



Supplementary Information for

**The PDK1-Foxo1 signaling in adipocytes controls systemic insulin sensitivity through the 5-lipoxygenase- leukotriene B4 axis**

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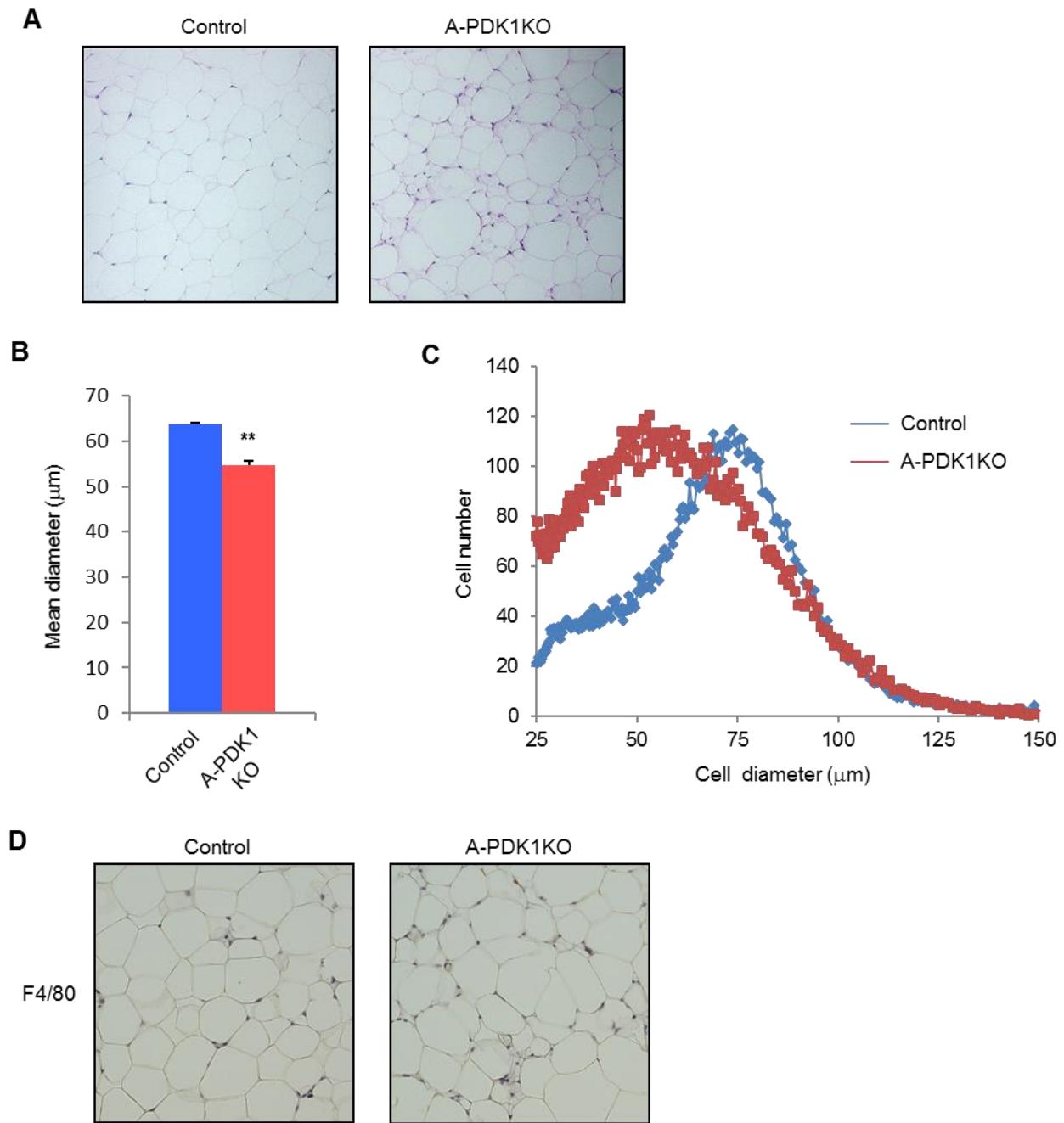
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**This PDF file includes:**

Figures S1 to S9

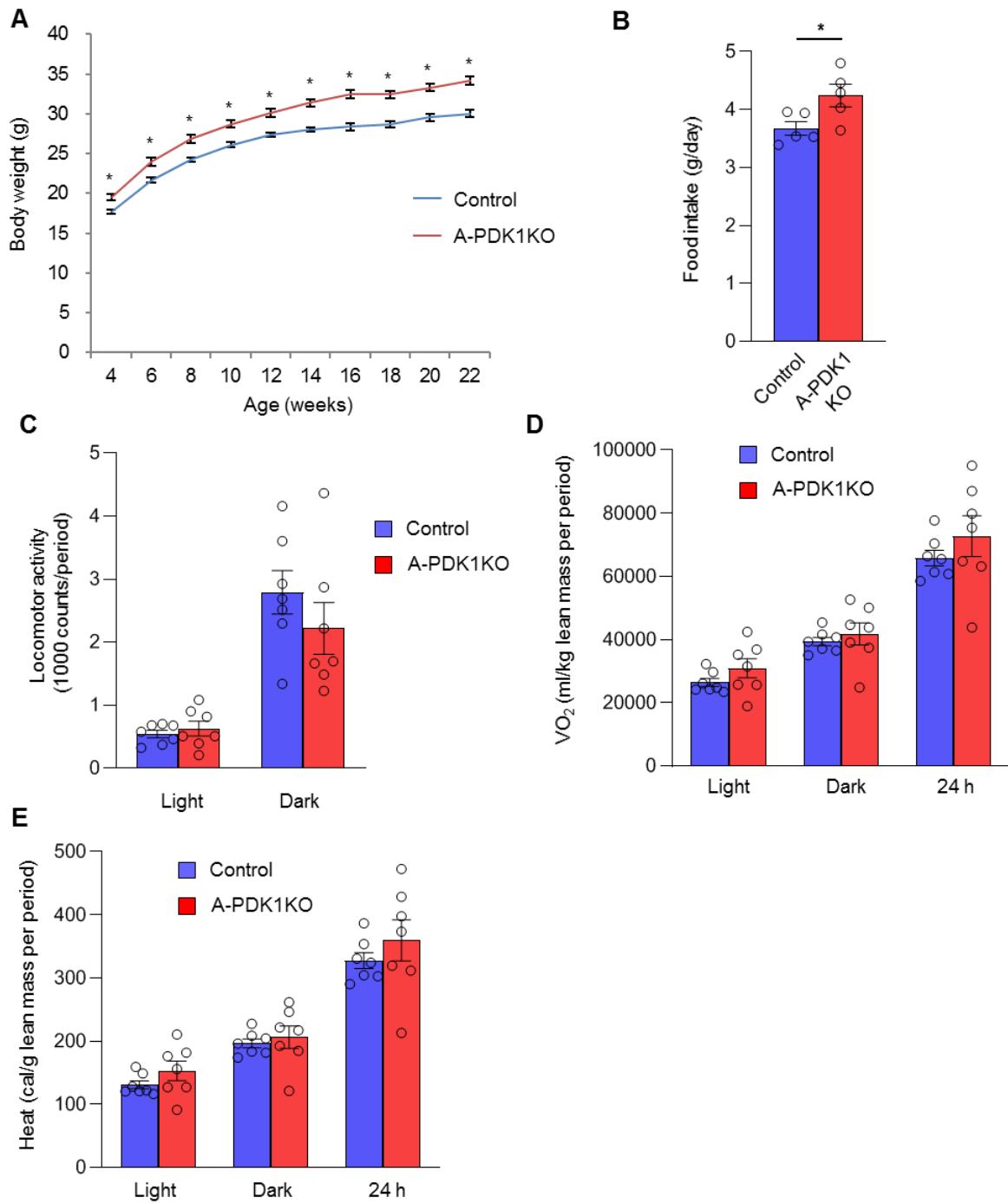
Tables S1 to S3

**Fig. S1**



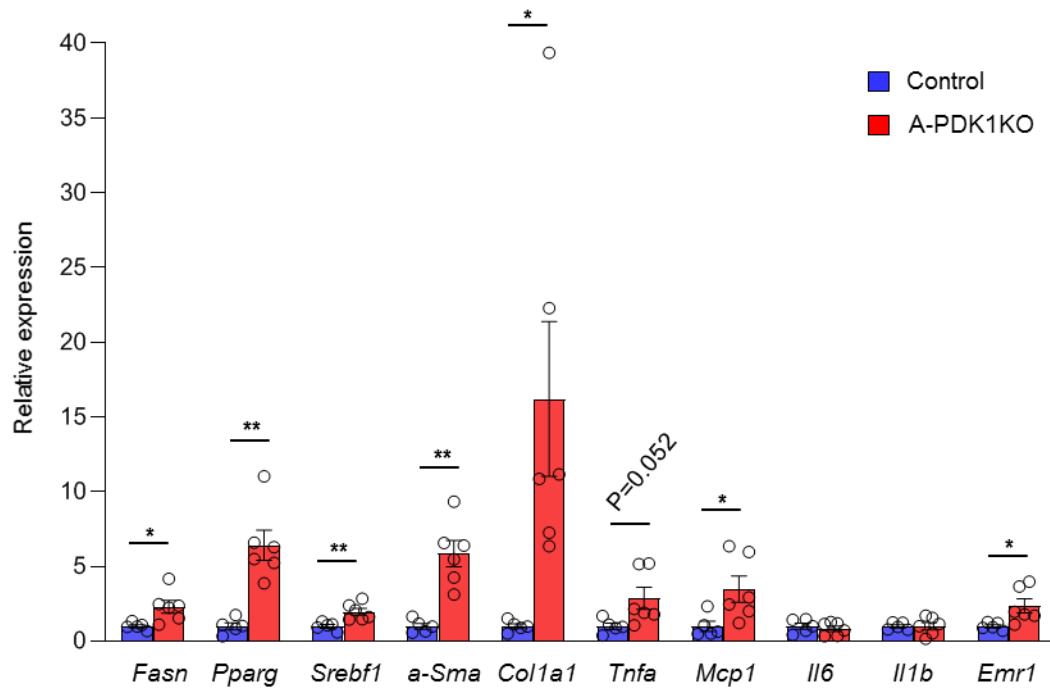
**Fig. S1.** Decreased adipocyte size in A-PDK1KO mice. (A) Hematoxylin-eosin staining of epididymal adipose tissue from control and A-PDK1KO mice. (B and C) Mean diameter of adipocytes (B) and distribution of adipocyte size (C) for epididymal adipose tissue from 20-week-old control or A-PDK1KO mice ( $n = 4$ ). Data in (B) are means  $\pm$  s.e.m. \*\* $P < 0.01$  versus control (Student's  $t$  test). (D) F4/80 immunohistochemistry of epididymal adipose tissue from control and A-PDK1KO mice.

**Fig. S2**



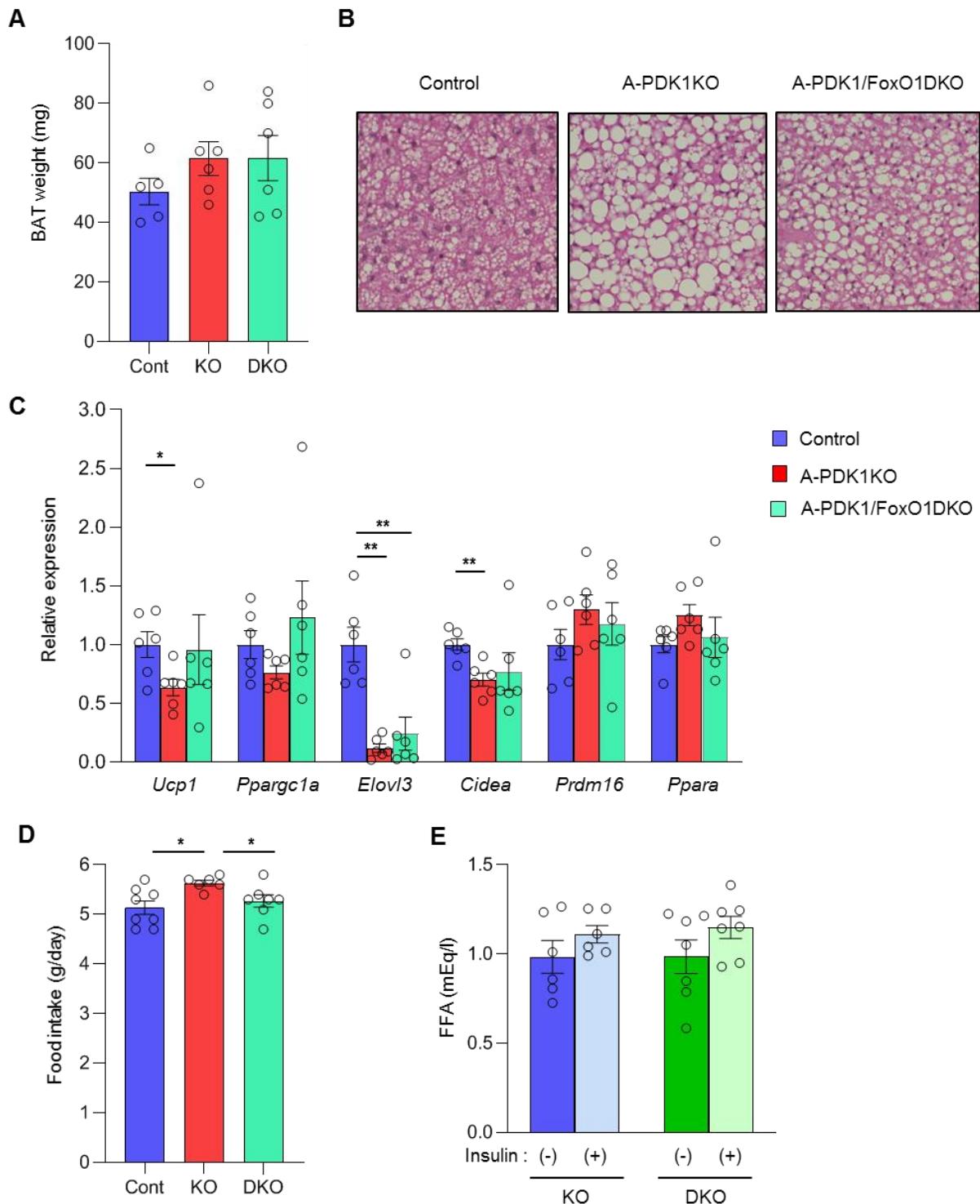
**Fig. S2.** Body weight, food intake, locomotor activity, and energy expenditure in A-PDK1KO mice. (A) Time course of body weight for control or A-PDK1KO mice ( $n = 7$  to 10). (B) Food intake for 15-week-old control or A-PDK1KO mice ( $n = 5$ ). (C-E) Locomotor activity (C), oxygen consumption ( $\text{VO}_2$ ) (D), and heat production (E) during light, dark, and 24-h periods for 14-week-old control or A-PDK1KO mice ( $n = 7$ ). All data are means  $\pm$  s.e.m. \* $P < 0.05$  versus corresponding control value (Student's  $t$  test).

**Fig. S3**



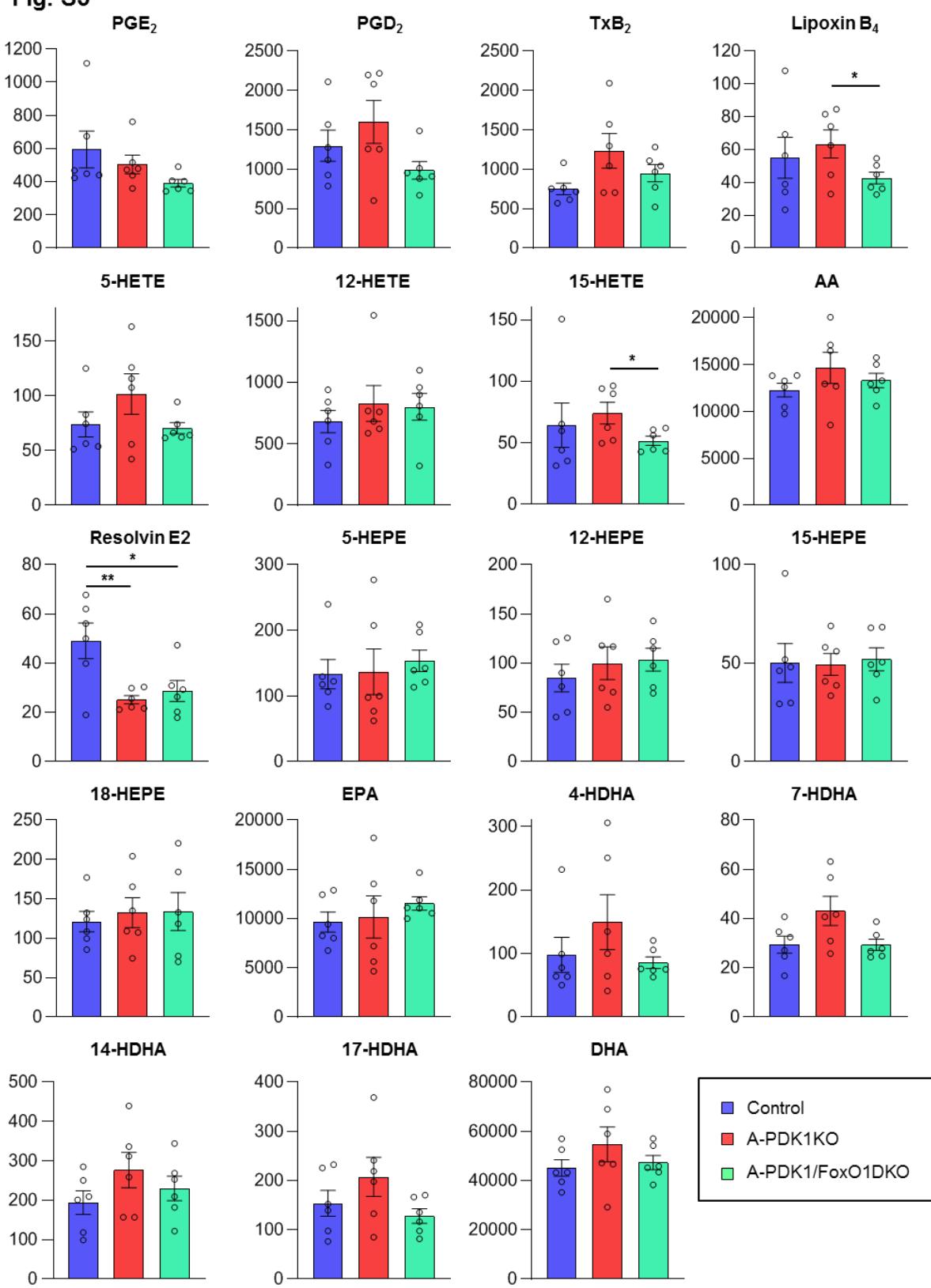
**Fig. S3.** Gene expression in the liver of A-PDK1KO mice. The abundance of mRNAs for genes related to lipogenesis, fibrosis, or inflammation in the liver of 37-week-old control or A-PDK1KO mice ( $n = 5-6$ ) was determined by Real-time PCR analysis. Data are means  $\pm$  s.e.m. \* $P < 0.05$ . \*\* $P < 0.01$  versus corresponding control value (Student's  $t$  test).

**Fig. S4**



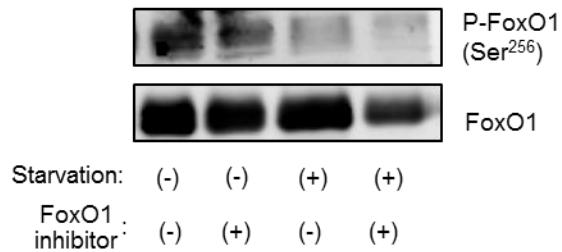
**Fig. S4.** BAT weight and histology, food intake, and lipolysis in A-PDK1KO and A-PDK1/FoxO1DKO mice. (A) BAT weight in control, A-PDK1KO, and A-PDK1/FoxO1DKO mice ( $n = 5$  or 6). (B) Hematoxylin-eosin staining of BAT from control, A-PDK1KO, and A-PDK1/FoxO1DKO mice. (C) Gene expression in BAT from control, A-PDK1KO, and A-PDK1/FoxO1DKO mice ( $n = 6$ ). (D) Food intake in control, A-PDK1KO, and A-

PDK1/FoxO1DKO mice ( $n = 6$  to 8) (E) Plasma FFA concentration in A-PDK1KO and A-PDK1/FoxO1DKO mice ( $n = 6$  or 7) measured 1 h after intraperitoneal injection of insulin (1 U/kg) or vehicle. All data are means  $\pm$  s.e.m. \* $P < 0.05$ . \*\* $P < 0.01$  versus corresponding control value (Student's t test).

**Fig. S5**

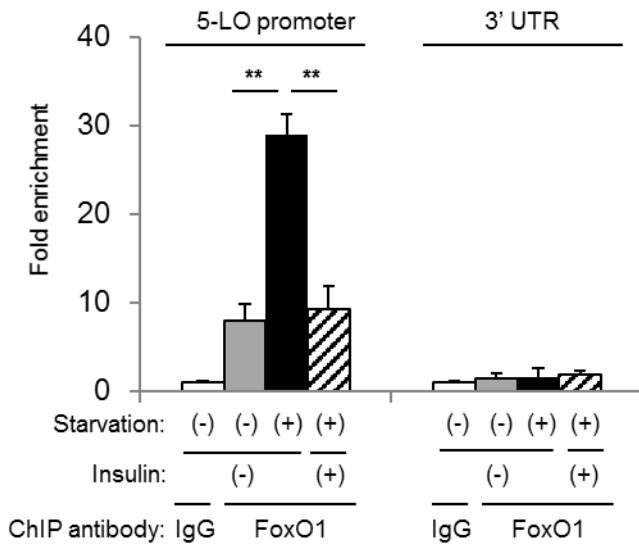
**Fig. S5.** Plasma concentrations of various lipid mediators in A-PDK1KO and A-PDK1/FoxO1DKO mice. The plasma concentrations of lipid mediators in 13-week-old control, A-PDK1KO, or A-PDK1/FoxO1DKO mice ( $n = 6$ ) were measured by LC-MS/MS analysis. All data are presented as picograms per milliliter and are means  $\pm$  s.e.m. \* $P < 0.05$ . \*\* $P < 0.01$  versus corresponding control value (Student's  $t$  test). PGE<sub>2</sub>, prostaglandin E<sub>2</sub>; PGD<sub>2</sub>, prostaglandin D<sub>2</sub>; TxB<sub>2</sub>, thromboxane B<sub>2</sub>; 5-HETE, 5-hydroxyeicosatetraenoic acid; 12-HETE, 12-hydroxyeicosatetraenoic acid; 15-HETE, 15-hydroxyeicosatetraenoic acid; AA, arachidonic acid; 5-HEPE, 5-hydroxyeicosapentaenoic acid; 12-HEPE, 12-hydroxyeicosapentaenoic acid; 15-HEPE, 15-hydroxyeicosapentaenoic acid; 18-HEPE, 18-hydroxyeicosapentaenoic acid; EPA, eicosapentaenoic acid; 4-HDHA, 4-hydroxydocosahexaenoic acid; 7-HDHA, 7-hydroxydocosahexaenoic acid; 14-HDHA, 14-hydroxydocosahexaenoic acid; 17-HDHA, 17-hydroxydocosahexaenoic acid; DHA, docosahexaenoic acid.

**Fig. S6**



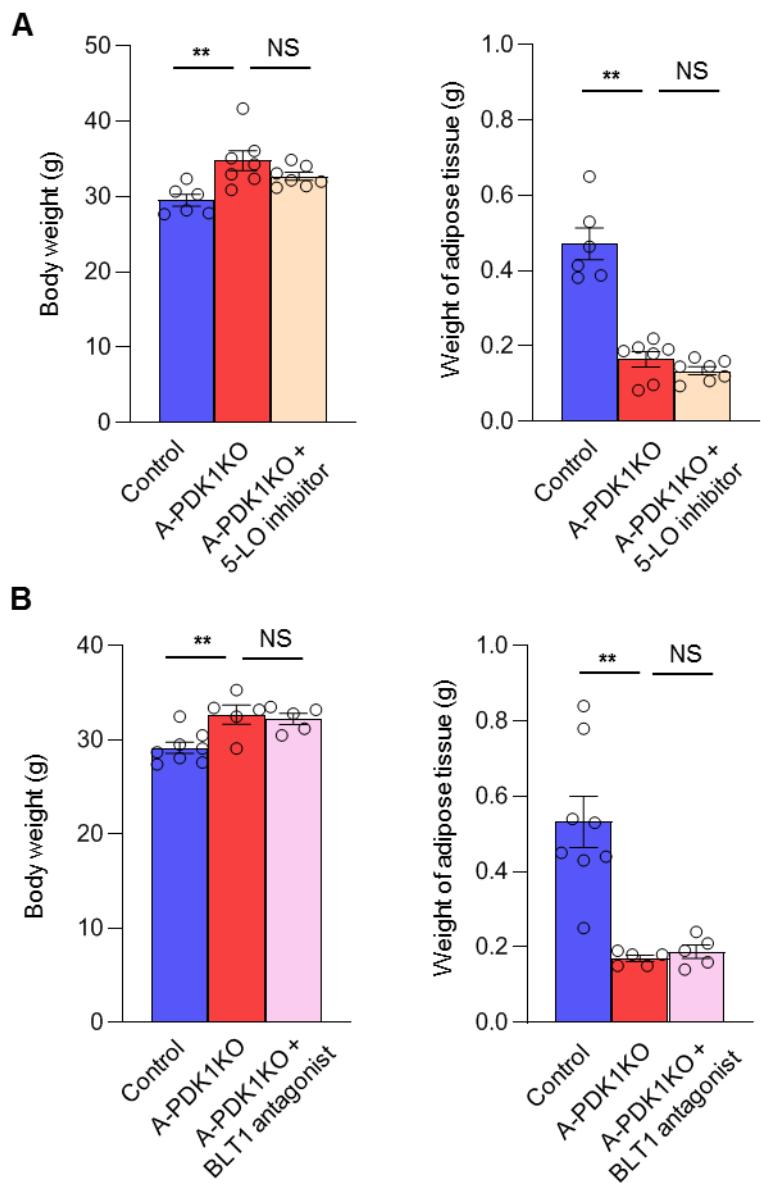
**Fig. S6.** Serum deprivation–induced down-regulation of FoxO1 phosphorylation in SV cells. SV cells isolated from C57BL/6 mice were exposed to AS1842856 (10  $\mu$ M) during serum deprivation for 24 h and were then subjected to immunoblot analysis of total and Ser<sup>256</sup>-phosphorylated forms of FoxO1.

**Fig. S7**



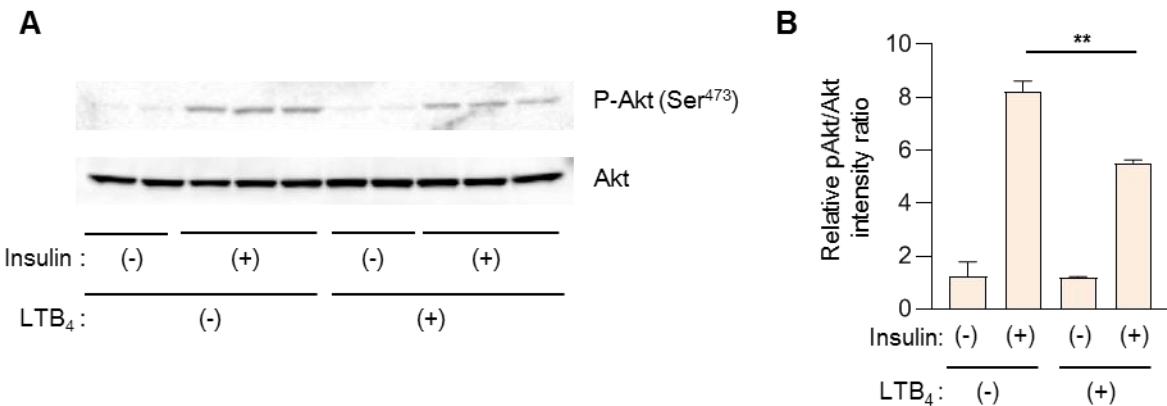
**Fig. S7.** FoxO1 binds to the 5-LO promoter in 3T3L1 adipocytes. ChIP analysis of FoxO1 binding to the 5-LO promoter in 3T3L1 adipocytes treated with (or without) insulin for 1 hour after serum starvation for 12 hours ( $n = 3$ ). Data are representative of three independent experiments. Data are means  $\pm$  s.e.m. \*\* $P < 0.01$  (Student's t test).

**Fig. S8**



**Fig. S8.** Body and adipose tissue weight in A-PDK1KO mice treated with 5-LO inhibitor zileuton or BLT1 antagonist CP105696. (A) Body and adipose tissue weight in control or A-PDK1KO mice ( $n = 6$  or 7) treated (or not) with zileuton for 12 weeks. (B) Body and adipose tissue weight in control or A-PDK1KO mice ( $n = 5$  to 8) treated (or not) with CP105696 for 12 weeks. All data are means  $\pm$  s.e.m. \*\*P < 0.01 (Student's t test).

**Fig. S9**



**Fig. S9.** LTB<sub>4</sub> suppresses insulin-dependent Akt phosphorylation in mouse primary hepatocytes. (A) Representative immunoblot of total and Ser473-phosphorylated forms of Akt in mouse primary hepatocytes stimulated with (or without) insulin after LTB<sub>4</sub> (100nM) or vehicle treatment for 1 hour. (B) Quantifications of experiments shown in panel (A). Data are representative of three independent experiments. Data are means  $\pm$  s.e.m. \*\*P < 0.01 (Student's t test).

**Table S1.** List of genes whose expression in epididymal adipose tissue was increased ( $\log_2(\text{KO}/\text{control ratio}) > 0.5$ ) in A-PDK1KO mice and normalized ( $\log_2(\text{DKO}/\text{control ratio}) < 0.2$ ) in A-PDK1/FoxO1DKO mice among genes with an expression signal of >30 in control mice. Data for the 5-LO gene (*Alox5*) are shown in red.

Gene symbol	Gene accession	Probe set ID	Control signal	KO signal	$\log_2(\text{KO}/\text{control})$	DKO signal	$\log_2(\text{DKO}/\text{control})$
Rnu1b1	NR_004412	17219206	100.6	166.9	0.73	111.7	0.15
Ankrd23	NM_153502	17222193	55.5	78.5	0.5	60.4	0.12
Elf3	NM_001163131	17227266	30.2	49.6	0.72	31.5	0.06
Prg4	NM_021400	17227892	88.5	185.2	1.07	85.9	-0.04
Akap12	NM_031185	17231423	305.5	481.5	0.66	318.1	0.06
Vnn1	NM_011704	17232162	61.7	142.9	1.21	37.3	-0.72
Elane	NM_015779	17235011	50.1	72.1	0.52	54.9	0.13
2210404O07Rik	ENSMUST00000105322	17235730	30.2	53.6	0.83	29.1	-0.05
Eid3	NM_025499	17235937	30.8	63.8	1.05	33.2	0.11
Rdh16	NM_009040	17238172	57.3	90.3	0.66	48.2	-0.25
Syne1	ENSMUST00000056571	17238904	38.9	60.1	0.63	44.2	0.18
Syne1	ENSMUST00000056571	17238930	72.5	111.1	0.62	83.2	0.2
Col18a1	NM_009929	17242232	83.4	125.1	0.59	91.8	0.14
Zfp781	NM_199062	17243460	76.1	112.1	0.56	55.8	-0.45
3230401D17Rik	ENSMUST00000104954	17249700	40	57.3	0.52	43.9	0.14
Lrrc48	ENSMUST00000108723	17250344	32.7	60.5	0.89	35.6	0.12
Adap2	ENSMUST0000021050	17253885	406.2	742.4	0.87	354.7	-0.2
Gngt2	ENSMUST00000036088	17255466	30.2	44.7	0.57	31	0.04
Spns2	NM_153060	17265672	174.5	248.4	0.51	189	0.11
Recql5	NM_130454	17272047	40.7	68.3	0.75	44	0.11
Mia2	NM_177321	17275718	42.7	83.8	0.97	47.5	0.16
Irf4	ENSMUST00000021784	17286295	82.3	140.5	0.77	68.9	-0.26
Gcnt2	NM_008105	17286707	121.3	200.4	0.72	127	0.07
Ankrd32	NM_134071	17294518	57	83.1	0.54	65.2	0.19
Selk	NM_019979	17298131	53.4	92.5	0.79	52	-0.04
Anxa8	NM_013473	17298775	66.8	101.7	0.61	56.6	-0.24
AY358078	AY358078	17299627	54.1	79.6	0.56	44	-0.3
1700047G03Rik	NR_040447	17310400	62.1	104.4	0.75	43.3	-0.52
Dnajc22	ENSMUST00000061295	17314729	33.1	46.9	0.5	34.2	0.05
Krt18	NM_010664	17315245	77.8	132	0.76	87.9	0.18
Egflam	NM_178748	17315763	54.2	79	0.54	51.8	-0.07
Kcnj15	ENSMUST00000113862	17327450	54.6	78.4	0.52	46.2	-0.24
Prm2	NM_008933	17328113	143.2	645.2	2.17	99.2	-0.53
Prm1	ENSMUST00000023144	17328118	35.6	79.8	1.16	31.8	-0.17
Ube2v2	NM_023585	17328425	46.1	72.4	0.65	52.8	0.2
Apod	NM_007470	17329759	195.4	276.4	0.5	183.8	-0.09
Gm609	NM_001005854	17330636	36.7	63	0.78	40.4	0.14
Prl3	NM_021495	17330773	43	61.2	0.51	47	0.13
Tmem45a	NM_019631	17331078	31.8	46.3	0.54	33.3	0.06
Cdkn1a	NM_007669	17335467	287.5	413.6	0.52	330.2	0.2
Gm16519	ENSMUST00000092011	17339390	70.8	122.1	0.79	75.3	0.09
Vit	NM_028813	17339824	66.6	98	0.56	63.7	-0.06
Thbs2	NM_011581	17341080	178.3	477.7	1.42	86.1	-1.05
Tcp11	NM_013687	17342810	30.4	51	0.74	29.1	-0.07
Ptk7	NM_175168	17345475	33.4	49.3	0.56	37.6	0.17
Tgif1	NM_001164075	17346936	42	63.6	0.6	45.1	0.1
Ankrd29	NM_001190371	17352763	105.4	156.9	0.57	102.9	-0.04
Ak3	NM_021299	17358498	35.4	51	0.53	35.8	0.01
BC021614	NM_144869	17361090	31.6	46.7	0.56	25.4	-0.32
Ms4a14	XM_357051	17362941	32.9	54.1	0.72	22.2	-0.56
Slc16a12	ENSMUST00000009522	17364139	107.4	180.2	0.75	101	-0.09
Gca	NM_145523	17371201	102.4	150.7	0.56	101.8	-0.01
Thbs1	NM_011580	17374488	202.7	461.3	1.19	170.3	-0.25
Optn	ENSMUST00000114996	17381330	110.9	201.4	0.86	116.8	0.07
1700026L06Rik	NM_027283	17383423	37.2	54	0.54	38.4	0.04
Fibin	NM_026271	17389157	34	53.4	0.65	36.3	0.09
Rnu1b1	NR_004412	17400568	100.6	166.9	0.73	111.7	0.15
Rnu1b1	NR_004412	17400579	100.6	166.9	0.73	111.7	0.15
Rnu1b1	NR_004412	17400588	100.6	166.9	0.73	111.7	0.15
Rnu1b1	NR_004412	17400590	100.6	166.9	0.73	111.7	0.15

**Table S1-continued.**

Gene symbol	Gene accession	Probe set ID	Control signal	KO signal	$\log_2(\text{KO}/\text{control})$	DKO signal	$\log_2(\text{DKO}/\text{control})$
Lef1	ENSMUST00000029611	17402662	36.9	59	0.68	35.9	-0.04
Cetn4	NM_145825	17404896	35	56.1	0.68	33.3	-0.07
Il6ra	NM_010559	17407138	392.1	619.4	0.66	370.5	-0.08
Rnu1b1	NR_004412	17408038	100.6	166.9	0.73	111.7	0.15
Rnu1b1	NR_004412	17408063	100.6	166.9	0.73	111.7	0.15
Rnu1b1	NR_004412	17408065	100.6	166.9	0.73	111.7	0.15
Synpo2	NM_080451	17410031	74.1	114.1	0.62	83.3	0.17
Acer2	NM_139306	17415219	154.2	297.9	0.95	147.2	-0.07
Inadl	NM_172696	17415635	31.6	46.1	0.54	32.9	0.06
Ttc39a	NM_001145948	17416862	37.6	53.4	0.51	41.9	0.15
Cldn19	NM_153105	17417898	31.9	51.7	0.7	35.1	0.14
Snord99	NR_028537	17419411	501.8	756.9	0.59	550.9	0.13
Hspg2	NM_008305	17420171	755.4	1125.8	0.58	814.5	0.11
Pla2g2d	NM_011109	17420530	154.8	332.7	1.1	167.7	0.12
Plekhf2	NM_175175	17423209	69.4	151.6	1.13	77.7	0.16
Rnu1b1	NR_004412	17425278	100.6	166.9	0.73	111.7	0.15
Cyp2j13	NM_145548	17427331	31.5	49.6	0.66	27.5	-0.2
Fam159a	NM_001099303	17428050	40	62.7	0.65	43.5	0.12
Nasp	NM_016777	17428659	46	67.6	0.55	49.6	0.11
Med18	NM_026039	17430853	30.9	48.1	0.64	31.7	0.04
Shroom3	NM_015756	17439138	45.8	67.5	0.56	51.9	0.18
Bmp3	NM_173404	17439535	85.5	142.1	0.73	93.5	0.13
Wdr66	BC138176	17442237	41.9	63.8	0.61	47.9	0.19
Fam20c	ENSMUST00000026972	17443901	96.4	156.5	0.7	98.6	0.03
Gm9899	NR_040427	17446752	34.6	50.8	0.55	37.9	0.13
Pdk4	NM_013743	17464654	287.5	490.8	0.77	307.5	0.1
Gprin3	ENSMUST00000051065	17467232	65.6	140.6	1.1	48.9	-0.42
Oxtr	ENSMUST00000165435	17469627	124.9	306.9	1.3	118.3	-0.08
<b>Alox5</b>	<b>NM_009662</b>	<b>17470031</b>	<b>46.8</b>	<b>69.2</b>	<b>0.56</b>	<b>52.1</b>	<b>0.15</b>
4931406P16Rik	BC060233	17476690	35.1	51.9	0.57	38.4	0.13
Stard10	ENSMUST00000163799	17480813	214.7	327.2	0.61	198.3	-0.11
Acsm3	NM_016870	17482310	160.9	308.3	0.94	103.9	-0.63
Olfr310	NM_001011520	17493116	48	68.9	0.52	46	-0.06
Defa3	NM_007850	17499757	35.4	55.4	0.65	37.9	0.1
Gse1	NM_198671	17506249	63	90.9	0.53	70.9	0.17
Ier2	NM_010499	17511130	33.3	47.7	0.52	32.7	-0.03
Ccdc153	NM_001081369	17516538	89.2	173.9	0.96	98	0.14
Lctl	NM_145835	17518278	40	60.3	0.59	35.5	-0.17
Elmod1	NM_177769	17527173	56.1	105.2	0.91	63	0.17
Morf4I	NM_001039147	17529647	68.3	99	0.54	60.1	-0.18
Zbtb38	ENSMUST00000152594	17529855	106.3	165.5	0.64	119.2	0.17
Gm14484	ENSMUST00000164729	17533307	34.7	51.5	0.57	39.1	0.17
Fmr1	NM_008031	17535208	600.3	929.1	0.63	528.6	-0.18
1700011M02Rik	NM_001243285	17536945	57.7	83.5	0.53	51.3	-0.17
A730046J19Rik	NR_040271	17538350	33.4	50.3	0.59	34.6	0.05
G530011O06Rik	NR_029457	17546212	43.8	88.1	1.01	48.3	0.14

**Table S2.** List of genes whose expression in epididymal adipose tissue was decreased ( $\log_2(\text{KO}/\text{control ratio}) < -0.5$ ) in A-PDK1KO mice and normalized ( $\log_2(\text{DKO}/\text{control ratio}) > -0.2$ ) in A-PDK1/FoxO1DKO mice among genes with an expression signal of >30 in control mice.

Gene symbol	Gene accession	Probe set ID	Control signal	KO signal	$\log_2(\text{KO}/\text{control})$	DKO signal	$\log_2(\text{DKO}/\text{control})$
Irs1	NM_010570	17214753	33.6	21.3	-0.66	43.5	0.37
Gm5258	XM_357111	17215101	34	24	-0.5	40.4	0.25
Mir3962	NR_039539	17221010	40.5	27.4	-0.57	44.5	0.13
Abcb6	ENSMUST00000027396	17224476	101.9	71.7	-0.51	101	-0.01
BC035947	BC138135	17224724	69.1	32.8	-1.08	104.3	0.59
Mndal	NM_001170853	17230067	61	36.4	-0.74	53.4	-0.19
Mir1981	NR_035502	17230750	65.2	39.2	-0.73	57.5	-0.18
Epm2a	ENSMUST00000069106	17231669	52.9	32	-0.73	49.7	-0.09
Vnn3	NM_011979	17232152	102.3	69.5	-0.56	97.4	-0.07
Echdc1	NM_025855	17232426	429.7	294.1	-0.55	404.4	-0.09
Rtn4ip1	NM_130892	17233039	60.8	42	-0.53	57.3	-0.08
Gnptab	NM_001004164	17236339	296.6	208.1	-0.51	269.2	-0.14
G630090E17Rik	NM_001173500	17240303	34	22.9	-0.57	34.1	0
Prdm1	NM_007548	17240645	37.5	26	-0.53	49	0.39
Slc16a7	ENSMUST00000063318	17245648	150.5	98	-0.62	237.8	0.66
B430319H21Rik	AK021026	17250849	60.9	27.5	-1.15	61	0
Fgf11	ENSMUST00000102585	17264960	52.5	31.3	-0.75	46.7	-0.17
Slc2a4	NM_009204	17265096	390.6	224.6	-0.8	417.9	0.1
Inca1	NM_001252485	17265365	112	73.4	-0.61	123.1	0.14
Pctp	ENSMUST00000020864	17267685	63	42.6	-0.57	56.6	-0.15
C630004H02Rik	NM_175454	17271861	60.5	40.8	-0.57	53.4	-0.18
Hpcal1	NM_016677	17274310	106.6	72.2	-0.56	104.5	-0.03
Gm5784	AK149188	17274369	69.6	45.5	-0.61	74.2	0.09
Ap4s1	NM_021710	17275392	57	39.2	-0.54	49.9	-0.19
Fam84a	NM_029007	17280041	36.1	23.3	-0.63	34.5	-0.07
Ifi27l2a	NM_029803	17283549	1669.5	952.3	-0.81	2138.6	0.36
Igh-VJ558	BC031703	17284314	101.6	69	-0.56	122.3	0.27
Ighm	AB067787	17284360	1162.6	684.2	-0.76	1463.2	0.33
Ighv1-53	AB069917	17284577	79.5	35.4	-1.17	82.3	0.05
Zfp493	NM_028402	17288338	33.7	23	-0.55	32.6	-0.05
Mblac2	NM_028372	17288903	124.4	83.6	-0.57	108.7	-0.19
Ankra2	NM_023472	17289396	45	31.8	-0.5	47.7	0.08
Aldh5a1	NM_172532	17291361	121.7	76	-0.68	117.5	-0.05
Rpp40	ENSMUST00000171686	17291854	50.5	35.2	-0.52	50.6	0
Muted	NM_139063	17291953	64.9	43.7	-0.57	57.6	-0.17
Dtnbp1	NM_025772	17292157	265	172	-0.62	253.5	-0.06
Fgf10	NM_008002	17296483	165.7	101.3	-0.71	145.8	-0.19
Ero1l	NM_015774	17299196	56.6	35.3	-0.68	51.1	-0.15
Trav9d-3	X01134	17300247	77.9	48.7	-0.68	120.2	0.63
Fhit	ENSMUST00000160340	17303474	41.1	28.1	-0.55	39.6	-0.05
Efs	NM_010112	17306524	41.8	25.4	-0.72	46.2	0.14
Prlr	NM_011169	17310259	60.9	34.1	-0.84	74.9	0.3
Cmbl	NM_181588	17310816	599.8	374.3	-0.68	571.2	-0.07
4930572J05Rik	NM_198607	17312191	62.3	41.3	-0.59	57.1	-0.13
Gcat	NM_013847	17312884	34.1	21	-0.7	36	0.08
9330020H09Rik	NR_028442	17314626	32.6	19.6	-0.74	28.9	-0.17
Hoxc4	NM_013553	17315538	45.7	32.3	-0.5	47.5	0.06
Angpt1	ENSMUST0000022921	17316780	216.6	124.9	-0.79	227.6	0.07
Oplah	ENSMUST00000171340	17318428	252.5	174.8	-0.53	244.9	-0.04
Tst	NM_009437	17318983	313.3	185.8	-0.75	313.9	0
Prodh	ENSMUST0000003620	17328842	107.3	71.6	-0.58	125.1	0.22
Iglv1	M94350	17329023	107.7	17	-2.66	269.2	1.32
Gm15760	NR_030670	17329149	65.2	43.3	-0.59	65.7	0.01
Ehhadh	NM_023737	17329220	216	122.3	-0.82	209.2	-0.05
Cyp4f17	NM_001101445	17335952	213.5	121.5	-0.81	235	0.14
Clpp	NM_017393	17338925	171.9	116.7	-0.56	172	0
Mir219-1	NR_029800	17343733	36.1	23.2	-0.64	31.5	-0.2
LOC100862363	XR_141834	17345004	33.6	22.9	-0.55	39	0.21
Lrg1	NM_029796	17346150	738.9	474.5	-0.64	681	-0.12
Mapre2	NM_001162941	17348933	143.4	98.3	-0.55	126.2	-0.18
Gm4013	NR_033452	17354071	203	138.9	-0.55	187.6	-0.11
Fibp	NM_001253832	17356434	156.4	110.5	-0.5	137.6	-0.18
Cd274	NM_021893	17358544	138.7	90.5	-0.62	168.9	0.28
O3far1	NM_181748	17359113	101.3	69.7	-0.54	97.2	-0.06
Gpam	ENSMUST00000086868	17365728	1674.5	1045.1	-0.68	1663.3	-0.01
Ivd	ENSMUST00000028807	17374648	537	354.5	-0.6	483.6	-0.15
Bcl2l11	NM_207680	17375961	46.9	30.7	-0.61	45.3	-0.05
Pygb	ENSMUST00000045441	17377498	846.2	591.5	-0.52	830.3	-0.03

**Table S2-continued**

Gene symbol	Gene accession	Probe set ID	Control signal	KO signal	$\log_2(\text{KO}/\text{control})$	DKO signal	$\log_2(\text{DKO}/\text{control})$
Rbm38	ENSMUST00000173393	17380199	103.1	71.6	-0.53	94.7	-0.12
Gm14391	ENSMUST00000151240	17380529	168.2	97.7	-0.78	191.3	0.19
Hnmt	NM_080462	17382203	329.5	222.5	-0.57	327.4	-0.01
Olf1226	NM_146967	17387912	36.1	23.2	-0.64	41.3	0.19
Tmem154	NM_177260	17398571	72.8	50.8	-0.52	69.6	-0.07
Gbp3	ENSMUST0000029935	17403237	85.6	46.9	-0.87	74.9	-0.19
Bche	NM_009738	17405908	334.2	210	-0.67	298.7	-0.16
Dcst1	NM_029974	17407049	53.5	37.6	-0.51	48.8	-0.13
Rbm12b	NM_028226	17411892	42.8	18.9	-1.18	41.7	-0.04
Tmem38b	NM_028053	17414250	54.4	37.1	-0.55	50.1	-0.12
Gm12824	NM_001085549	17417090	228.3	150.8	-0.6	229.3	0.01
Mycbp	ENSMUST00000030400	17418241	263.8	180.1	-0.55	239.8	-0.14
Mecr	NM_025297	17419332	85.3	57.5	-0.57	77.1	-0.15
Hnrnph2	NM_019868	17421170	49.2	34.7	-0.5	43.9	-0.17
Gm13152	ENSMUST00000063704	17421491	32.2	18	-0.84	28.1	-0.2
2810432D09Rik	NM_027278	17424293	53.2	35.7	-0.57	52.8	-0.01
Gm568	BC028561	17425120	49	31.9	-0.62	43.8	-0.16
Bnc2	NM_172870	17426929	339.5	211	-0.69	327.7	-0.05
Gm12597	NM_206870	17427067	33.6	23.8	-0.5	33.3	-0.01
Cdkn2a	NM_009877	17427147	41.4	27.3	-0.6	36.9	-0.16
Cdkn2c	NM_007671	17428217	266.3	143.9	-0.89	284.6	0.1
Zbtb48	NM_133879	17433412	49.8	33.1	-0.59	49.3	-0.02
Rasl11b	NM_026878	17438189	68.7	38.8	-0.82	61.3	-0.16
Igj	NM_152839	17449447	34.7	17.2	-1.02	63.9	0.88
Cdkl2	ENSMUST00000086978	17449609	50.7	34.4	-0.56	47.5	-0.1
Agpat9	ENSMUST00000092990	17450196	149.9	83.7	-0.84	167	0.16
AB010352	AB010352	17450950	41.8	28.6	-0.55	46.1	0.14
Try4	NM_011646	17457731	63.8	41.6	-0.62	58.2	-0.13
Plekha8	NM_001164361	17458734	49.2	32	-0.62	44.5	-0.14
Retsat	ENSMUST00000070597	17459676	416.5	255.2	-0.71	399	-0.06
Asns	ENSMUST00000031766	17464718	317.5	214.4	-0.57	331.2	0.06
Igkv4-91	X88903	17467398	69.8	36.9	-0.92	78.7	0.17
Elmod3	NM_144917	17467782	322.2	197.4	-0.71	291.9	-0.14
Wbp1	ENSMUST00000032111	17468102	204.9	136.4	-0.59	186	-0.14
Gys2	NM_145572	17472497	81.6	51.4	-0.67	74.8	-0.13
Bhlhe41	ENSMUST00000032386	17472760	82	57.5	-0.51	89	0.12
Isoc2a	NM_001101598	17473402	106.9	65.6	-0.7	95.1	-0.17
Zfp28	NM_175247	17473603	48.7	32.3	-0.59	42.6	-0.19
Ptgir	NM_008967	17474217	33.5	21.9	-0.61	37.9	0.18
Il28b	NM_177396	17475863	42	28.2	-0.58	38.4	-0.13
Dbp	ENSMUST00000080885	17477979	733.9	483.8	-0.6	801.4	0.13
Sez6l2	ENSMUST00000123117	17483192	48.4	26.7	-0.86	45.2	-0.1
Hcst	NM_011827	17489046	36.4	22.7	-0.68	37.8	0.06
Cpeb1	NM_001252525	17492754	106.7	75	-0.51	94.9	-0.17
Hbb-b1	NM_008220	17494221	200	123.7	-0.69	227.9	0.19
Coro1a	ENSMUST00000106364	17496376	63.7	39.9	-0.68	61.5	-0.05
Fadd	ENSMUST00000033394	17498461	63	43.1	-0.55	55.4	-0.18
Gm15315	NM_001177528	17499796	81.6	50.4	-0.69	77.1	-0.08
Car7	NM_053070	17504454	55.1	38.5	-0.52	49.4	-0.16
Cog4	NM_133973	17505648	483.9	322.6	-0.59	482.5	0
Ednra	NM_010332	17510685	552.5	354.4	-0.64	500.1	-0.14
Ces1f	NM_144930	17511731	502.2	216.7	-1.21	533.2	0.09
Ddx28	NM_028038	17512630	35.8	25	-0.52	34.8	-0.04
Ldhd	NM_027570	17513135	185	120.8	-0.61	180.8	-0.03
Gm6484	NM_001080940	17515335	122.1	84.6	-0.53	123.1	0.01
2310047B19Rik	NM_025870	17515371	47.3	32.9	-0.52	56.2	0.25
Opcml	ENSMUST00000115243	17515653	33.4	22.8	-0.55	33.2	-0.01
9030425E11Rik	ENSMUST00000034522	17516352	416.9	286.6	-0.54	452.2	0.12
C920006O11Rik	NR_040401	17519644	43.3	26.1	-0.73	42.5	-0.03
Cish	ENSMUST00000085102	17521300	49.5	24.9	-0.99	47.4	-0.06
Muc16	AK003577	17524311	42	23.6	-0.83	39.3	-0.1
Anln	NM_028390	17524969	75.3	50.7	-0.57	66.8	-0.17
Rbm15b	NM_175402	17530802	43.4	29.4	-0.56	38.1	-0.19
Gm19971	XR_106302	17533823	62.7	44	-0.51	67.5	0.11
Plxna3	NM_008883	17535841	31.7	22.3	-0.5	32.1	0.02
C1gal1c1	NM_021550	17541217	56.2	39.5	-0.51	56.6	0.01
2310047B19Rik	NM_025870	17548156	84.4	55.2	-0.61	81.3	-0.06
4930412F12Rik	AK015120	17548675	42.8	27.6	-0.64	42.4	-0.02
Gm6625	XM_003085369	17548690	298.4	210.4	-0.5	328.2	0.14

**Table S3.** List of lipid mediators detectable by LC-MS/MS-based metabololipidomics.

Arachidonic acid-origin			
Prostanoids	Leukotrienes	Lipoxins	Pathway markers
PGE <sub>2</sub>	LTB <sub>4</sub>	LXA <sub>4</sub>	5-HETE
PGD <sub>2</sub>	Δ6-trans-LTB <sub>4</sub>	LXB <sub>4</sub>	12-HETE
PGF <sub>2α</sub>	12-epi-Δ6-trans-LTB <sub>4</sub>	5,15-diHETE	15-HETE
8-iso-PGF <sub>2α</sub>	5,12-diHETE	AT-LXA <sub>4</sub>	Arachidonic acid
6-keto-PGI <sub>2</sub>	5,6-diHETE	AT-LXB <sub>4</sub>	
PGJ <sub>2</sub>	20-OH-LTB <sub>4</sub>		
Δ12-PGJ <sub>2</sub>	20-COOH-LTB <sub>4</sub>		
15-deoxy-Δ12,14-PGJ <sub>2</sub>	LTC <sub>4</sub>		
TxB <sub>2</sub>	LTD <sub>4</sub>		
	LTE <sub>4</sub>		

DHA-origin			
D-series resolvins	Protectin	Maresin	Pathway markers
RvD1	PD1	MaR1	4-HDHA
RvD2	AT-PD1	Δ12-trans-MaR1	7-HDHA
RvD3	Δ15-trans-PD1	7-epi-Δ12-trans-MaR1	14-HDHA
RvD4	10-epi-Δ15-trans-PD1	4,14-diHDHA	17-HDHA
RvD5	10,17-diHDHA	7,14-diHDHA	DHA
RvD6		13,14-diHDHA	
AT-RvD1			
AT-RvD2			
AT-RvD3			
AT-RvD4			
AT-RvD5			

EPA-origin				
Prostanoids	Leukotrienes	Lipoxins	E-series resolvins	Pathway markers
PGE <sub>3</sub>	LTB <sub>5</sub>	LXA <sub>5</sub>	RvE1	5-HEPE
PGD <sub>3</sub>	LTC <sub>5</sub>	LXB <sub>5</sub>	RvE2	12-HEPE
PGF <sub>3α</sub>	LTD <sub>5</sub>	5,15-diHEPE	RvE3	15-HEPE
TxB <sub>3</sub>	LTE <sub>5</sub>			18-HEPE EPA