Supplementary Table 1. Characteristics of the four selected tagSNPs in *PCAT1*

TagSNPs	Chr	Position (hg19)	Allele (Ref > Alt)	ASN freq[a]	Location in PCAT1
rs16901904	8	128027502	T > C	0.21	intron
rs1902432	8	128024811	A > G	0.44	5'UTR
rs710886	8	128026860	C > T	0.50	intron
rs4871771	8	128029101	A > T	0.64	intron

[a] The allele frequency in Asian population were obtained from HaploReg v4.1(http://archive.broadinstitute.org/mammals/haploreg/haploreg.php).

Supplementary Figure legends

Supplementary Fig.1 DNA sequencing and transient transfection of *PCAT1* overexpression plasmid.

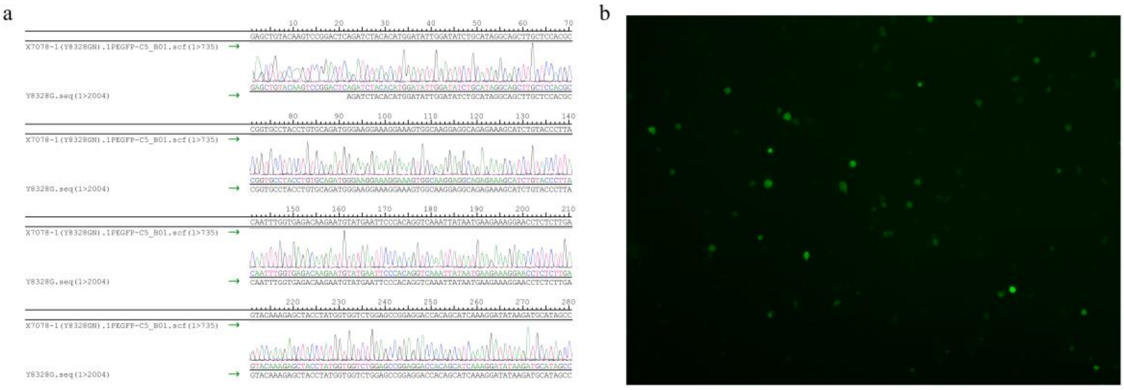
Supplementary Fig.2 Differentially expressed Genes between DU145 cells treated with *PCAT1* overexpression vector and NC vector.

(a) Heatmap shows that the gene expression pattern from DU145 cells transfected with *PCAT1* overexpression vector is significantly different from that from DU145 cell transfected with NC vector. The values are color coded using a green-red scale. Red indicates up-regulated genes and the green means down-regulated genes.

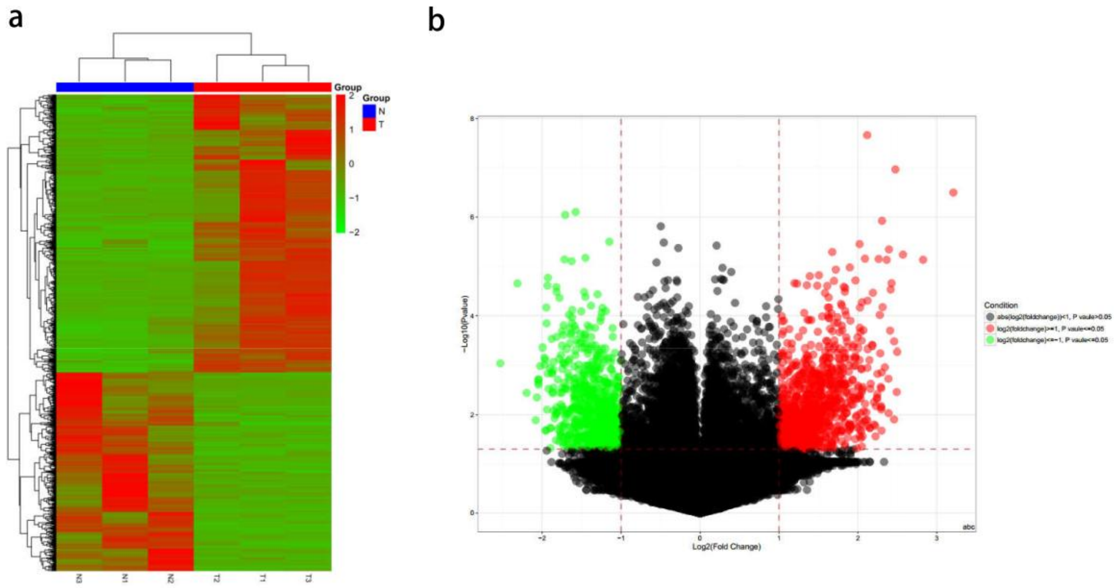
(b) Volcano plot shows the differentially expressed genes between DU145 cells transfected with overexpression of *PCAT1* or NC vector. The red and green dot means significantly up-regulated and down-regulated genes, respectively.

Supplementary Fig.3 KEGG pathway analysis. Significantly enriched pathways ($P < 0.05$) are presented. The size of each circle means the number of differentially expressed gene enriched in the corresponding pathway.

Supplementary Fig.1



Supplementary Fig.2



Supplementary Fig.3