Supplementary information

Egr1 deficiency induces browning of inguinal subcutaneous white adipose tissue in mice

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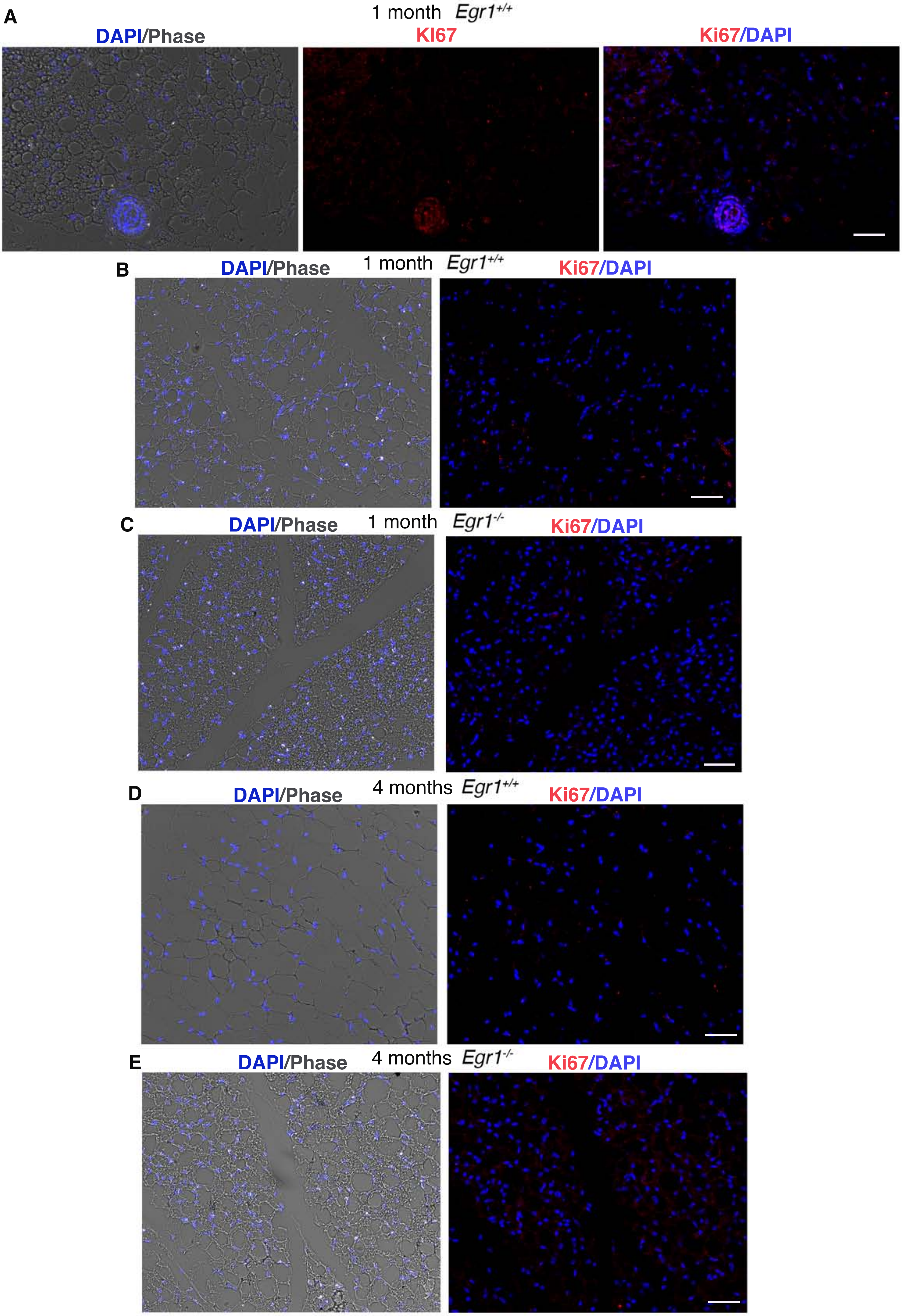
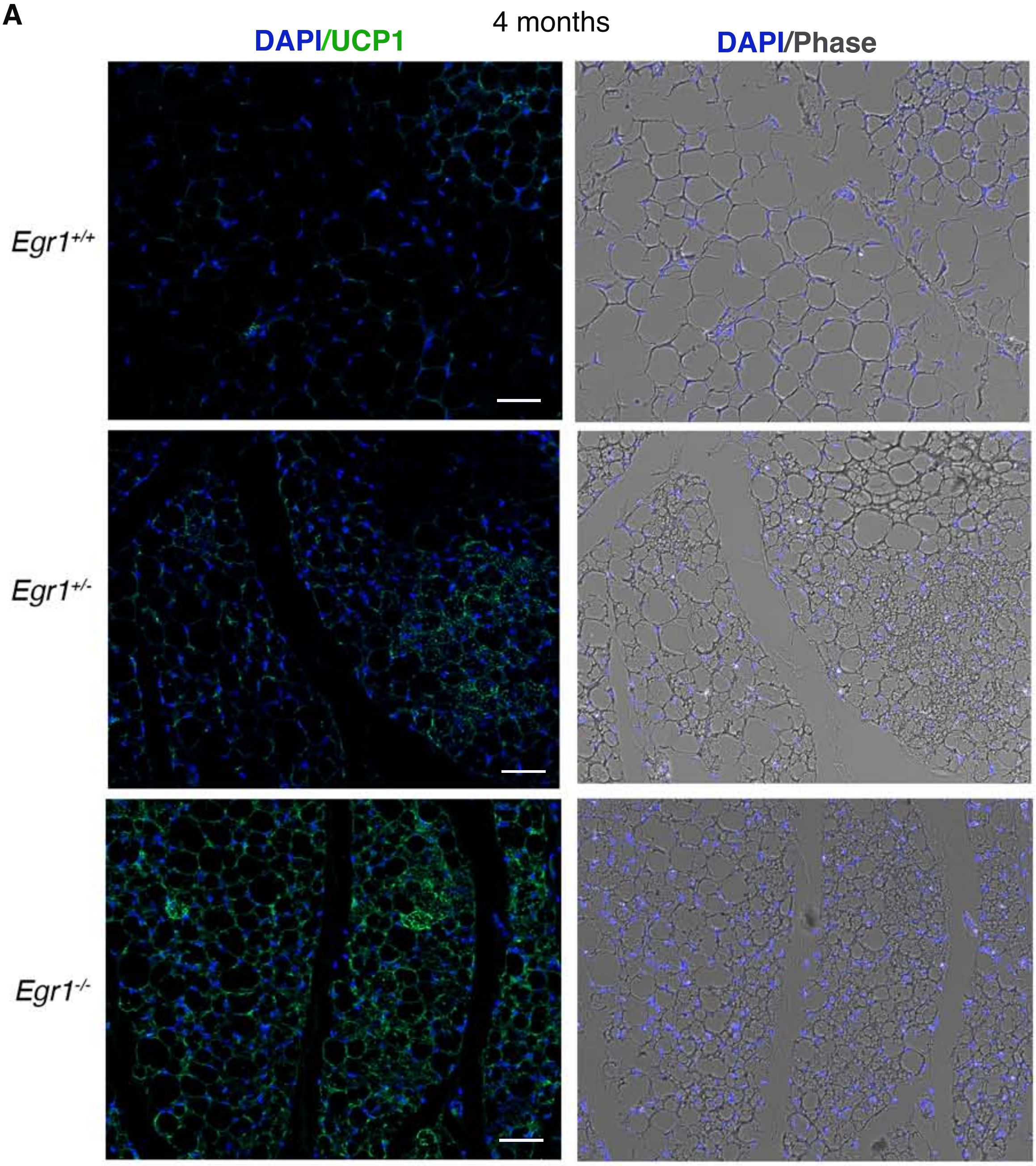
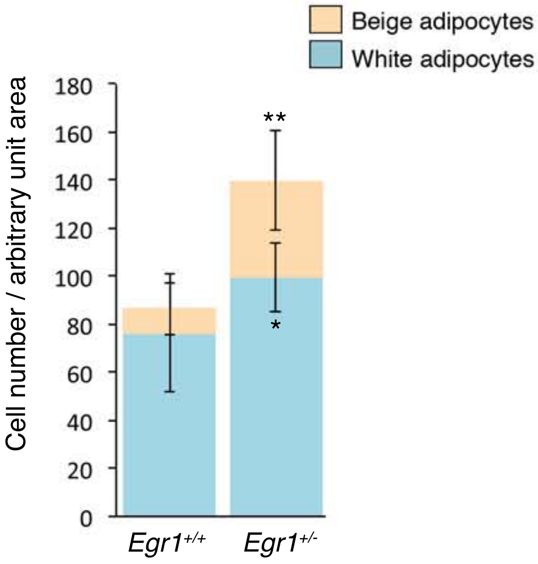
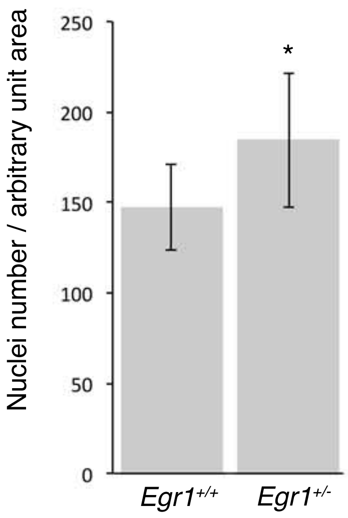

A
1 month *Egr1*+/+
DAPI/Phase
KI67
Ki67/DAPI
B
DAPI/Phase
1 month *Egr1*+/+
Ki67/DAPI
C
DAPI/Phase
1 month *Egr1*-/-
Ki67/DAPI
D
DAPI/Phase
4 months *Egr1*+/+
Ki67/DAPI
E
DAPI/Phase
4 months *Egr1*-/-
Ki67/DAPI



B Number of beige and white adipocytes



C DAPI-stained cell counting



List of up-regulated genes in the ingWAT of postnatal Egr1-/- mice

Contig	log2FoldChar	Fold Change	padj	Description
Genes expressed in adipose tissue derived- mesenchymal stem cells				
Gnas	0.471	1.386	3.94E-02	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus
Genes expressed during adipocytes (white/beige) differentiation				
Cebpb	0.583	1.498	2.03E-02	CCAAT/enhancer binding protein (C/EBP), beta
Ppara	0.682	1.604	9.66E-03	peroxisome proliferator activated receptor alpha
Genes expressed in beige differenciated adipocytes: metabolism and thermogenic genes				
Acacb	0.747	1.679	2.57E-03	acetyl-Coenzyme A carboxylase beta
Acadm	0.508	1.422	3.32E-02	acyl-Coenzyme A dehydrogenase, medium chain
Acadvl	0.504	1.418	3.47E-02	acyl-Coenzyme A dehydrogenase, very long chain
Aco2	0.628	1.546	6.26E-03	aconitase 2, mitochondrial
Acot11	1.171	2.251	1.92E-07	acyl-CoA thioesterase 11
Apoc1	0.605	1.521	9.48E-03	apolipoprotein C-I
bscl2	0.479	1.394	2.18E-02	BSCL2, seipin lipid droplet biogenesis associated
Chchd10	0.502	1.416	4.64E-02	coiled-coil-helix-coiled-coil-helix domain containing 10
Cidea	0.818	1.763	6.35E-04	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A
Cisd3	0.664	1.584	1.91E-02	CDGSH iron sulfur domain 3
Clstn3	0.725	1.653	1.78E-02	calsyntenin 3
Cluh	0.552	1.466	1.01E-02	clustered mitochondria (cluA/CLU1) homolog
Coq6	0.684	1.607	4.08E-03	coenzyme Q6 monooxygenase
Cox5a	0.694	1.618	2.10E-03	cytochrome c oxidase subunit Va
Cox8b	0.670	1.591	2.10E-03	cytochrome c oxidase subunit VIIIb
Cpn2	0.809	1.752	5.18E-03	carboxypeptidase N, polypeptide 2
Cpt1b	0.620	1.537	2.54E-02	carnitine palmitoyltransferase 1b, muscle
Cs	0.645	1.563	3.97E-03	citrate synthase] [Gene Type: protein-coding]
Cspg4	0.563	1.478	2.63E-02	chondroitin sulfate proteoglycan 4
Cyc1	0.486	1.401	4.44E-02	cytochrome c-1
Dhrs11	0.804	1.746	2.96E-03	dehydrogenase/reductase (SDR family) member 11

Dhrs9	0.971	1.961	9.52E-04	dehydrogenase/reductase (SDR family) member 9
Dio2	1.421	2.677	4.63E-09	deiodinase, iodothyronine, type II
Elovl6	0.536	1.450	4.30E-02	ELOVL family member 6, elongation of long chain fatty acids (yeast)]
Etfa	0.525	1.439	2.03E-02	electron transferring flavoprotein, alpha polypeptide
Etfdh	0.506	1.420	3.34E-02	electron transferring flavoprotein, dehydrogenase
Gpd1	0.675	1.596	5.58E-03	glycerol-3-phosphate dehydrogenase 1 (soluble)
Gpd2	0.783	1.721	5.70E-04	glycerol phosphate dehydrogenase 2, mitochondrial
Hadhb	0.642	1.561	5.77E-03	hydroxyacyl-Coenzyme A dehydrogenase, beta subunit
Idh3a	0.586	1.501	1.02E-02	isocitrate dehydrogenase 3 (NAD+) alpha
Idh3g	0.497	1.411	2.36E-02	isocitrate dehydrogenase 3 (NAD+), gamma
Kcnk3	0.625	1.543	1.13E-02	potassium channel, subfamily K, member 3
Kng2	0.785	1.723	8.74E-03	kininogen 2
Ldhb	0.719	1.646	2.83E-03	lactate dehydrogenase B
Letmd1	0.747	1.679	1.41E-03	LETM1 domain containing 1
Lrg1	0.659	1.579	1.50E-02	leucine-rich alpha-2-glycoprotein 1
Mdh2	0.565	1.479	1.62E-02	malate dehydrogenase 2, NAD (mitochondrial)
Mecr	0.547	1.461	1.04E-02	mitochondrial trans-2-enoyl-CoA reductase
Mlxipl	0.706	1.632	3.11E-03	MLX interacting protein-like
Mrap	0.684	1.606	1.42E-03	melanocortin 2 receptor accessory protein
Nampt	0.678	1.600	1.42E-03	nicotinamide phosphoribosyltransferase
Nrg4	0.454	1.370	2.75E-02	neuregulin 4
Ntrk3	0.619	1.536	8.33E-03	neurotrophic tyrosine kinase, receptor, type 3
Nudt7	0.494	1.409	4.56E-02	nudix (nucleoside diphosphate linked moiety X)-type motif 7
Ogdh	0.653	1.572	2.81E-03	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
Oplah	0.563	1.477	7.75E-03	5-oxoprolinase (ATP-hydrolysing)
Otop1	0.748	1.679	8.21E-04	otopetrin 1
Pald1	0.491	1.405	2.54E-02	phosphatase domain containing, paladin 1
Pank1	0.815	1.759	1.97E-04	pantothenate kinase 1
Plin5	0.817	1.762	1.46E-04	perilipin 5
Pm20d1	1.052	2.074	2.36E-04	peptidase M20 domain containing 1
Ppargc1a	0.870	1.827	6.30E-04	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
Ppargc1b	0.792	1.732	3.45E-04	peroxisome proliferative activated receptor, gamma, coactivator 1 beta

Ptp4a1	0.445	1.362	3.55E-02	protein tyrosine phosphatase 4a1
Sh2b2	0.621	1.538	5.44E-03	SH2B adaptor protein 2
Slc25a20	0.540	1.454	3.06E-02	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20
Slc25a22	0.611	1.527	2.35E-02	solute carrier family 25 (mitochondrial carrier, glutamate), member 22
Slc25a42	0.860	1.815	1.26E-06	solute carrier family 25, member 42
Slc25a51	0.539	1.453	8.47E-03	solute carrier family 25, member 51
Slc36a2	0.750	1.682	1.70E-04	solute carrier family 36 (proton/amino acid symporter), member 2
Slc4a4	0.490	1.404	6.12E-03	solute carrier family 4 (anion exchanger), member 4
Sucla2	0.626	1.543	8.09E-03	succinate-Coenzyme A ligase, ADP-forming, beta subunit
Suclg1	0.541	1.455	2.33E-02	succinate-CoA ligase, GDP-forming, alpha subunit]
Ucp1	1.050	2.071	1.18E-07	uncoupling protein 1 (mitochondrial, proton carrier)

Genes expressed in White adipose metabolism

Adra1a	1.056	2.079	2.95E-08	adrenergic receptor, alpha 1a
Adrbk2	0.641	1.559	4.79E-03	adrenergic, beta, receptor kinase 2
Chst3	0.588	1.503	4.61E-02	carbohydrate (chondroitin 6/keratan) sulfotransferase 3
Cmtm4	0.550	1.464	1.84E-02	CKLF-like MARVEL transmembrane domain containing 4
Cntfr	0.723	1.651	2.22E-02	ciliary neurotrophic factor receptor
Cntnap1	0.656	1.576	4.44E-02	contactin associated protein-like 1
Crat	0.504	1.418	1.90E-02	carnitine acetyltransferase
Ctse	1.659	3.157	2.07E-10	cathepsin E
Dcun1d3	0.512	1.426	4.08E-02	DCN1, defective in cullin neddylation 1, domain containing 3
Dgat2	0.647	1.566	1.19E-02	diacylglycerol O-acyltransferase 2
Gk	1.074	2.106	1.74E-09	glycerol kinase
Gys1	0.553	1.468	1.97E-02	glycogen synthase 1, muscle
Helz2	0.518	1.432	1.97E-02	helicase with zinc finger 2, transcriptional coactivator
Hk2	0.804	1.746	3.42E-04	hexokinase 2
Mif4gd	0.509	1.423	3.01E-02	MIF4G domain containing/serum leptin-interacting protein 1
Pdp2	0.583	1.498	2.75E-02	pyruvate dehyrogenase phosphatase catalytic subunit 2
Pnpla3	0.819	1.764	6.72E-04	patatin-like phospholipase domain containing 3
Ppip5k1	0.531	1.445	2.06E-02	diphosphoinositol pentakisphosphate kinase 1
Ppp1r10	0.462	1.377	4.01E-02	protein phosphatase 1, regulatory subunit 10

Rtn4ip1	0.531	1.445	4.47E-02	reticulon 4 interacting protein 1
Syt12	0.777	1.714	1.13E-02	synaptotagmin XII
Tfrc	1.189	2.280	1.18E-07	transferrin receptor
Tysnd1	0.553	1.467	4.20E-02	trypsin domain containing 1
Genes involved in inflammation in adipose tissue				
Cdkn1a	0.654	1.574	3.55E-02	cyclin-dependent kinase inhibitor 1A (P21)
Ifit1	0.795	1.735	2.54E-02	interferon-induced protein with tetratricopeptide repeats 1
Il15ra	0.483	1.398	3.95E-02	interleukin 15 receptor, alpha chain
Il2rb	0.810	1.753	1.43E-02	interleukin 2 receptor, beta chain
Irf7	0.702	1.626	2.54E-02	interferon regulatory factor 7
Tmem38b	0.501	1.415	4.29E-02	transmembrane protein 38B
Tob1	0.524	1.438	5.25E-03	transducer of ErbB-2.1
Tob2	0.698	1.623	2.79E-03	transducer of ERBB2, 2
Traf4	0.591	1.506	4.93E-02	TNF receptor associated factor 4
Usp2	0.642	1.560	2.59E-02	ubiquitin specific peptidase 2
Genes expressed in other cell types within the adipose tissue				
Adam11	0.633	1.550	2.79E-02	a disintegrin and metallopeptidase domain 11
Bst2	0.705	1.630	3.55E-02	bone marrow stromal cell antigen 2
Cnnm2	0.614	1.530	4.39E-02	cyclin M2
Cd79a	0.672	1.594	4.61E-02	CD79A antigen
Cdh2	0.611	1.527	1.73E-02	cadherin 2
Csrnp1	0.715	1.641	2.05E-02	cysteine-serine-rich nuclear protein 1
Dlat	0.505	1.419	3.96E-02	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
Dlst	0.510	1.424	2.62E-02	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
Fggy	0.717	1.644	1.35E-02	FGGY carbohydrate kinase domain containing
Gramd1b	0.566	1.480	1.40E-02	GRAM domain containing 1B
Pax5	0.687	1.610	3.11E-02	paired box 5
Perm1	0.712	1.638	1.05E-02	PPARGC1 and ESRR induced regulator, muscle 1
Sbk1	0.594	1.509	1.13E-02	SH3-binding kinase 1
Sec61a2	0.536	1.450	1.90E-02	Sec61, alpha subunit 2 (S. cerevisiae)

Trim67	1.374	2.591	2.58E-11	tripartite motif-containing 67

Genes with unidentified function or Non coding RNA

1110001J03Rik	0.744	1.675	5.77E-03	
Ctcflos	0.673	1.594	3.80E-03	CCCTC-binding factor (zinc finger protein)-like, opposite strand (ncRNA)
Fam126b	0.440	1.357	2.16E-02	family with sequence similarity 126, member B
Fam210a	0.507	1.422	2.96E-02	family with sequence similarity 210, member A
Fam73b	0.689	1.613	1.32E-03	family with sequence similarity 210, member A
Gdap10	0.950	1.932	8.41E-07	ganglioside-induced differentiation-associated-protein 10 (ncRNA)
Gm10032	0.754	1.686	3.59E-02	predicted gene 10032 (ncRNA)
Gm37674	0.680	1.603	3.98E-02	-
Gm37783	0.725	1.653	2.14E-02	-
Gm38357	0.680	1.602	1.22E-02	-
Gm42428	0.765	1.699	1.23E-02	-
Gm42614	0.944	1.924	1.42E-03	-
Gm42895	0.741	1.671	2.52E-02	-
Gm43605	0.772	1.707	2.14E-02	-
Gm8822	2.452	5.473	5.82E-23	ARP3 actin-related protein 3 homolog pseudogene
Gm9899	0.668	1.589	1.98E-02	predicted gene 9899 (ncRNA)
RP23-82I13.6	0.813	1.757	1.34E-03	-

GOTERM_BP_DIRECT	**Up regulated genes in the inguinal subcutaneous adipose tissue of 2-week-old *Egr1*$^{-/-}$ mice**	
	Enrichment scores / P-values	**Genes**
NADH Metabolic process	**95.2/** 3.3^{E}-11	*Dlst* dihydrolipoamide S-succinyltransferase *Gpd2* glycerol phosphate dehydrogenase 2, mitochondrial *Gpd1* glycerol-3-phosphate dehydrogenase 1 (soluble) *Idh3a* isocitrate dehydrogenase 3 (NAD+) alpha *Idh3g* isocitrate dehydrogenase 3 (NAD+), gamma *Mdh2* malate dehydrogenase 2, NAD (mitochondrial) *Ogdh* oxoglutarate (alpha-ketoglutarate) dehydrogenase
Tricarboxylic acid cycle	**53.4/** 1.1^{E}-13	*Aco2* aconitase 2, mitochondrial *Cs* citrate synthase *Dlat* dihydrolipoamide S-acetyltransferase *Dlst* dihydrolipoamide S-succinyltransferase *Idh3a* isocitrate dehydrogenase 3 (NAD+) alpha *Idh3g* isocitrate dehydrogenase 3 (NAD+), gamma *Mdh2* malate dehydrogenase 2, NAD (mitochondrial) *Ogdh* oxoglutarate (alpha-ketoglutarate) dehydrogenase *Suclg1* succinate-CoA ligase, GDP-forming, alpha subunit *Sucla2* succinate-Coenzyme A ligase, ADP-forming, beta subunit
Brown fat cell differentiation	**23.4** /5.7^{E}-5	*Cebpb* CCAAT/enhancer binding protein (C/EBP), beta *Sh2b2* SH2B adaptor protein 2 *Lrg1* leucine-rich alpha-2-glycoprotein 1 *Mrap* melanocortin 2 receptor accessory protein *Nudt7* nudix -type motif 7 *Ucp1* uncoupling protein 1
Fatty acid metabolic process	**9.9** /7.1^{E}-7	*Elovl6* elongation of long chain fatty acids, member 6 *Acacb* acetyl-Coenzyme A carboxylase beta *Acot11* acyl-CoA thioesterase 11

		Acadm acyl-Coenzyme A dehydrogenase, medium chain *Acadvl* acyl-Coenzyme A dehydrogenase, very long chain *Crat* carnitine acetyltransferase *Cpt1b* carnitine palmitoyltransferase 1b *Hadhb* hydroxyacyl-Coenzyme A dehydrogenase *Mecr* mitochondrial trans-2-enoyl-CoA reductase *Ppara* peroxisome proliferator activated receptor alpha
Metabolic process	**4.9/** 6 .9^{E}-7	*Acacb* acetyl-Coenzyme A carboxylase beta *Aco2* aconitase 2, mitochondrial *Acadm* acyl-Coenzyme A dehydrogenase, medium chain *Acadvl* acyl-Coenzyme A dehydrogenase, very long chain *Dhrs11* dehydrogenase/reductase (SDR family) member 11 *Dhrs9* dehydrogenase/reductase (SDR family) member 9 *Dlat* dihydrolipoamide S-acetyltransferase *Dlst* dihydrolipoamide S-succinyltransferase *Gys1* glycogen synthase 1, muscle *Hk2* hexokinase 2 Hadhb hydroxyacyl-Coenzyme A dehydrogenase Ogdh oxoglutarate (alpha-ketoglutarate) dehydrogenase Pnpla3 patatin-like phospholipase domain containing 3 Pm20d1 peptidase M20 domain containing 1 Suclg1 succinate-CoA ligase, GDP-forming, alpha subunit) Sucla2 succinate-Coenzyme A ligase, ADP-forming, beta subunit
Lipid metabolic process	**4.7** /8.3^{E}-6	Bscl2 Berardinelli-Seip congenital lipodystrophy 2 Elovl6 elongation of long chain fatty acids, member 6 Acacb acetyl-Coenzyme A carboxylase beta Acadm acyl-Coenzyme A dehydrogenase, medium chain Acadvl acyl-Coenzyme A dehydrogenase, very long chain) Crat carnitine acetyltransferase Cpt1b carnitine palmitoyltransferase 1b Cidea cell death-inducing DNA fragmentation factor, alpha subunit-like effector A

		Dgat2 diacylglycerol O-acyltransferase 2 Hadhb hydroxyacyl-Coenzyme A dehydrogenase Mecr mitochondrial trans-2-enoyl-CoA reductase Pnpla3 patatin-like phospholipase domain containing 3 Plin5 perilipin 5 Ppara peroxisome proliferator activated receptor alpha

List of down-regulated genes in the ingWAT of postnatal Egr1-/- mice

Gene symbol	Log2 (Fold Ch	Fold Change	padj	Description
Extracellular matrix, cytoskeleton and adhesion genes				
Adamts2	-0.488	0.713	3.83E-02	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2
Adamtsl4	-0.557	0.680	4.61E-02	ADAMTS-like 4
Adgrd1	-0.617	0.652	3.91E-02	adhesion G protein-coupled receptor D1
Adgre1	-0.622	0.650	1.23E-02	adhesion G protein-coupled receptor E1
Antxr1	-0.520	0.697	1.51E-02	anthrax toxin receptor 1
Aspn	-0.698	0.616	1.64E-03	asporin
Apcdd1	-0.517	0.699	4.18E-02	adenomatosis polyposis coli down-regulated 1
Cdh11	-0.555	0.681	3.46E-02	cadherin 11
Ckap4	-0.552	0.682	2.14E-02	cytoskeleton-associated protein 4
Col14a1	-0.692	0.619	2.01E-05	collagen, type XIV, alpha 1
Col1a1	-0.549	0.684	8.29E-03	collagen, type I, alpha 1
Col1a2	-0.522	0.696	8.78E-03	collagen, type I, alpha 2
Col3a1	-0.549	0.684	6.47E-03	collagen, type III, alpha 1
Col5a2	-0.598	0.661	1.95E-03	collagen, type V, alpha 2
Dab2	-0.555	0.681	1.76E-02	disabled 2, mitogen-responsive phosphoprotein
Dbn1	-0.598	0.661	4.64E-02	drebrin 1
Dcn	-0.790	0.578	7.84E-06	decorin
Ddr2	-0.548	0.684	7.24E-03	discoidin domain receptor family, member 2
Dpt	-0.641	0.641	4.05E-03	dermatopontin
Dpysl3	-0.669	0.629	1.08E-03	dihydropyrimidinase-like 3
Ecm2	-0.541	0.688	3.83E-02	extracellular matrix protein 2, female organ and adipocyte specific
Efemp1	-0.735	0.601	1.15E-03	epidermal growth factor-containing fibulin-like extracellular matrix protein 1
Fap	-0.600	0.660	4.05E-03	fibroblast activation protein
Fbn1	-0.781	0.582	7.58E-05	fibrillin 1
Fmr1	-0.504	0.705	2.61E-02	fragile X mental retardation syndrome 1
Fn1	-0.676	0.626	2.04E-04	fibronectin 1
Fndc1	-0.535	0.690	4.21E-02	fibronectin type III domain containing 1
Itgbl1	-0.604	0.658	4.20E-02	integrin, beta-like 1

Lum	-0.741	0.598	1.50E-05	lumican
Mmp14	-0.478	0.718	3.95E-02	matrix metallopeptidase 14 (membrane-inserted)
Mmp2	-0.464	0.725	3.66E-02	matrix metallopeptidase 2]
Mmp23	-0.630	0.646	8.69E-03	matrix metallopeptidase 23
Pcdh20	-0.697	0.617	2.37E-02	protocadherin 20
Pcdhb14	-0.749	0.595	5.51E-03	protocadherin beta 14
Pcolce2	-0.771	0.586	4.73E-03	procollagen C-endopeptidase enhancer 2
Postn	-0.615	0.653	1.21E-03	periostin, osteoblast specific factor
Srpx2	-0.799	0.575	1.77E-03	sushi-repeat-containing protein, X-linked 2
Thbs3	-0.575	0.671	2.05E-02	thrombospondin 3
Timp2	-0.537	0.689	2.54E-02	tissue inhibitor of metalloproteinase 2
Tppp3	-0.667	0.630	1.26E-02	tubulin polymerization-promoting protein family member 3
Vcan	-0.646	0.639	1.13E-02	versican
Vnn3	-0.663	0.632	1.94E-02	vanin 3

Genes involved in adipose tissue metabolism and adipocyte metabolism (cell signalling/cell cycle/transcription)

Aebp1	-0.710	0.611	2.34E-04	Adipocyte Enhancer binding protein 1
Akr1c14	-0.858	0.552	8.06E-04	aldo-keto reductase family 1, member C14
Akr1c18	-0.921	0.528	1.21E-04	aldo-keto reductase family 1, member C18
Alb	-0.734	0.601	3.66E-03	albumin
Aldh1a3	-0.752	0.594	2.10E-03	aldehyde dehydrogenase family 1, subfamily A3
Atp2b4	-0.494	0.710	2.54E-02	ATPase, Ca++ transporting, plasma membrane 4
Atpif1	-0.513	0.701	1.98E-02	ATPase inhibitory factor 1
Casp1	-0.667	0.630	3.32E-02	caspase 1
Ces1f	-0.635	0.644	2.05E-03	Carboxylesterase 1F
Clec3b	-0.711	0.611	8.48E-03	C-type lectin domain family 3, member b
Cyb5r3	-0.659	0.633	3.79E-03	cytochrome b5 reductase 3
Cygb	-0.532	0.692	2.01E-02	cytoglobin
Dnm1	-0.633	0.645	8.04E-03	dynamin 1
Gas7	-0.735	0.601	1.91E-04	growth arrest specific 7
Gatm	-0.537	0.689	3.59E-02	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
Ggh	-0.605	0.658	4.70E-03	gamma-glutamyl hydrolase

Ghr	-0.596	0.662	3.79E-03	growth hormone receptor
Glb1l2	-0.507	0.704	4.59E-03	galactosidase, beta 1-like 2
Gnai1	-0.472	0.721	3.65E-02	guanine nucleotide binding protein (G protein), alpha inhibiting 1
Gpc3	-0.487	0.714	3.25E-02	glypican 3
Gulp1	-0.528	0.693	3.52E-02	GULP, engulfment adaptor PTB domain containing 1]
Hmgn3	-0.683	0.623	1.97E-02	high mobility group nucleosomal binding domain 3
Kdelr3	-0.670	0.629	1.56E-02	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
Klf14	-1.097	0.468	2.34E-04	Kruppel-like factor 14
Klhl13	-0.755	0.592	2.40E-04	kelch-like 13
Lpar1	-0.578	0.670	4.70E-03	lysophosphatidic acid receptor 1
Lrrc17	-0.727	0.604	4.94E-04	leucine rich repeat containing 17
Lrrn4cl	-0.752	0.594	1.56E-03	LRRN4 C-terminal like
Mcm6	-0.593	0.663	1.50E-02	minichromosome maintenance complex component 6
Mfap2	-0.841	0.558	3.58E-03	microfibrillar-associated protein 2
Mfap4	-0.832	0.562	1.69E-03	microfibrillar-associated protein 4
Morf4l2	-0.480	0.717	2.85E-02	mortality factor 4 like 2
Mpz	-0.558	0.679	3.91E-02	myelin protein zero
Mrc1	-0.615	0.653	3.79E-03	mannose receptor, C type 1
Mrc2	-0.484	0.715	3.23E-02	mannose receptor, C type 2
Nr5a2	-0.721	0.607	2.01E-02	nuclear receptor subfamily 5, group A, member 2
Nrk	-0.733	0.601	3.11E-03	Nik related kinase
Nxnl1	-0.757	0.592	2.05E-02	nucleoredoxin-like 1
Olfml1	-0.746	0.596	2.38E-03	olfactomedin-like 1
Olfml2b	-0.654	0.636	1.57E-02	olfactomedin-like 2B
Opcml	-0.716	0.609	5.75E-03	opioid binding protein/cell adhesion molecule-like
P4hb	-0.433	0.741	2.22E-02	prolyl 4-hydroxylase, beta polypeptide
Palm	-0.509	0.703	4.28E-02	paralemmin
Peg10	-0.696	0.617	2.35E-02	paternally expressed 10
Pi15	-0.614	0.653	5.75E-03	peptidase inhibitor 15
Pi16	-0.632	0.645	2.98E-02	peptidase inhibitor 16
Plekha4	-0.746	0.596	8.18E-04	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4
Plscr4	-0.743	0.598	5.77E-03	phospholipid scramblase 4

Plxdc2	-0.624	0.649	5.96E-04	plexin domain containing 2
Ptgfrn	-0.761	0.590	1.12E-04	prostaglandin F2 receptor negative regulator
Qpct	-0.739	0.599	2.36E-03	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)
Rab3il1	-0.556	0.680	4.84E-02	RAB3A interacting protein (rabin3)-like 1
Rab7b	-0.763	0.589	2.10E-03	RAB7B, member RAS oncogene family
Rassf8	-0.441	0.737	3.24E-02	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8
Rcan2	-0.716	0.609	7.24E-03	regulator of calcineurin 2
Rcn1	-0.567	0.675	2.99E-03	reticulocalbin 1
Rcn3	-0.582	0.668	3.00E-02	reticulocalbin 3, EF-hand calcium binding domain
Rnase4	-0.589	0.665	2.81E-02	ribonuclease, RNase A family 4
S100a10	-0.487	0.714	3.46E-02	S100 calcium binding protein A10 (calpactin)
S100a6	-0.584	0.667	2.54E-02	S100 calcium binding protein A6 (calcyclin)
Scara5	-0.585	0.667	1.97E-02	scavenger receptor class A, member 5
Sh3d19	-0.509	0.703	2.47E-02	SH3 domain protein D19
Slc5a3	-0.692	0.619	5.61E-03	solute carrier family 5 (inositol transporters), member 3
Smarca1	-0.685	0.622	1.61E-02	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, m1
Sncg	-0.889	0.540	1.12E-04	synuclein, gamma
Srpx2	-0.799	0.575	1.77E-03	sushi-repeat-containing protein, X-linked 2
Tceal8	-0.585	0.667	7.35E-03	transcription elongation factor A (SII)-like 8
Tmeff2	-0.610	0.655	2.47E-02	transmembrane protein with EGF-like and two follistatin-like domains 2
Tmem100	-0.969	0.511	1.29E-04	transmembrane protein 100
Tpsb2	-0.691	0.620	4.72E-02	tryptase beta 2
Ugdh	-0.575	0.672	1.23E-02	UDP-glucose dehydrogenase
Ugt8a	-0.662	0.632	6.15E-03	UDP galactosyltransferase 8A

Genes involved in adipocytes differentiation

Ahnak2	-0.684	0.623	2.46E-03	AHNAK nucleoprotein 2
Arhgef25	-0.561	0.678	2.33E-02	Rho guanine nucleotide exchange factor (GEF) 25
Camk2n1	-0.589	0.665	4.21E-02	calcium/calmodulin-dependent protein kinase II inhibitor 1
Cdkn1c	-0.592	0.663	4.51E-03	cyclin-dependent kinase inhibitor 1C (P57)
Ctsk	-0.636	0.643	7.85E-03	cathepsin K
Ctsl	-0.434	0.740	3.01E-02	cathepsin L

Eid1	-0.489	0.712	3.65E-02	EP300 interacting inhibitor of differentiation 1
Ffar2	-0.624	0.649	6.28E-03	free fatty acid receptor 2
Medag	-0.615	0.653	1.13E-02	mesenteric estrogen dependent adipogenesis
Pros1	-0.448	0.733	4.44E-02	protein S (alpha)
Prrx1	-0.492	0.711	3.04E-02	paired related homeobox 1

Genes involved in inflammation, immune response or expressed in blood cells

Aif1l	-0.665	0.631	1.88E-02	allograft inflammatory factor 1-like
Akap12	-0.681	0.624	2.79E-03	A kinase (PRKA) anchor protein (gravin) 12
Alcam	-0.513	0.701	1.62E-02	activated leukocyte cell adhesion molecule
Anxa1	-0.603	0.658	1.58E-02	annexin A1
Anxa3	-0.505	0.704	2.75E-02	annexin A3
C1qtnf7	-0.767	0.588	5.88E-03	C1q and tumor necrosis factor related protein 7
C3ar1	-0.611	0.655	2.59E-02	complement component 3a receptor 1
Car8	-0.700	0.616	6.74E-03	carbonic anhydrase 8
Cd209f	-0.825	0.564	2.79E-03	CD209f antigen
Cd248	-0.839	0.559	3.42E-04	CD248 antigen, endosialin
Cd34	-0.625	0.649	3.35E-03	CD34 antigen
Cfh	-0.825	0.565	3.42E-04	complement component factor h
Cma1	-0.744	0.597	7.75E-03	chymase 1, mast cell
Commd1	-0.559	0.679	3.57E-02	COMM domain containing 1
Cp	-0.748	0.596	1.36E-03	ceruloplasmin
Cpa3	-0.626	0.648	3.68E-02	carboxypeptidase A3, mast cell
Dse	-0.548	0.684	1.50E-02	dermatan sulfate epimerase
Efhd1	-0.704	0.614	1.19E-02	EF hand domain containing 1
Emilin2	-0.609	0.656	2.00E-02	elastin microfibril interfacer 2
F13a1	-0.695	0.618	4.99E-03	coagulation factor XIII, A1 subunit
Fcgr3	-0.626	0.648	2.01E-02	Fc receptor, IgG, low affinity III
Fcrls	-0.786	0.580	1.13E-02	Fc receptor-like S, scavenger receptor]
Folr2	-0.812	0.570	6.29E-03	folate receptor 2 (fetal)
Frmd4b	-0.498	0.708	3.51E-02	FERM domain containing 4B]
Hba-a1	-0.694	0.618	9.93E-03	hemoglobin alpha, adult chain 1

Il1rl2	-0.549	0.683	3.59E-02	interleukin 1 receptor-like 2
Mal	-0.582	0.668	4.44E-02	myelin and lymphocyte protein, T cell differentiation protein
Morc4	-0.619	0.651	2.11E-02	microrchidia 4
Pf4	-0.730	0.603	6.34E-03	platelet factor 4
Plat	-0.716	0.609	2.10E-03	plasminogen activator, tissue
Ppic	-0.551	0.682	1.46E-02	peptidylprolyl isomerase C
Prnp	-0.468	0.723	3.47E-02	prion protein
Serpinb6a	-0.684	0.622	5.76E-04	serine (or cysteine) peptidase inhibitor, clade B, member 6a
Serpinf1	-0.556	0.680	1.43E-02	serine (or cysteine) peptidase inhibitor, clade F, member 1
Sulf1	-0.532	0.692	1.61E-02	sulfatase 1
Wbp5	-0.683	0.623	2.34E-04	WW domain binding protein 5
Genes encoding secreted molecules				
Bmp3	-0.633	0.645	4.01E-02	bone morphogenetic protein 3
Ccdc80	-0.849	0.555	1.09E-04	coiled-coil domain containing 80
Chrdl1	-0.891	0.539	1.20E-04	chordin-like 1
Crispld1	-0.709	0.612	6.15E-03	cysteine-rich secretory protein LCCL domain containing 1
Fgf2	-0.576	0.671	1.56E-02	fibroblast growth factor 2
Fstl1	-0.762	0.590	1.73E-04	follistatin-like 1
Igf1	-0.710	0.611	2.04E-04	insulin-like growth factor 1
Igf2	-0.719	0.608	1.08E-03	insulin-like growth factor 2
Igfbp5	-0.511	0.702	2.00E-02	insulin-like growth factor binding protein 5
Igfbp6	-0.777	0.583	5.58E-03	insulin-like growth factor binding protein 6
Lep	-0.507	0.704	2.18E-02	leptin
Nucb2	-0.607	0.657	5.82E-03	nucleobindin 2
Rarres2	-0.610	0.655	1.97E-02	retinoic acid receptor responder (tazarotene induced) 2
Retnla	-0.779	0.583	5.44E-03	resistin like alpha
Sema3b	-0.605	0.658	1.88E-02	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B
Sema3d	-0.677	0.625	2.55E-03	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D
Sfrp2	-0.796	0.576	2.10E-03	secreted frizzled-related protein 2
Sfrp4	-1.293	0.408	3.35E-08	secreted frizzled-related protein 4
Smoc1	-0.542	0.687	1.18E-02	SPARC related modular calcium binding 1

Sparc	-0.490	0.712	2.03E-02	secreted acidic cysteine rich glycoprotein
Wnt2	-0.711	0.611	2.35E-02	wingless-type MMTV integration site family, member 2

Genes with unidentified function in the adipose tissue and non coding RNAs

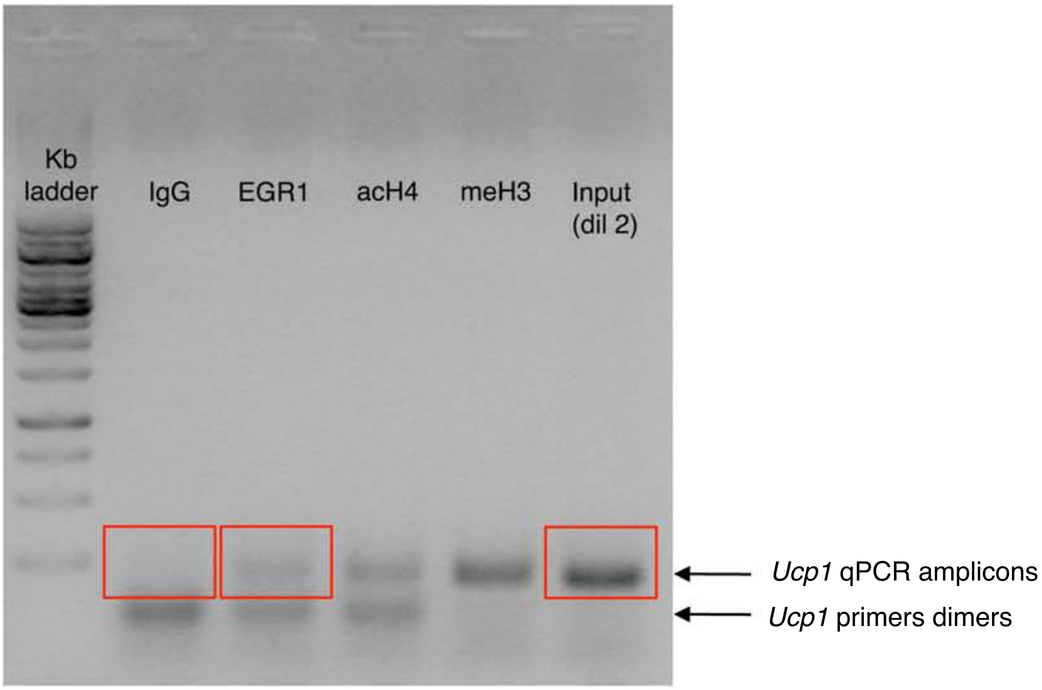
AW551984	-0.645	0.640	4.93E-02	expressed sequence AW551984
Bcas1	-0.663	0.632	3.66E-02	breast carcinoma amplified sequence 1
C130074G19	-0.522	0.696	3.25E-02	RIKEN cDNA C130074G19 gene
Fam102b	-0.688	0.621	1.04E-03	family with sequence similarity 102, member B]
Fam114a1	-0.554	0.681	4.41E-02	family with sequence similarity 114, member A1
Fam171b	-0.759	0.591	1.58E-02	family with sequence similarity 171, member B
Gm10093	-0.809	0.571	2.36E-02	histone deacetylase 1 pseudogene
H19	-0.825	0.565	2.04E-04	H19, imprinted maternally expressed transcript (ncRNA)
Snhg18	-0.615	0.653	4.61E-02	small nucleolar RNA host gene 18 (ncRNA)
Zeb2os	-0.805	0.573	4.55E-03	inc finger E-box binding homeobox 2, opposite strand (ncRNA)

Genes with function described in other cell types

Gap43	-0.917	0.529	1.58E-03	growth associated protein 43
Kcnk2	-0.757	0.592	2.13E-02	potassium channel, subfamily K, member 2
Nbl1	-0.724	0.606	1.76E-02	neuroblastoma, suppression of tumorigenicity 1
Net1	-0.781	0.582	1.42E-03	neuroepithelial cell transforming gene 1
Nov	-0.859	0.551	1.77E-03	nephroblastoma overexpressed gene
Nrep	-0.517	0.699	3.95E-02	neuronal regeneration related protein
Ogn	-0.702	0.615	2.08E-03	osteoglycin
Plp1	-0.579	0.669	8.66E-03	proteolipid protein (myelin) 1
Sbsn	-0.727	0.604	3.65E-02	suprabasin
Sgms2	-0.650	0.637	2.34E-02	sphingomyelin synthase 2

GOTERM_BP_DIRECT	**Down regulated genes in the inguinal subcutaneous adipose tissue of 2-week-old *Egr1*$^{-/-}$ mice**	
	Enrichment scores / P-values	**Genes**
Collagen fibril organization	**23.8**/ 2.4^{E}-10	*Adamts2* a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2 *Col1a1* collagen, type I, alpha 1 *Col1a2* collagen, type I, alpha 2 *Col3a1* collagen, type III, alpha 1 *Col5a2* collagen, type V, alpha 2 *Col14a1* collagen, type XIV, alpha 1 *Dpt* dermatopontin *Ddr2* discoidin domain receptor family, member 2 *Lum* lumican *Sfrp2* secreted frizzled-related protein 2
Collagen catabolic process	**21.1**/ 8^{E}-5	*Adamts2* a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2 *Ctsk* cathepsin K *Mrc2* mannose receptor, C type 2 *Mmp14* matrix metallopeptidase 14 *Mmp2* matrix metallopeptidase 2
Extracellular matrix organization	**6.7**/ 6.1^{E}-4	*Adamtsl4* ADAMTS-like 4 *Smoc1* SPARC related modular calcium binding 1 *Ccdc80* coiled-coil domain containing 80 *Ecm2* extracellular matrix protein 2, female organ and adipocyte specific *Fn1* fibronectin 1 *Olfml2b* olfactomedin-like 2B *Postn* periostin
Ossification	**6.5**/ 2.2^{E}-3	*Bmp3* bone morphogenetic protein 3 *Chrdl1* chordin-like 1 *Ddr2* discoidin domain receptor family, member 2 *Igf2* insulin-like growth factor 2

		Lrrc17 leucine rich repeat containing 17 *Mmp14* matrix metallopeptidase 14
Wound healing	**5.6**/ 3.4^{E}-2	*Col1a1* collagen, type I, alpha 1 *Col3a1* collagen, type III, alpha 1 *Fgf2* fibroblast growth factor 2 *Fn1* fibronectin 1
Positive regulation of MAPK cascade	**4.5**/ 2.6^{E}-2	*Igf1* insulin-like growth factor 1 *Igf2* insulin-like growth factor 2 *Lep* leptin *Lpar1* lysophosphatidic acid receptor 1 *Timp2* tissue inhibitor of metalloproteinase 2
Cell adhesion	**3.2**/ 1.6^{E}-4	*Cd34* CD34 antigen *Alcam* activated leukocyte cell adhesion molecule *Cdh11* cadherin 11 *Col14a1* collagen, type XIV, alpha 1 *Dpt* dermatopontin *Emilin2* elastin microfibril interfacer 2 *Fap* fibroblast activation protein *Fn1* fibronectin 1 *Mfap4* microfibrillar-associated protein 4 *Nov* nephroblastoma overexpressed gene *Postn* periostin *Pcdh20* protocadherin 20 *Pcdhb14* protocadherin beta 14 *Srpx2* sushi-repeat-containing protein, X-linked 2 *Thbs3* thrombospondin 3 *Vcan* versican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IgG
EGR1
acH4
meH3
Input (dil 2)
Ucp1 qPCR amplicons
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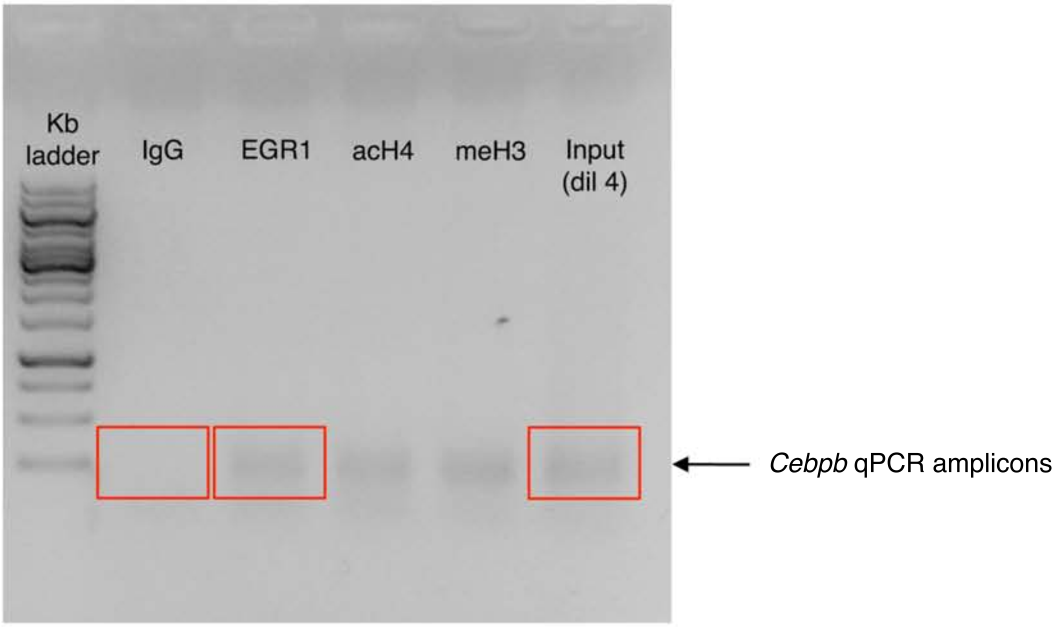
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IgG
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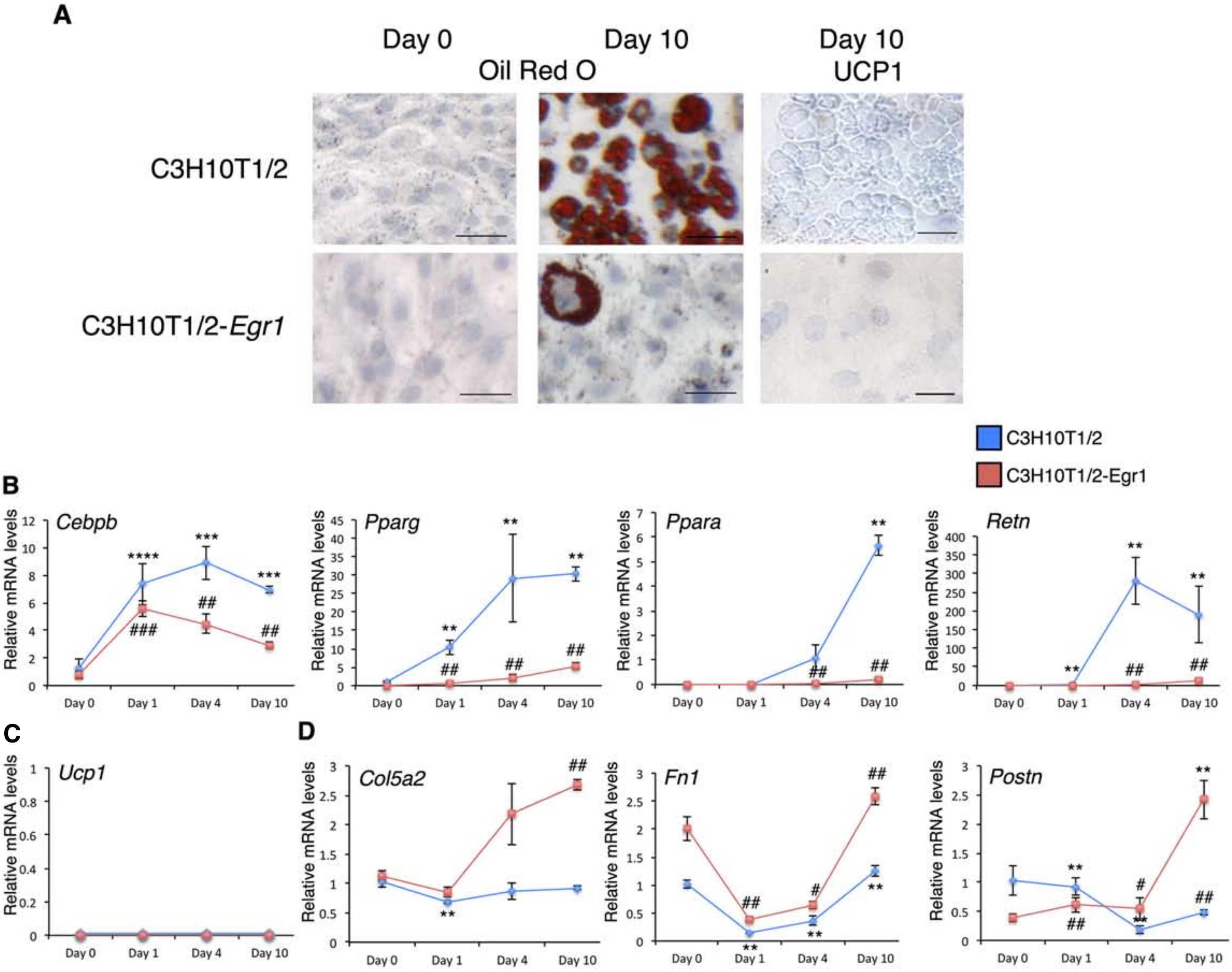
acH4
meH3
Input (dil 4)
Cebpb qPCR amplicons


A
Day 0
Day 10
Oil Red O
Day 10
UCP1
C3H10T1/2
C3H10T1/2-Egr1
C3H10T1/2
C3H10T1/2-Egr1
B
Cebpb
Pparg
Ppara
Retn
Relative mRNA levels
Day 0
Day 1
Day 4
Day 10
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##
##
C
Ucp1
D
Col5a2
Fn1
Postn
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For RT-qPCR analysis		
Gene name	**Forward Primer**	**Reverse Primer**
Cebpb	5’- CGCCTTTAGACCCATGGAAG	5’- AGGCAGTCGGGCTCGTAGTAG
Ppara	5’-AACATCGAGTGTCGAATATGTGG	5’- CCGAATAGTTCGCCGAAAGAA
Pparg	5’- TCGGTGATGCACTGCCTATG	5’- GAGAGGTCCACAGAGCTGATT
Ppargc1a	5’- TGGACGGAAGCAATTTTTCA	5’- TTACCTGCGCAAGCTTCTCT
Dio2	5’- CTTCTCTACCACCACCTTC	5’- CATCTTCACCCAGTTTAACC
Pank1	5’- GTTCGCCCAGCATGATTCTC	5’- CTTAACCAGGGTTCCACCGAT
Cidea	5’- ACTTCCTCGGCTGTCTCAATGTCA	5’- TCAGCAGATTCCTTAACACGGCCT
Ucp1	5’- GGGCATTCAGAGGCAAATCAGCTT	5’- ACACTGCCACACCTCCAGTCATTA
Cox8b	5’- AGCCAAAACTCCCACTTCC	5’- TCTCAGGGATGTGCAACTTC
Plin5	5’- CAGAGCAAACACCGTACCCAG	5’- GGGATGGAAAGTAGGGCTAGG
Ogdh	5’- TATGGCCTACACGAGTCTGAC	5’- CCAGCCGACGGATGATCTCA
Sucla2	5’- ACCCTTTCGCTGCATGAATAC	5’- CTGTGCCTTTATCACAACATCCT
Col1a1	5’- TGGAGAGAGCATGACCGAT	5’- GAGCCCTCGCTTCCGTACT
Col5a2	5’- ACAGGTGAAGTGGGATTCTCA	5’- CCATAGCACCCATTGGACCA
Col14a1	5’- TGGAGTATTGGGAGGTTCAACT	5’- TGCCACTCTATTCTGGGGTCC
Fn1	5’- CACGTACCTCTTCAAAGTCTTTG	5’- GGATTGCTTTCCCTGCCCT

Postn	5’- TGGTATCAAGGTGCTATCTGCG	5’- AATGCCCAGCGTGCCATAAA
Dcn	5’- CTATGTGCCCCTACCGATGC	5’- CAGAACATGCACCACTCGAAG
Mmp2	5’- CAAGTTCCCCGGCGATGTC	5’- TTCTGGTCAAGGTCACCTGTC
Retn	5’- GCCATCGACAAGAAGATCAA	5’- CTTCCCTCTGGAGGAGACTG
ßactin	5’- GATCTGGCACCACACCTTCT	5’- GGGGTGTTGAAGGTCTCAAA
Rplp0	5’- ACCTCCTTCTTCCAGGCTTT	5’- CTCCCACCTTGTCTCCAGTC
For ChIP-qPCR analysis		
Promoter name	**Forward Primer**	**Reverse Primer**
Cebpb	5’- GAGGGAACTCAGAAGCAAAGT	5’- AGCCCTCCACCCTATGTAT
Ppargc1a	5’- GCCTATGAGATCCACGGAAAG	5’- GTCTCCTTGGCAGTAGAGAATG
Ucp1	5’- TGTGGCCAGGGCTTTGGGAGT	5’- AGATTGCCCGGCACTTCTGCG
Gapdh	5’- CAGGAGCCCAGGGAAGATACAAATA	5’- ACGCATACACATATACAACCAGTCA

Supplementary Figure legends

Supplementary Figure 1. Cell proliferation in *Egr1*$^{+/+}$ and *Egr1*$^{-/-}$ mice. SC-WATs of 1-month-old (A,B,C) and 4-months-old (D,E) *Egr1*$^{+/+}$ and *Egr1*$^{-/-}$ mice were sectioned transversely and immuno-stained with KI67 (red). Nuclei were visualized with DAPI (blue). Individual channel or merged channels are indicated in each panel. (**A**) Ki67+ cells were visualized in vessels of SC-WATs of 1-month-old *Egr1*$^{+/+}$ mice. Ki67+ cells were barely observed in SC-WATs of 1 and 4 month *Egr1*$^{+/+}$ mice, as in SC-WATs of 1 and 4-month-old *Egr1*$^{-/-}$ mice. These results indicate that proliferation is not modified in SC-WATs of *Egr1*$^{-/-}$ mice at 1 and 4 months of age compared to control mice. Scale bars in A,B,C and D, 50 μm.

Supplementary Figure 2. SC-WAT browning in heterozygous *Egr1*$^{+/-}$ mice. (**A**) SC-WATs of 4-month-old *Egr1*$^{+/+}$, *Egr1*$^{+/-}$ and *Egr1*$^{-/-}$ mice were sectioned and immuno-stained with UCP1 antibody. Nuclei were visualized with DAPI. Phase, individual or merged channels are indicated in each panels. *Egr1*$^{+/-}$ mice exhibit an intermediate browning of their SC-WAT compared to *Egr1*$^{+/+}$ and *Egr1*$^{-/-}$ mice. (**B**) White and beige adipocyte number was counted in arbitrary unit areas of transverse sections of SC-WAT of 4 month-old Egr1$^{+/+}$ (N=13) and *Egr1*$^{+/-}$ (N=8) mice. Graphs show means of sections for each sample ± standard deviations. Asterisks indicate the p-values obtained using the Mann-Whitney test, comparing beige or white adipocyte number between mutant and control mice * $P<0.05$, **$P<0.01$. (**C**) Cell number in SC-WAT in *Egr1*$^{+/+}$ and *Egr1*$^{+/-}$ mice. Number of nuclei (DAPI-positive cells) was counted in arbitrary unit areas of transverse sections of SC-WAT of 4 month-old *Egr1*$^{+/+}$ (N=11) and *Egr1*$^{+/-}$ (N=8) mice. Graphs show means of sections for each sample ± standard deviations. Asterisks indicate the p-values obtained using the Mann-Whitney test, comparing beige or white adipocyte number between mutant and control mice * $P<0.05$.

Supplementary Figure 3. List of upregulated genes in the inguinal subcutaneous adipose tissue of 2-week-old *Egr1*$^{-/-}$ mice versus wild-type mice.

Supplementary Figure 4. Gene Ontology analysis of the upregulated genes in the inguinal subcutaneous adipose tissue of *Egr1*$^{+/+}$ versus *Egr1*$^{-/-}$ 2-week-old mice using the DAVID Bioinformatics Resources 6.8.

Supplementary Figure 5. List of downregulated genes in the inguinal subcutaneous adipose tissue of 2-week-old *Egr1*$^{-/-}$ mice versus wild-type mice.

Supplementary Figure 6. Gene Ontology analysis of downregulated genes in the inguinal subcutaneous adipose tissue of *Egr1*$^{+/+}$ versus *Egr1*$^{-/-}$ 2-week-old mice using the DAVID Bioinformatics Resources 6.8.

Supplementary Figure 7. Full scan of the gels used in Figure 3E. Boxed regions correspond to the bands used in the Figure 3E.

Supplementary Figure 8. *Egr1* gain-of-function decreases white adipose tissue differentiation in mouse mesenchymal stem cells. (**A**) C3H10T1/2 and C3H10T1/2-*Egr1* cells subjected to white adipocyte differentiation for 10 days were stained with Oil Red O and Hematoxilin/Eosin at Day 0 (confluence) and Day 10, or immuno-stained with UCP1 antibody and counterstained with Hematoxilin/Eosin at Day 10. UCP1 was never expressed in cells cultured in white adipocyte differentiation medium. Scale bars: Oil red O staining 50 μm, UCP1 immunostaining 25 μm. (**B-D**) RT-qPCR analysis of the expression levels for the generic adipocyte differentiation genes *Cebpb, Pparag, Ppara*, the white differentiation marker *Retn* (**B**), the thermogenic marker *Ucp1* (**C**), the extracellular matrix genes *Col5a2*, *Fn1* and *Postn* (**D**), in C3H10T1/2 and C3H10T1/2-*Egr1* cells subjected to 10 days of white adipocyte differentiation conditions. *Egr1* repressed the expression of *Cepbb*, *Pparg Ppara* and *Retn*, involved in the white adipocyte differentiation program and activated the expression of ECM genes, *Col5a2*, *Fn1* and *Postn* during white adipocyte differentiation. *Ucp1* expression was not detected in cells cultured in white differentiation conditions. For each time point, graphs show means ± standard deviations of 6 samples. The p values were calculated using the Mann-Withney test. The relative mRNA levels were calculated using the $2\wedge^{-\Delta\Delta\mathrm{Ct}}$ method. Asterisks indicate the p-values of gene expression levels in C3H10T1/2-*Egr1* cells or C3H10T1/2 cells compared to Day 0 (*Cebpb*, *Pparg*, *Col5a2*, *Fn1* and *Postn*) or from the first day of gene detection (*Ppara* and *Retn*), **P<0.01, ***P<0,001, ****P<0,0001. # indicate the p-values of gene expression levels in C3H10T1/2-*Egr1* versus C3H10T1/2 cells, for each time point,; # P<0.05, ## P<0.01, ### P<0.001

Supplementary Table 1. List of primers used for quantitative PCR.