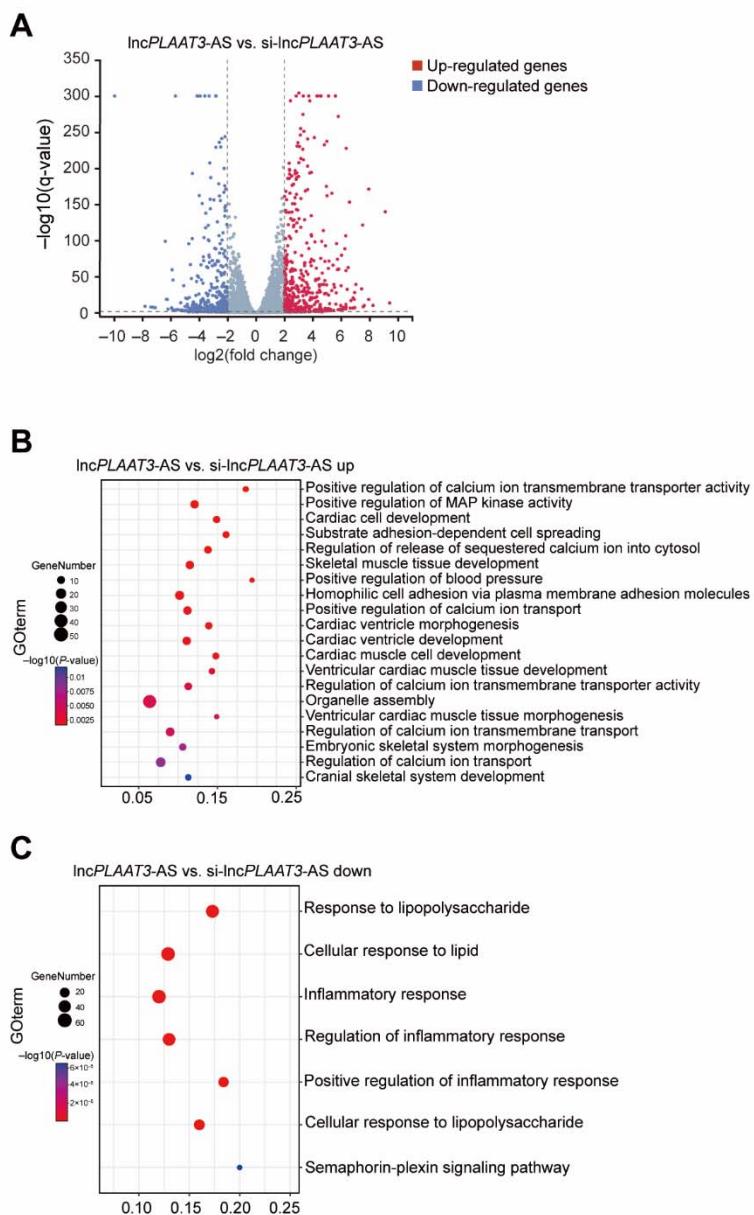
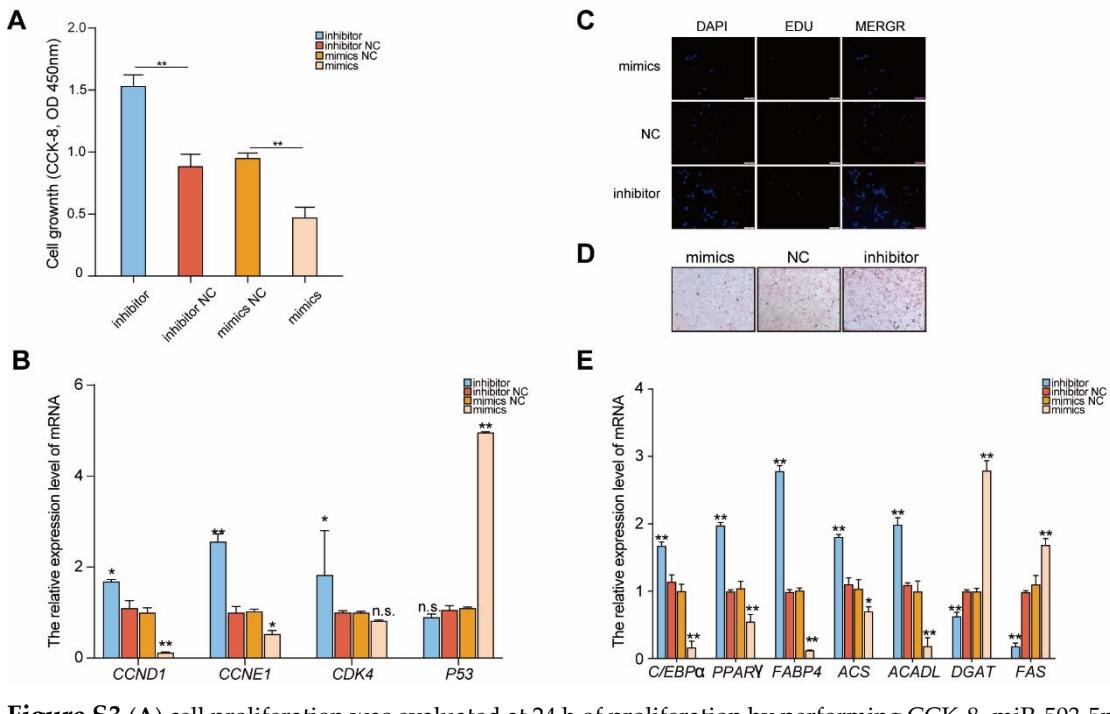


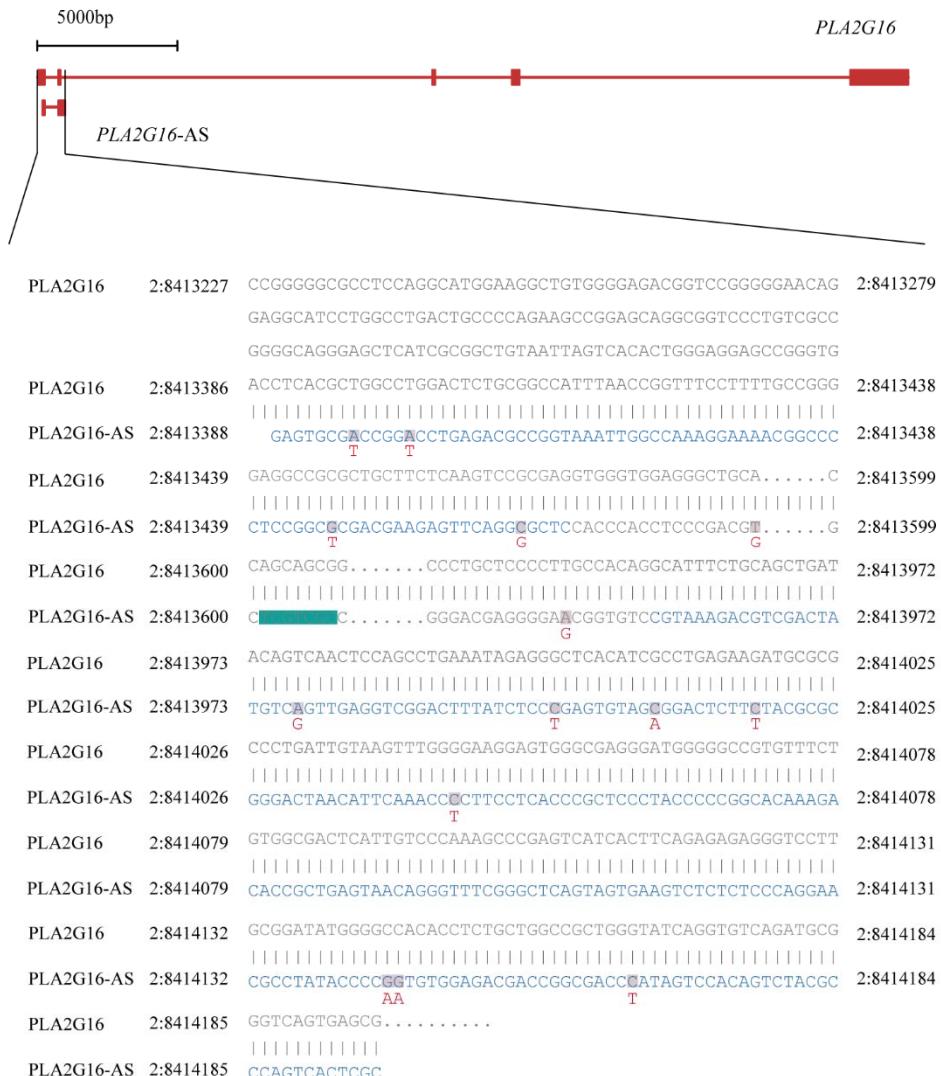
**Figure S1 (A)** mRNA sequencing data reads quality statistics; **(B)** Boxplot of mRNA sequencing expression in transfected cells.



**Figure S2** (A) Differentially expressed gene volcano plot; (B-C) The top 20 KEGG pathways of differential genes. Sequentially for IncPLAAT3-AS vs si-IncPLAAT3-AS differential genes with up-regulated expression, IncPLAAT3-AS vs si-IncPLAAT3-AS differential genes with down-regulated expression.



**Figure S3** (A) cell proliferation was evaluated at 24 h of proliferation by performing CCK-8, miR-503-5p mimic negative control for miR-503-5p mimic NC, miR-503-5p inhibitor negative control for miR-503-5p inhibitor NC; (B) qRT-PCR analysis of genes related with cell cycle; (C) Representative images illustrating the EdU of PK15 cells to transfected with miRNA-503-5p mimics or miRNA-503-5p inhibitor; (D) Cells were stained with oil red O, NC is negative control; (E) The expression levels of gene-related adipogenic, fatty acid oxidation and fatty acid transportation synthesis were measured by qRT-PCR. Scale bars 50 $\mu$ m. All results are presented as means  $\pm$  SEM ( $n = 3$ ). \*  $P < 0.05$ ; \*\*  $P < 0.01$ , n.s. no significant difference.



**Figure S4** The single nucleotide mutation site of lncPLAAT3-AS SNP, red is the mutated base, and the green area is the binding region of lncPLAAT3-AS and miR-503-5p. We used ISWINE database ([http://iswine.omics.pro/pigDNA/dna/index?access\\_token=null&lang=en\\_US](http://iswine.omics.pro/pigDNA/dna/index?access_token=null&lang=en_US)) to predict the biological effect of the significant SNPs on lncRNAs.