Up-regulation of miR-187 modulates the advances of oral carcinoma by targeting BARX2 tumor suppressor

Supplementary Materials

Supplementary Table S1: Clinicopathological parameters of the OSCC

|   | 56 |
|---|----|
| T1, 2 | 19 |
| T3, 4 | 37 |
| N0 | 34 |
| N1 | 13 |
| N2 | 9 |
| Stage I, II | 15 |
| Stage III, IV | 41 |

Supplementary Table S2: Primary antibodies

| Antibodies | Molecular Weight (kDa) | Dilution | Company & Cat # |
|------------|------------------------|----------|----------------|
| BARX2 (S-13) | 43 | 1:200 | Santa Cruz Biotech; sc-68144 |
| cMyc (9E10) | 67 | 1:1000 | Santa Cruz Biotech; sc-40 |
| Dab2 | 85 | 1:200 | BD Biosciences; 610465 |
| FIH | 40 | 1:1000 | Santa Cruz Biotech; Sc-26219 |
| GAPDH | 36 | 1:2000 | Santa Cruz; sc-32233 |
| Tubulin | 50 | 1:5000 | Sigma-Aldrich; T51681 |

Supplementary Table S3: The primers used to generate reporter constructs by PCR amplification

BCL6 reverse: CCGAAGCTTTCAGTCCCTTGTTGCTG
DYRK2 forward: CCGTCTAGAGATCTGGTCGGTAAAGG
DYRK2 reverse: CCGAAGCTTCCACTTCAACCATTGTCAC
FAM80B forward: CCGTCTAGGCGACATCAGCAGCACATTTC
FAM80B reverse: CCGAAGCTTCTCTGTCAGACCTACATTTTC
GRIA3 forward: CCGTCTAGAAGAGAAAATCGACGAACACG
GRIA3 reverse: CCGAAGCTTTGATGTGGTCATTGTCGC
HIPK3 forward: CCGTCTAGAATGGGAGCAGCAAGATCCAG
HIPK3 reverse: CCGAAGCTTGGAAACCGGTATTACATGCAG

Forward and reverse; direction.
Supplementary Table S4: BARX2 3'UTR sequence and reporter construct

Forward primer : 5′ GCGACTAGTCCAGTCATCAAAGCAGAGAG 3′
Reverse primer : 5′ GCGACGCGTGACCTTGAGCAGTAGGATAG 3′

>`ENST00000281437 utr3:KNOWN_protein_coding
AGTAAAACCCTTTTGAGGAAGAGGAGACTGGGGAGAAGGGAAAA
GAGAGAGAGGCAGAGTGGAGAGAGAAAACCTCCAGAGGCCA
GTAAACTCGGCGGAGAGATCTACCCGTCCTCCCTCCCTCCACAGTT
ACCCTTGGCCCTTGCTACTCGCAAGCATTGGACAAAAAGACCTTGCTTGCTTG
GGCCTGTACCTCCTGAAGAGGCTGCTTATGCTGATGATGCCCTTGATTTA
AGGAGAGAGGCCTGAGTCCTGCCCCAGCTGGGTTGACCGCTG
TAGGGCTGGTCTATGTGGCAAGCCCTATATCTTAGCTGACCATGCAGTTGAAA
GTGCTTATGCTCTCCTCCTGACCTCGTGGGAGCCAGTCATCAAAGCA
GAGAGACGTGGCGGCATGTGGGACATGACGGCCAGTCTCCTTGCTGACTCT
AGCATTATTTCGTATGTATTGTTTTAAAAAGAATTTTGTGGTTTGTAATT
TTTTGGGGGGGAGGAGGGTCGACATGGGGGTAGCTGAGTCTGAGTTG
TTAGAAATGTCTTCTGAATCAAAGTTTTGTTTTGAAAGACAGTGTCCTTGTGTA
CCCAATTATAAGATGGCTCATAAGCCCAGGACTGAATAGCTTTGTTTTTT
TTTTTGTCTTGTCTTATATCCATTTACCATGCTGCTGCATGTCG
CATTATGGAAACCTAAGCTTTGAGGTTATTTTCTACTCTACTGGCTCA
GGTCTACCCAGATCTGATTTTTCATAAAAAACATTTGTGACCTTCGGC
ATAAAATGGGTTAGGTCCATCCCTGAAAACATGCAATTGAGATATGTTCA
GATAAATTTTTATTTAATAAAAATTAATATTTTCAAAA

*miR-187 binding site underlined.