

Figure S1. Transfection efficiency of anti-miR-411-5p was verified using reverse transcription-quantitative PCR. (A) HSC-3 and (B) SCC15 cells were infected with lentiviral vectors to establish stable cell lines that expressed short hairpin RNA against miR-411-5p (anti-miR-411-5p). Compared with the empty vector (anti-ctrl), the miR-411-5p expression was downregulated in the anti-miR-411-5p group. \* $P < 0.05$ . miR, microRNA; ctrl, control.

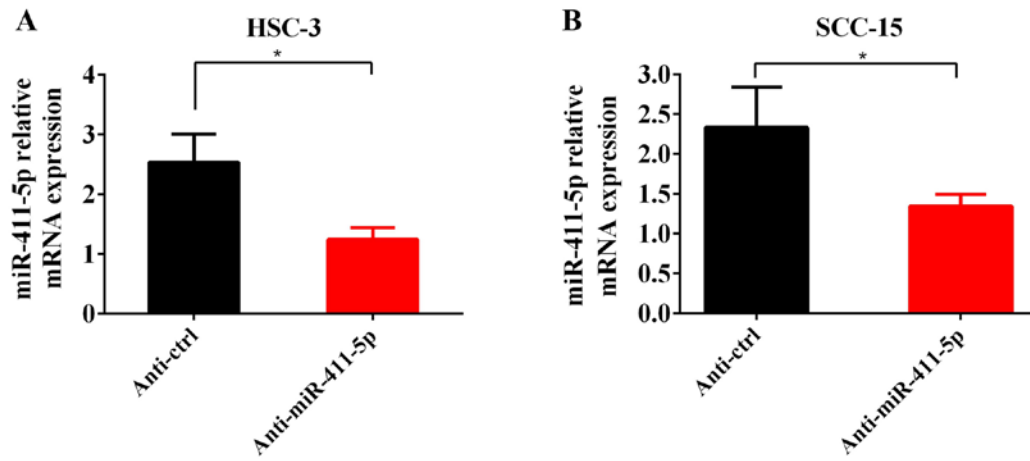


Figure S2. miR-411-5p has minimal effects on head and neck squamous cell carcinoma cell proliferation *in vitro*. (A) Cell Counting Kit-8 and (B) colony formation assays were used to analyze the proliferation of HSC-3 and SCC-15 cells transfected with miR-411-5p mimics, miR-411-5p inhibitor or the respective NCs. miR, microRNA; NC, negative control; ns, not significant.

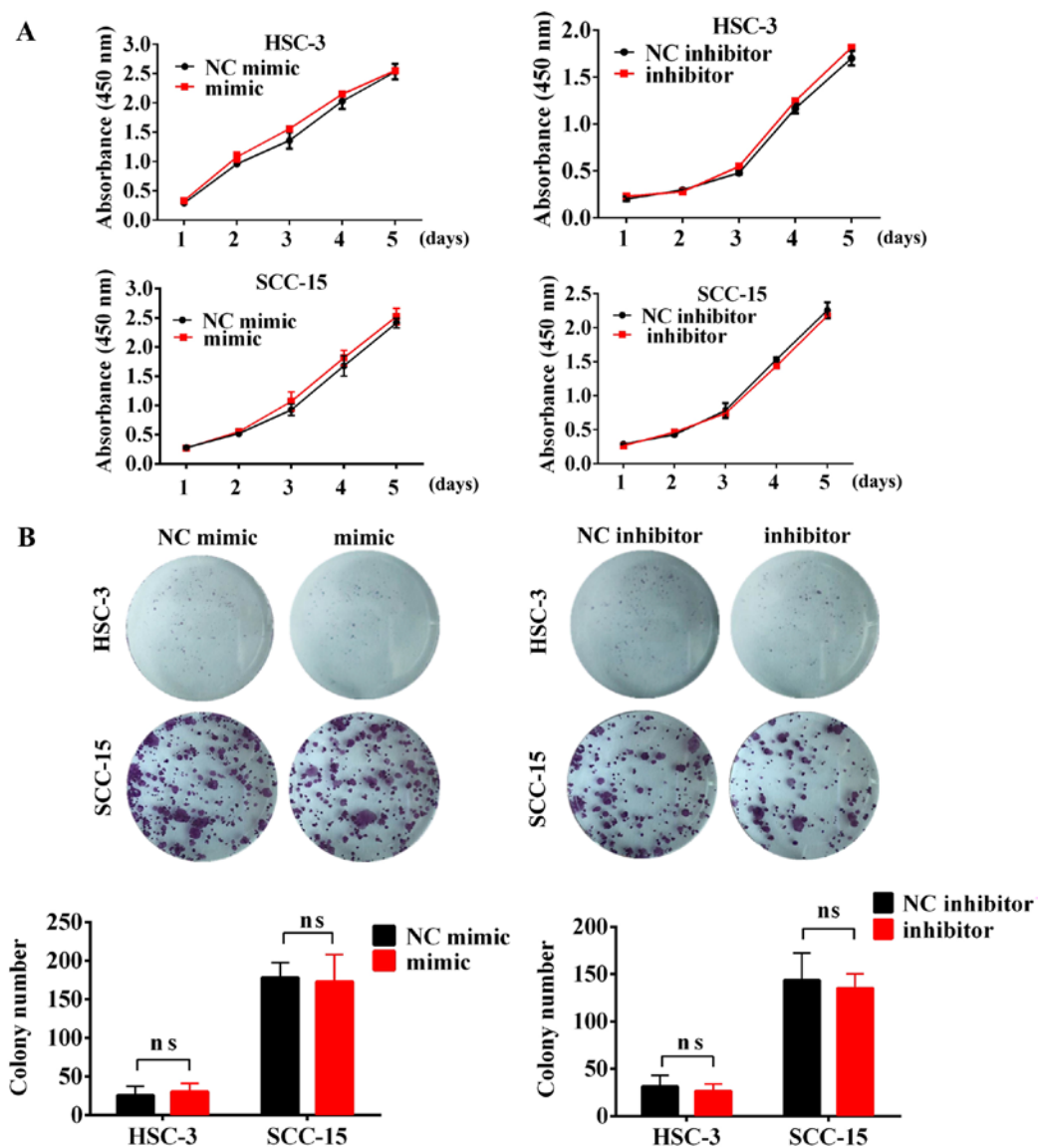


Table SI. Association between the expression of miR-411-5p and clinicopathological characteristics in patients with HNSCC in TCGA databases.

| Clinicopathological characteristics | Number of cases, n | miR-411-5p expression, n |     | P-value            |
|-------------------------------------|--------------------|--------------------------|-----|--------------------|
|                                     |                    | High                     | Low |                    |
| Age, years                          |                    |                          |     |                    |
| ≥55                                 | 274                | 138                      | 136 | >0.999             |
| <55                                 | 104                | 52                       | 52  |                    |
| Sex                                 |                    |                          |     |                    |
| Male                                | 277                | 138                      | 139 | 0.817              |
| Female                              | 101                | 52                       | 49  |                    |
| Differentiation                     |                    |                          |     |                    |
| Well                                | 43                 | 20                       | 23  | 0.630              |
| Moderate + poor                     | 335                | 170                      | 165 |                    |
| T stage                             |                    |                          |     |                    |
| T1 + TII                            | 119                | 60                       | 59  | >0.999             |
| TIII + TIV                          | 259                | 130                      | 129 |                    |
| Clinical stage                      |                    |                          |     |                    |
| I-II                                | 80                 | 42                       | 38  | 0.706              |
| III-IV                              | 298                | 148                      | 150 |                    |
| LNM                                 |                    |                          |     |                    |
| LNM(-)                              | 160                | 69                       | 91  | 0.022 <sup>a</sup> |
| LNM(+)                              | 218                | 121                      | 97  |                    |

<sup>a</sup>P<0.05. miR, microRNA; HNSCC, head and neck squamous cell carcinoma; LNM, lymph node metastasis; T, tumor; TCGA, The Cancer Genome Atlas.

Table SII. Multivariate Cox regression analysis of different clinicopathological characteristics in TCGA databases.

| Clinicopathological characteristics         | Univariate analysis | Multivariate analysis |       |              |
|---------------------------------------------|---------------------|-----------------------|-------|--------------|
|                                             | P-value             | P-value               | HR    | 95% CI       |
| Sex (female vs. male)                       | 0.191               | 0.252                 | 0.817 | 0.579, 1.154 |
| Age, years ( $\geq 55$ vs. $< 55$ )         | 0.157               | 0.071                 | 1.417 | 0.971, 2.067 |
| Pathological grade (well vs. moderate/poor) | 0.162               | 0.176                 | 1.436 | 0.851, 2.425 |
| Tumor stage (TI + II vs. TIII + IV)         | 0.056               | 0.188                 | 1.495 | 0.822, 2.721 |
| LNM (positive vs. negative)                 | $< 0.001^a$         | $< 0.001^a$           | 1.911 | 1.335, 2.735 |
| Clinical stage (CI-II vs. CIII-IV)          | 0.149               | 0.477                 | 0.774 | 0.382, 1.568 |
| miR-411-5p expression (high vs. low)        | 0.002 <sup>a</sup>  | 0.019 <sup>a</sup>    | 1.478 | 1.066, 2.048 |

<sup>a</sup>P<0.05. miR, microRNA; LNM, lymph node metastasis; TCGA, The Cancer Genome Atlas; HR, hazard ratio.