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Supplemental Information

circFLT1 and lncCCPG1 Sponges miR-93 to Regulate the Proliferation and Differentiation of Adipocytes by Promoting lncSLC30A9 Expression

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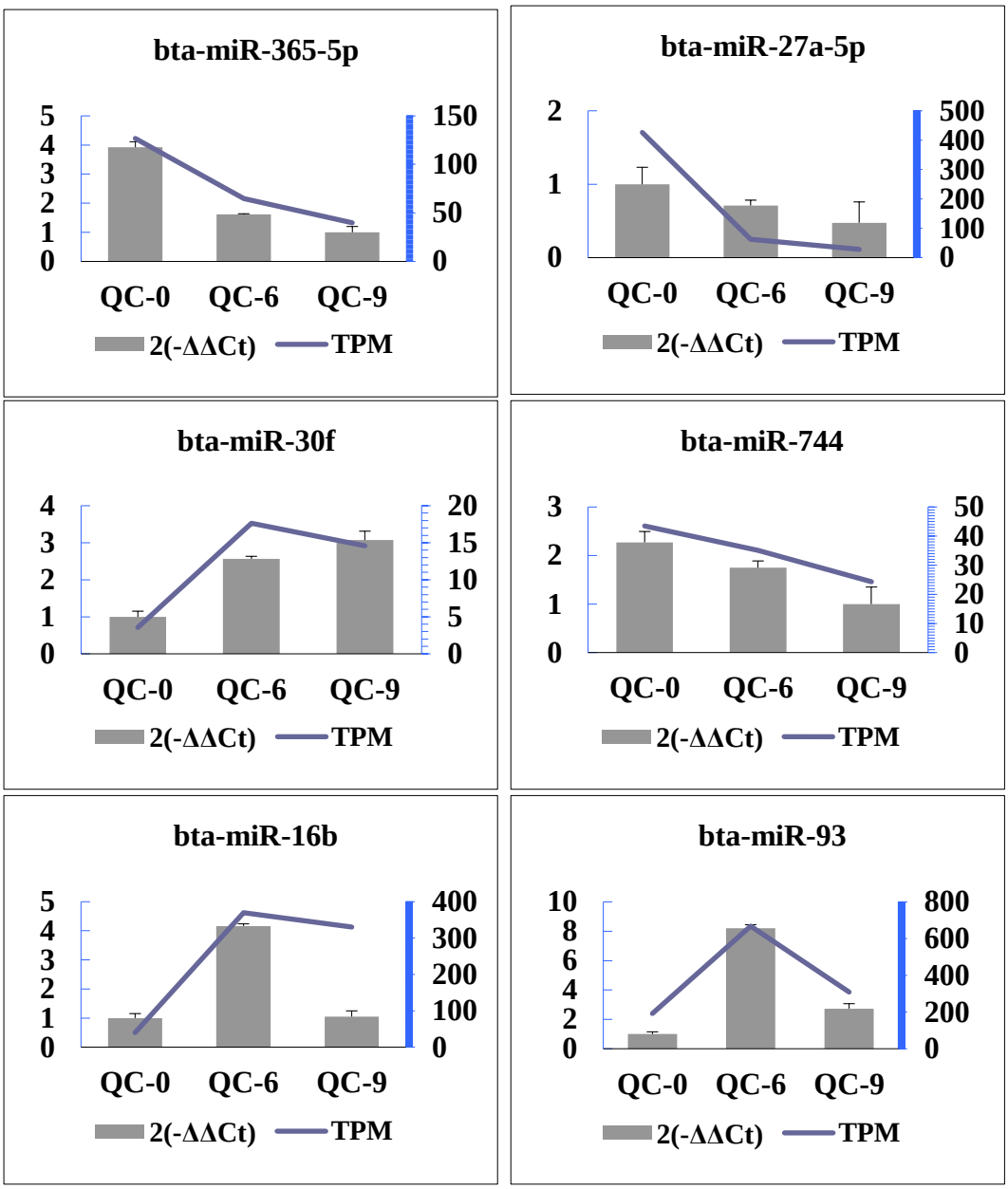
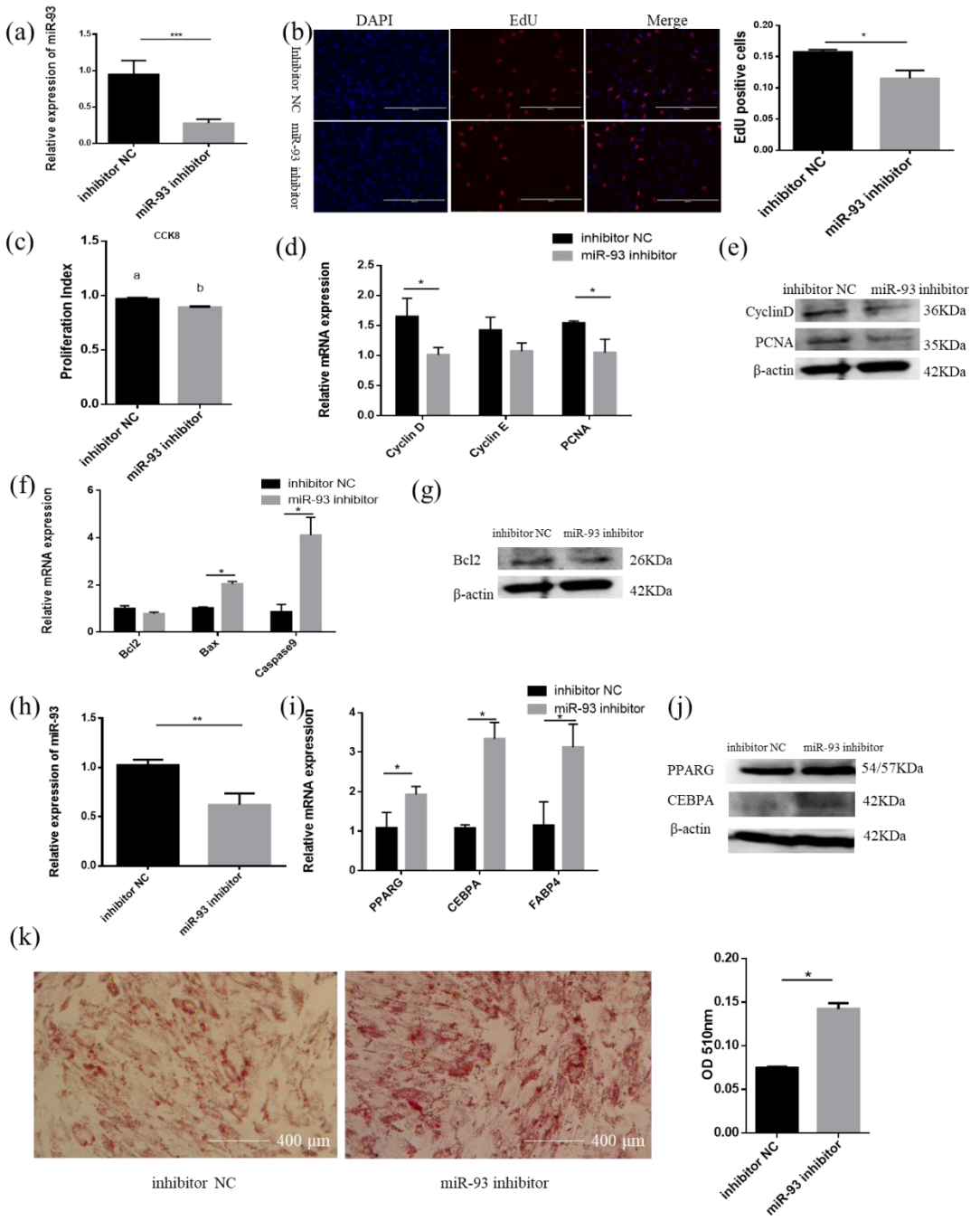
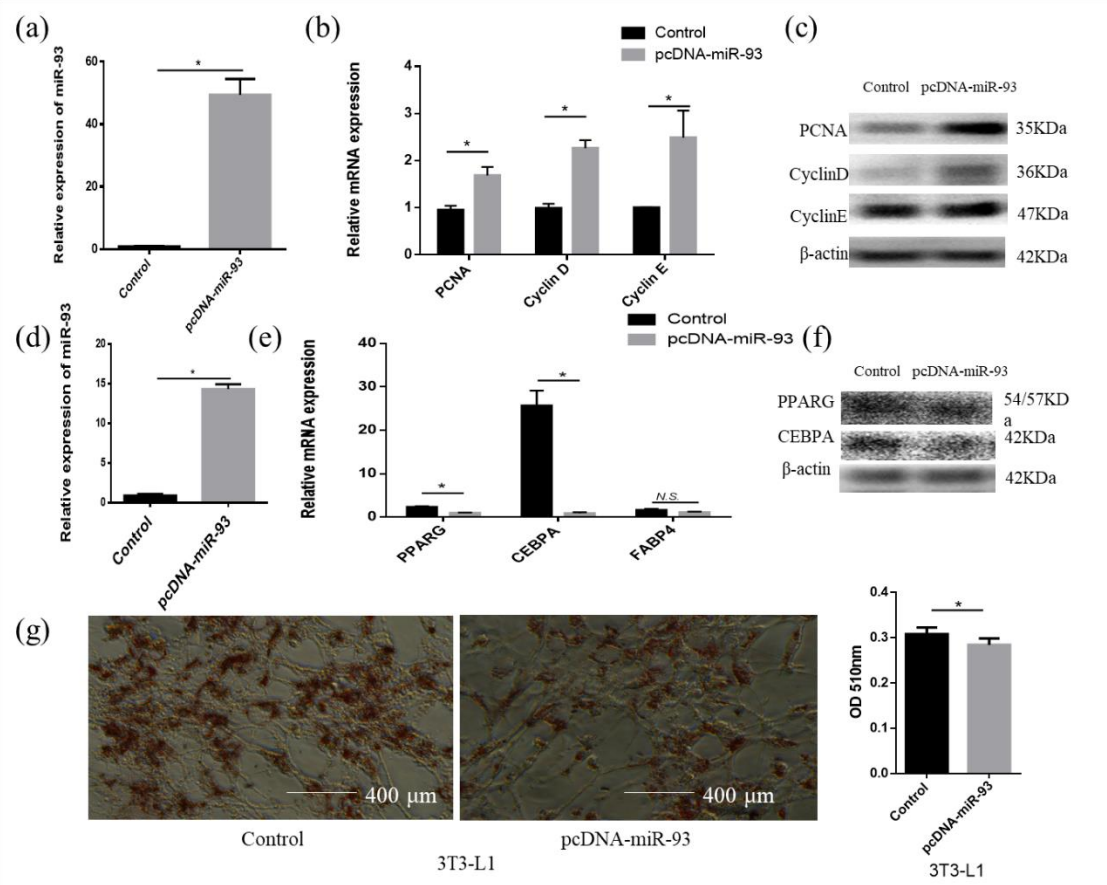


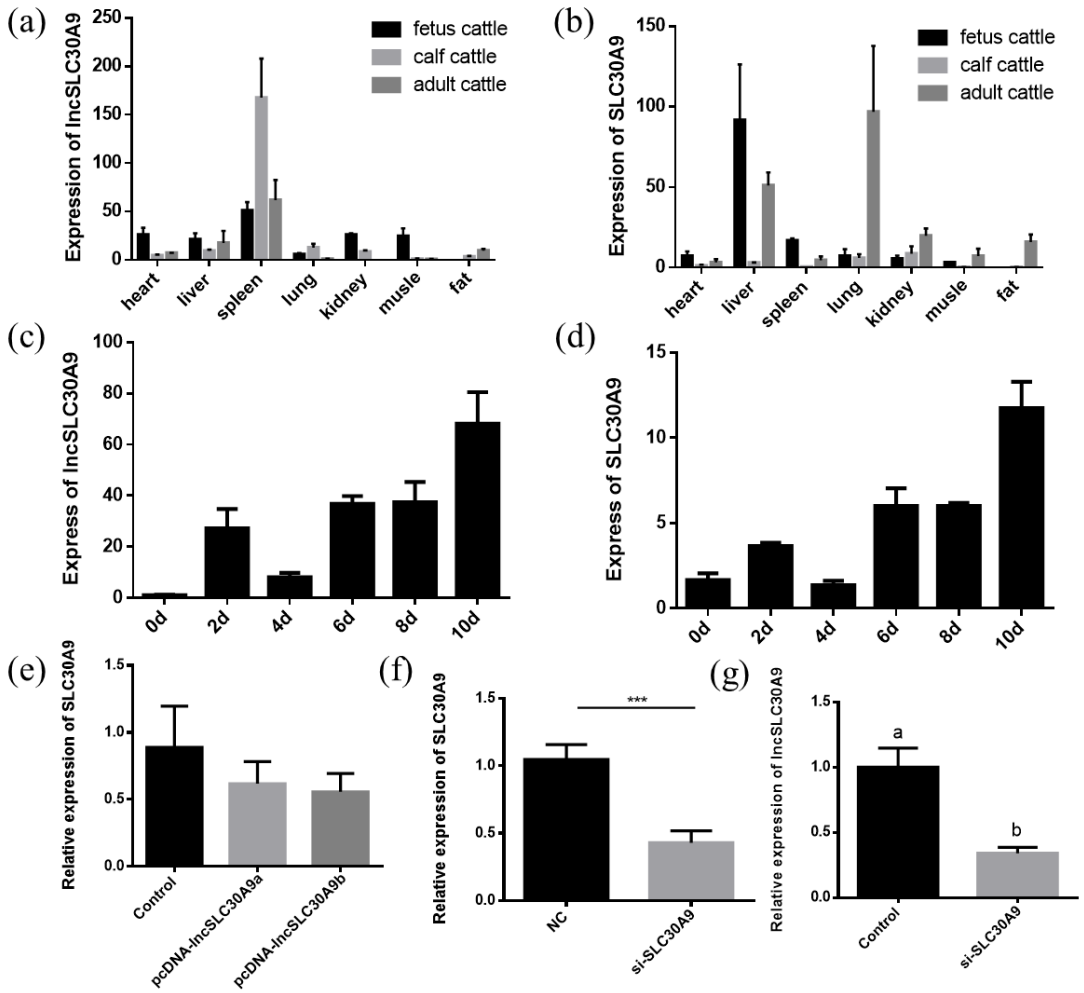
Supplementary Figure 1. RT-qPCR verified the sequencing results.



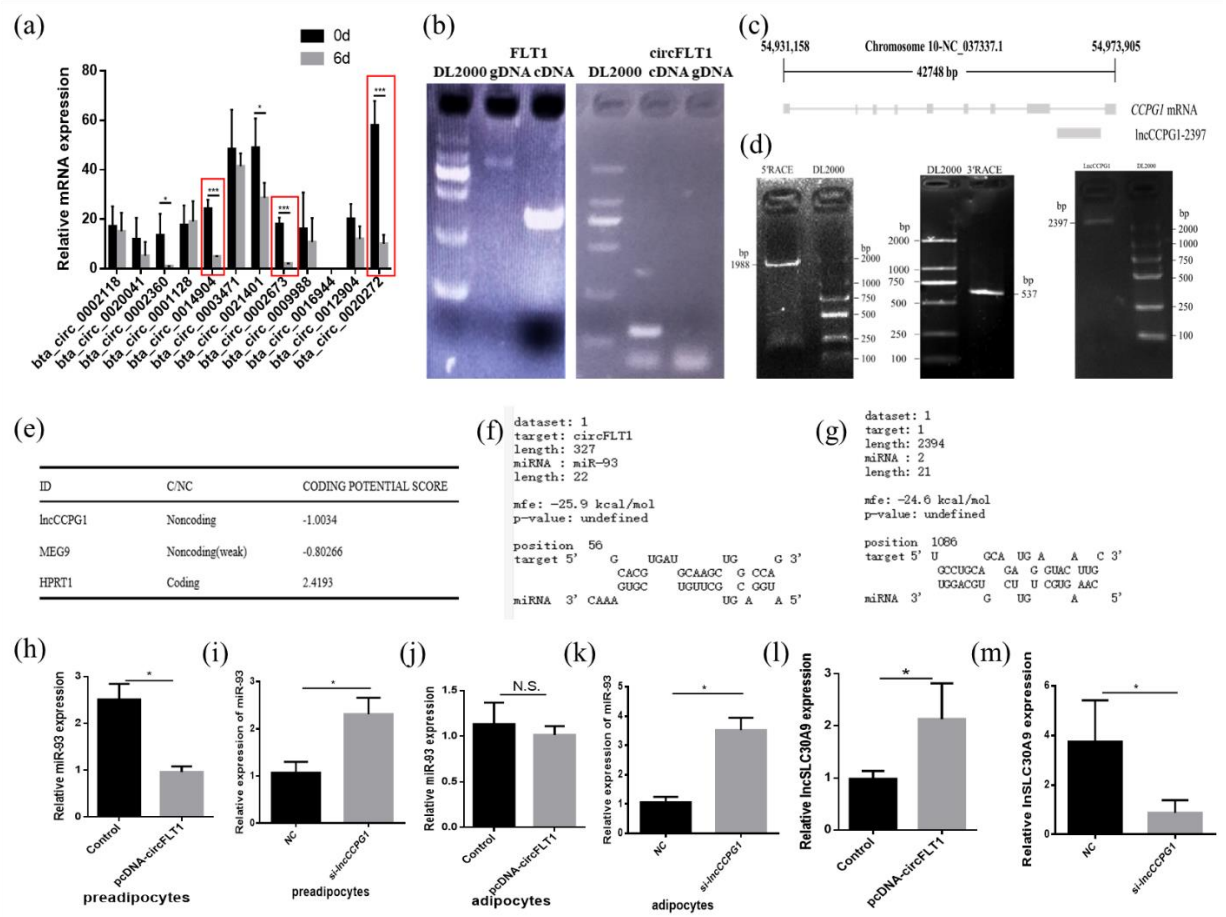
Supplementary Figure 2. Effect of miR-93 on proliferation, apoptosis, and differentiation of adipocytes. (a) Know down efficiency of miR-93; (b) Cell proliferation was measured with 5-ethynyl-20-deoxyuridine (EdU); (c) Cell proliferation index was measured by cell counting kit-8 (CCK-8) assay; (d)(e) The expression of proliferation marker genes were measured by real-time qPCR and western blotting. (f)(g) The expression of apoptosis marker genes were measured by real-time qPCR and western blotting. (h) Know down efficiency of miR-93;(i,j) The mRNA and protein expression of cell differentiation markers were measured by real-time qPCR and western blotting. (k) Oil red O staining was used to detect the production of lipid droplet. Values are mean ± SEM for three biological replicates, the different letters (a, b) means $P < 0.05$; *$P < 0.05$; **$P < 0.01$; ***$P < 0.01$.



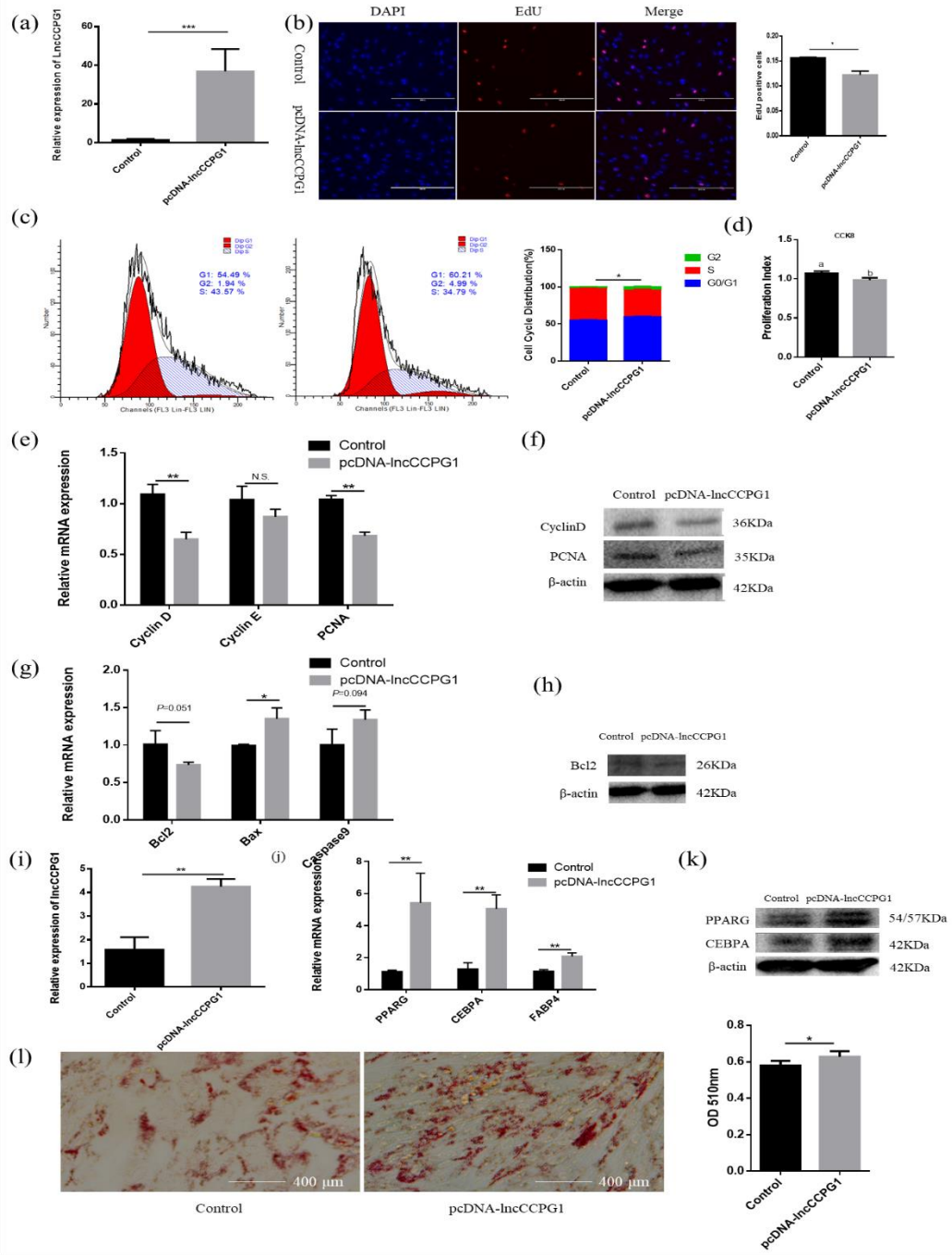
Supplementary Figure 3. Effect of miR-93 overexpression on 3T3-L1 cell proliferation and differentiation. (a) Overexpression efficiency of miR-93. (b,c) Expression of the proliferation marker genes were measured with real-time qPCR and western blotting. (d) Overexpression efficiency of miR-93. (e,f) The mRNA and protein expression of cell differentiation markers were measured with real-time qPCR and western blotting. (g) Oil Red O staining was used to detect the production of lipid droplet. Values are presented as mean ± SEM for three biological replicates, $*P < 0.05$.



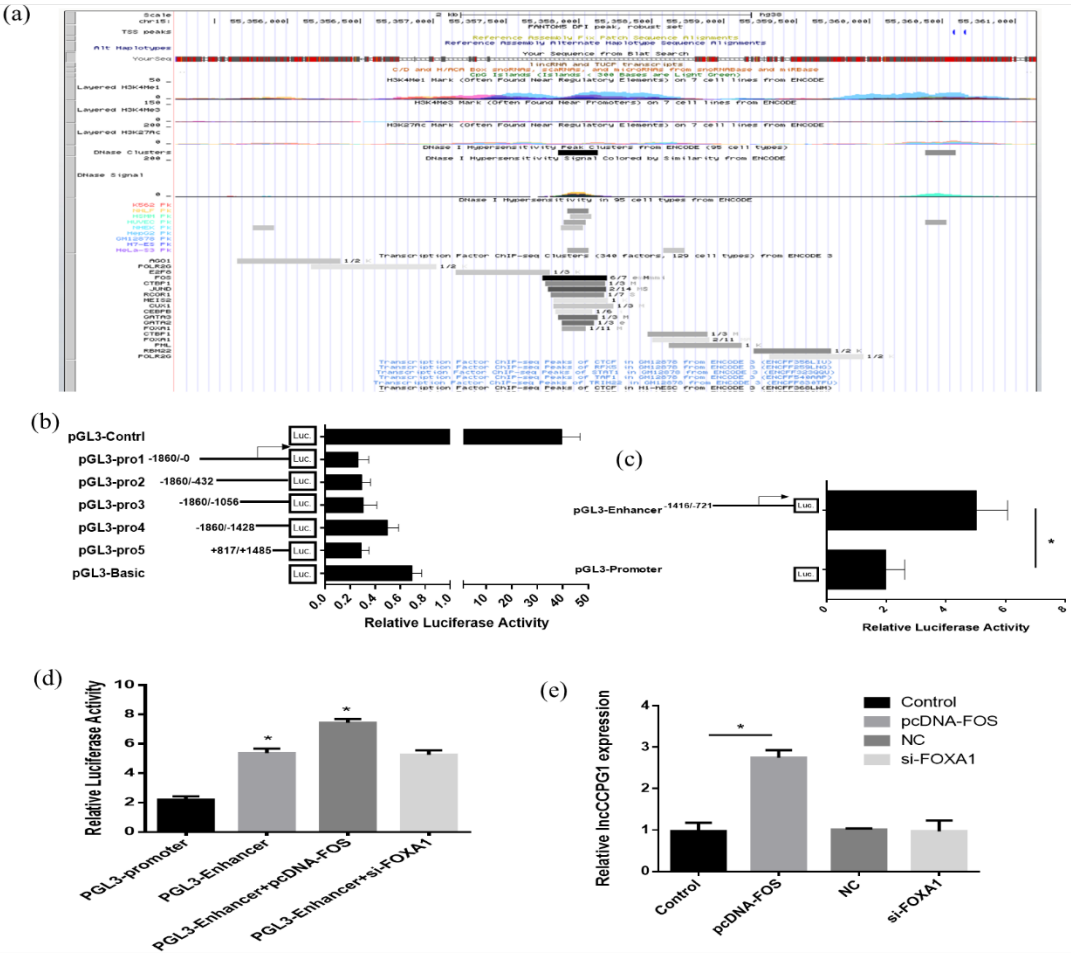
Supplementary Figure 4. Expression pattern of lncSLC30A9 and its maternal gene SLC30A9. (a) LncSLC30A9 tissue expression profile. (b) SLC30A9 tissue expression profile. (c) LncSLC30A9 was expressed at different time series. (d) SLC30A9 was expressed at different time series. (e) The influence of lncSLC30A9 on the expression of SLC30A9. (f) Know down efficiency of SLC30A9. (g) The influence of SLC30A9 on the expression of lncSLC30A9. Values are presented as mean ± SEM for three biological replicates. Different letters (a, b) indicate significant differences $P < 0.05$; ****$P < 0.001$*.



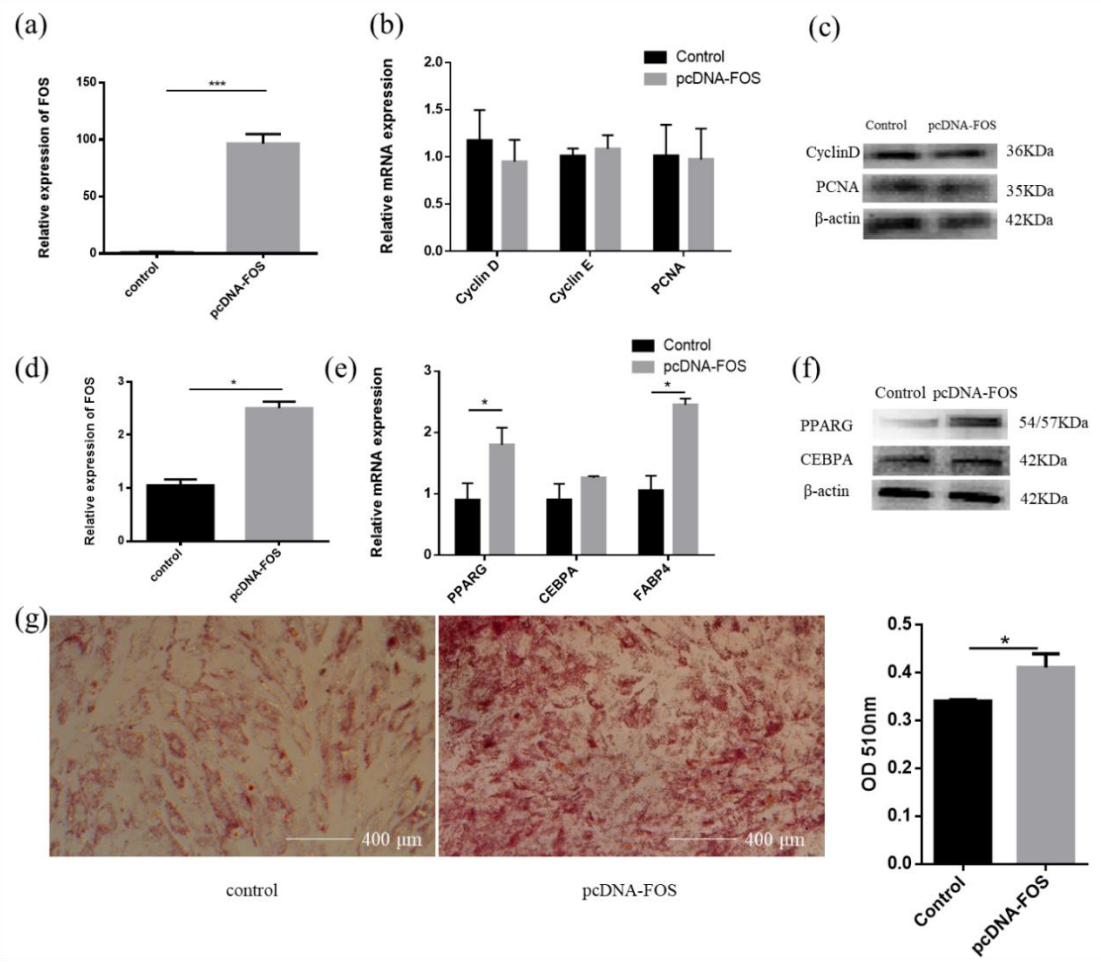
Supplementary Figure 5. circFLT1 and lncCCPG1 identification and interaction analysis. (a) circFLT1 screening. (b) Authenticity of circFLT1 verification. (c) Genomic structures of lncCCPG1. (d) The 5'RACE and 3'RACE analyses demonstrated the full length of lncCCPG1. (e) The RNA sequences of lncCCPG1 were processed by the Coding Potential Calculator (CPC) program and were predicted to be non-coding RNAs. (f,g) The RNAhybrid tool predicted the miR-93 binding sites at one distinct position in circFLT1 and lncCCPG1. (h-k) circFLT1 overexpression or lncCCPG1 knockdown effect the relative abundance of miR-93. (l,m) circFLT1 overexpression or lncCCPG1 knockdown effect the relative abundance of lncSLC30A9. Values are presented as mean ± SEM for three biological replicates, *$P < 0.05$; ***$P < 0.001$.



Supplementary Figure 6. Effect of lncCCPG1 on proliferation, apoptosis, and differentiation of adipocytes. (a) Overexpression efficiency of lncCCPG1; (b) Cell proliferation was measured with 5-ethynyl-20-deoxyuridine (EdU); (c) cell phase analyzed by flow cytometry; (d) Cell proliferation index was measured by cell counting kit-8 (CCK-8) assay; (e,f) The expression of proliferation marker genes were measured by real-time qPCR and western blotting. (g,h) The expression of apoptosis marker genes were measured by real-time qPCR and western blotting. (i) Overexpression efficiency of lncCCPG1; (j,k) The mRNA and protein expression of cell differentiation markers were measured by real-time qPCR and western blotting. (l) Oil red O staining was used to detect the production of lipid droplet. Values are mean ± SEM for three biological replicates, the different letters (a, b) means $P < 0.05$; *$P < 0.05$; **$P < 0.01$.



Supplementary Figure 7. Fluorescence activity analysis and transcription factor validation. (a) Sequence analysis by UCSC. (b) Promoter activity analysis. (c) Enhancer activity analysis. (d) Effects of overexpression of FOS and knock down of FOXA1 on enhancer activity. (e) Effects of overexpression of FOS and knockdown of FOXA1 on expression of lncCCPG1. Values are mean ± SEM for three biological replicates, $*P < 0.05$.



Supplementary Figure 8. Effect of *FOS* on proliferation and differentiation of adipocytes. (a) Overexpression efficiency of *FOS*; (b) (c) The expression of proliferation marker genes were measured by real-time qPCR and western blotting. (d) Overexpression efficiency of *FOS*; (e,f) The mRNA and protein expression of cell differentiation markers were measured by real-time qPCR and western blotting. (g) Oil red O staining was used to detect the production of lipid droplet. Values are mean ± SEM for three biological replicates, $*P < 0.05$; $***P < 0.001$.

Supplementary Table 1. Primers sequence for PCR and qRT-PCR
(submitted as a separate file)

Supplementary Table 2. The primary antibody and secondary antibody

Antibody name	**Purpose**	**Source**	**Catalogue Number**
Actin	primary antibody	Abbkine	WL01372
PPARG	primary antibody	Wanleibio	WL01800
CEBPA	primary antibody	Wanleibio	WL01899
PCNA	primary antibody	Wanleibio	WL02809
CyclinD1	primary antibody	Wanleibio	WL01435a
CyclinE	primary antibody	Wanleibio	WL01072
Bcl-2	primary antibody	Wanleibio	WL01556
AKT	primary antibody	Wanleibio	WL0003b
pAKT	primary antibody	Wanleibio	WLP001a
Goat Anti-Rabbit	secondary antibody	BOSTER	BA1041

LncRNA and circRNA sequence information

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FLT1-327nt

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Note: Red represents the joint sequence