**Supplementary Table 1.** The characteristics of included 13 patients undergoing nephrectomy due to renal cancers.

|  |  |
| --- | --- |
| characteristics |  Values |
| Age (years), mean±SD (range) | 58.5±8.1 (45-69) |
| Gender (M/F) | 8/5 |
| Hydronephrosis degree\*, n, % |  |
| None or mild |  11(84.6%) |
| moderate | 2(15.4%) |
| Comorbidities, n (%) |  |
| Renal insufficiency |  1(7.6%) |
| Hypertension | 2(15.4%) |
| Diabetes mellitus |  3(23.0%) |
| Tumor size (cm), mean±SD | 5.1±0.9 (3.1-6.7) |

\* The Society of Fetal Urology grading system was used to determine the hydronephrosis degree, and those with severe hydronephrosis were routinely excluded in current study. M, male; F, female; SD, standard deviation.

**Supplementary Table 2.** Primer sequences for plasmid construction to overexpress *NEAT1* and *EGR1*

|  |  |  |
| --- | --- | --- |
| Gene | Forward primer 5′–3′ | Reverse primer 5′–3′ |
| *NEAT1*(NR\_028272.1) | TCCAACTTTGTGCCAACCGGTGGAGTTAGCGACAGGGAGG | CTGCCACGCATGCCACAGGAATTTCTAATGAGTTTAGAACT |
| *EGR1* | TCAATATATCAACCGGTATGGCCGCGGCCAAGGCCGAGATG | GACTGGACAGTCCACAGGAATTGCAAATTTCAATTGTCCT |

**Supplementary Table 3.** ShRNA sequences designed for *NEAT1* and *BMP2*

|  |  |  |
| --- | --- | --- |
| Gene |  | shRNA sequences |
| *NEAT1*(NR\_028272.1) | Len-sh1-*NEAT1* | Sense: 5’- -3’ CCGGGGGACAACATTGACCAACGCCTCGAGGCGTTGGTCAATGTTGTCCCTTTTTG |
| Anti-sense: 5’- -3’ AATTCAAAAAGGGACAACATTGACCAACGCCTCGAGGCGTTGGTCAATGTTGTCCC |
| Len-sh2-*NEAT1* | Sense: 5’- -3’ CCGGGGCAGGTCTAGTTTGGGCATCTCGAGATGCCCAAACTAGACCTGCCTTTTTG |
| Anti-sense: 5’- -3’ AATTCAAAAAGGCAGGTCTAGTTTGGGCATCTCGAGATGCCCAAACTAGACCTGCC |
| Len-sh3-*NEAT1* | Sense: 5’- -3’ CCGGGGAAGCTTGGCAAGGAGACCTCGAGGTCTCCTTGCCAAGCTTCCTTTTTG |
| Anti-sense: 5’- -3’ AATTCAAAAAGGAAGCTTGGCAAGGAGACCTCGAGGTCTCCTTGCCAAGCTTCC |
| *BMP2* | Len-sh1- *BMP2* | Sense: 5’- -3’ CCGGTCCAAGAGACATGTTAGGATACTCGAGTATCCTAACATGTCTCTTGGATTTTTG |
| Anti-sense: 5’- -3’ AATTCAAAAATCCAAGAGACATGTTAGGATACTCGAGTATCCTAACATGTCTCTTGGA |
| Len-sh2- *BMP2* | Sense: 5’- -3’ CCGGAAGGCCATTGCTAGTAACTTTCTCGAGAAAGTTACTAGCAATGGCCTTTTTTTG |
| Anti-sense: 5’- -3’ AATTCAAAAAAAGGCCATTGCTAGTAACTTTCTCGAGAAAGTTACTAGCAATGGCCTT |
| Len-sh3- *BMP2* | Sense: 5’- -3’ CCGGAAACGTCAAGCCAAACACAAACTCGAGTTTGTGTTTGGCTTGACGTTTTTTTTG |
| Anti-sense: 5’- -3’ AATTCAAAAAAAACGTCAAGCCAAACACAAACTCGAGTTTGTGTTTGGCTTGACGTTT |
| Len-sh-ctrl | Involved in the kit |

**Supplementary Table 4.** Sequences of Mimic and inhibitor for miRNAs

|  |  |
| --- | --- |
| Gene | Sequences 5′–3′ |
| MiR-129-5p-mimic | CUUUUUGCGGUCUGGGCUUGC |
| MiR-129-5p-inhibitor | GCAAGCCCAGACCGCAAAAAG |
| NC-mimic | Involved in the kit |
| NC-inhibitor | Involved in the kit |

**Supplementary Table 5.** Primer sequences for qRT-PCR

|  |  |  |
| --- | --- | --- |
| **Gene** | **Forward primer 5′–3′** | **Reverse primer 5′–3′** |
| *NEAT1*(NR\_028272.1) | GGCAGGTCTAGTTTGGGCAT | CCTCATCCCTCCCAGTACCA |
| *NEAT1*(NR\_131012.1) | CCTGTCTTGCACTGTGGACT | ACACGGCTACCACACAGATG |
| *RUNX2* | CACCATGTCAGCAAAACTTCTT | TCACGTCGCTCATTTTGC |
| *BMP2* | GTGGACAAGACTCGGGATGAAA | ATCACGTAATGCCTGCTGTG |
| *OCN* | CTTTGTGTCCAAGCAGGA | CTGAAAGCCGATGTGGTCAG |
| *EGR1* | TGCTAAAGGGAAAGGGGAA | TTGGGGAAGGGGAAGTG |
| *GAPDH* | AACGTGTCAGTGGTGGACCTG | AGTGGGTGTCGCTGTTGAAGT |
| miR-129-5p | CTTTTTGCGGTCTGGGCTTGC | Involved in the kit |
| miR-140-5p | GCGCAGTGGTTTTACCCTATGGTAG |
| miR-3187-3p | TATATATTGGCCATGGGGCTGCG |
| miR-541-3p | TGGTGGGCACAGAATCTGGAC |
| miR-576-5p | GCGCGATTCTAATTTCTCCACGTCTTT |
| miR-654-5p | TGGTGGGCCGCAGAACAT |
| *U6* | Involved in the kit |

**Supplementary Table 6.** The details of primary antibodies used in Western Blotting (WB)

|  |  |  |  |
| --- | --- | --- | --- |
| **Antibody** | **Calculated molecular weight** | **Dilution ratio** | **Company (Cat No.)** |
| GAPDH | 36Kd | 1:5000 | Proteintech, China(60004-1-Ig) |
| LaminA/C | 65/70Kd | 1:5000 | Proteintech, China(10298-1-AP) |
| OCN | 11Kd | 1:3000 | Abcam, UK (ab133612) |
| RUNX2 | 55-62Kd | 1:3000 | CST, USA (#12556) |
| BMP2 | 45Kd | 1:2000 | Servicebio, China(18933-1-AP) |
| EGR1 | 58Kd | 1:3000 | Abcam, UK (ab55160) |
| AGO2 | 100Kd | 1:4000 | Millipore, USA(cs204386) |

**Supplementary Table 7.** Primer sequences for CHIP-qPCR

|  |  |  |
| --- | --- | --- |
| **EGR1-bound sites (E-BS)** | **Forward primer 5′–3′** | **Reverse primer 5′–3′** |
| E-BS1 (192bp) | CCTTGTTTGCGGTGCAATGA | AGGCGAATTAGGCACTTGCT |
| E-BS2 (106bp) | GGGAAATAAGAGGCCAGACCC | TCCCTGCTCTCAAAGGAGAGAT |
| E-BS3 (245bp) | TACTCCAGTGCACCCCCAT | CGATGCGGAGCACCTACTG |
| Positive control (For *GAPDH*; 110bp) | Involved in the kit | Involved in the kit |

**Supplementary Table 8.** The transcription factors (TFs) binding to the promoter of *BMP2* predicted by FIMO software, JASPAR and HOCOMOCO datasets, and RNA-Protein Interaction Prediction (RPISeq; http://pridb.gdcb.iastate.edu/RPISeq/#) was used to predict whether these TFs bind to *NEAT1*.

|  |  |  |  |
| --- | --- | --- | --- |
| **TF** | **Prediction using RF (Random Forests) classifier** | **Prediction using SVM (Support Vector Machine) classifier** | **SUM** |
| EGR1 | 0.95 | 0.93 | 1.88 |
| POU2F1 | 0.95 | 0.92 | 1.87 |
| CTCF | 0.95 | 0.92 | 1.87 |
| SP3 | 0.95 | 0.91 | 1.86 |
| ZNF263 | 0.9 | 0.95 | 1.85 |
| POU1F1 | 0.95 | 0.9 | 1.85 |
| KLF5 | 0.9 | 0.93 | 1.83 |
| KLF9 | 0.9 | 0.92 | 1.82 |
| SP2 | 0.85 | 0.96 | 1.81 |
| RBPJ | 0.85 | 0.96 | 1.81 |
| POU2F2 | 0.9 | 0.91 | 1.81 |
| ZEB1 | 0.9 | 0.91 | 1.81 |
| SP1 | 0.9 | 0.89 | 1.79 |
| E2F1 | 0.8 | 0.96 | 1.76 |
| EBF1 | 0.85 | 0.91 | 1.76 |
| TFAP2A | 0.8 | 0.92 | 1.72 |
| CTCFL | 0.85 | 0.84 | 1.69 |
| TFAP2C | 0.75 | 0.93 | 1.68 |
| TBX21 | 0.85 | 0.81 | 1.66 |

**Supplementary Table 9.** The predicted sites of EGR1 binding to the promoter of *BMP2*.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strand** | **Score** | **P-Value** | **Q-Value** | **Matched\_Sequence** | **Motif\_Web** |
| + | 16.3462 | 1.72E-06 | 0.0232 | GCGCCGCCGCCGCC | http://jaspar.genereg.net/matrix/MA0162.2 |
| + | 14.3462 | 7.23E-06 | 0.0455 | CCCCCACCCCCTTT | http://jaspar.genereg.net/matrix/MA0162.2 |
| - | 13.6909 | 9.52E-06 | 0.0514 | CGGGGTGTGGGAAGCGG | http://hocomoco11.autosome.ru/motif/EGR1\_HUMAN.H11MO.0.A |