**Supplementary materials:**

**Supplementary Table 1 The RT-PCR primer sequences and target sequences of siLPGAT1**

|  |  |  |  |
| --- | --- | --- | --- |
|  | Name | Sequence | Product Size |
| RT-PCR | LPGAT1 Forward | AGCGGTTCTGGTATATCGAAGG | 161 bp |
| LPGAT1 Reverse | TCCTGTTGCCTGATGATTCAC |
| CRLS1 Forward | AGCAGTCCAGTTAATCTTGGTG | 148 bp |
| CRLS1 Reverse | AGTCTTCCGGCCATAATGATAGT |
| LPCAT1 Forward | TTACCTTCAAACCTGGTGCATT | 131 bp |
| LPCAT1 Reverse | CGTGAGCCACAGGATTTCC |
| LPCAT4 Forward | GGCCTTTATCGTCCTCTTTCTC | 93 bp |
| LPCAT4 Reverse | CATCCTGTAATTGGCTCCTGAAG |
| LCLAT1 Forward | AACCATCGGACAAGAATGGAC | 108 bp |
| LCLAT1 Reverse | AGGAACACCTTTGAGACTCGC |
| GPAM Forward | GAGATGTGCATAAGGGCATGT | 77 bp |
| GPAM Reverse | AATTGCCTCTTGTACTCTACTGC |
| GAPDH Forward | AGAAGGCTGGGGCTCATTTG | 258 bp |
| GAPDH Reverse | AGGGGCCATCCACAGTCTTC |
| Knockdown | siLPGAT1-1 sense | GUUCAUGGAGACUUCUUUAUATT |  |
| siLPGAT1-1 antisense | UAUAAAGAAGUCUCCAUGAACTT |  |
| siLPGAT1-2 sense | GCGAGAAACAAGUCAGGCAUUTT |  |
| siLPGAT1-2 antisense | AAUGCCUGACUUGUUUCUCGCTT |  |
| siLPGAT1-3 sense | CCUUACCACUUGGCUCUAUTT |  |
| siLPGAT1-3 antisense | AUAGAGCCAAGUGGUAAGGTC |  |

**Supplementary Table 2 univariate cox analyses**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **ID** | **HR** | **HR.95L** | **HR.95H** | **P value** |
| **Age** | 1.012414 | 0.99575 | 1.029357 | 0.145103174 |
| **Gender** | 1.08451 | 0.78743 | 1.493671 | 0.61937912 |
| **Stage** | 1.655573 | 1.426762 | 1.921079 | 3.07E-11 |
| **T** | 1.535725 | 1.25942 | 1.872647 | 2.24E-05 |
| **N** | 1.699193 | 1.419914 | 2.033402 | 7.17E-09 |
| **LPGAT1** | 1.028699 | 1.007628 | 1.05021 | 0.007370464 |

**Supplementary Table 3 multivariate cox analyses**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **ID** | **HR** | **HR.95L** | **HR.95H** | **P value** |
| **Age** | 1.01648 | 0.999793 | 1.033445 | 0.052939 |
| **Gender** | 0.934506 | 0.672784 | 1.298041 | 0.686188 |
| **Stage** | 1.441411 | 1.160318 | 1.790599 | 0.000955 |
| **T** | 1.183391 | 0.960214 | 1.45844 | 0.114291 |
| **N** | 1.20727 | 0.947081 | 1.53894 | 0.128274 |
| **LPGAT1** | 1.026472 | 1.004216 | 1.049221 | 0.019485 |

**Supplementary Table 4 GO functional enrichment analyses results for the H1299 cells knockdown of LPGAT1**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Category** | **GOID** | **Description** | **BgRatio** | **pvalue** | **geneName** | **Count** |
| BP | GO:0046471 | phosphatidylglycerol metabolic process | 29/17639 | 9.65E-10 | LPGAT1/LPCAT4/LPCAT1/LCLAT1/CRLS1 | 5 |
| BP | GO:0036148 | phosphatidylglycerol acyl-chain remodeling | 18/17639 | 1.77E-08 | LPGAT1/LPCAT4/LPCAT1/CRLS1 | 4 |
| BP | GO:0006654 | phosphatidic acid biosynthetic process | 41/17639 | 5.72E-07 | LPCAT4/LPCAT1/LCLAT1/GPAM | 4 |
| BP | GO:0046473 | phosphatidic acid metabolic process | 42/17639 | 6.31E-07 | LPCAT4/LPCAT1/LCLAT1/GPAM | 4 |
| BP | GO:0008654 | phospholipid biosynthetic process | 285/17639 | 5.87E-06 | LPGAT1/LPCAT4/LPCAT1/LCLAT1/GPAM/CRLS1 | 6 |
| BP | GO:0046890 | regulation of lipid biosynthetic process | 179/17639 | 9.92E-06 | LPGAT1/LPCAT1/GPAM/CEACAM1/STAR | 5 |
| BP | GO:0006650 | glycerophospholipid metabolic process | 366/17639 | 2.43E-05 | LPGAT1/LPCAT4/LPCAT1/LCLAT1/GPAM/CRLS1 | 6 |
| BP | GO:0046474 | glycerophospholipid biosynthetic process | 242/17639 | 4.23E-05 | LPCAT4/LPCAT1/LCLAT1/GPAM/CRLS1 | 5 |
| BP | GO:0045017 | glycerolipid biosynthetic process | 274/17639 | 7.63E-05 | LPCAT4/LPCAT1/LCLAT1/GPAM/CRLS1 | 5 |
| BP | GO:0046486 | glycerolipid metabolic process | 458/17639 | 8.48E-05 | LPGAT1/LPCAT4/LPCAT1/LCLAT1/GPAM/CRLS1 | 6 |



**Supplementary Figure 1:** (A-B) Protein expression levels of LPGAT1 in the four cell lines (PC9, NCI-H23, A549, H1299) and the corresponding gray value intensity. (C) Real-time quantitative PCR was used to detect the mRNA expression of LPGAT1 knockdown in A549 cells, and then judge the interference effect of target sites. Dunnett t-test. 🞷🞷🞷*p*<0.001. (D-E) A549 cell proliferation was detected by Cell Counting Kit-8 assay, n=3. Two-way ANOVA. 🞷*p*<0.05, 🞷🞷🞷🞷*p*<0.0001. (F) Supplementary data of H1299 cell cycle assay. (G-H) The cell cycles in control and LPGAT1-knockdown groups were detected by flow cytometry, and the results were statistically analyzed, n=3. Unpaired two-tailed t-test; 🞷🞷🞷*p*<0.001(G1 phase), ns, *p*=0.3325(S phase), ns, *p*=0.5348(G2/M phase). (I) The A549 cell apoptosis in control and LPGAT1-knockdown groups was detected by flow cytometry, n=3. (J) Statistical results of A549 cell apoptosis assay. Unpaired two-tailed t-test. 🞷🞷🞷*p*<0.001.



**Supplementary Figure 2:** (A) Supplementary data of H1299 cell apoptosis assay. (B) H1299 cells infected by siRNA and the efficiencies were 93.6%(siCtrl) and 94.1%(siLPGAT1), respectively. (C) *In vivo* imaging of tumor-bearing mice in control and LPGAT1-knockdown groups, n=3. Scale bars: 1 cm. (D) Tumor size was measured in both control and LPGAT1 groups. Scale bars: 1 cm.