|  |
| --- |
| **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 |