|  |  |  |  |
| --- | --- | --- | --- |
| **Supplementary Table S1**  Correlation between Rad50 expression and clinicopathological characteristics | | | |
|  | | | |
| **Clinicopathological Variables** | **Number** | **Rad50 expression**  **Low level High level** | ***P* value a** |
| **Age (years)** |  |  |  |
| <56 | 73 | 43 30 | 0.1230 |
| ≥56 | 78 | 56 22 |  |
| **Stage** |  |  |  |
| Early (stagesⅠ-Ⅱ) | 36 | 27 9 | 0.2282 |
| Advanced (stages Ⅲ-Ⅳ) | 115 | 72 43 |  |
| **Lymph nodes metastasis** |  |  |  |
| Negative | 25 | 21 4 | 0.0410 |
| Positive | 28 | 16 12 |  |
| **Omentum metastasis** | | | |
| Negative | 81 | 61 20 | 0.0365 |
| Positive | 70 | 41 29 |  |
| **CA 125 in serum (U/mL)** |  |  |  |
| <600 | 61 | 44 17 | 0.2217 |
| ≥600 | 90 | 55 35 |  |
| a Independent-samples t-test. | | | |

**Supplementary Table S2**

Primers and siRNA sequences used in this study

|  |  |  |
| --- | --- | --- |
| method | name | sequence(5 ′—3 ′) |
| qPCR | MYC-F | CTACCCTCTCAACGACAGCA- |
| qPCR | MYC-R | AGAGCAGAGAATCCGAGGAC |
| qPCR | RAD50-F | GCTTGTTGAACAGGGTCGTC |
| qPCR | RAD50-R | TCACTGAATGGTCCACGCTC |
| qPCR | NBS1-F | GTCTAGCAGCCCCGGTTAC |
| qPCR | NBS1-R | GTATGGTTCTCCTCCTGCCG |
| qPCR | MRE11-F | CAGAGGAGTCTGCTTCTGCC |
| qPCR | MRE11-R | ACCAGTGTCTGCTCTTCCTCT |
| qPCR | GAPDH-F | CAGAACATCATCCCTGCCTCTAC |
| qPCR | GAPDH-R | TTGAAGTCAGAGGAGACCACCTG |
| ChIP-PCR | RAD50-ChIP-F | AGCACCTAGCCCTCTGCTTC |
| ChIP-PCR | RAD50-ChIP -R | CAAAGCCGT-AGCCACAATG |
| si-RNA | si-MYC | CGUCCAAGCAGAGGAGCAA |
| si-RNA | si-CARD9-1 | GGGUAGAGCAAGACAAGUU |
| si-RNA | si-CARD9-2 | CCAACUAUGAAGAGUCCAU |
| si-RNA | si-Rad50 | CGCCUAAAGAACGACAUAGAA |
| si-RNA | negative control | UUCUCCGAACGUGUCACGU |