

SUPPLEMENTARY DATA

Supplementary Table 1. Expression of key metabolic genes in skeletal muscle (quadriceps) following fat mass clamping. Cd36: cluster of differentiation 36, Cpt1b: carnitine palmitoyltransferase 1B, Fabp4: fatty acid binding protein 4, Acacb: Acetyl-CoA carboxylase 2, Slc2a1: solute carrier family 2, facilitated glucose transporter member 1 (GLUT1), Slc2a4: Solute carrier family 2, facilitated glucose transporter member 4 (GLUT4), Gys1: Glycogen synthase, Pygm: Glycogen phosphorylase, Hk2: Hexokinase 2, Ldha: Lactate dehydrogenase A, Pfkkm: 6-phosphofructokinase (muscle type), Acadl: acyl-Coenzyme A dehydrogenase (long chain), Hadha: hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit, Hadhb: beta-ketothiolase, Atp5b: ATP synthase subunit beta, Cox4i1: Cytochrome c oxidase subunit 4 isoform 1, Cox5a: cytochrome c oxidase subunit Va, Cox5b: cytochrome c oxidase subunit Vb, Sdhhd: succinate dehydrogenase complex, subunit D, Ucp2: uncoupling protein 2, Ucp3: uncoupling protein 3, Nr4a3: nuclear receptor subfamily 4, group A, member 3. Mice were fasted for 16 h prior to tissue collection. All mice are male n= 8 per group. All data are represented as mean +/- SEM. SD, standard diet; HFD, high-fat diet; FMC, fat mass clamped. a: p<0.05 vs SD, b: p<0.05 vs HFD.

Gene Function	Gene	SD		HFD		FMC	
		Mean	SEM	Mean	SEM	Mean	SEM
Fatty Acid Transport	Cd36	1.00	0.16	3.58 ^a	0.83	0.77 ^b	0.18
	Cpt1b	1.00	0.20	1.71 ^a	0.23	0.33 ^{a,b}	0.08
	Fabp4	1.00	0.11	2.85 ^a	0.53	1.01 ^b	0.16
Lipogenesis	Acacb	1.00	0.20	1.72 ^a	0.26	2.40 ^a	0.25
Glucose Uptake	Slc2a1	1.00	0.19	1.31	0.30	0.53 ^b	0.02
	Slc2a4	1.00	0.20	1.37	0.30	0.47 ^b	0.07
Glycogen Metabolism	Gys1	1.00	0.24	1.56	0.19	0.31 ^{a,b}	0.14
	Pygm	1.00	0.19	1.28	0.26	0.88	0.24
Glycolysis & Lactate production	Hk2	1.00	0.21	0.87	0.16	0.47	0.09
	Ldha	1.00	0.15	2.21 ^a	0.37	0.82 ^b	0.16
	Pfkkm	1.00	0.22	0.84	0.09	0.33 ^{a,b}	0.09
Mitochondrial β -Oxidation	Acadl	1.00	0.12	2.52 ^a	0.47	0.36 ^b	0.12
	Hadha	1.00	0.15	2.12 ^a	0.36	0.41 ^b	0.11
	Hadhb	1.00	0.18	1.96 ^a	0.34	0.51 ^b	0.08
Oxidative Phosphorylation	Atp5b	1.00	0.16	1.67 ^a	0.23	0.67 ^b	0.16
	Cox4i1	1.00	0.22	1.46	0.22	1.27	0.45
	Cox5a	1.00	0.18	1.18	0.18	0.37 ^{a,b}	0.13
	Cox5b	1.00	0.25	1.89	0.46	0.61 ^b	0.12
	Sdhhd	1.00	0.23	1.51	0.26	0.59 ^a	0.07
	Ucp2	1.00	0.31	0.70	0.11	0.15 ^b	0.01
	Ucp3	1.00	0.20	0.75	0.11	5.37 ^{a,b}	1.03
SNS activity	Nr4a3	1.00	0.25	2.51	1.10	6.84 ^{a,b}	0.89

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Supplementary Table 2. Expression of key metabolic genes in epididymal white adipose tissue following fat mass clamping. Fatp1: solute carrier family 27 (fatty acid transporter), member 1, Cd36: cluster of differentiation 36, Fabb4: fatty acid binding protein 4, Fabb5: fatty acid binding protein 5, Fasn: fatty acid synthase, Scd1: stearoyl-CoA desaturase 1, Scd2: stearoyl-CoA desaturase 2, Acac: acetyl-CoA carboxylase alpha, Cd68: cluster of differentiation 68, Tnf: tumor necrosis factor, Il10: interleukin 10, Ccl2: chemokine (C-C motif) ligand 2, Itgax: integrin, alpha X, Il6: interleukin 6, Slc2a1: solute carrier family 2, facilitated glucose transporter member 1 (GLUT1), Slc2a4: Solute carrier family 2, facilitated glucose transporter member 4 (GLUT4), Lep: Leptin, Adipoq: adiponectin, C1Q and collagen domain containing, Retn: resistin. Mice were fasted for 16 h prior to tissue collection. All mice are male n= 8 per group. All data are represented as mean +/- SEM. SD, standard diet; HFD, high-fat diet; FMC, fat mass clamped. a: p<0.05 vs SD, b: p<0.05 vs HFD.

Gene Function	Gene	SD		HFD		FMC	
		Mean	SEM	Mean	SEM	Mean	SEM
Fatty Acid Transport	Fatp1	1.00	0.17	0.79	0.08	0.45	0.07
	Cd36	1.00	0.18	1.24	0.10	0.77	0.23
	Fabb4	1.00	0.20	0.63	0.06	0.56	0.16
	Fabb5	1.00	0.24	2.14	0.16	1.09	0.32
Fatty Acid Synthesis	Fasn	1.00	0.22	1.09	0.10	1.95	0.55
	Scd1	1.00	0.21	0.79	0.11	1.65	0.56
	Scd2	1.00	0.28	2.79	0.30	2.75	1.09
	Acac	1.00	0.17	0.59	0.05	1.43	0.35
Inflammation	Cd68	1.00	0.15	13.88 ^a	1.53	1.23 ^b	0.47
	Tnf	1.00	0.37	7.39 ^a	1.17	1.93 ^b	0.88
	Il10	1.00	0.28	9.71 ^a	2.56	2.17 ^b	0.88
	Ccl2	1.00	0.25	10.58 ^a	1.41	1.69 ^b	0.61
	Itgax	1.00	0.15	35.87 ^a	3.08	1.25 ^b	0.36
	Il6	1.00	0.57	1.94	0.44	1.27	0.46
Glucose Transport	Slc2a1	1.00	0.20	1.23	0.10	0.81	0.13
	Slc2a4	1.00	0.18	0.39	0.03	0.96	0.28
Metabolism regulation	Lep	1.00	0.20	2.93	0.23	1.29	0.39
	Adipoq	1.00	0.22	0.33	0.03	0.64	0.19
	Retn	1.00	0.22	0.23	0.02	1.41	0.44

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Supplementary Table 3. Expression of key metabolic genes in liver following fat mass clamping. Fabp1: fatty acid binding protein 1, Cd36: cluster of differentiation 36, Lpl: lipoprotein lipase, Scd1: stearoyl-CoA desaturase 1, Fasn: fatty acid synthase, Srebf1: sterol regulatory element binding transcription factor 1, Acaca: acetyl-CoA carboxylase alpha, Acox1: acyl-CoA oxidase 1, palmitoyl, Crota: carnitine O-octanoyltransferase, Cpt1b: carnitine palmitoyltransferase 1B, Ppara: peroxisome proliferator-activated receptor alpha, Ppargc1a: peroxisome proliferator-activated receptor gamma, coactivator 1 alpha, Il10: interleukin 10, Il6: interleukin 6, Tlr4: toll-like receptor 4, Tnf: tumor necrosis factor, Gsta2: glutathione S-transferase alpha 2, Por: P450 (cytochrome) oxidoreductase, Hmox1: heme oxygenase (decycling) 1, Acly: ATP citrate lyase, Gck: glucokinase (hexokinase 4), Hk2: Hexokinase 2, Me1: malic enzyme 1, Pdk4: pyruvate dehydrogenase kinase, isozyme 4, G6pc: glucose-6-phosphatase, catalytic subunit, Pck1: phosphoenolpyruvate carboxykinase 1, Pklr: pyruvate kinase (liver). Mice were fasted for 16 h prior to tissue collection. All mice are male n= 8 per group. All data are represented as mean +/- SEM. SD, standard diet; HFD, high-fat diet; FMC, fat mass clamped. a: p<0.05 vs SD, b: p<0.05 vs HFD.

Gene Function	Gene	SD		HFD		FMC	
		Mean	SEM	Mean	SEM	Mean	SEM
Fatty Acid Transport	Fabp1	1.00	0.25	1.09	0.23	0.87	0.13
	CD36	1.00	0.15	9.05 ^a	1.86	1.28 ^b	0.21
	Lpl	1.00	0.25	1.41 ^a	0.24	0.52 ^b	0.06
Fatty Acid Synthesis	Scd1	1.00	0.24	1.67	0.38	1.10	0.16
	Fasn	1.00	0.31	1.87 ^a	0.30	2.79 ^{a,b}	0.26
	Srebf1	1.00	0.16	1.36	0.32	0.95	0.13
	Acaca	1.00	0.18	1.09	0.19	0.87	0.09
Fatty Acid Oxidation	Acox1	1.00	0.22	1.54	0.25	1.21	0.11
	Crot	1.00	0.15	1.50 ^a	0.39	0.57	0.11
	Cpt1a	1.00	0.19	1.26	0.21	0.78	0.10
Lipid Metabolism	Ppara	1.00	0.23	1.09	0.23	0.76	0.08
	Ppargc1a	1.00	0.24	1.04	0.24	0.85	0.12
Inflammation	Il10	1.00	0.39	1.41	0.39	1.03	0.37
	Il6	1.00	0.56	0.19	0.09	0.53	0.25
	Tlr4	1.00	0.07	1.99 ^a	0.31	0.89 ^b	0.08
	Tnf	1.00	0.43	3.76 ^a	0.75	0.97 ^b	0.25
	Gsta2	1.00	0.16	3.24 ^a	1.17	0.50 ^b	0.08
	Por	1.00	0.36	0.66	0.11	0.77	0.12
TCA/Glycolysis	Hmox1	1.00	0.16	1.78 ^a	0.28	0.97 ^b	0.09
	Acly	1.00	0.22	2.36 ^a	0.76	2.28 ^a	0.32
	Gck	1.00	0.13	2.26 ^a	0.29	2.26 ^a	0.39
	Hk2	1.00	0.47	2.27 ^a	0.61	0.53 ^b	0.09
	Me1	1.00	0.23	1.75	0.44	1.38	0.19
Gluconeogenesis	Pdk4	1.00	0.27	2.11 ^a	0.37	0.86 ^b	0.16
	G6pc	1.00	0.17	0.88	0.18	0.82	0.21
	Pck1	1.00	0.22	0.45 ^a	0.10	0.89 ^b	0.14
	Pklr	1.00	0.17	1.54	0.30	1.00	0.15