males		Females		
n	8	10	13	9	
Avg. body mass on 12th week of HFD (g)	36.5	34.7	23	28.4	
t-test (p-value) from body mass at 12th week on HFD	0.4579 (ns)		0.0009 (***)		
Avg. Age on 12th week of HFD (weeks)	17.1	19.5	16.3	19.3	
Outliers removed by ROUT analysis	0	0	0	0	
(G,H) OGTT (retroorbital blood taken prior to glc administration)	Males		Females		
n	6	6	12	6	
Avg. body mass on 12th week of HFD (g)	36.5	35.7	23.7	27.8	
t-test (p-value) from body mass at 12th week on HFD	0.7214 (ns)		0.0169 (*)		
Avg. Age on 12th week of HFD (weeks)	17.5	19.3	16.3	19.5	
Outliers removed by ROUT analysis	0	0	0	0	
					Females
Figure 3: Plasma lipid and lipoproteins	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	*10A+/+ (WT): 11 fast + OGTT, 1: fast only (92% fast + OGTT, 8% fast only)*
(A,D) Plasma FFA	Males		Females		*10A-/- (KO), FFA: 4: fast + OGTT, 4: fast only (50% fast + OGTT, 50% fast only)*
n	7 (all done by lab kit)	6 (all done by lab kit)	12 (11 done by Core, 1 done by lab kit)	8 (7 done by Core, 1 done by lab kit)	*10A-/- (KO). TG, chol: 4: fast + OGTT, 8: fast only (33% fast + OGTT, 67% fast only)*
Avg. body mass on 12th week of HFD (g)	34.2	37.2	23.1	27.9	
t-test (p-value) from body mass at 12th week on HFD	0.2427 (ns)		0.0014(**)		
Avg. Age on 12th week of HFD (weeks)	17.4	19.2	16.6	19.5	
Outliers removed by ROUT analysis	0	0	0	4	
(B,E) Plasma Chol	Males		Females		
n	8 (all done by lab kit)	6 (all done by lab kit)	12 (11 done by Core, 1 done by lab kit)	12 (7 done by Core, 5 done by lab kit)	
Avg. body mass on 12th week of HFD (g)	34.6	35.5	23.1	26.3	
t-test (p-value) from body mass at 12th week on HFD	0.5880 (ns)		0.0243 (*)		
Avg. Age on 12th week of HFD (weeks)	17.5	19.2	16.6	19.3	
Outliers removed by ROUT analysis	0	0	0	0	
(C,F) Plasma TG	Males		Females		
n	9 (all done by lab kit)	7 (all done by lab kit)	12 (11 done by Core, 1 done by lab kit)	12 (7 done by Core, 5 done by lab kit)	
Avg. body mass on 12th week of HFD (g)	34.4	37	23.1	26.3	
t-test (p-value) from body mass at 12th week on HFD	0.2138 (ns)		0.0243 (*)		
Avg. Age on 12th week of HFD (weeks)	17.6	19.1	16.6	19.3	
Outliers removed by ROUT analysis	0	0	0	0	
(G-I) Lipoprotein fractionation	Males		Females, chol		
n	N/A	N/A	6	6	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23.8	29.2	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0274 (*)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	16.3	19.3	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
	Males		Females, TG		
n	N/A	N/A	6	7	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23.8	28.6	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0372 (*)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	16.3	19.3	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
Figure 4: Plasma lipidomics and VF RNASeq	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(A,B) Plasma lipidomics	Males		Females		
n	N/A	N/A	ique mice (4 unpooled samples, 1 pooled sam	nique mice (3 unpooled samples, 2 pooled samples)	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	22.9	28.4	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0068 (**)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	16.5	19.4	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
(C) VF RNASeq	Males		Females		*10A+/+ (WT): 2: fast + OGTT, 1: fast only (67% fast + OGTT, 33% fast only)*
n	N/A	N/A	3	3	*10A-/- (KO): 1: fast + OGTT, 2: fast only (33% fast + OGTT, 67% fast only)*
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23.3	31.5	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0261 (*)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	17.3	19.3	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
Figure 5: Liver signaling (WB analysis)	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(A,B,C) DGAT and AMPK	Males		Females		*10A+/+ (WT): 2: fast + OGTT, : 5 fast only (29% fast + OGTT, 71 % fast only)*
n	N/A	N/A	7	7	*10A-/- (KO): : 4 fast + OGTT, : 3 fast only (57% fast + OGTT,43% fast only)*
Avg. body mass on 12th week of HFD (g)	N/A	N/A	22.9	27.6	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0142 (*)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	16.7	19.1	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
(D,E) IRB, IRS1, Akt, etc...	Males		Females		*10A+/+ (WT): 2: fast + OGTT, : 6 fast only (25% fast + OGTT, 75% fast only)*
n	N/A	N/A	8	8	*10A-/- (KO): : 4 fast + OGTT, : 4 fast only (50% fast + OGTT,50 % fast only)*
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23	27.3	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0118 (*)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	16.9	19.1	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
Figure 6: 10A Expression (WB & IF)	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	IHC: n=tissues from different mice imaged in the same session where the representative image was imag
(A) 10A Expression in Mouse tissues (WB)	Males		Females (fed HFD for 12 weeks)		
n	2 (vas def, heart:1, testes: 1)	2 (vas def, heart:1, testes: 1)	1 (brain, liver, VF)	1 (brain, liver, VF)	
Body mass at sacrifice (g)	N/A	N/A	27	25	
t-test (p-value) from body mass at 12th week on HFD	N/A		N/A		
Age (weeks)	7.5	8	19	19	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
(B) 10A Expression in Testes & Vas deferens (IF)	Males		Females		
n	1	1	N/A	N/A	
Body mass at sacrifice (g)	26	25	N/A	N/A	
t-test (p-value) from body mass at 12th week on HFD	N/A		N/A		
Age (weeks)	11	11	N/A	N/A	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
(C) 10A Expression in Liver	Males		Females (Liver)		
n	N/A	N/A	3	1	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	24	22	
t-test (p-value) from body mass at 12th week on HFD	N/A		N/A		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	18.7	21	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
(C) 10A Expression in VF	Males		Females (VF)		
n	N/A	N/A	3	2	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	24	23	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.7345 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	18.7	19.5	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
Figure 7: EC signaling	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(E,F) Mouse Aorta	Males		Females (all normal chow)		
n	N/A	N/A	5	4	
Avg. Body mass at sacrifice (g)	N/A	N/A	23.8	22.8	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.5209 (ns)		
Avg. Age (weeks)	N/A	N/A	20.4	17.8	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
Supp. Figure 1: Body length & tissue mass	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(A) Body length	Males		Females		
n	11	5	17	14	
Avg. body mass on 12th week of HFD (g)	34.7	36	23.7	27.3	
t-test (p-value) from body mass at 12th week on HFD	0.6672 (ns)		0.0666 (ns)		
Avg. Age on 12th week of HFD (weeks)	17.9	19.4	16.7	19.6	
Outliers removed by ROUT analysis	0	0	0	0	
(B) Tissue mass	Males		Females (12 weeks of HFD)		
n	N/A	N/A	3-5	7	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23.6	23.1	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.7344 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	18.4	19.1	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
(C) T30 Serum Insulin	Males		Females		
n	4	4	8	6	
Avg. body mass on 12th week of HFD (g)	37.3	28.1	22.9	27.8	
t-test (p-value) from body mass at 12th week on HFD	0.5431 (ns)		0.0099 (**)		
Avg. Age on 12th week of HFD (weeks)	17.3	15.4	15.9	19.5	
Outliers removed by ROUT analysis	0	0	0	0	
(D) T60 Serum Insulin	Males		Females		
n	6	5	8	6	
Avg. body mass on 12th week of HFD (g)	36.5	35.1	20.7	27.8	
t-test (p-value) from body mass at 12th week on HFD	0.5790 (ns)		0.0270 (*)		
Avg. Age on 12th week of HFD (weeks)	17.5	19.2	14.1	19.5	
Outliers removed by ROUT analysis	0	0	0	0	
Supp. Figure 2: Sable data	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(A) Body length	Males		Females		
n	N/A	N/A	7	13	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	24.4	25.6	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.5296 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	19.7	19.1	
Outliers removed	N/A	N/A	1	0	
Supp. Figure 3: Normal chow studies	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(A) Weight gain	Males		Females		
n	N/A	N/A	4	7	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	20.8	21.6	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.2943 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	20	19.7	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
B,C, D, E F) % Lean, % Fat, Body length, FBG, Fasting plasma insulir	Males		Females		
n	N/A	N/A	4	4	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	20	21.5	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.4772 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	20	20	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
Supp. Figure 4: Inheritance pattern studies	Maternal Inh. 10a +/-	Paternal Inh. 10a +/-	Maternal Inh. 10a +/-	Paternal Inh. 10a +/-	
(A, B, C, E) Weight gain, %Lean, %Fat, FBG	Males		Females		
n	7	10	10	6	
Avg. body mass on 12th week of HFD (g)	35.9	32.5	25.4	25.6	
t-test (p-value) from body mass at 12th week on HFD	0.1405 (ns)		0.9105 (ns)		
Avg. Age on 12th week of HFD (weeks)	17.1	17.8	16.8	17.7	
Outliers removed by ROUT analysis	0	0	0	0	
(D) Body length	Males		Females		
n	4	11	N/A	N/A	
Avg. body mass on 12th week of HFD (g)	33	32.3	N/A	N/A	
t-test (p-value) from body mass at 12th week on HFD	0.7165 (ns)		N/A		
Avg. Age on 12th week of HFD (weeks)	17.6	17.8	N/A	N/A	
Outliers removed by ROUT analysis	0	0	N/A	N/A	
(F) Fasting plasma insulin	Males		Females		
n	6	10	5	2	
Avg. body mass on 12th week of HFD (g)	33	32.5	26	27.3	
t-test (p-value) from body mass at 12th week on HFD	0.7744 (ns)		0.7049 (ns)		
Avg. Age on 12th week of HFD (weeks)	17.6	17.8	16	17	
Outliers removed by ROUT analysis	0	0	0	0	
Supp. Figure 5: Liver lipids	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(A, B, E, F, G, H*) Liver FFA, T Chol, TG, Cer, PL, Lipid fold change*	Males		Females		* TG: (16:1/16:0), (18:w7/18:0), (18:1w9/19:0), PL: (16:1/16:0), (18:1w7/18:0)
n	N/A	N/A	14-16	7	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23.1	28.5	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0006 (***)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	16.3	19.6	
Outliers removed by ROUT analysis	N/A	N/A	FFA: 1, TG:2	0	
(C,D, I*) Liver Chol Est, Chol un-est, Lipid fold change*	Males		Females		*CE: (18:1w7/18:0)
n	N/A	N/A	6	6	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	23.8	27.8	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0551 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	17	19.2	
Outliers removed by ROUT analysis	N/A	N/A	0	0	
(J, K) Liver Oil Red O	Males		Females		
n	N/A	N/A	6	10	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	22.7	28.1	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.0059 (**)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	17	19.4	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
(K) Lipid droplet size	Males		Females		
n	N/A	N/A	2	3	
Avg. body mass on 12th week of HFD (g)	N/A	N/A	25.5	24.8	
t-test (p-value) from body mass at 12th week on HFD	N/A		0.5993 (ns)		
Avg. Age on 12th week of HFD (weeks)	N/A	N/A	19	19.3	
Outliers removed by ROUT analysis	N/A	N/A	3	1	
Supp. Figure 6: 10A Expression (WB, IF)	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(B) 10A expression in heart (IF)	Males		Females		
n	N/A	N/A	1	1	n=tissues from different mice imaged in the same session where the representative image was imaged
Body mass on 12th week of HFD (g)	N/A	N/A	22	24	
t-test (p-value) from body mass at 12th week on HFD	N/A		N/A		
Age on 12th week of HFD (weeks)	N/A	N/A	19	19	
Outliers removed by ROUT analysis	N/A	N/A	N/A	N/A	
Supp. Figure 8: Aorta eNOS (WB)	10A+/+ (WT)	10A-/- (KO)	10A+/+ (WT)	10A-/- (KO)	
(C,D) 10A Expression in Mouse Aorta	Males		Females		
n	2 (both on HFD)	4 (1 on HFD)	N/A	N/A	
Body mass on 12th week of HFD (g)	30	27.8	N/A	N/A	
t-test (p-value) from body mass at 12th week on HFD	0.3177 (ns)		N/A		
Age on 12th week of HFD (weeks)	19	13	N/A	N/A	
Outliers removed by ROUT analysis	0	0	N/A	N/A	

Supplemental Table 2

Pathway Kegg

geneSet	description	size	overlap	expect	enrichmentRatio	pValue	FDR
g.jp/kegg-bin/show_pathway? mmu04972+13487+1878	Pancreatic secretion	103	5	0.809063	6.179985	0.0012387	0.393894
tp://www.kegg.jp/kegg-bin/show_pathway? mmu00730+	Thiamine metabolism	15	2	0.117825	16.974359	0.0059725	0.566786
gg-bin/show_pathway? mmu04080+110902+11555+126	Neuroactive ligand-receptor interaction	289	7	2.270091	3.083577	0.0072516	0.566786
www.kegg.jp/kegg-bin/show_pathway? mmu05150+1351	Staphylococcus aureus infection	56	3	0.439879	6.820055	0.0095348	0.566786
www.kegg.jp/kegg-bin/show_pathway? mmu00561+2355	Glycerolipid metabolism	61	3	0.479154	6.261034	0.0120409	0.566786
tp://www.kegg.jp/kegg-bin/show_pathway? mmu04964+	Proximal tubule bicarbonate reclamation	22	2	0.17281	11.573427	0.0126837	0.566786
g.jp/kegg-bin/show_pathway? mmu04145+12845+1499	Phagosome	181	5	1.421752	3.516787	0.0135801	0.566786
p://www.kegg.jp/kegg-bin/show_pathway? mmu00790+1	Folate biosynthesis	26	2	0.20423	9.792899	0.0174897	0.566786
www.kegg.jp/kegg-bin/show_pathway? mmu04976+1384	Bile secretion	71	3	0.557704	5.379198	0.018093	0.566786
://www.kegg.jp/kegg-bin/show_pathway? mmu00650+2	Butanoate metabolism	27	2	0.212085	9.430199	0.0187942	0.566786

Significantly differential expressed genes in Pancreatic secretion

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000041193.15	Pla2g5	327.6929	0	0	21.6047666
ENSMUSG00000007107.6	Atp1a4	258.5906	0	0.000001	4.8748642
ENSMUSG00000071553.10	Cpa2	196.022	0	1.2E-06	3.7086972
ENSMUSG00000020431.5	Adcy1	104.9107	0.00022	0.020501	0.3598145
ENSMUSG00000001225.12	Slc26a3	29.11604	0.00024	0.021209	3.9715976

Significantly differential expressed genes in Thiamine metabolism

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000026817.14	Ak1	1358.032	0.000292	0.023143	2.018769
ENSMUSG00000028766.10	Alpl	237.0382	0.000518	0.034247	2.843773

Significantly differential expressed genes in Neuroactive ligand-receptor interaction

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000056380.13	Gpr50	56.43242	1.47E-05	0.003859	571.2601672
ENSMUSG00000040495.4	Chrm4	14.01271	2.69E-05	0.005626	25.0694979
ENSMUSG00000043017.9	Ptgir	400.5867	5.13E-05	0.008149	2.345606
ENSMUSG00000044338.9	Aplnr	803.3216	0.00076	0.04297	2.7616563
ENSMUSG00000021478.6	Drd1	52.58807	0.0009	0.048217	0.2768258
ENSMUSG00000022041.10	Chrna2	169.0929	0.000918	0.048854	2.1544465
ENSMUSG00000045730.4	Adrb2	637.536	0.000944	0.049661	0.4256661

Significantly differential expressed genes in Staphylococcus aureus infection

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000069441.3	Dsg1a	61.66929	4E-07	0.000233	5.596025
ENSMUSG00000061928.6	Dsg1b	20.82076	2.61E-05	0.00562	19.302742
ENSMUSG00000026580.16	Selp	210.5568	0.00073	0.04214	2.465355

Significantly differential expressed genes in Glycerolipid metabolism

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000024768.5	Lipf	231.5996	0	0	16.1785033
ENSMUSG00000012187.13	Mogat1	674.7383	0.000242	0.021213	0.4207309
ENSMUSG00000020258.16	Glyctk	130.4926	0.000281	0.022637	2.285067

Significantly differential expressed genes in Proximal tubule bicarbonate reclamation

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000007107.6	Atp1a4	258.5906	0	0.000001	4.874864
ENSMUSG00000010064.15	Slc38a3	708.3462	0.000883	0.048032	2.559326

Significantly differential expressed genes in Phagosome

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000031849.9	Comp	138.805	0.000068	0.009699	2.5941413
ENSMUSG00000020695.14	Mrc2	2506.892	0.00012	0.013829	2.7056454
ENSMUSG00000067201.11	H2-M9	240.8505	0.000181	0.017773	0.4219105
ENSMUSG00000028238.6	Atp6v0d2	208.2672	0.000195	0.018484	4.0684324
ENSMUSG00000026390.7	Marco	155.7569	0.000613	0.037129	2.3528541

Significantly differential expressed genes in Folate biosynthesis

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000006764.8	Tph2	959.1933	1E-07	5.16E-05	22.049261
ENSMUSG00000028766.10	Alpl	237.0382	0.000518	0.034247	2.843773

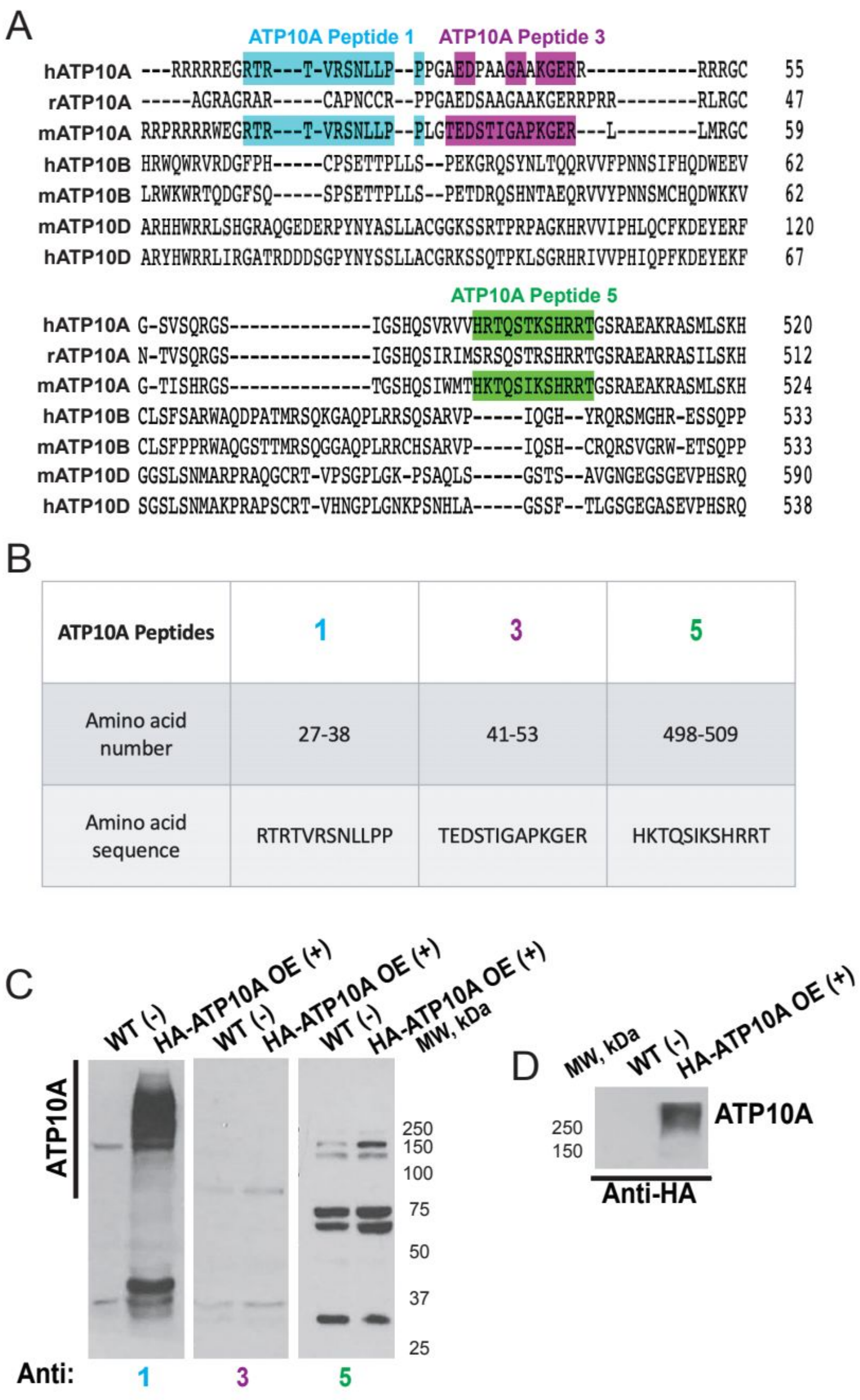
Significantly differential expressed genes in Bile secretion

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000007107.6	Atp1a4	258.5906	0	0.000001	4.8748642
ENSMUSG00000038776.13	Ephx1	4746.016	9.4E-06	0.002761	2.0548225

Significantly differential expressed genes in Butanoate metabolism

Stable IDs	Feature_gene_name	baseMean	pvalue	padj	FoldChange
ENSMUSG00000057880.12	Abat	3895.093	1E-07	4.84E-05	2.4992921
ENSMUSG00000030972.6	Acsm5	1971.103	0.000482	0.032604	0.4485598

Appendix C: Supplemental Figures for Chapter 3



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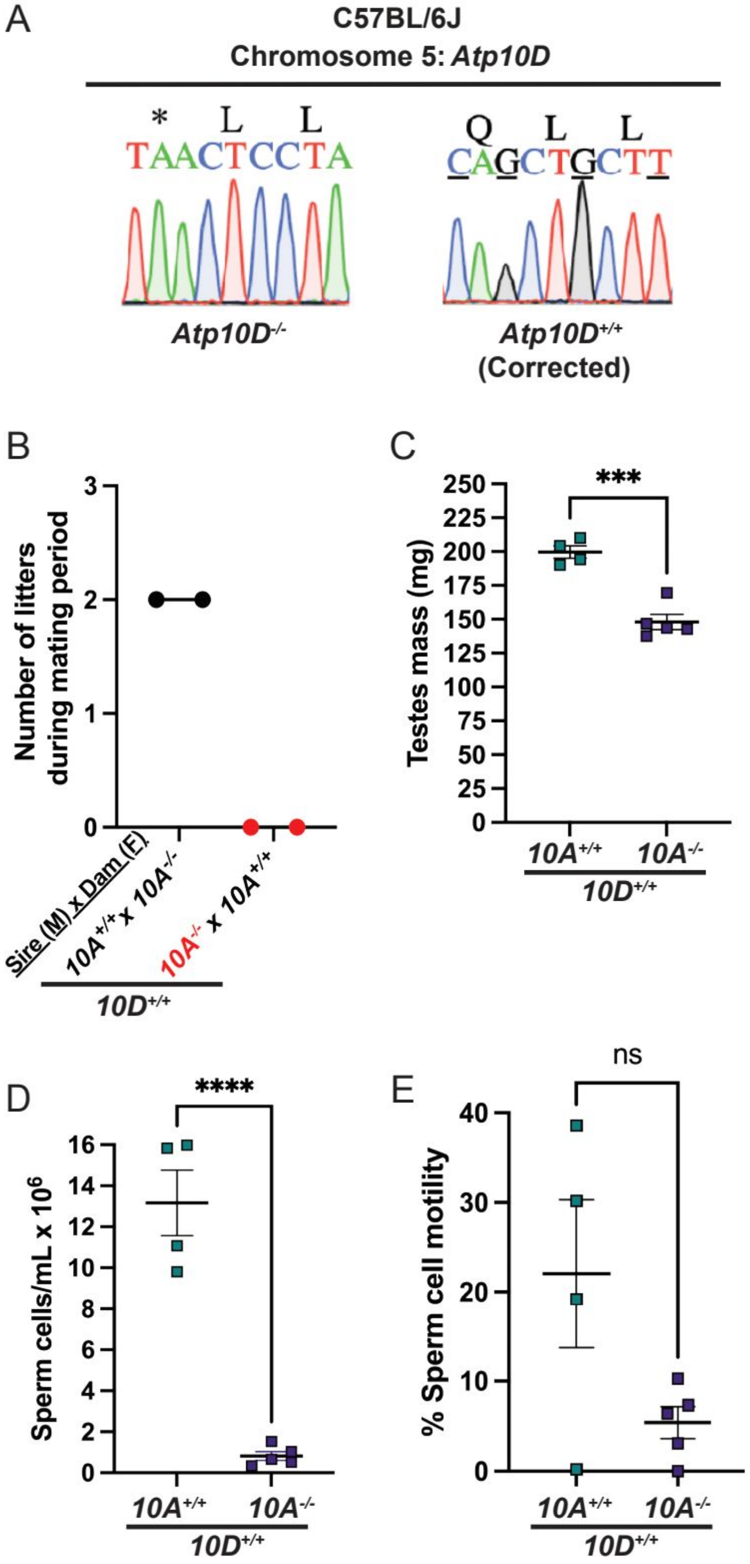
hATP10A ---RRRRREGRTR---T-VRSNLLP--PPGAEDPAAGAAKGERR-----------RRRGC  55
rATP10A -----AGRAGRAR-----CAPNCCR--PPGAEDSAAGAAKGERRPRR--------RLRGC  47
mATP10A RRPRRRRWEGRTR---T-VRSNLLP--PLGTEDSTIGAPKGER---L--------LMRGC  59
hATP10B HRWQWRVRDGFPH-----CPSETTPLLS--PEKGRQSYNLTQQRVVFPNNSIFHQDWEEV  62
mATP10B LRWKWRTQDGFSQ-----SPSETTPLLS--PETDRQSHNTAEQRVVYPNNSMCHQDWKKV  62
mATP10D ARHHWRRLSHGRAQGEDERPYNYASLLACGGKSSRTPRPAGKHRVVIPHLQCFKDEYERF  120
hATP10D ARYHWRRLIRGATRDDDSGPYNYSSLLACGRKSSQTPKLSGRHRIVVPHIQPFKDEYEKF  67

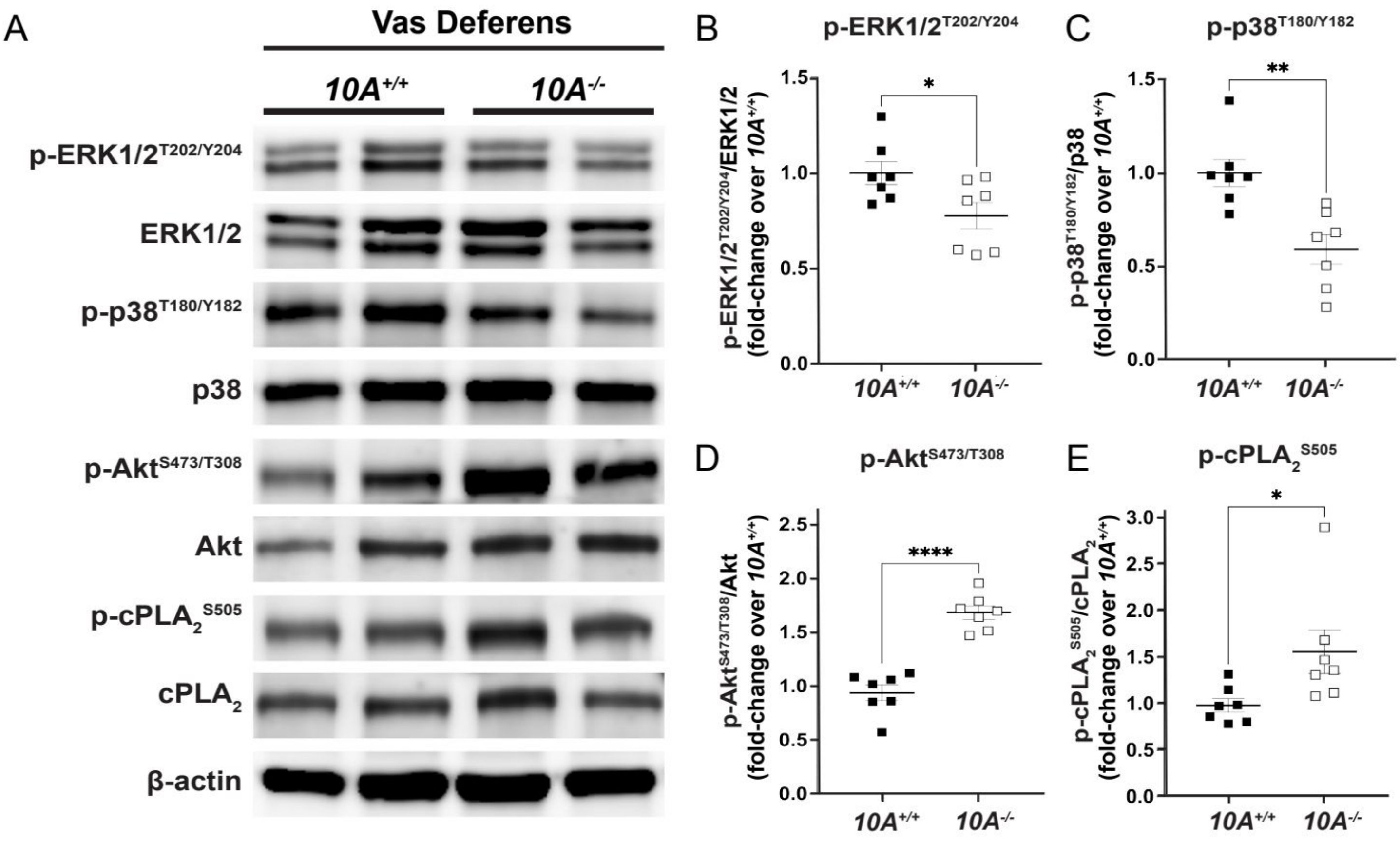
hATP10A G-SVSQRGS--------------IGSHQSVRVVHRTQSTKSHRRTGSRAEAKRASMLSKH  520
rATP10A N-TVSQRGS--------------IGSHQSIRIMSRSQSTRSHRRTGSRAEARRASILSKH  512
mATP10A G-TISHRGS--------------TGSHQSIWMTHKTQSIKSHRRTGSRAEAKRASMLSKH  524
hATP10B CLSFSARWAQDPATMRSQKGAQPLRRSQSARVP-----IQGH--YRQRSMGHR-ESSQPP  533
mATP10B CLSFPPRWAQGSTTMRSQGGAQPLRRCHSARVP-----IQSH--CRQRSVGRW-ETSQPP  533
mATP10D GGSLSNMARPRAQGCRT-VPSGPLGK-PSAQLS-----GSTS--AVGNGEGSGEVPHSRQ  590
hATP10D SGSLSNMAKPRAPSCRT-VHNGPLGNKPSNHLA-----GSSF--TLGSGEGASEVPHSRQ  538
```

ATP10A Peptides	1	3	5
Amino acid number	27-38	41-53	498-509
Amino acid sequence	RTRTVRSNLLPP	TEDSTIGAPKGER	HKTQSIKSHRRT

Supplemental Figure 9. Validation of ATP10A antibody: expression of ATP10A in HeLa cells with over-expressed HA-ATP10A. (A) Alignments of human (h), rat (r), and mouse (m) ATP10A, ATP10B, and ATP10D created using Clustal Omega with the ATP10A peptides that were chosen for antibody production highlighted. These peptides were chosen based on conservation between mouse and human ATP10A orthologs and lack of conservation with ATP10B and ATP10D paralogs. (B) Table indicating the sequences of the ATP10A peptides that were injected into rabbits to produce antibodies, peptides are color-coded according to the colors of the peptides in (A). (C,D) Representative images of total cell lysates from HeLa cells with (+) or without (-) over-expressed (OE) human HA-ATP10A (40 µg total protein) that were subjected to Western immunoblot analyses for expression of ATP10A using antibody produced against (C) ATP10A peptides or (D) HA. Peptides are color-coded according to the colors of the peptides in (A).



Supplemental Figure 10. Reintroduction of *Atp10D* does not rescue infertility, smaller testes, or low sperm cell count in *Atp10A* deficient mice. (A) Sequencing was performed to validate the genotype of the *Atp10D* mice. Briefly, CRISPR was used to replace the premature stop codon found in the *Atp10D* sequence in C57BL/6J mice (*, *Atp10D*$^{-/-}$ mice) to glutamine that is found in other mouse strains (Q, *Atp10D*$^{+/+}$ (corrected) mice). The underlined nucleotides indicate CRISPR-mediated changes to the DNA sequence, for the purposes of changing the amino acid or introducing restriction digest cut sites for genotyping purposes. (B) Mating studies were done by housing pairs of mice together (without separating) for approximately 9 weeks and recording the number of litters produced. (See supplemental table 1 for more details). (C) The wet mass of testes was measured in 14-21-week-old mice, ***P=0.0002. (D) Sperm cells collected from the caput epididymis were counted using a hemocytometer, ****P<0.0001. (E) % Sperm cell motility was measured using the equation: motile sperm/total sperm counted. P-value by unpaired t-test.



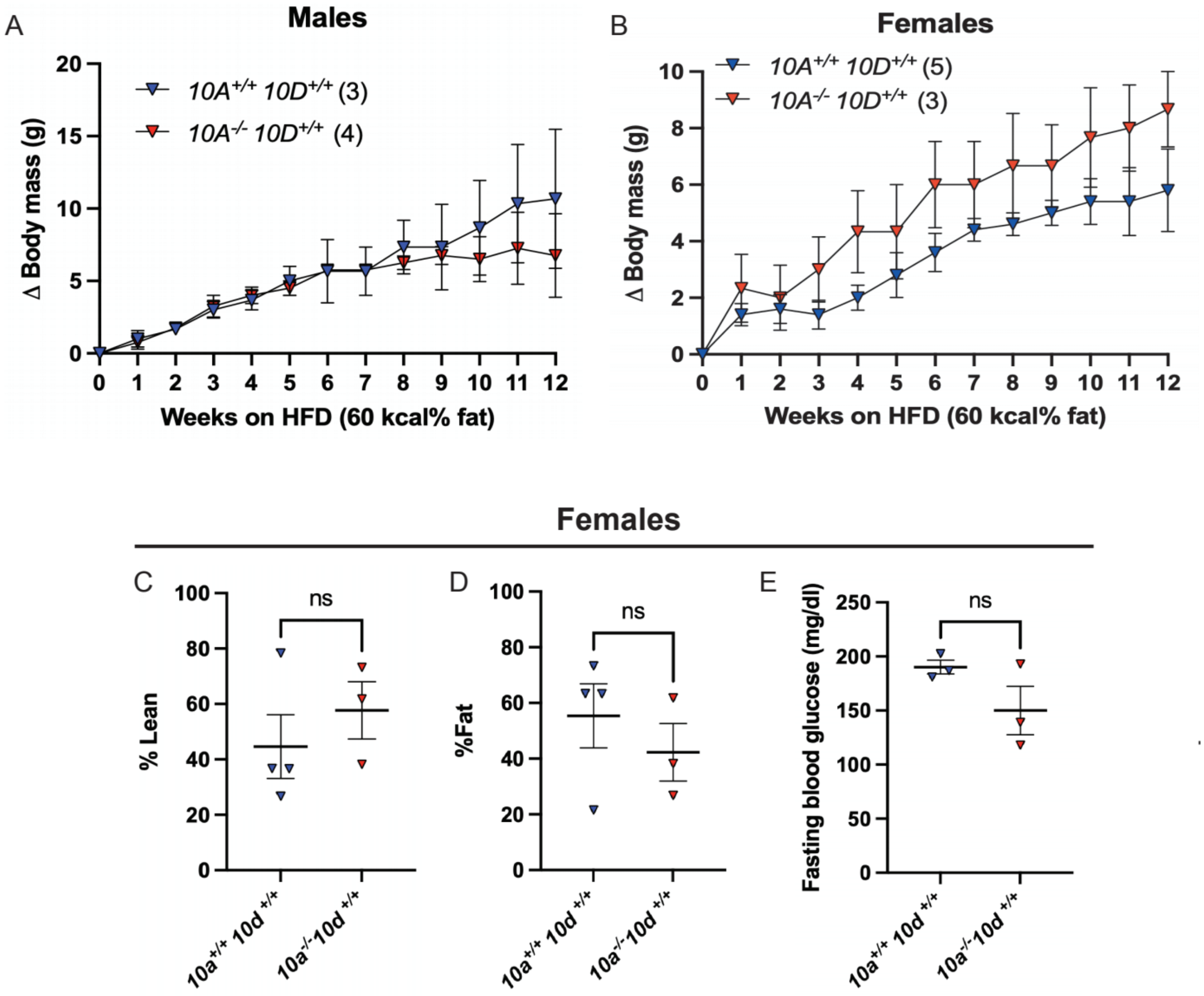
Supplemental Figure 11. *Atp10A* deficiency results in changes to signaling in the vas deferens. Total tissue lysates from vas deferens from the *10A*$^{+/+}$ and *10A*$^{-/-}$ mice were subjected to Western immunoblot analysis. (A) Representative blots for total and/or phosphorylated ERK1/2, p38, Akt, and cPLA$_2$. (B-E) The phosphoproteins were normalized to their respective total protein, β-actin levels, and total protein from *10A*$^{+/+}$ samples. Mean measurements of 4-6 independent experiments are shown. P value by unpaired t-test. (*10A*$^{+/+}$ n=7, *10A*$^{-/-}$ n=7, B: *P=0.0313, C: **P= 0.0024, D: ****P<0.0001, E: *P=0.0376).

Appendix D. Supplemental Table for Chapter 3

Supplemental Table 3

Figure 9 (all 10D -/-)	***10A+/+ (WT)***	***10A-/- (KO)***	
(A) Vas deferens WB			
n	1	1	
Body mass at sacrifice (g)	*did not measure*	*did not measure*	
Age at sacrifice (weeks)	7	8	
Outliers removed by ROUT analysis	N/A	N/A	
(B) Testes WB			
n	1	1	
Body mass at sacrifice (g)	23	24	
Age at sacrifice (weeks)	8	8	
Outliers removed by ROUT analysis	N/A	N/A	
(C) Vas deferens IF			
n	1	2	
Avg. body mass at sacrifice (g)	26	28.5	
Avg. age at sacrifice (weeks)	11	15	
Outliers removed by ROUT analysis	N/A	N/A	
(D) Testes IF			
n	2	2	
Avg. body mass at sacrifice (g)	27.5	28.5	
Avg. age at sacrifice (weeks)	17	17	
Outliers removed by ROUT analysis	N/A	N/A	
(E) Mating studies	Red text= Sire is 10A -/-		
Order: Sire (M) x Dam (F)	**Average time parents housed together (weeks)**		**Average pups per litter**
10A +/+ x 10A +/+ (1 pair)	20.9		6
10A +/+ x 10A -/- (2 pairs)	6.6		5
10A -/- x 10A +/+ (3 pairs)	9.8		N/A
10A +/- x 10A -/- (1 pair)	19.6		6
10A -/- x 10A +/- (3 pairs)	15.9		8.5
10A +/- x 10A +/- (5 pairs)	12		7.1
10A -/- x 10A -/- (3 pairs)	10.9		N/A
Figure 10 (all 10D -/-)	***10A+/+ (WT)***	***10A+/- (Het)***	***10A-/- (KO)***
(A) Testes mass (mg), (B), Sperm cells/mL, (C) % sperm cell motility			
n	9	2	14
Avg. body mass at sacrifice (g)	26.8	25	26.7
Avg. age at sacrifice (weeks)	13.8	10.5	12
Outliers removed by ROUT analysis	0	0	0
Figure 11 (all 10D -/-)	***10A+/+ (WT)***	***10A-/- (KO)***	
(C) Seminiferous tubule scoring			
n	6	12	
Avg. body mass at sacrifice (g)	26	26.8	
Avg. age at sacrifice (weeks)	12.2	11.6	
Outliers removed by ROUT analysis	N/A	N/A	
Figure 12 (all 10D -/-)	***10A+/+ (WT)***	***10A-/- (KO)***	
(B) Plasma T			
n	16	18	
Avg. body mass at sacrifice (g)	33.5	33.8	
Avg. age at sacrifice (weeks)	14.1	15.4	
Outliers removed by ROUT analysis	3	1	
(C) LH	***10A+/+ (WT)***	***10A-/- (KO)***	
n	11	17	
Avg. body mass at sacrifice (g)	26	27	
Avg. age at sacrifice (weeks)	11.5	11.1	
Outliers removed by ROUT analysis	0	1	
(D) FSH	***10A+/+ (WT)***	***10A-/- (KO)***	
n	11	18	
Avg. body mass at sacrifice (g)	26	27	
Avg. age at sacrifice (weeks)	11.5	11.1	
Outliers removed by ROUT analysis	1	0	
(E) Inhibin B	***10A+/+ (WT)***	***10A-/- (KO)***	
n	11	15	
Avg. body mass at sacrifice (g)	26	27.3	
Avg. age at sacrifice (weeks)	11.5	11.1	
Outliers removed by ROUT analysis	0	0	
Figure 13 (Testes, all 10D -/-)	***10A+/+ (WT)***	***10A-/- (KO)***	
n	6-8	6-8	
Avg. body mass at sacrifice (g)	27.4	28	
Avg. age at sacrifice (weeks)	14.5	14.1	
Outliers removed by ROUT analysis	0	LHR: 1, pAkt: 1	
Supplemental Figure 10 (All 10D +/+)			
(A) Mating studies	Red text= Sire is 10A -/-		
Order: Sire (M) x Dam (F)	**Average time parents housed together (weeks)**		**Average pups per litter**
10A +/+ x 10A -/- (2 pairs)	8.9		5.8
10A -/- x 10A +/+ (2 pairs)	9.1		N/A
(B,C,D) Testes mass, Sperm cells/mL, sperm cell motility	***10A+/+, 10D +/+***	***10A-/-, 10D +/+***	
n	4	5	
Avg. body mass at sacrifice (g)	29.8	29.4	
Avg. age at sacrifice (weeks)	18.5	17.8	
Outliers removed by ROUT analysis	0	0	
Supplemental Figure 11 (Vas deferens, all 10D -/-)	***10A+/+ (WT)***	***10A-/- (KO)***	
n	4-7	4-7	
Avg. body mass at sacrifice (g)	15.4	15	
Avg. age at sacrifice (weeks)	27.9	28.6	
Outliers removed by ROUT analysis	0	0	

Appendix E: Supplemental Figure for Chapter 5



Supplemental Figure 12. Metabolic parameters in the 10A Deficient, 10D Correction mouse model (A, B) Weight gain of (A) male and (B) female $10A^{+/+}10D^{+/+}$ and $10A^{-/-}10D^{+/+}$ over the course of 12 weeks on a HFD (60 kcal% fat, Ad lib feeding). P value by 2-way ANOVA with Sidak's multiple comparison. (C) Lean and (D) fat body mass were normalized to the sum of lean mass and fat mass to calculate % Lean and % Fat mass ($10A^{+/+}10D^{+/+}$ n=4, $10A^{+/+}10D^{-/-}$ n=3). (E) Fasting blood glucose was measured after a 5 hour fast, via a glucometer ($10A^{+/+}10D^{+/+}$ n=3, $10A^{+/+}10D^{-/-}$ n=3). (C-E) P value by unpaired t-test. Average body mass (g) at end of HFD: Males: $10A^{+/+}10D^{+/+}$: 36 g, $10A^{-/-}10D^{+/+}$: 33.3 g, Females: $10A^{+/+}10D^{+/+}$: 24.5 g, $10A^{+/+}10D^{+/+}$: 29 g

Appendix F: Supplemental Tables for Chapter 6

Supplemental Table 4

	Primer sequence (5' to 3')	
Target	**F**	**R**
Pla2g5	TGG GGT TCT GAG ATG TCA CT	TCT TCC TCC TGT CTT GTT GC
SCD1	CTGTACGGGATCATACTGGTTC	GCCGTGCCTTGTAAGTTCTG
LPL	TGG CAT AAG TCA GGT CCA TT	GAG CCA TGT CTT CAA CTG CT
Pla2g6	ATC CAC ACA GCC ATG AAG TT	TGT TCC CTG AGG AGC TAG TG
FAS	GCGATGAAGAGCATGGTTTAG	GGCTCAAGGGTTCCATGTT
DGAT1	CCA GGT GGT GTC TCT GTT TC	AGA TGA TTG TGG CCA GGT TA
DGAT2	CTGTGCTCTACTTCACCTGGCT	CTGGATGGGAAAGTAGTCTCGG
PPARa	GCCTGTCTGTCGGGATGT	GGCTTCGTGGATTCTCTTG
PPARg	GCCCTTTGGTGACTTTATGGA	GCAGCAGGTTGTCTTGGATG
LXRa	CCGACAGAGCTTCGTCC	CCCACAGACACTGCACAG
Srebpc1	CGCGGAAGCTGTCGGGGTAG	AAATGTGCAATCCATGGCTCCGTGGTC
CGI58	GGT TAA GTC TAG TGC AGC	AAG CTG TCT CAC CAC TTG
Cyp7a1	cca ggg aga tgc tct gtg ttc	acc cag aca gcg ctc ttt gat
	AGCAACTAAACAACCTGCCAGTAC TA	GTCCGGATATTCAAGGATGCA
Cyp8b1	GCCTTCAAGTATGATCGGTTCCT	GATCTTCTTGCCCGACTTGTAGA
Hprt1 (housekeeping gene)	GCTGACCTGCTGGATTACAT	TTGGGGCTGTACTGCTTAAC

Supplemental Table 5

Visceral Fat, Females, 12 weeks after HFD feeding									
qPCR results						RNA sequencing results (*10A+/+ n=* 3, *10A-/-* n=3)			
	Sample size (n)								
Target	***10A+/+***	***10A-/-***	**p-value (unpaired t-test of Relative mRNA level (2^-ΔΔCq))**	**Significant (Y or N)**		**Target**	***log2FoldChange***	**p-value**	**Significant (Y or N)**
Pla2g5	2	4	0.2526	N		Pla2g5	4.433277742	2.03E-17	Y
SCD1	2	4	0.8275	N		SCD1	0.355620653	0.242335	N
LPL	3	4	0.7678	N		LPL	0.294114678	0.123495	N
Pla2g6	3	4	0.8143	N		Pla2g6	0.234601663	0.309316	N
FAS	3	4	0.9077	N		FAS	-0.099676899	0.588441	N
DGAT1	3	4	0.6299	N		DGAT1	0.017153228	0.933198	N
DGAT2	3	4	0.6174	N		DGAT2	0.439107779	N/A	N/A
PPARa	2	4	0.3831	N		PPARa	not found in data	---	---
PPARg	3	4	0.3658	N		PPARg	not found in data	---	---
LXRa	3	4	0.824	N		LXRa	not found in data	---	---
SREBP-1C	2	4	0.824	N		Srebpc1	not found in data	---	---
CGI58	2	4	0.824	N		CGI58	not found in data	---	---

Liver qPCR Results, Females, 12 weeks after HFD feeding				
	Sample size (n)			
Target	***10A+/+***	***10A-/-***	**p-value (unpaired t-test of Relative mRNA level (2^-ΔΔCq))**	**Significant (Y or N)**
PPARg	4	4	0.0474	Y *
FAS	4	3	0.0067	Y **
SCD1	4	5	0.4074	N
Cyp7a1	4	4	0.7601	N
Cyp8b1	4	4	0.1477	N
LPL	4	3	0.2685	N