Supplementary Fig. S1: The bioluminescence images of orthotopic tumors
Supplementary Fig. S2: CircME1 promotes ccRCC metastasis in vivo
Supplementary Fig. S3: circME1 enhances tumor growth and metastasis via ME1.

A

B

C

D

E

F

Vector+DMSO  circME1+DMSO  circME1+ME1 inhibitor

Vector+DMSO  circME1+DMSO  circME1+ME1 inhibitor

Vector+DMSO  circME1+DMSO  circME1+ME1 inhibitor
Supplementary Fig. S4: circME1 enhances sunitinib resistance and glycolysis of ccRCC cells via ME1.
**Supplementary Table 1**: Association of circME1 expression with clinicopathological information in ccRCC.

| Variable       | Total (%) | circME1 expression | P value |
|----------------|-----------|---------------------|---------|
|                |           | Low                 | High    |         |
|                |           | (Total,%)           | (%)     |         |
|                |           | 47 (33.6%)          | 49 (35.0%) | 0.716  |
|                |           | 23 (16.4%)          | 21 (15.0%) |         |
| Sex            | Male      | 96 (68.6%)          | 47 (33.6%) | 49 (35.0%) | 0.716 |
|                | Female    | 44 (31.4%)          | 23 (16.4%) | 21 (15.0%) |         |
| Age (Median, range) | 53 (18-80) | 50.5 (26-80) | 54.5 (18-80) | 0.403 |
| T stage        | 1         | 82 (58.6%)          | 47 (33.6%) | 35 (25.0%) | 0.029 |
|                | 2         | 25 (17.9%)          | 12 (8.6%) | 13 (9.3%) | 1/2 VS 3/4 |
|                | 3         | 26 (18.5%)          | 9 (6.4%) | 17 (12.1%) |         |
|                | 4         | 7 (5.0%)            | 2 (1.4%) | 5 (3.6%) |         |
| N stage        | 0         | 127 (90.7%)         | 67 (47.9%) | 60 (42.8%) | 0.042 |
|                | 1         | 13 (9.3%)           | 3 (2.1%) | 10 (7.2%) |         |
| M stage        | 0         | 129 (92.1%)         | 68 (48.6%) | 61 (43.5%) | 0.028 |
|                | 1         | 11 (7.9%)           | 2 (1.4%) | 9 (6.5%) |         |
| AJCC stage     | I         | 78 (55.7%)          | 45 (32.1%) | 33 (23.6%) | 0.006 |
|                | II        | 19 (13.6%)          | 11 (7.9%) | 8 (5.7%) | I/II VS III/IV |
|                | III       | 28 (20.0%)          | 11 (7.9%) | 17 (12.1%) |         |
|                | IV        | 15 (10.7%)          | 3 (2.1%) | 12 (8.6%) |         |
| Fuhrman grade  | 1         | 27 (19.3%)          | 12 (8.6%) | 15 (10.7%) | 0.025 |
|                | 2         | 82 (58.6%)          | 48 (34.3%) | 34 (24.3%) | 1/2 VS 3/4 |
|                | 3         | 25 (17.8%)          | 8 (5.7%) | 17 (12.1%) |         |
|                | 4         | 6 (4.3%)            | 2 (1.4%) | 4 (2.9%) |         |
**Supplementary Table 6:** Primers, shRNA sequences and U1 AMO sequence used in this study

| Primers      | Sequence                        |
|--------------|---------------------------------|
| circME1-F    | GGGAACCGAAAAATGAGGACTT          |
| circME1-R    | ACCTGGATCTCCTGACTGTT            |
| ME1-F        | TGGTGTTGCATTCTCAGAACA           |
| ME1-R        | GAACATTCTGCTTTGCTAGTGGAT        |
| ACTB-F       | CCTGGCAACCCAGCACAAT             |
| ACTB-R       | GGGCCGGAACCTCGTACA             |
| ChIP-A-F     | AATGGCTTCTTCAGCTAGGC           |
| ChIP-A-R     | TCTCCCTCAAGGCAACATT            |
| ChIP-B-F     | CAATGAAAGGTGTGATTTAACTTCA     |
| ChIP-B-R     | TGTTAACTGGGCCTTATCACAAAAGA    |
| ChIP-C-F     | GGAAGGCCCTGAAAGACTGCT          |
| ChIP-C-R     | TCAAGGTTAGGTTGGCAAA            |
| ChIP-D-F     | ATCCCCCTAGGTTGCTGAGG           |
| ChIP-D-R     | GGCATGCCCCTAAAACGCCAGT         |

| shRNA (target sequence) | Sequence                        |
|-------------------------|---------------------------------|
| sh-circME1#1            | AACCGAAAATGAGGACCTTG           |
| sh-circME1#2            | ACGGAAAAATGAGGACCTTG          |

| U1 AMO | Sequence                        |
|--------|---------------------------------|
|        | GGTATCTCCCTGCCAGGTAAGTAT        |