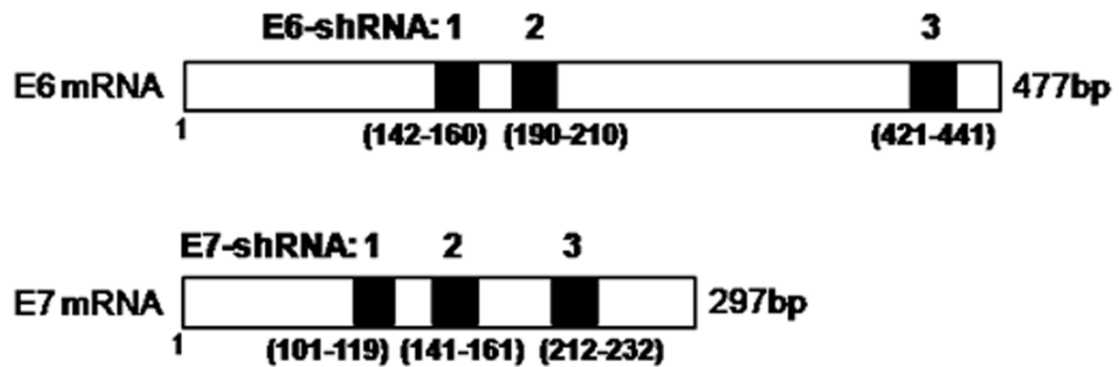


E6 and E7 gene silencing results in decreased methylation of tumor suppressor genes and induces phenotype transformation of human cervical carcinoma cell lines

Supplementary Material



Supplementary Figure 1. Sketch map of the location of specific shRNAs on E6 and E7 genes of HPV16.

Supplementary Table 1. Sequences selected for generating shRNAs.

| shRNA | Oligonucleotides sequence (5'-3') |
|---------|--|
| E6-1 | F: AATTCGAGGTATATGACTTTGCTTTTCAAGAGAAAGCAAAGTCATATACCTCTTTTTTG R: GATCCAAAAAAGAGGTATATGACTTTGCTTTCTCTTGAAAAGCAAAGTCATATACCTCG |
| E6-2 | F: AATTCGGGAATCCATATGCTGTATGTTTCAAGAGAACATACAGCATATGGATTCCCTTTTTTG R: GATCCAAAAAAGGGAATCCATATGCTGTATGTTCTCTTGAAACATACAGCATATGGATTCCCG |
| E6-3 | F: AATTCGGTCGATGTATGTCTTGTTGCTTCAAGAGAGCAACAAGACATACATCGACCTTTTTTG R: GATCCAAAAAAGGTCGATGTATGTCTTGTTGCTCTCTTGAAGCAACAAGACATACATCGACCG |
| E7-1 | F: AATTCAGGAGGATGAAATAGATGGTTCAAGAGACCATCTATTTTCATCCTCCTTTTTTTG R: GATCCAAAAAAGGAGGATGAAATAGATGGTCTCTTGAACCATCTATTTTCATCCTCCTG |
| E7-2 | F: AATTCGGACAGAGCCCATTACAATATTTCAAGAGAATATTGTAATGGGCTCTGTCTTTTTTG R: GATCCAAAAAAGGACAGAGCCCATTACAATATTCTCTTGAATATTGTAATGGGCTCTGTCCG |
| E7-3 | F: AATTCGCACACACGTAGACATTTCGTATTCAAGAGATACGAATGTCTACGTGTGTGCTTTTTTG R: GATCCAAAAAAGCACACACGTAGACATTTCGTATCTCTTGAATACGAATGTCTACGTGTGTGCG |
| Control | F: AATTCTTCTCCGAACGTGTCACGTTTCAAGAGAACGTGACACGTTCCGGAGAATTTTTTG R: GATCCAAAAAATTCTCCGAACGTGTCACGTTCTCTTGAACGTGACACGTTCCGGAGAAG |

Supplementary Table 2. The primers for genes examined in our study.

| Primer | Primer sequence (5'-3') | Useage |
|----------------|--|---------------|
| E6 | F: CAGCAATACAACAAACCG | RT-PCR |
| | R: GCAACAAGACATACATCG | Q-PCR |
| E7 | F: CAGAGGAGGAGGATGAAATAG | RT-PCR |
| | R: AGGTCTTCCAAAGTACGAATG | Q-PCR |
| DNMT1 | F: CCACCATCACATCTCATT R: GGTCTAGCAACTCGTTCTC | Q-PCR |
| DNMT3A | F: GCGGAGGTCGGGAGAAC R: CGATGGCTCCACCTGGC | Q-PCR |
| DNMT3B | F: AGACACCAGGCATCTCAAT R: TCTTCGGCCTCTGATCTC | Q-PCR |
| DNMT3L | F: TCTGTTTGAGGGAGGGAT R: GTAGCATCGGGTGCAATC | Q-PCR |
| SPARC | F: GCCCAGTTCATCACCATTTCT R: TCCCAGAGAACTGACAGTCCGT | Q-PCR |
| TFPI2 | F: CTGTGCTCTGCCAATGTGACTC R: TGCAATCCTCCCTGCTAACAA | Q-PCR |
| RRAD | F: ACTCAGTGACGGACAAGGG R: CCTCATCCACCGAGACCT | Q-PCR |
| SFRP1 | F: AAGTTTCGGTTCCTATGAGCCC R: AAAATCGCCGTCTCTCTCAGG | Q-PCR |
| MT1G | F: TTGCAATGGACCCCACTG R: ACTTCTCCGATGCCCTTT | Q-PCR |
| NMES1 | F: TGACCAAATGACGAGCCCT R: CAGAAGCATTTCCGCACACT | Q-PCR |
| β -actin | F: CCATCGTCCACCGCAAAT R: GCTGTCACCTTCACCGTTCC | Q-PCR |
| SPARC | F: TGGAGGGGAGATAGATTTAGTTT R: CAAAACCTCCCTCCCTTACAC | MS-HRM |
| TFPI2 | F: TGGGGAGAGAAGTTTTTGGGA R: ATCAACCACCCCTCAAACCTC | MS-HRM |
| RRAD | F: ATTTAGGGTTTTAGGTTGGATTGGT R: ATCCCCTCACCTACTACCTCTACTTC | MS-HRM |
| SFRP1 | F: GTTTTATTTTGGGGTTTGGAGGTTT R: CAAACCAACAATAAATACCCCTACTCA | MS-HRM |
| MT1G | F: ATGGTGTTTGGGAATTTGGT R: AAACCTTACACTTAACCCATCTCCT | MS-HRM |
| NMES1 | F: GTAGAATGTTTTGTAGGGGG R: CTACAAATAAAAACTCACCTAAAC | MS-HRM |