

S1. Table. Clinical details of the HNSCC and OPM cell lines used in this study.

Cell line	Primary lesion site	Stage	Source of cell line	Reference
B16	Lateral Tongue	T2 N0	Recurrent tumour	31, 32
B22	Lateral Tongue	T4 N3	LN metastasis	31, 32
B56	Lateral Tongue	T4 N1	Primary tumour	31, 32
T4	Floor of mouth	T4 N0	Primary tumour	34, 35
H357	Lateral Tongue	T1 N0	Primary tumour	33
D19	Lateral tongue	Severe dysplasia	N/A	34, 35
D20	Lateral tongue	Moderate dysplasia	N/A	34, 35
D4	Ventral tongue	Moderate dysplasia	N/A	34, 35
D35	Ventral tongue	Severe dysplasia	N/A	34, 35

All cell lines are HPV negative.

S2. Table. Clinical and pathological details of the 25 HNSCC samples in the TMA used for HOXB9 IHC. FOM = Floor of mouth, RM = retromolar, BM = buccal mucosa.

Case	Age/Gender	Diagnosis	Site
1	68M	SCC, Moderately differentiated	Tongue
2	67F	SCC, Moderately differentiated	FOM
3	48M	SCC, Moderately differentiated	FOM
4	51M	SCC, Moderately differentiated	Tongue
5	52M	SCC, Moderately differentiated	RM
6	51M	SCC, Moderately differentiated	RM
7	44M	SCC, Moderately differentiated	Tongue
8	64F	SCC, Moderately differentiated	Tongue
9	47M	SCC, Well differentiated	Tongue
10	76F	SCC, Moderately differentiated	Tongue
11	40F	SCC, Moderately differentiated	Tongue
12	73M	SCC, Well differentiated	Tongue
13	80M	SCC, Well differentiated	Gingiva
14	52F	SCC, Moderately differentiated	RM
15	79M	SCC, Well differentiated	Palate
16	46F	SCC, Moderately differentiated	Tongue
17	77M	SCC, Poorly differentiated	Tongue
18	65M	SCC, Moderately differentiated	Palate
19	62M	SCC, Moderately differentiated	FOM
20	63M	SCC, Well differentiated	RM
21	74F	SCC, Moderately differentiated	FOM
22	69M	SCC, Moderately differentiated	Gingiva
23	64M	SCC, Moderately differentiated	Gingiva
24	47M	SCC, Moderately differentiated	BM
25	36M	SCC, Well differentiated	Tongue

S3. Table. Clinical pathological details of HNSCC samples used for Laser capture microdissection FOM = Floor of mouth, RM = retromolar, BM = buccal mucosa.

Case	Age/Gender	Diagnosis	Site
1	52F	SCC, Moderately differentiated	Tongue
2	59M	SCC, Moderately differentiated	Tongue
3	71M	SCC, Moderately differentiated	RM
4	68F	SCC, Moderately differentiated	Gingiva
5	65F	SCC, Moderately differentiated	Palate
6	90M	SCC, Moderately differentiated	BM
7	79F	SCC, Moderately differentiated	BM
8	83F	SCC, Poorly differentiated	Gingiva
9	58F	SCC, Poorly differentiated	FOM
10	72F	SCC, Poorly differentiated	Tongue
11	53M	SCC, Moderately differentiated	BM
12	53M	SCC, Poorly differentiated	Gingiva
13	85F	SCC, Moderately differentiated	Tongue
14	56M	SCC, Moderately differentiated	Tongue
15	71M	SCC, Moderately differentiated	Gingiva
16	72F	SCC, Poorly differentiated	BM

S4. Table. A full list of qPCR primers used in this study.

HOX gene name	Product length (bp)	Primer sequence
HOXA1	153	F: 5' CTGGCCTGGCTACGTATAA 3' R: 5' TCCAACCTTCCCTGTTTTGG 3'
HOXB1	157	F: 5' TTCAGCAGAACTCCGGCTAT 3' R: 5' CCTCCGTCTCCTTCTGATTG 3'
HOXD1	232	F: 5' TTCAGCACCAAGCAACTGAC 3' R: 5' TAGTGGGGTTGTTCCAGAG 3'
HOXA2	176	F: 5' TTCAGCAAAATGCCCTCTCT 3' R: 5' TAGGCCAGCTCCACAGTTCT 3'
HOXB2	258	F: 5' CTCCCAAAATCGCTCCATTA 3' R: 5' GAAAGGAGGAGGAGGAGGAA 3'
HOXA3	227	F: 5' ACCTGTGATAGTGGGCTTGG 3' R: 5' ATACAGCCATTCCAGCAACC 3'
HOXB3	299	F: 5' TATGGCCTCAACCACCTTTC 3' R: 5' AAGCCTGGGTACCACCTTCT 3'
HOXD3	176	F: 5' CAGCCTCCTGGTCTGAACTC 3' R: 5' ATCCAGGGGAAGATCTGCTT 3'
HOXA4	271	F: 5' CCCTGGATGAAGAAGATCCA 3' R: 5' AATTGGAGGATCGCATCTTG 3'
HOXB4	155	F: 5' TCTTGGAGCTGGAGAAGGAA 3' R: 5' GTTGGGCAACTTGTGGTCTT 3'
HOXC4	276	F: 5' CGCTCGAGGACAGCCTATAC 3' R: 5' GCTCTGGGAGTGGTCTTCAG 3'
HOXD4	173	F: 5' TCAAATGTGCCATAGCAAGC 3' R: 5' TCCATAGGGCCCTCCTACTT 3'
HOXA5	193	F: 5' CCGGAGAATGAAGTGGAAAA 3' R: 5' ACGAGAACAGGGCTTCTTCA 3'
HOXB5	189	F: 5' AAGGCCTGGTCTGGGAGTAT 3' R: 5' GCATCCACTCGCTCACTACA 3'
HOXC5	268	F: 5' CAGTTACACGCGTACCAGA 3' R: 5' AGAGAGGAAAGGCGAAAAGG 3'
HOXA6	158	F: 5' AAAGCACTCCATGACGAAGG 3' R: 5' TCCTTCTCCAGCTCCAGTGT 3'
HOXB6	184	F: 5' ATTCCTTCTGGCCCTCACT 3' R: 5' GGAAGGTGGAGTTCACGAAA 3'
HOXC6	190	F: 5' AAGAGGAAAAGCGGGAAGAG 3' R: 5' GGTCCACGTTTACTCCCTA 3'
HOXA7	285	F: 5' TGGTGTAATCTGGGGGTGT 3' R: 5' TCTGATAAAGGGGCTGTTG 3'
HOXB7	249	F: 5' CAGCCTCAAGTTCGGTTTTTC 3' R: 5' CGGAGAGGTTCTGCTCAAAG 3'
HOXB8	265	F: 5' GTAGGCTTCAGCTGGGACTG 3' R: 5' GGGAGCCTTTGCTTAAATCC 3'
HOXC8	150	F: 5' CTCAGGCTACCAGCAGAACC 3' R: 5' TTGGCGGAGGATTTACAGTC 3'
HOXD8	290	F: 5' TCAAATGTTTCCGTGGATGA 3' R: 5' GCTCTGGGCTCCTTTTTTC 3'

HOXA9	203	F: 5' AATAACCCAGCAGCCAACTG 3' R: 5' ATTTTCATCCTGCGGTTCTG 3'
HOXB9	198	F: 5' TAATCAAAGACCCGGCTACG 3' R: 5' CTACGGTCCCTGGTGAGGTA 3'
HOXC9	190	F: 5' AGACGCTGGAAGTGGAGAAG 3' R: 5' AGGCTGGGTAGGGTTTAGGA 3'
HOXD9	236	F: 5' TCCCCATGTTTCTGAAAAG 3' R: 5' GGGCTCCTCTAAGCCTCACT 3'
HOXA10	159	F: 5' AACTGGAGCTGGAGAAGGA 3' R: 5' GATCCGGTTTTCTCGATTCA 3'
HOXC10	289	F: 5' CGCCTGGAGATTAGCAAGAC 3' R: 5' GGTCCTTGGGAAGGAGAGTC 3'
HOXD10	154	F: 5' GCTCCTTCAACCAACATT 3' R: 5' AAATATCCAGGGACGGGAAC 3'
HOXA11	279	F: 5' CGCTGCCCTATACCAAGTA 3' R: 5' GTCAAGGGCAAAATCTGCAT 3'
HOXC11	186	F: 5' CGGAACAGCTACTCCTCTG 3' R: 5' CAGGACGCTGTTCTTGTGA 3'
HOXD11	253	F: 5' GGGGCTACGCTCCCTACTAC 3' R: 5' GCTGCCTCGTAGAACTGGTC 3'
HOXC12	180	F: 5' CAAGCCCTATTCGAAGTTGC 3' R: 5' GCTTGCTCCCTCAACAGAAG 3'
HOXD12	201	F: 5' CGTTCCCCCTATCTCCTAC 3' R: 5' CTTGGGCGCATAGAACTTA 3'
HOXA13	176	F: 5' GGATATCAGCCACGACGAAT 3' R: 5' ATTATCTGGGCAAAGCAACG 3'
HOXB13	234	F: 5' CTTGGATGGAGCCAAGGATA 3' R: 5' CCGCCTCAAAGTAACCATA 3'
HOXC13	170	F: 5' GTGGAAATCCAAGGAGGACA 3' R: 5' TTGTTGAGGGACCCACTCTC 3'
HOXD13	265	F: 5' GGGGATGTGGCTCTAAATCA 3' R: 5' AACCTGGACCACATCAGGAG 3'
β -actin	182	F: 5' ATGTACCCTGGCATTGCCGAC 3' R: 5' GACTCGTCATACTCTGCTTG 3'
MAMDC2	187	F: 5' ATGCTGTAAAGGGGCGTCCTCCTG 3' R: 5' CCTGCTTGCCAAAGGAGGTATCCA 3'

S5. Table. Gene ontology enrichment analysis demonstrating significantly enriched GO biological processes on manipulation of miR-196a expression.

Term	Count	%	P Value	Genes	Fold Enrichment
GO:0033554: Cellular response to stress	16	0.78	0.002	<i>C9ORF102, ZAK, SMC5, SIRT7, FOXO3, HSPA1L, RFC3, DCLRE1B, PSEN1, STAC, BTG2, GSK3B, MUS81, EIF2B3, FANCA, ERCC1</i>	2.5
GO:0015837: Amine transport	7	0.34	0.002	<i>SLC1A4, SLC6A9, PSEN1, SLC38A7, SLC36A4, CLN8, CRYM</i>	5.2
GO:0006974: Response to DNA damage stimulus	12	0.59	0.004	<i>HSPA1L, RFC3, C9ORF102, DCLRE1B, PSEN1, ZAK, BTG2, MUS81, SMC5, FOXO3, FANCA, ERCC1</i>	2.8
GO:0046942: Carboxylic acid transport	7	0.34	0.007	<i>SLC1A4, SLC6A9, PSEN1, SLC38A7, ABCC3, SLC36A4, CLN8</i>	4.2
GO:0006281: DNA repair	9	0.44	0.016	<i>HSPA1L, RFC3, C9ORF102, DCLRE1B, BTG2, MUS81, SMC5, FANCA, ERCC1</i>	2.8
GO:0045892: Negative regulation of transcription, DNA-dependent	10	0.49	0.020	<i>HOXC8, SBNO2, EHMT1, ARID4A, E2F6, SIRT7, SKIL, ZNF254, DNAJB6, CRYM</i>	2.5
GO:0010558: Negative regulation of macromolecule biosynthetic process	13	0.64	0.022	<i>SBNO2, EHMT1, ARID4A, E2F6, CENPF, SIRT7, ZNF254, EIF4EBP1, HOXC8, SKIL, EIF2B3, CRYM, DNAJB6</i>	2.1
GO:0021532: Neural tube patterning	3	0.15	0.023	<i>PSEN1, GBX2, RPGRIP1L</i>	12.5
GO:0009612: Response to mechanical stimulus	4	0.20	0.026	<i>BTG2, MGP, DNAH1, TIMP3</i>	6.2
GO:0010629: Negative regulation of gene expression	12	0.59	0.029	<i>HOXC8, SBNO2, EHMT1, ARID4A, E2F6, BNIP3L, CENPF, SIRT7, SKIL, ZNF254, DNAJB6, CRYM</i>	2.1
GO:0032318: Regulation of Ras GTPase activity	5	0.24	0.031	<i>FICD, SH3D20, C6ORF170, EVI5L, TBC1D20</i>	4.2

The total number of significantly differentially expressed genes entered into this analysis was 353. Analysis generated by analysis of the gene list in DAVID (<http://david.abcc.ncifcrf.gov>).