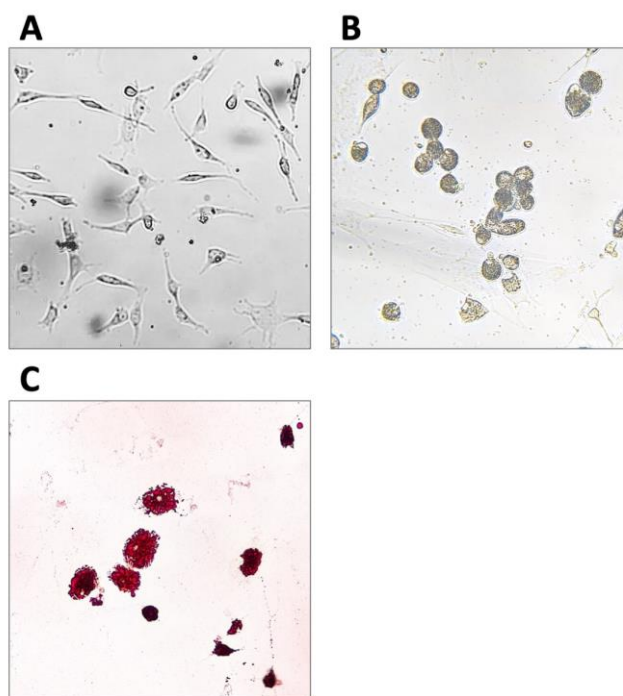
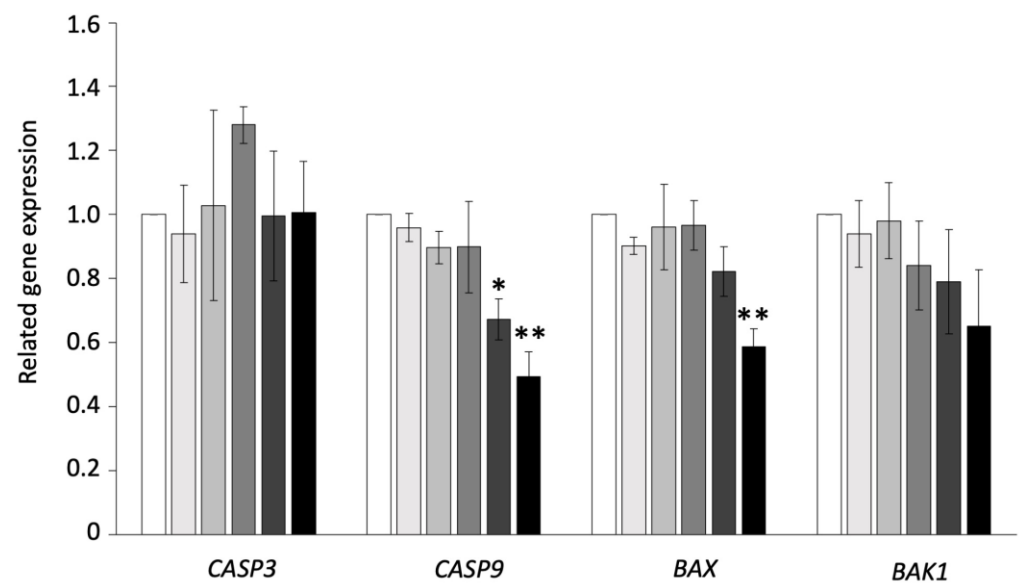


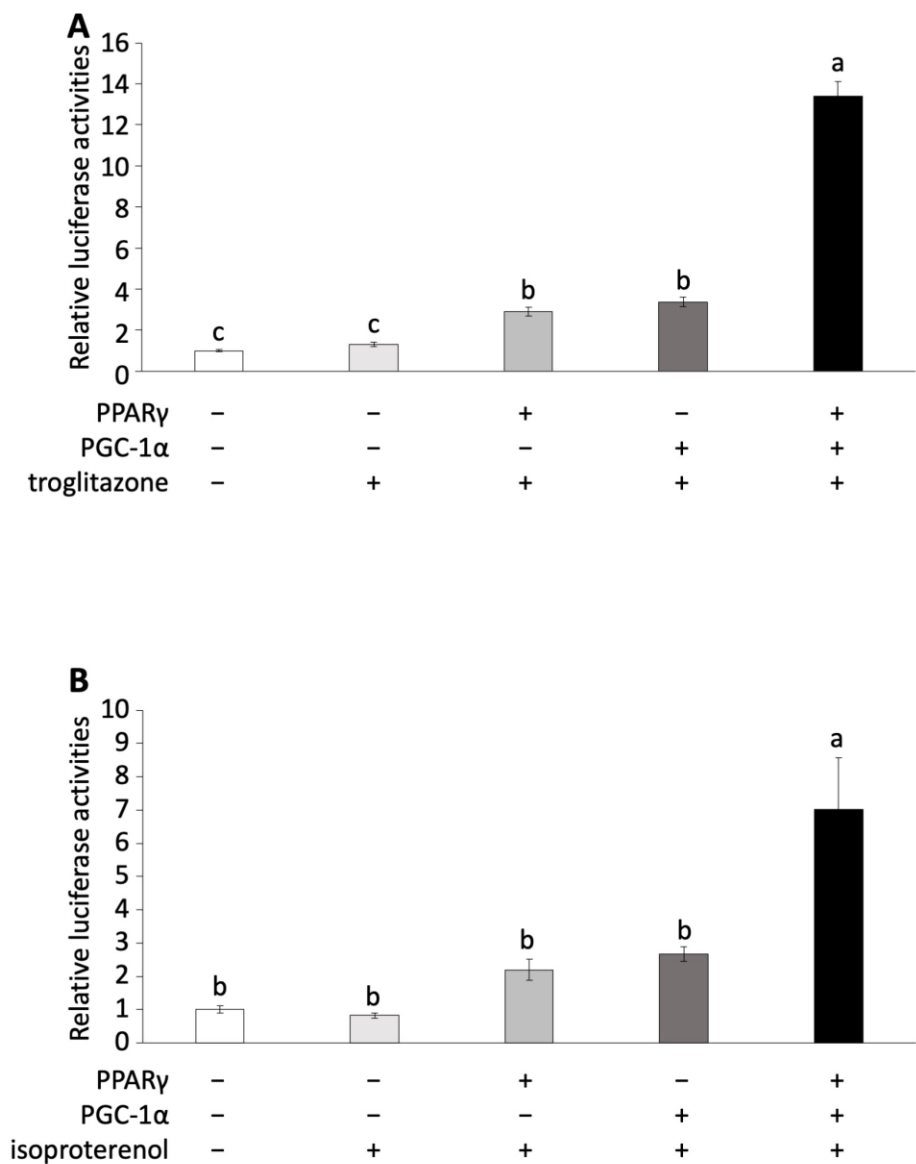
Supplementary Materials



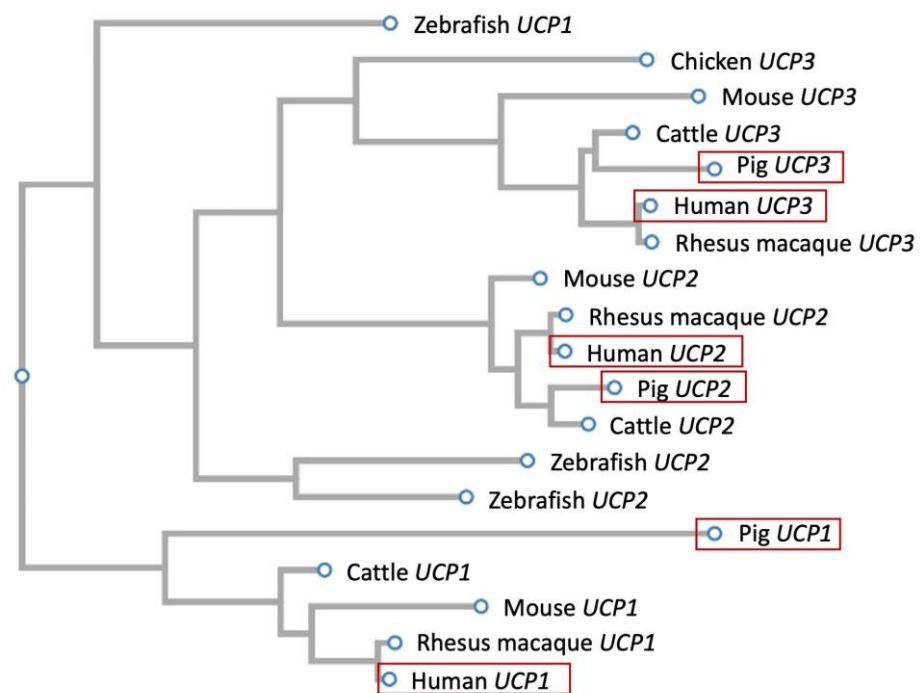
Supplementary Figure S1. Cell morphology changes demonstrating success of the pig adipocyte dedifferentiation-redifferentiation process prior to browning experiments. (A) Dedifferentiation of mature adipocytes to DFAT resulted in a fibroblast-like cell morphology. (B) Redifferentiation of DFAT to adipocytes resulted in a rounded cell morphology. (C) Staining of lipid using Oil Red O.



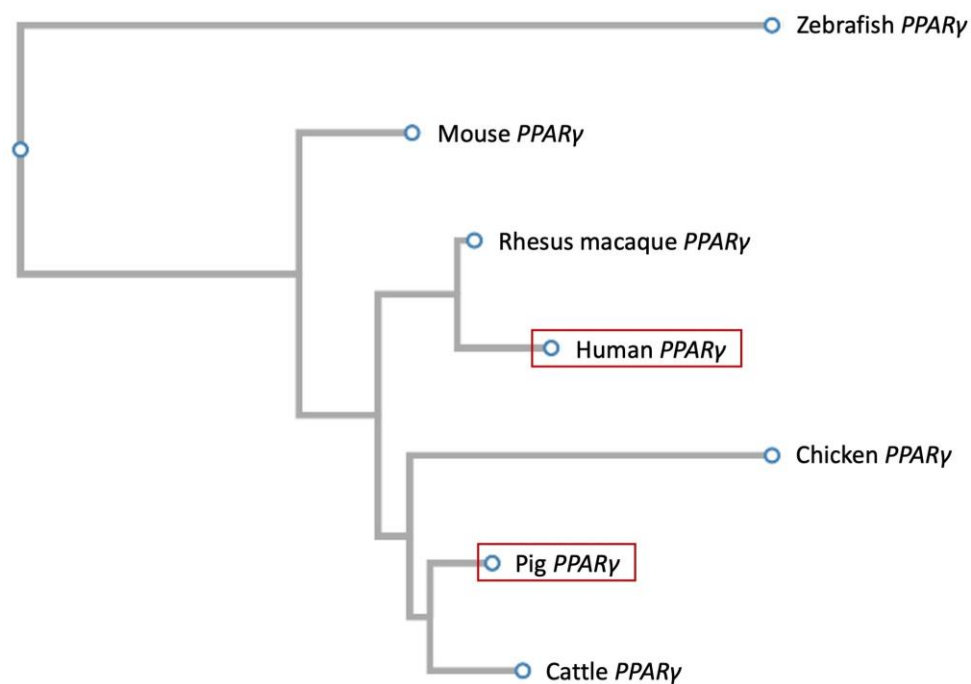
Supplementary Figure S2. Gene expressions related to apoptosis of pig redifferentiated adipocytes after isoproterenol administration. The values of the treatment and control groups were compared. The experiments were conducted 4 times. Each color indicates a concentration of isoproterenol: (□) control, (□) 0.01 μM , (□) 0.1 μM , (■) 1 μM , (■) 10 μM , and (■) 100 μM . The values are shown as mean \pm SEM. * $p < 0.05$ and ** $p < 0.01$.



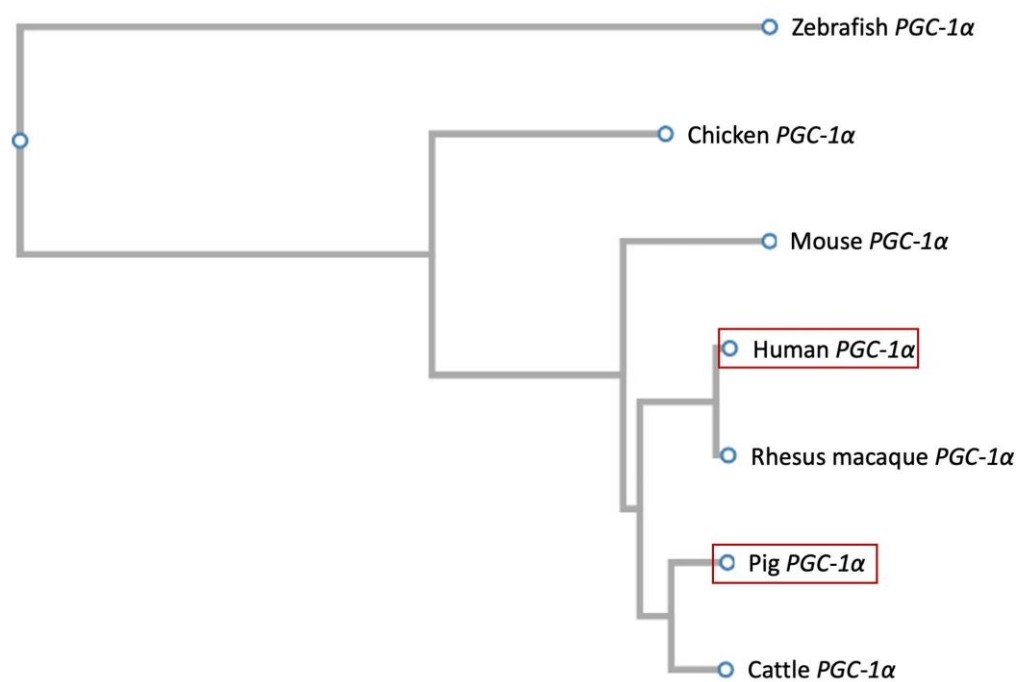
Supplementary Figure S3. Luciferase assay of pig UCP promoter region and alignment analysis. (A) Luciferase assay using Hela cells transfected with *PPAR γ* or/and *PGC-1 α* with/without 5 μ M troglitazone. The experiments were conducted 4 times. (B) Luciferase assay using Hela cells transfected with *PPAR γ* or/and *PGC-1 α* with 1 μ M isoproterenol. The experiments were conducted thrice. The values are shown as mean \pm SEM. Significant differences are indicated by different signs.



Supplementary Figure S4. Tree diagram of UCP family mRNA sequences in vertebrates. The red-line boxes indicate pig and human genes.



Supplementary Figure S5. Tree diagram of *PPARγ* mRNA sequences in vertebrates. The redline boxes indicate pig and human genes.



Supplementary Figure S6. Tree diagram of *PGC-1α* mRNA sequences in vertebrates. The redline boxes indicate pig and human genes.

Supplementary Table S1. Primer pairs used in the analysis of gene expressions.

Gene		Primer	Product Length (bp)	Annealing Temperature (°C)	Accession Number
<i>PGC-1α</i>	F	CATGTGCAACCAGGACTCTG	133	60	NM_213963
	R	GCTGTCTGTATCCAAGTCGTTC			
<i>PPARγ</i>	F	AGGACTACCAAAGTGCCATCAAA	142	60	NM_214379
	R	GAGGCTTTATCCCCACAGACAC			
<i>UCP1</i>	F	GCAGGGCAGACAGGTAAGC	134	60	XM_021100543.1
	R	CAAATAGTCCCGCCAAACCA			
<i>UCP2</i>	F	CCTCAGTGTGAGACCTGACGAA	148	60	NM_214289
	R	CTGTGGCCTTGAATCCAACCA			
<i>UCP3</i>	F	ATTCCAGGCCAGCATAACACG	165	60	NM_214049
	R	GTCACCATCTCGGCACAGTT			
<i>CS</i>	F	GGCTGACCTTATACCTAAGGAGC	230	60	NM_214276.1
	R	GTTCTTCCCCACCCTTAGCC			
<i>CASP3</i>	F	TGTGGGATTGAGACGGACAG	131	60	NM_214131.1
	R	GATCCGTCCTTTGAATTTGCGCC			
<i>CASP9</i>	F	CCAGTGGACATTGGTTCTGGA	247	60	XM_003127618.4
	R	TGGCAGTCAGGTTGCACTTC			
<i>BAX</i>	F	GCCTCAGGATGCATCTACCAA	170	60	XM_003127290.5
	R	AGTTGAAGTTGCCGTCAGCA			
<i>BAK1</i>	F	CTAGAACCTAGCAGCACCATGG	156	60	XM_021098603.1
	R	GGAGGCGATCTTGGTGAAGTAC			
<i>ACTB</i>	F	AGATCAAGATCATCGCGCCTC	159	60	DQ845171.1
	R	AGTCCGCCTAGAAGCATTTC			

Supplementary Table S2. Alignment scores of thermogenesis genes among mammals.

	Pig Human	Pig Mouse	Pig Cattle	Human Mouse	Human Cattle	Mouse Cattle
<i>PPARγ</i>	85	84	86	84	78	76
<i>PGC-1α</i>	91	90	95	86	90	88
<i>UCP1</i>	30	29	33	70	80	72
<i>UCP2</i>	84	79	86	83	84	80
<i>UCP3</i>	73	52	82	68	86	76

Alignment scores were calculated using mRNA sequences of *PPAR γ* , *PGC-1 α* , *UCP1*, *UCP2*, and *UCP3* in pigs, humans, mice, and cattle. The heights of the alignment scores indicate the homology of mRNA between two species.

Supplementary Table S3. Alignment scores of the promoter regions in the UCP family among mammals.

	Pig Human	Pig Mouse	Pig Cattle	Human Mouse	Human Cattle	Mouse Cattle
<i>UCP1</i>	53	6	66	18	46	5
<i>UCP2</i>	5	3	5	22	53	3
<i>UCP3</i>	23	18	25	21	60	19

Alignment score calculations in the promoter region used the sequence of 1,000 bp upstream from the transcriptional start site in *UCP1*, *UCP2*, and *UCP3*.