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| **Table S1.** Sequences of PCR primers used in this study. |
| Gene | Primer | Taregt Length |
| PLCE1 | For:5’-aggaagagagGTTGGGTATATTGATGGGGTTTAAT-3’Rev:5’-cagtaatacgactcactatagggagaaggctACCCCTAAAAACCATCCTTTCTAAC-3’ | 320bp |

“For”: Forward, “Rev”: Reverse.

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| **Table S2** Compare the CpG sites methylation of PLCE1 between ESCC and and NCAT tissues |
| CpG Site | ESCC | Normal | Z | *P* |
| N | 说明: 1 | N | 说明: 1 |
| CpG\_2 | 59 | 0.2025±0.1518 | 48 | 0.3238±0.1245 | -4.498 | **0.000\*\*\*** |
| CpG\_3 | 131 | 0.0950±0.0708 | 104 | 0.0897±0.0582 | -0.017 | 0.986 |
| CpG\_4 | 132 | 0.0651±0.0702 | 104 | 0.0599±0.0541 | -0.336 | 0.737 |
| CpG\_5.6 | 129 | 0.1184±0.0594 | 104 | 0.1389±0.0839 | -2.073 | **0.038\*** |
| CpG\_7.8 | 123 | 0.0807±0.0493 | 101 | 0.1052±0.0604 | -3.588 | **0.000\*\*\*** |
| CpG\_9.10 | 131 | 0.0720±0.0512 | 104 | 0.0937±0.0584 | -2.931 | **0.003\*\*** |

N stand for the number of analyzed CpG units; \* represents *P*<0.05，\*\* indicates *P*<0.01，\*\*\* depicts *P*<0.001.

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|  **Table S3** Correlation between DNA methylation andPLCE1 expression in ESCC tissues |
| CpG Site | N | PLCE1 methylation 说明: 1 | PLCE1 expression 说明: 1 | *r* | *P* |
| CpG\_2 | 59 | 0.2025±0.1518 | 6.0339±3.0341 | -0.267 | **0.041\*** |
| CpG\_5.6 | 129 | 0.1184±0.0594 | 6.1938±2.9582 | -0.216 | **0.003\*\*** |
| CpG\_7.8 | 123 | 0.0807±0.0493 | 6.2114±2.9456 | -0.118 | 0.193 |
| CpG\_9.10 | 131 | 0.0720±0.0512 | 6.1603±2.9478 | -0.140 | 0.112 |

Bivariate correlation analysis (two-sided), N stand for the number of analyzed CpG units; \* represents *P*< 0.05, \*\* indicates *P*< 0.01.

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| **Table S4** Correlation between the expression and promoter methylation of PLCE1 in ESCC tissues |
| PLCE1 Expression  | N | Amplicon Methylation | *χ2* | *P* |
| Hypomethylated | Methylated |
| High | 70 | 49(70.0%) | 21(30.0%) | 3.932 | **0.047\*** |
| Low | 62 | 33(53.2%) | 29(46.8%) |

N stand for the number of analyzed patients; \*\* represents *P*<0.001.