Table S1: OXPHOS pathway gene list impacted by ATRA

Probe Name	Gene Symbol	Protein name	Fold change	P-value
A_51_P387334	1110020P15Rik	Cytochrome b-c1 complex subunit 9	1.19	0.04
A_52_P674489	Atp5a1	ATP synthase subunit alpha, mitochondrial	1.35	4.00 E-05
A_51_P207636	Atp5b	ATP synthase subunit beta, mitochondrial	1.45	1.9 E-05
A_51_P378087	Atp5c1	ATP synthase subunit gamma, mitochondrial	1.23	0.007
A_51_P302588	Atp5d	ATP synthase subunit delta, mitochondrial	1.31	1.26 E-04
A_52_P631514	Atp5f1	ATP synthase subunit b, mitochondrial	2.51	8.18 E-08
A_51_P294849	Atp5g3	ATP synthase lipid-binding protein, mitochondrial	1.58	3.14 E-04
A_51_P264186	Atp5h	ATP synthase subunit d, mitochondrial	1.55	6.94 E-05
A_51_P100866	Atp5j	ATP synthase-coupling factor 6, mitochondrial	1.44	1.40 E-05
A_51_P224216	Atp5j2	ATP synthase subunit f, mitochondrial	1.62	1.00 E-05
A_51_P301289	Atp5k	ATP synthase subunit e, mitochondrial	1.71	1.27 E-07
A_52_P75415	Atp5l	ATP synthase subunit g,	1.36	0.06

		mitochondrial		
A_51_P365521	Atp5o	ATP synthase subunit O, mitochondrial	1.32	8.79 E-05
A_51_P323880	COX2	Cytochrome c oxidase subunit 2	1.41	0.003
A_51_P335900	Cox5a	Cytochrome c oxidase subunit 5A, mitochondrial	1.56	1.48 E-07
A_51_P141123	Cox5b	Cytochrome c oxidase subunit 5B, mitochondrial	1.26	0.029
A_51_P311540	Cox6a1	Cytochrome c oxidase subunit 6A1, mitochondrial	1.80	3.59 E-04
A_51_P509997	Cox6a2	Cytochrome c oxidase subunit 6A2, mitochondrial	1.68	1.28 E-05
A_51_P448032	Cox6b1	Cytochrome c oxidase subunit 6B1	1.29	0.005
A_51_P343323	Cox6c	Cytochrome c oxidase subunit 6C	1.36	6.67 E-05
A_51_P148612	Cox7a1	Cytochrome c oxidase polypeptide 7A1, mitochondrial	1.54	4.24 E-04
A_52_P37894	Cox7a2	Cytochrome c oxidase polypeptide 7A2, mitochondrial	1.42	5.08 E-04
A_51_P160664	Cox7b	Cytochrome c oxidase subunit 7B, mitochondrial	1.63	3.81 E-06
A_52_P136153	Cox7c	Cytochrome c oxidase	1.59	2.36 E-09

		subunit 7C, mitochondrial		
A_52_P528726	Cox8a	Cytochrome c oxidase subunit 8A, mitochondrial	1.28	0.036
A_52_P423814	Cox8b	Cytochrome c oxidase subunit 8B, mitochondrial	2.84	3.97 E-08
A_51_P295610	Cyc1	Cytochrome c1, heme protein, mitochondrial	1.48	8.66 E-04
A_51_P163587	Cycs	Cytochrome c, somatic	3.63	3.36 E-08
A_51_P245525	ND4L	NADH dehydrogenase 4L, mitochondrial	1.40	3.22 E-04
A_51_P472405	Ndufa1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	1.66	1.48 E-07
A_51_P272123	Ndufa10	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	1.30	0.002
A_51_P279854	Ndufa11	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	1.68	2.96 E-07
A_51_P458540	Ndufa12	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	1.84	1.51 E-06
A_51_P384946	Ndufa2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	1.60	1.64 E-06

A_51_P431772	Ndufa3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	2.21	1.50 E-10
A_52_P552832	Ndufa4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	2.04	8.63 E-09
A_51_P170156	Ndufa5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	1.46	3.22 E-05
A_52_P217474	Ndufa6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	1.75	1.25 E-07
A_51_P263756	Ndufa7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	1.32	8.40 E-04
A_51_P475502	Ndufa8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	1.31	3.57 E-05
A_51_P280492	Ndufa9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	1.55	7.77 E-06
A_51_P208801	Ndufab1	Acyl carrier protein, mitochondrial	1.42	0.003
A_51_P516615	Ndufb10	NADH dehydrogenase [ubiquinone] 1 beta	1.71	2.28 E-06

		subcomplex subunit 10		
A_51_P205573	Ndufb11	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	1.28	2.68 E-04
A_51_P361184	Ndufb2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial	1.20	0.007
A_51_P160744	Ndufb3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	1.52	5.46 E-06
A_51_P434269	Ndufb4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	1.33	1.56 E-04
A_51_P201904	Ndufb5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	1.21	0.02
A_52_P210338	Ndufb6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	1.56	2.12 E-05
A_51_P519276	Ndufb7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	1.28	0.006
A_51_P247873	Ndufb8	NADH dehydrogenase	1.63	1.78 E-05

		[ubiquinone] 1 beta subcomplex subunit mitochondrial		
A_51_P177552	Ndufb9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	1.44	0.001
A_52_P254795	Ndufc1	NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial	1.56	3.40 E-05
A_51_P357459	Ndufc2	NADH dehydrogenase [ubiquinone] 1 subunit C2	2.46	3.76 E-07
A_51_P379597	Ndufs1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	1.14	0.002
A_51_P393761	Ndufs2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	1.21	0.003
A_51_P395014	Ndufs3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	1.27	1.13 E-04
A_51_P388696	Ndufs4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	1.45	3.86 E-04
A_51_P214916	Ndufs5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	1.24	0.003

A_51_P335077	Ndufs6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	1.50	8.45 E-07
A_51_P364671	Ndufs7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1.90	3.21 E-07
A_51_P247441	Ndufs8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	1.78	7.02 E-05
A_51_P261470	Ndufv2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	1.72	1.44 E-06
A_52_P170054	Ndufv3	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	1.93	1.92 E-07
A_52_P458708	Sdha	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1.42	0.001
A_51_P234853	Sdhb	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.20	0.003
A_51_P260871	Sdhd	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial	1.42	2.62 E-06
A_51_P300143	Uqcr	Cytochrome b-c1 complex subunit 10	1.25	0.029

A_51_P109828	Uqcrc1	Cytochrome b-c1 complex subunit 1, mitochondrial	1.33	7.86 E-04
A_51_P128648	Uqcrc2	Cytochrome b-c1 complex subunit 2, mitochondrial	1.36	6.63 E-04
A_51_P361951	Uqcrfs1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	1.68	1.80 E-09
A_52_P541875	Uqcrh	Cytochrome b-c1 complex subunit 6, mitochondrial	1.88	1.82 E-07
A_52_P370484	Uqcrq	Cytochrome b-c1 complex subunit 8	1.83	4.21 E-05

Table S2: Gene expression in ATRA-treated 3T3-L1 adipocytes exposed to RAR antagonist AGN 193109

	-ATRA		**+ATRA**	
	vehicle	**AGN**	**vehicle**	**AGN**
Gene Name				
Ppargc1α	1.00 ± 0.04	1.11 ± 0.06	1.93 ± 0.26*	1.67 ± 0.20*
Ppargc1β	1.00 ± 0.04	1.09 ± 0.07	2.37 ± 0.12*	1.69 ± 0.18*$^{\#}$
Nrf2	1.00 ± 0.04	0.88 ± 0.03$^{\#}$	1.32 ± 0.05*	1.13 ± 0.08*$^{\#}$
Tfam	1.00 ± 0.07	0.75 ± 0.04$^{\#}$	1.06 ± 0.03	0.98 ± 0.03*
Pparα	1.00 ± 0.06	0.93 ± 0.10	2.07 ± 0.32*	2.26 ± 0.41*
Ucp1	0.16 ± 0.05	0.29 ± 0.10	1.00 ± 0.06*	0.52 ± 0.15$^{\#}$
Cyp26b1	1.00 ± 0.06	0.85 ± 0.16	218 ± 29*	93.5 ± 17*$^{\#}$
Aco	1.00 ± 0.04	0.92 ± 0.04	1.70 ± 0.07*	1.45 ± 0.08*$^{\#}$

Differentiated 3T3-L1 cells were pre-incubated with RAR antagonist (AGN 193109; 10 μM) for 1 hour and next treated with ATRA for 24 h (2 μM). Control cells received an equal volume of vehicle (DMSO + ethanol). Values of gene expression were normalized to the mean value in vehicle-treated control cells (equal to 1), except for UCP1 gene expression, which was normalized to the mean value in the ATRA-treated cells. Expression values between cells were compared by Student t-test; p-values < 0.05 (indicated by * for the effect of ATRA and $^{\#}$ for the effect of antagonist) were considered as significant.

Table S3: Gene expression in ATRA-treated 3T3-L1 adipocytes exposed to PPARδ antagonist GSK0660

	-ATRA		**+ATRA**	
	vehicle	**GSK**	**vehicle**	**GSK**
Gene Name				
Ppargc1α	1.00 ± 0.08	1.38 ± 0.10	2.90 ± 0.67*	1.82 ± 0.34
Ppargc1β	1.00 ± 0.06	1.33 ± 0.12	2.52 ± 0.24*	1.84 ± 0.18*
Nrf2	1.00 ± 0.04	1.05 ± 0.05	1.39 ± 0.12*	1.32 ± 0.15
Tfam	1.00 ± 0.15	0.98 ± 0.11	1.04 ± 0.04	1.06 ± 0.08
Pparα	1.00 ± 0.12	1.01 ± 0.10	3.52 ± 0.25*	3.55 ± 0.61*
Ucp1	0.37 ± 0.04	1.74 ± 0.23$^{\#}$	1.00 ± 0.12*	3.31 ± 0.98$^{\#}$
Cyp26b1	1.00 ± 0.13	2.62 ± 0.52	348 ± 25*	307 ± 25*
Aco	1.00 ± 0.04	1.28 ± 0.07	1.56 ± 0.12*	1.62 ± 0.16

Differentiated 3T3-L1 cells were pre-incubated with PPARδ antagonist (GSK0660; 10 μM) for 1 hour and next treated with ATRA for 24 h (2 μM). Control cells received an equal volume of vehicle (DMSO + ethanol). Values of gene expression were normalized to the mean value in vehicle-treated control cells (equal to 1), except for UCP1 gene expression, which was normalized to the mean value in the ATRA-treated cells. Expression values between cells were compared by Student t-test; p-values < 0.05 (indicated by * for the effect of ATRA and $^{\#}$ for the effect of antagonist) were considered as significant.