

Original Article

Deregulation of paralogous 13 HOX genes in oral squamous cell carcinoma

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Abstract: Many oncogenic drivers related to the pathogenesis of OSCC have identified, but the discovery of new molecular markers for early detection of this cancer, remains one the main goals of clinical research. HOX genes regulate normal embryonic development, cell differentiation and other critical processes in eukaryotic cell life. Several studies have demonstrated that the deregulation of HOX genes play a significant role in cancer development and progression. In this study, we built a prognostic TMA with 119 OSCC samples, representative of deep and superficial part of the tumour, to investigate, the paralogous 13 HOX proteins expression, correlating them with clinic-pathological parameters, outcomes and therapy information. Our results show an aberrant expression of HOX A13 and HOX D13 in OSCC pathogenesis and tumour progression. HOX A13 overexpression is related to an OSCC better prognosis ($P=0.029$) and better therapy response in patients treated with both radiotherapy and chemotherapy ($P=0.015$). HOX D13 overexpression is inversely related to an overall survival ($P=0.004$). These data highlight the potential prognostic role of HOX paralogous group 13 genes in OSCC.

Keywords: Paralogous 13 HOX genes, OSCC, tumour progression

Introduction

Oral squamous cell carcinoma (OSCC) is the sixth most common cancer worldwide with a 5-year survival rate of 60%. In particular, it represents 4% of all malignancies in men and 2% in women. The majority of OSCC patients present with an advanced stage of the disease, not only because the clinical manifestations are difficult to define but also for the absence of early diagnosis tools [1]. The understanding of the molecular mechanisms related to the pathogenesis and progression of this disease could allow to improve life expectancy, quality of life, disease-free survival of the patients and to establish new and more effective therapeutic strategies [2, 3].

Homeobox genes regulate normal embryonic development, cell differentiation and other critical processes in eukaryotic cell life [4]. Several members of the Dlx family are essential for normal development of the jaw, skull, and inner ear [5], while Pax3 and Pax 7 homeodomain pro-

teins are crucial for the differentiation of mesodermal precursors into muscle cells [6]. Several studies have demonstrated that in particular the genes belonging to Class I homeobox genes, defined HOX genes in humans, play a crucial role in neoplastic transformation in several human tissues [7, 8]. Specifically, the genes belonging to HOX paralogous group 13 seem to carry out a relevant role in both tumour development and progression. We have recently demonstrated the aberrant expression of all paralogous group 13 HOX genes, HOX A13, HOX B13, HOX C13 and HOX D13, in thyroid cancer [9]. Moreover, we have identified a significant prognostic role of *HOX D13* in pancreatic cancer [10], a *HOX A13* gene deregulation in liver carcinogenesis [11] and an abnormal overexpression of *HOX C13* in metastatic melanoma and in de-differentiated and well-differentiated liposarcoma [12, 13]. Finally, we have also showed the aberrant expression of *HOX B13* in bladder tumorigenesis and progression [14]. Data on the role played by HOX genes in oral cancers are still few, and most refer to epigen-

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etic alterations, in particular hypermethylation and hypomethylation of HOX genes promoters [15].

In this study we have analyzed paralogous 13 HOX genes expression, by immunohistochemistry, in a series of 119 OSCC samples included in a prognostic Tissue Micro Array (TMA), highlighting the main role of HOX A13 and HOX D13 in pathogenesis and tumor progression of OSCC.

Material and methods

OSCC patients

One hundred nineteen patients admitted to the National Cancer Institute "Giovanni Pascale" of Naples, between 1998 and 2011, were recruited in this study. All patients had provided written informed consent for the use of samples according to the institutional regulations and the study was approved by the ethics committee of the National Cancer Institute "G. Pascale".

All OSCC cases have been reviewed according to WHO/ISUP 2007 classification criteria, using standard tissue sections. Medical records have been reviewed for clinical information, including histologic parameters assessed on standard H&E-stained slides.

TMA building

A Prognostic-Tumor Array was constructed using 119 tumor tissue samples. Two cores from different areas, one superficial and one representative of the deep invasion, were arrayed in a recipient block. All tumors and controls were reviewed by two experienced pathologists (RF and SL). Discrepancies for the same case were resolved in a joint analysis. Tissue cylinders with a diameter of 1 mm were punched from morphologically representative tissue areas of each 'donor' tissue block and brought into one recipient paraffin block (3 × 2.5. cm) using a semi-automated tissue array (Galileo TMA).

Immunohistochemistry analysis

Immunohistochemical staining was carried out on slides from formalin-fixed, paraffin embedded tissues, in order to evaluate the expression of HOX A13, HOX B13, HOX C13 and HOXD13.

Paraffin slides was deparaffinized in xylene and rehydrated through graded alcohols. Antigen retrieval was performed with slides heated in 0.01 M citrate buffer (pH 6.0.) in a bath for 20 min at 97°C. After antigen retrieval, the slides were allowed to cool. The slides were rinsed with TBS and the endogenous peroxidase was inactivated with 3% hydrogen peroxide. After protein block (BSA 5% in PBS 1 ×), the slides were incubated with primary antibody to human HOX A13 (dilution 1:200, cod. Ab-106503, Abcam, Cambridge, UK), HOX B13 (dilution 1:300, cod. ab28575, Abcam, Cambridge, UK), HOX C13 (dilution 1:1200, cod. ab55251, Abcam, Cambridge, UK), HOX D13 (dilution 1:100, cod. Ab19866, Abcam, Cambridge, UK) overnight. Sections were incubated with mouse anti-rabbit or goat anti-mouse secondary IgG biotinylated secondary antibody for 30 min. Immunoreactivity was visualized by means of avidin-biotin-peroxydase complex kit reagents (Novocastra, Newcastle, UK) as the chromogenic substrate. Finally, sections were weakly counterstained with haematoxylin and mounted.

Evaluation of immunostaining

Antigen expression was independently evaluated by two experienced pathologists (RF/SL) using light microscopy. For paralogous 13 HOX genes nuclear and cytoplasmic localization were considered. All values of immunostaining were expressed only in percentage terms of positive cells. The percentage of positive cancer cells was evaluated in each sample by counting the number of positive cells over the total cancer cells in 10 non-overlapping fields using × 400 magnification.

RNA extraction and analysis

Total RNA was isolated from selected FFPE samples collected from the National Cancer Institute "Fondazione G. Pascale" Institutional Bio-Bank. For RNA extraction, 4 sections at 10 µm thick were cut from each FFPE tissue block. Total RNA was extracted using High pure FFPE RNA Micro Kit (Roche Molecular Biochemicals, Mannheim, Germany) following the manufacturer's instructions. A total of 1 µg RNA was subjected to cDNA synthesis for 1 hour at 37°C using the Ready To Go You-Primer First-Strand Beads kit (Amersham Biosciences Europe GmbH, Freiburg, Germany) in a reaction mixture

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Table 1. Main clinical features of the patients arranged in the prognostic OSCC TMA

	Overall Population (119)
Age at the diagnosis	
<45	4\119
>45	115\119
Gender	
M	83\119
F	36\119
Grading	
G1	20\119
G2	66\119
G3	33\119
Overall free disease survival	40\85
Death	42\85
No follow-up	37\119
Recurrence	3\85
Tumor staging	
T1-2	75\119
T3-4	44\119
Lymph Node metastases	78\119
Distant metastases	1\119
No metastasis	40\119
THERAPY	
Chemotherapy	29\89
Radiotherapy	60\89
Chemo-therapy+Radiotherapy	27\89
No Therapy information	20\119
Primary anatomical Site	
Tongue	71\119
Other sites	45\119
Lips	3\119

containing 0.5 µg random hexamers (GeneAmp RNA PCR Random Hexamers Set N808-0127 Applied Biosystems, Foster City, CA).

Quantitative real-time PCR

Quantitative RT-PCR was performed in a LightCycler system (Roche Molecular Biochemicals, Mannheim, Germany) using TaqMan® analysis. In this system, all reactions have been run in glass capillaries in a volume of 20 µl with 4 µl of The LightCyclerTaqMan Master Mix (Roche Molecular Biochemicals), 2 µl of cDNA and 1 µl of specific TaqMan Gene Expression Assays for human HOX A13, HOX B13, HOX C13, HOX D13 (RealTime Designer Assay, Roche Molecular Biochemicals) according to the manufacturer's directions. All reactions were

performed in triplicate. The thermal cycling conditions included a step of 20 sec at 95°C followed by a 40 cycles of 95°C for 1 sec and 60°C for 20 sec. The comparative C_t method was employed to determine the human HOX genes variation, using TaqMan Endogenous Controls Human ACTB (β -actin) Endogenous Control (Real Time Designer Assay, Roche Molecular Biochemicals) as reference gene. Final amounts of target were determined as follows: target amount = 2^{-C_t} , where $C_t = (C_t(\text{HOX genes}) - C_t(\text{ACTB}))_{\text{sample}} - (C_t(\text{HOX genes}) - C_t(\text{ACTB}))_{\text{calibrator}}$. Data were expressed as mean \pm standard deviation (SD, n=3).

Statistical analysis

Only a percentage of immunoreactive cells was considered for the evaluation of paralogous 13 HOX IHC expression on TMA samples. Kruskal-Wallis test was applied to identify differences in median expression values of each marker between two groups of OSCC (superficial and deep side). Wilcoxon signed-rank test was used to study the correlation between the nuclear and cytoplasmic expression in the paralogous 13 HOX group genes because of nonparametric and paired values.

The association between HOX A13, HOX B13, HOX C13 and HOX D13 with the clinic-pathological data was conducted using the χ^2 test considering the median of expression for each marker as cut-off. The Pearson χ^2 test was used to determine whether a relationship exists between the variables included in the study, while the value Pearson's R represents a measure of linear association between the variables. The level of significance was defined as $P < 0.05$. Overall Survival (OS) curves were calculated using the Kaplan-Meier method. OS was defined as the time from diagnosis (first biopsy) to death by any cause or until the most recent follow-up.

All the statistical analyses were carried out using MedCalc 12.7.

Results

Clinic pathological features of OSCC patients

The main clinic pathological characteristics of the patients included in the TMA are reported in **Table 1**. 119 patients aged between 31 and 92 years (mean age 70 years). 78 patients had lymph node metastases at diagnosis and 1

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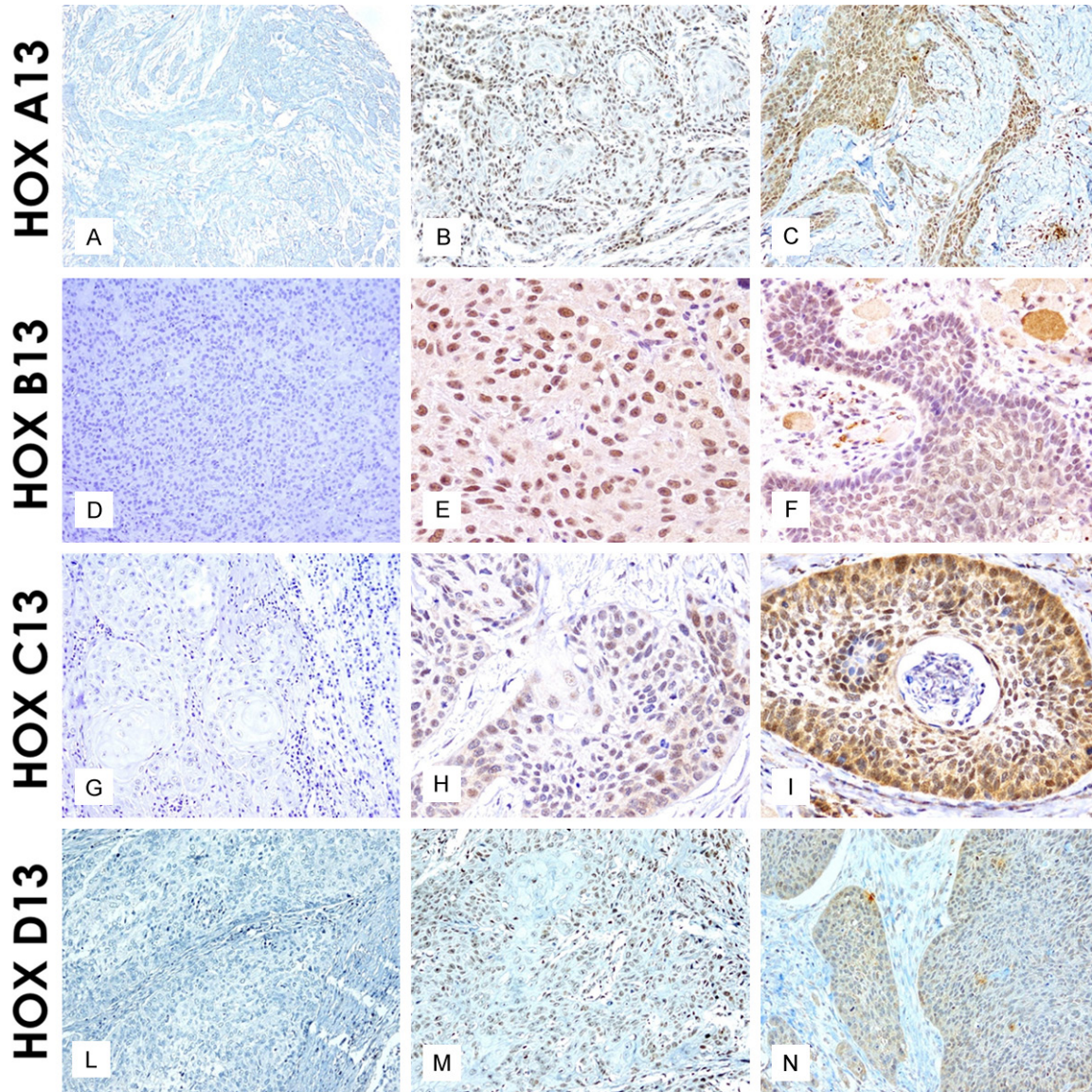


Figure 1. Paralogous group 13 *HOX* protein localization in OSCC samples: Negative, Weak and Strong *HOX A13* nuclear and cytoplasmic expression (20 ×) respectively (A-C); Negative, Weak and strong *HOX B13* nuclear and cytoplasmic expression (20 × and 40 ×) respectively (D-F); Negative, Weak and Strong *HOX C13* nuclear and cytoplasmic expression (20 × and 40 ×) respectively (G-I); Negative, Weak and strong *HOX D13* nuclear and cytoplasmic expression (40 ×) respectively (L-N).

patient had distant metastases. Furthermore, 29 patients were submitted to adjuvant chemotherapy, 60 to radiotherapy, and 27 to radio and chemotherapy. All selected patients were treated with chemotherapy after surgery and none of them had received the drug in the neoadjuvant therapy. Finally, the appearance of local recurrence was observed in 3 cases, 42 patients died over an average period of 24 months. The follow up of 37 patients was not available. Regarding the histopathological grading, 20 cases were well-differentiated squamous cell carcinoma (G1), 66 squamous cell

carcinomas were moderately differentiated (G2) and 33 cases were poorly differentiated carcinomas (G3). The tongue, with 71 cases, was the most affected location, followed by oral floor with 12 cases, lip with 3 cases and other sites with 33 cases.

IHC paralogous 13 HOX expression in OSCC patients series

The immunohistochemical analysis mainly revealed a nuclear localization of paralogous 13 *HOX*, whereas a cytoplasmic localization

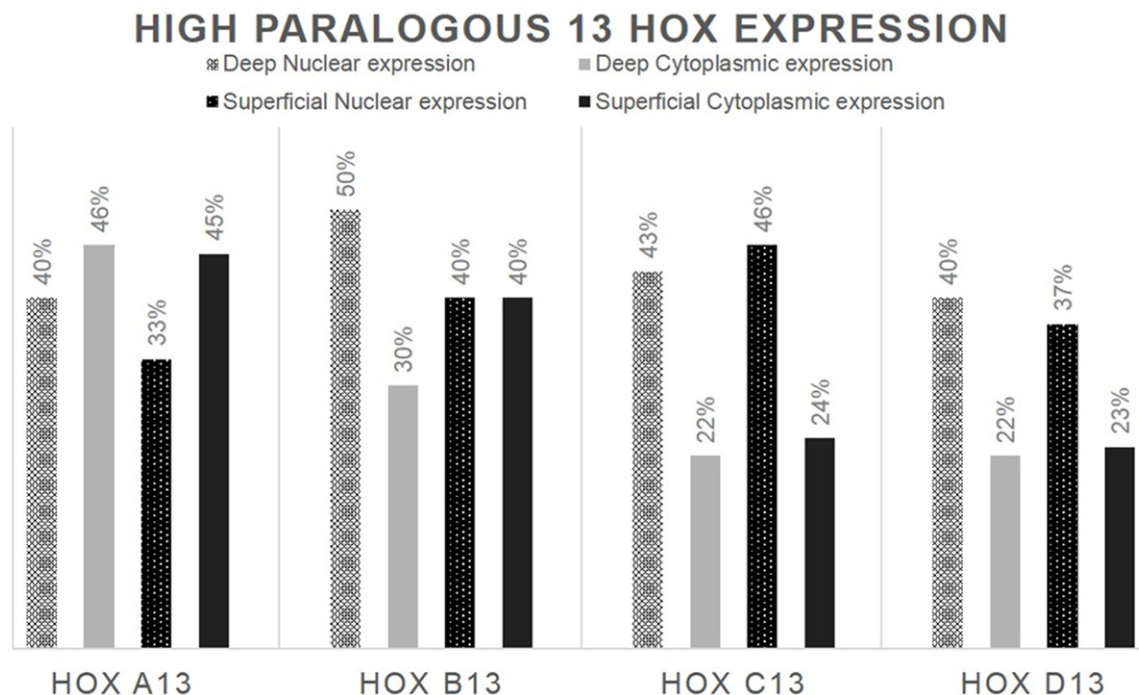


Figure 2. Percentage distribution of paralogous 13 HOX high expression in the deep and superficial margin of the lesion.

was observed only in some areas. Generally, paralogous 13 HOX protein was detected in nucleus of normal cells. HOXA13 and HOXD13 were expressed in normal basal epithelium instead, HOXB13 stained normal peritumoral epithelium. HOXC13 is not expressed in normal tissue. We evaluated both the cytoplasmic and nuclear positivity and, for statistical associations, we considered them separately in the deep and superficial part of cancer (schematically shown in **Figures 1** and **2**). In the deep part of the lesion, the immunohistochemical analysis of HOXA13 showed an increased cytoplasmic and nuclear expression in 46% and 40% of cases respectively. Even in the superficial side of lesion HOXA13 was abundantly localized in cytoplasmic (45%) compare nuclear (33%) expression. HOXB13 showed a high nuclear detection in the deep portion of the cancer. In detail, in the deep side, HOXB13 expression was nuclear in 50% of cases and cytoplasmic in 30%; in the superficial side of tumor, HOXB13 expression was nuclear in 40% and cytoplasmic in 38% of cases. HOXC13 nuclear expression increased in the superficial portion of the lesion. In detail, in the superficial side of the tumor, it showed nuclear positivity in 46% of cases and cytoplasmic in 24%; in the deep side of the tumor, nuclear positivity was present in 43% of cases and cytoplasmic in

22%. HOXD13 showed a high nuclear expression. In detail, in the deep side of the cancer, HOXD13 expression was nuclear in 40% of cases and cytoplasmic in 22%; in the superficial side of tumor, its expression was nuclear in 37% of cases and cytoplasmic in 23%. The only cytoplasmic expression has been proven on selected samples by Real Time PCR (data not shown).

Relation between paralogous 13 HOX expression and clinic pathological features of OSCC patients series

We considered both cytoplasmic and nuclear positivity in the deep and superficial margin of the tumor for statistical associations. In general, tumor samples stained more consistently for paralogous 13 HOX proteins, compared to non-neoplastic areas.

All IHC HOX expression data were statistically analyzed and all elaborations are schematized in Supplementary Tables 1, 2, 3, 4.

At first, the Immunohistochemical HOX expression data were statistically analyzed using tumor deep and superficial parameters. In detail, aberrant HOX A13 cytoplasmic superficial expression appeared associated ($P < 0.044$) with different anatomic sites of OSCC samples.

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Table 2. Mean and median of cytoplasmic and nuclear paralogous HOX expression

	HOXA13Nucl	HOXA13Cyto	HOXB13Nucl	HOXB13Cyto	HOXC13Nucl	HOXC13Cyto	HOXD13Nucl	HOXD13Cyto
N Valid	94	94	94	94	94	94	94	94
Missing	0	0	0	0	0	0	0	0
Mean	37.8723	38.3777	27.0213	5.7979	20.1117	13.4574	27.1277	4.4415
Median	40.0000	45.0000	25.0000	.0000	15.0000	10.0000	15.0000	.0000

Its expression increased in lips. There is a trend of statistical association between superficial cytoplasmic expression of HOXC13 and anatomic site. In fact, the tongue site showed an aberrant cytoplasmic expression in superficial tumor side. Finally, a strong statistical significance has been shown for cytoplasmic deep expression ($P=0.0.01$) of HOX D13, that significantly increases with tumor size (data not shown). Subsequently, we gathered in a single value the paralogous HOX expression of deep and superficial cores, as there were no significant differences between cytoplasmic and nuclear expressions related to the depth of the tumor. **Table 2** reports the mean and median of cytoplasmic and nuclear paralogous HOX expression. We have also standardized the series. In fact, the new data encompassed only 94 patients with all paralogous protein expressions and all clinical information (missing expression data for 15 cases). The new HOX expression data were statistically analyzed and all elaborations are schematized in **Table 3**. This second analysis showed no significant differences with the previous one. Only HOX C13 expression was significantly correlated with male gender ($P=0.0.06$) and deep invasion ($P=0.0.45$).

Relation between paralogous 13 HOX expression and survival of OSCC patients series

The paralogous 13 HOX expression influenced the prognosis of OSCC differently. Indeed, the overall survival of 94 OSCC patients associated to paralogous 13 HOX proteins positivity was statistically significant, in particular for HOXA13, HOXB13 and HOXD13 (**Figures 3A, 4A, 6A**). The first assessments showed that the overexpression of HOX A13 was significantly associated with a better prognosis at 60 months ($P=0.029$). (**Figure 3A**). In addition, patients with high HOXA13 expression, treated only with surgery, showed a better overall survival ($P=0.038$) (**Figure 3B**). Patients undergone chemo and radiotherapy with HOXA13 positivity were heavily associated with a better survival ($P=0.015$) (**Figure 3D**). Regarding

HOXB13, its expression was associated with a low overall survival (trend of statistical association, $P=0.076$) (**Figure 4A**) and, in the same way, its expression in patients undergone chemo and radiotherapy was associated with a poor overall survival (**Figure 4D**). No significant changes of overall survival associated to HOXC13 expression were found, as shown in **Figure 5A-D**. Instead HOXD13 expression was significantly associated with a worse prognosis ($P=0.029$), as shown in **Figure 6A** and HOXD13 expression in patients undergone radio therapy was associated with a low overall survival ($P=0.004$).

Discussion

Squamous cell carcinoma of the oral cavity is one of the most common malignancies in the population, but its diagnosis is often late for the body location in which it occurs and for the irregularity with which patients yet consult specialists [1]. The molecular mechanisms associated with the pathogenesis and evolution of this disease are poorly understood, although some indications in the literature suggest to direct the attention on the role of HOX genes. Early studies, carried out on small numbers of cases, suggested the aberrant expression of several HOX genes in oral dysplasia and OSCC [16]. In particular, the overexpression of HOX B7 was significantly correlated to T and N stages and ki67 in OSCC patients [17]. Molecular and immunohistochemical studies also highlighted the progressive increase of expression of HOX A5 from non-tumor epithelium to carcinoma [18]. Moreover, Hunter *et al*, through transcriptomic analysis of cell cultures representative of OSCC development, showed a dysregulation of expression of several HOX genes, in particular of HOX D10 [19]. More recently, the transfection of HOX D10 gene in an OSCC cellular model caused a decrease in cell invasion but an increase of proliferation, adhesion and migration of tumor cells [20].

In this study we have focused the attention on HOX genes of paralogous group 13, which activ-

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Table 3. Correlation between paralogous group 13 (HOXA-HOXB-HOXC-HOXD) expression and main clinical features of 94 patients

Main clinical-pathological characteristics	HOXA13		Pearson Chi-Square	Pearson's R	HOXB13		Pearson Chi-Square	Pearson's R	HOXC13		Pearson Chi-Square	Pearson's R	HOXD13		Pearson Chi-Square	Pearson's R	
	Weak or Negative expression	Positive expression			Weak or Negative expression	Positive expression			Weak or Negative expression	Positive expression			Weak or Negative expression	Positive expression			
Age	≤68	36.7%	63.3%	0.512	0.083	24.5%	75.5%	0.315	0.111	49.0%	51.0%	0.146	0.159	20.4%	79.6%	0.113	-0.169
	>69	28.9%	71.1%			15.6%	84.4%			33.3%	66.7%			35.6%	64.4%		
Gender	F	35.7%	64.3%	0.811	0.038	21.4%	78.6%	1	0.020	64.3%	35.7%	0.006	0.301	17.9%	82.1%	0.212	-0.143
	M	31.8%	68.2%			19.7%	80.3%			31.8%	68.2%			31.8%	68.2%		
Site	Lip	0	100%	0.624	-0.061	0	100%	0.319	0.072	0	100%	0.345	-0.029	0	100%	0.427	0.038
	Tongue	33.9%	66.1%			25%	75%			44.6%	55.4%			32.1%	67.9%		
	Other	34.3%	65.7%			14.3%	85.7%			40%	60%			22.9%	77.1%		
Deep invasion	≤5	26.7%	73.3%	0.766	-0.093	20%	80%	1	-0.002	66.7%	33.3%	0.045	0.223	20%	80%	0.548	-0.075
	>6	34.2%	65.8%			20.3%	79.7%			36.7%	63.3%			29.1%	70.9%		
Grading	1	16.7%	83.3%	0.236	-0.093	27.8%	72.2%	0.541	0.114	38.9%	61.1%	1	-0.114	27.8%	72.2%	1	0.004
	2	38.9%	61.1%			20.4%	79.6%			42.6%	57.4%			27.8%	72.2%		
	3	31.8%	68.2%			13.6%	86.4%			40.9%	59.1%			27.3%	72.7%		
T	1	31.3%	68.8%	0.406	-0.003	25%	75%	0.544	0.144	50%	50%	0.284	0.031	43.8%	56.3%	0.261	0.204
	2	37.5%	62.5%			25%	75%			42.5%	57.5%			30%	70%		
	3	16.7%	83.3%			16.7%	83.3%			22.2%	77.8%			22.2%	77.8%		
	4	40%	60%			10%	90%			50%	50%			15%	85%		
Staging	1	20%	80%	0.217	-0.094	30%	70%	0.749	0.107	50%	50%	0.908	0.049	50%	50%	0.224	0.180
	2	39.1%	60.9%			21.7%	78.3%			39.1%	60.9%			34.8%	65.2%		
	3	18.2%	81.8%			22.7%	77.3%			45.5%	54.5%			18.2%	81.8%		
	4	41%	59%			15.4%	84.6%			38.5%	61.5%			23.1%	76.9%		

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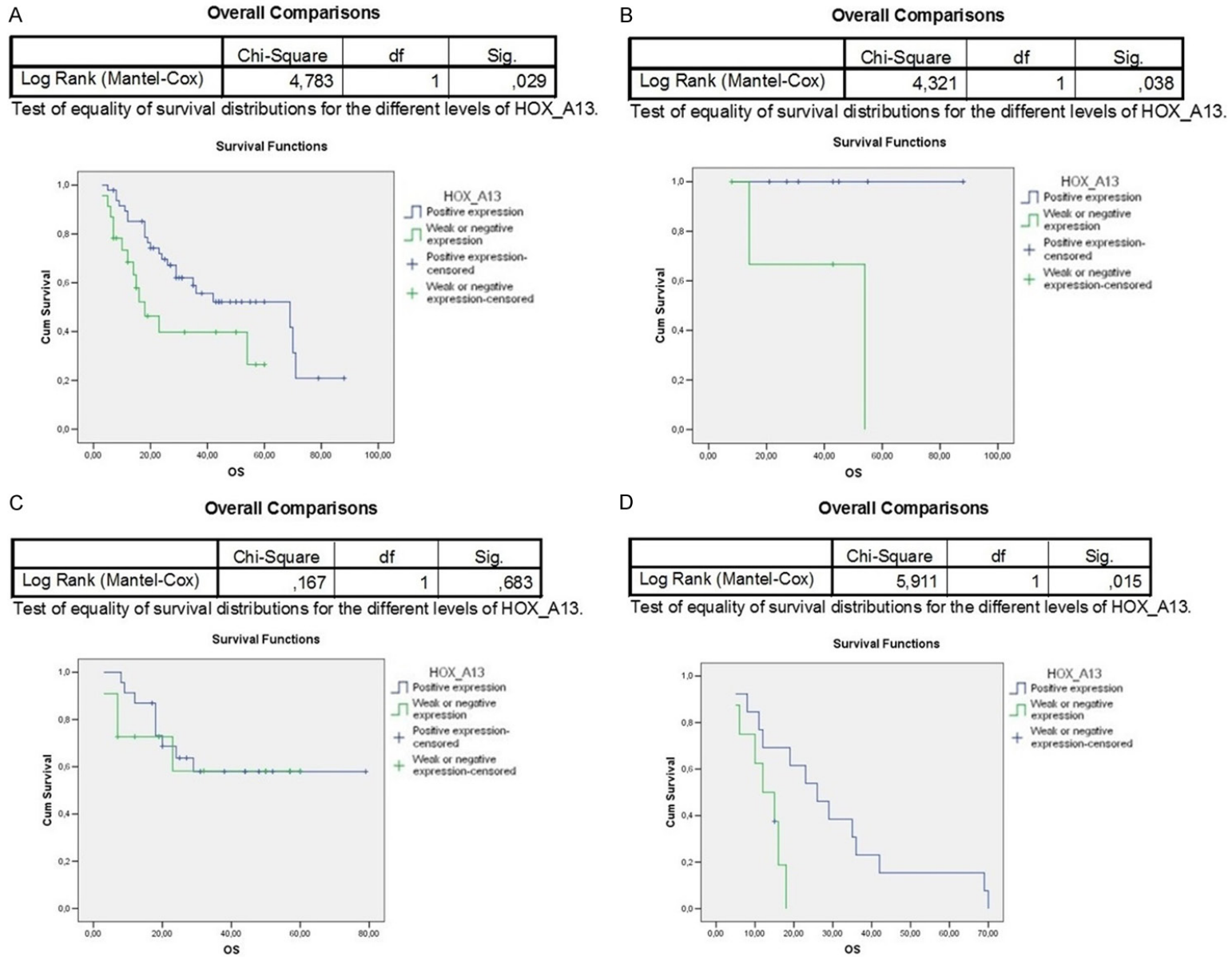


Figure 3. Kaplan-Meier curves analysis to evaluate overall survival according to HOXA13 expression in A. 94 OSCC patients; in B. Patients without treatment; C. Patients treated only with radiotherapy; D. Patients treated with chemo/radiotherapy.

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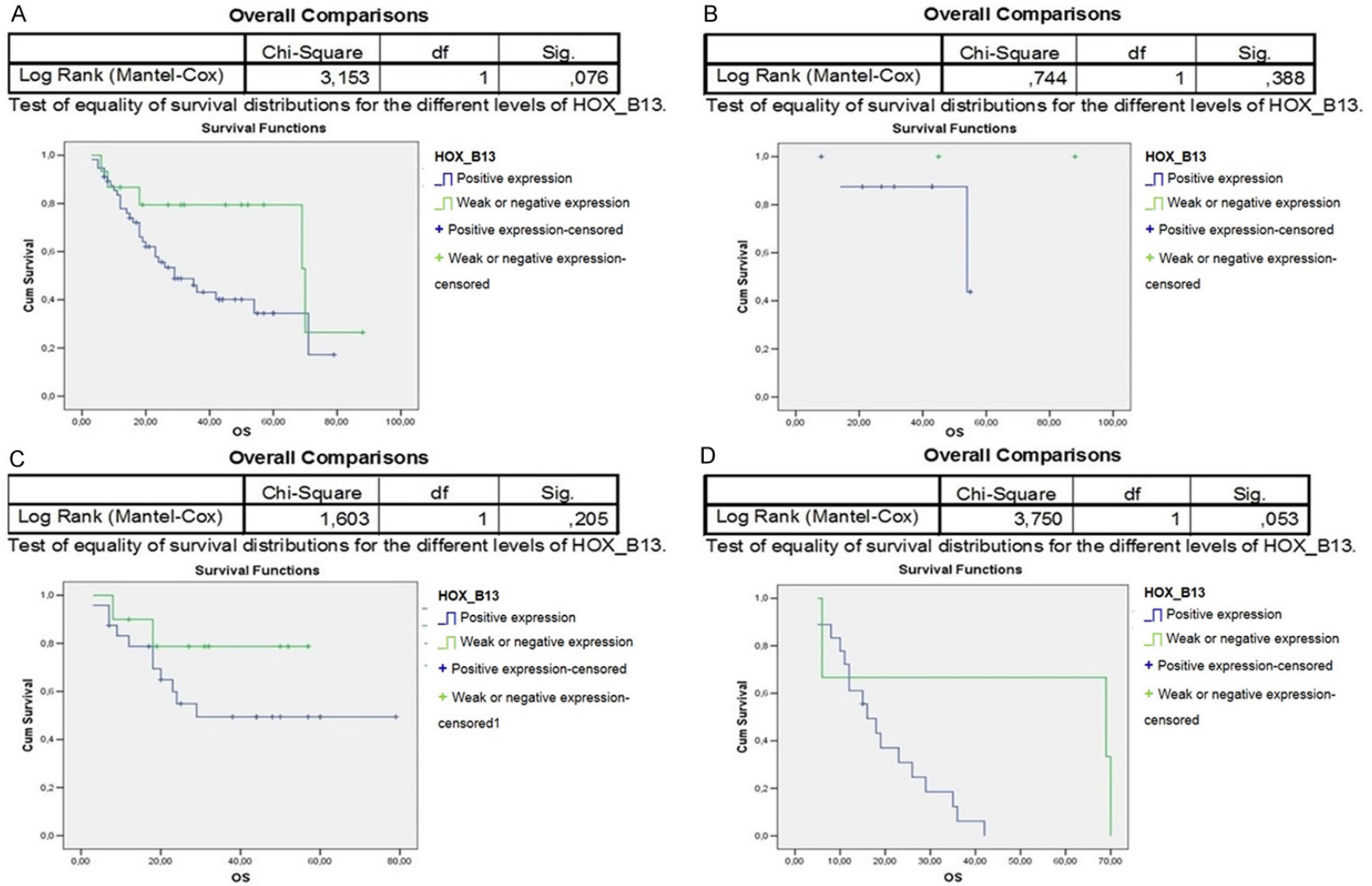


Figure 4. Kaplan-Meier curves analysis to evaluate overall survival according to HOXB13 expression in A. 94 OSCC patients; in B. Patients without treatment; C. Patients treated only with radiotherapy; D. Patients treated with chemo/radiotherapy.

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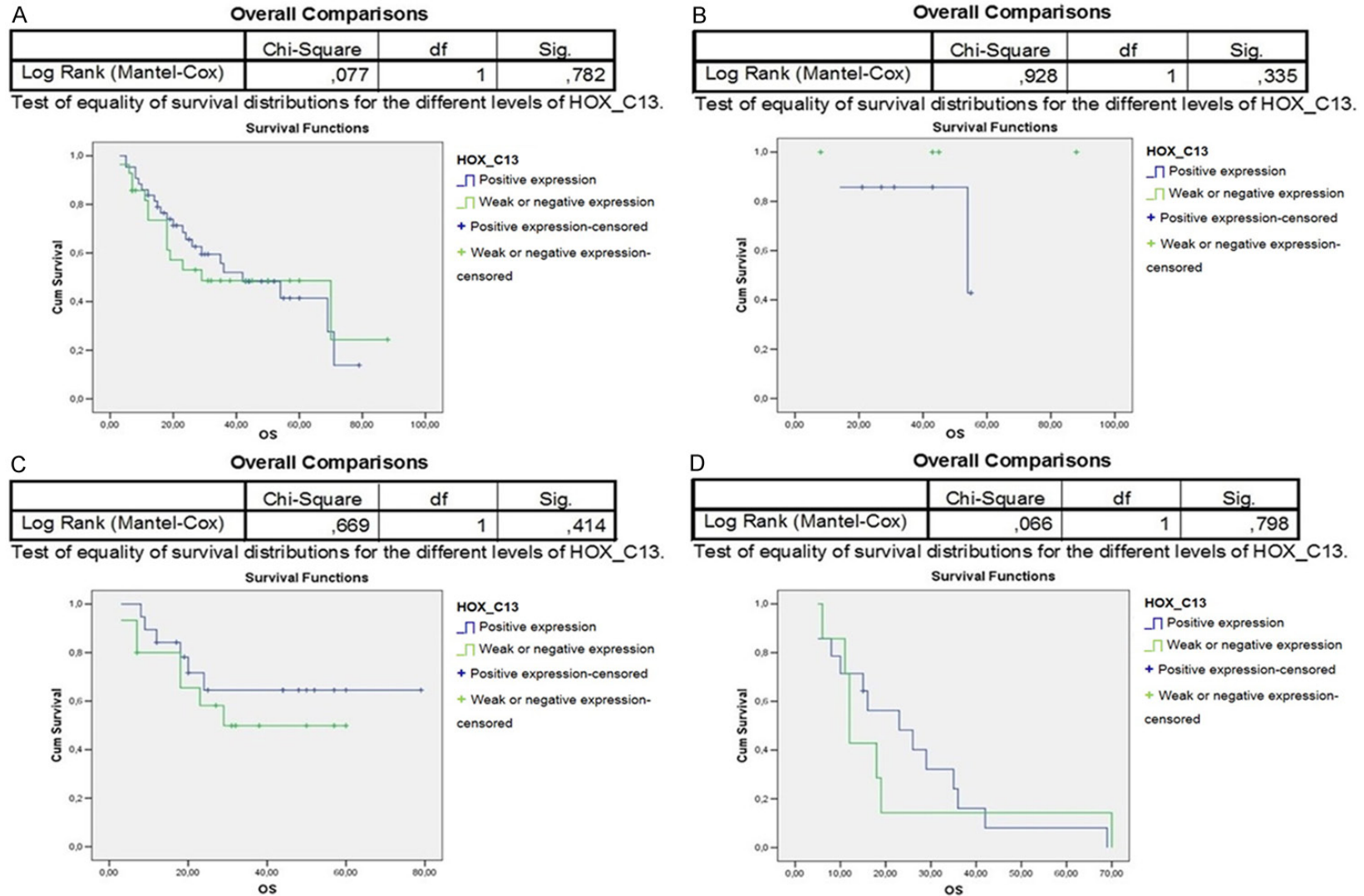


Figure 5. Kaplan-Meier curves analysis to evaluate overall survival according to HOXC13 expression in A. 94 OSCC patients; in B. Patients without treatment; C. Patients treated only with radiotherapy; D. Patients treated with chemo/radiotherapy.

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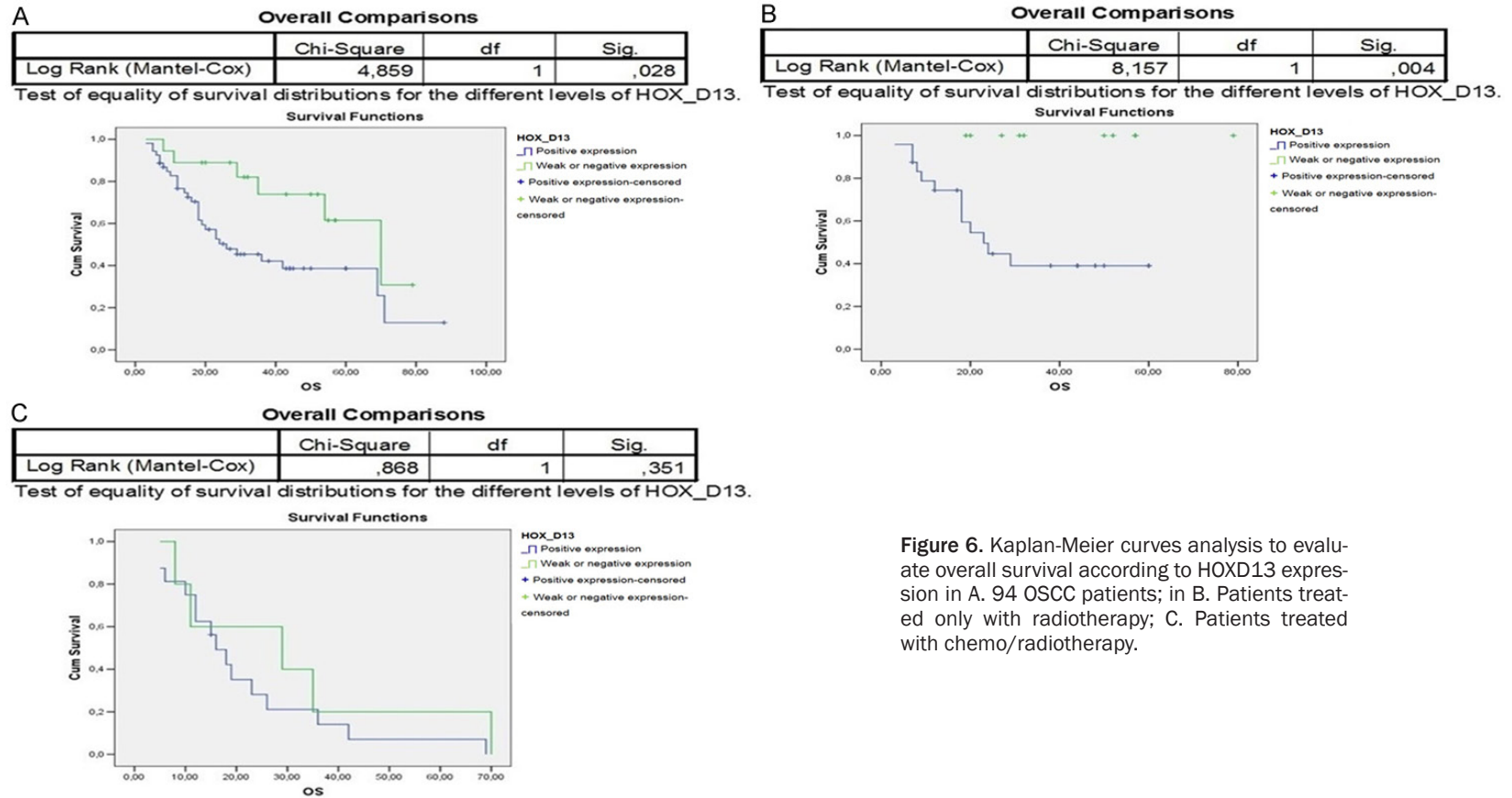


Figure 6. Kaplan-Meier curves analysis to evaluate overall survival according to HOXD13 expression in A. 94 OSCC patients; in B. Patients treated only with radiotherapy; C. Patients treated with chemo/radiotherapy.

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ity is correlated to cell proliferation and their deregulation is often associated with tumor evolution [9-14]. We analyzed paralogous 13 HOX proteins expression in a Prognostic-Tumor Array including 119 OSCC samples. HOX A13, HOX B13, HOX C13 and HOX D13 protein localization appeared prevalently nuclear but some areas showed also a cytoplasmic localization. This different sub cellular localization has been tested by analysis of mRNA transcripts for each of the 4 HOX genes. Cytoplasmic localization was previously described, and in some tumor types has represented an unfavorable prognostic factor during tumor progression [14]. In our OSCC series HOXB13 showed a high nuclear expression in the deep side of cancer, and only a trend of statistical association with a low overall survival of patients. HOXC13 nuclear expression increased in the superficial margin of the lesion. HOX B13 and HOXC13 do not display significant associations with other clinic pathological parameters in OSCC, despite HOX B13 has been associated with tumor evolution and progression of several hormone-dependent tumors, such as prostate, ovarian and breast cancers [21-23], while the prognostic role of HOX C13 was recently described in metastatic melanoma [12]. The most interesting results seem to be associated with HOX A13 and HOX D13 proteins expression in OSCC. Aberrant HOX A13 expression increased in lip, and in the superficial side of the lesion; HOXA13 was detected with a prevalent cytoplasmic (45%) compare to nuclear expression (33%). The most consistent data showed the strong HOX A13 expression significantly associated with a better prognosis at 60 months. This appears real in both patients treated only with surgery and those undergoing chemo and radiotherapy with an even stronger statistical significance. HOX A13 expression has been previously associated with progression of esophageal squamous cell carcinoma (ESCC), and it was involved in the pathogenesis of gastric cancer and hepatocarcinoma (HCC) [11, 24]. More recently, the up-regulation of HOX A13 and the long non-coding RNA, HOTTIP, located in physical contiguity with HOXA13 and that directly controls the HOXA locus gene expression, were associated with HCC patients' clinical progression and were able to predict clinic outcome and therapeutic response [25]. Moreover, HOXA13 knockdown reduces HOTTIP expression in liver cancer-derived cell lines

[26]. To date all the evidence reported in literature emphasize the prognostic role of HOX A13, highlighting its overexpression associated with tumor progression. In OSCC, the role of HOX A13 seems to follow an opposite trend. The overexpression of the marker appears protective in patients with OSCC, making to hypothesize a potential role as tumor suppressor. Regarding HOX D13 expression, a strong cytoplasmic expression, in deep side of the tumor, was detected, that gradually increased with tumor size.

HOXD13 expression appeared significantly associated with a worse prognosis and in patients undergoing radiotherapy it was strongly associated with a low overall survival. In detail, the cytoplasmic HOX D13 expression appeared inversely related to overall survival of OSCC patients, highlighting its role as tumor progression marker. Also for this gene, its activity in tumor pathogenesis and evolution is often described in an opposite manner. In fact, the downregulation of HOX D13, during tumor progression, was previously demonstrated in pancreatic cancer. HOXD13 homeoprotein expression not only decreased from normal to pancreatic tumor tissues but its de-regulation was strongly associated with clinic outcome [10]. This effect on outcome was independent from the T or N stage of the patients at the time of diagnosis. On the contrary, as in OSCC, HOX D13 expression gradually increased from normal tissue until thyroid cancers [9]. In conclusion, our data strongly highlight that HOXA13 tumor expression could be a good prognosis marker, instead HOXD13 and HOXB13 expression could be the worst prognosis markers, suggesting the potential prognostic value of paralogous 13 HOX genes in squamous cell carcinoma of the oral cavity. Their deregulation, also in OSCC, supports the important role of HOX genes in tumor evolution and suggests the development of new potential therapies targeted against the activities of these genes.

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Disclosure of conflict of interest

None.

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HOX genes and oral squamous cell carcinoma

Supplementary Table 1. Correlation between nuclear or cytoplasmic HOXA13 expression and main clinical features in deep and superficial margin of the lesion

Crosstabs		HOXA13 Deep nuclear expression		P value	HOXA13 Deep cytoplasmic expression		P value	HOXA13 Superficial nuclear expression		P value	HOXA13 Superficial cytoplasmic expression		P value
		≤40	41+		≤40	41+		≤40	41+		≤40	41+	
Median expression		≤40	41+		≤40	41+		≤40	41+		≤40	41+	
Grading	G1	11	6	0.168	11	6	0.458	8	9	0.274	6	11	0.343
		64.70588	35.29412		64.70588	35.29412		47.05882	52.94118		35.29412	64.70588	
	G2	29	27		27	29		32	14		26	20	
	G3	51.78571	48.21429	48.21429	51.78571	69.56522	30.43478	56.52174	43.47826				
		19	7	15	11	19	10	15	14				
		73.07692	26.92308	57.69231	42.30769	65.51724	34.48276	51.72414	48.27586				
Lymphonode metastasis	N0	27	18	0.6	23	22	0.685	26	14	1	20	20	0.834
		60	40		51.11111	48.88889		65	35		50	50	
	N2+	32	21		30	23		33	18		27	24	
	I	60.37736	39.62264	56.60377	43.39623	64.70588	35.29412	52.94118	47.05882				
		4	4	3	5	4	3	1	6				
	II	50	50	37.5	62.5	57.14286	42.85714	14.28571	85.71429				
	III	17	9	16	10	16	6	12	10				
		65.38462	34.61538	61.53846	38.46154	72.72727	27.27273	54.54545	45.45455				
	IV	12	13	10	15	12	9	10	11				
	IV	48	52	40	60	57.14286	42.85714	47.61905	52.38095				
		26	14	24	16	27	15	24	18				
		65	35	60	40	64.28571	35.71429	57.14286	42.85714				
T	1	7	7	0.813	7	7	0.771	8	5	0.555	6	7	0.98
		50	50		50	50		61.53846	38.46154		46.15385	53.84615	
	2	28	18		27	19		28	13		21	20	
	3	60.86957	39.13043	58.69565	41.30435	68.29268	31.70732	51.21951	48.78049				
		12	6	8	10	9	9	9	9				
	4	66.66667	33.33333	44.44444	55.55556	50	50	50	50				
	F	12	9	11	10	14	6	11	9				
		57.14286	42.85714	52.38095	47.61905	70	30	55	45				
	Gender	18	13	16	15	19	8	14	13				
	M	58.06452	41.93548	51.6129	48.3871	70.37037	29.62963	51.85185	48.14815				
		41	27	37	31	40	25	33	32				
	Age	60.29412	39.70588	54.41176	45.58824	61.53846	38.46154	50.76923	49.23077				
<68		31	20	0.84	29	22	0.549	34	16	0.513	27	23	0.676
		60.78431	39.21569		56.86275	43.13725		68	32		54	46	
	>68	28	20		24	24		25	17		20	22	
		58.33333	41.66667	50	50	59.52381	40.47619	47.61905	52.38095				

HOX genes and oral squamous cell carcinoma

Chemotherapy	No	30	18	1	29	19	0.22	33	10	0.273	23	20	0.624
		62.5	37.5		60.41667	39.58333		76.74419	23.25581		53.48837	46.51163	
	Yes	16	9		11	14		16	10		12	14	
		64	36		44	56		61.53846	38.46154		46.15385	53.84615	
Radiotherapy	No	6	6	0.341	5	7	0.357	8	4	0.734	5	7	0.54
		50	50		41.66667	58.33333		66.66667	33.33333		41.66667	58.33333	
	Yes	40	21		35	26		41	16		30	27	
		65.57377	34.42623		57.37705	42.62295		71.92982	28.07018		52.63158	47.36842	
Anatomic site	Lip	2	1	1	0	3	0.154	2	1	0.111	0	3	0.044
		66.66667	33.33333		0	100		66.66667	33.33333		0	100	
	Toungue	35	24		34	25		30	24		25	29	
		59.32203	40.67797		57.62712	42.37288		55.55556	44.44444		46.2963	53.7037	
	Other	22	15		19	18		27	8		22	13	
		59.45946	40.54054		51.35135	48.64865		77.14286	22.85714		62.85714	37.14286	

HOX genes and oral squamous cell carcinoma

Supplementary Table 2. Correlation between nuclear or cytoplasmic HOXB13 expression and main clinical features in deep and superficial margin of the lesion

Crosstabs		HOXB13 Deep nuclear expres- sion		P value	HOXB13 Deep cytoplasmic expression		P value	HOXB13 Superficial nuclear expression		P value	HOXB13 Superficial cytoplasmic expression		P value		
		≤30	31+		≤0	1+		≤30	31+		≤0	1+			
Median ex- pression		≤30	31+		≤0	1+		≤30	31+		≤0	1+			
Grading	G1	11	8	0.383	14	5	1	10	10	0.623	13	6	0.544		
		57.89473684	42.10526316		73.68421053	26.31578947		52.63158	47.36842		68.42105	31.57895			
	G2	34	26	56.66666667	43	17	71.66666667	34	19	65.38462	28	24	34.61538	53.84615	46.15385
		56.66666667	43.33333333		71.66666667	28.33333333		65.38462	34.61538		53.84615	46.15385			
	G3	11	16	40.74074074	19	8	70.37037037	17	11	60.71429	16	12	39.28571	57.14286	42.85714
		40.74074074	59.25925926		70.37037037	29.62962963		60.71429	39.28571		57.14286	42.85714			
Lymphonode metastasis	N0	29	21	0.329	36	14	1	26	19	0.54	27	18	0.83		
		58	42		72	28		57.77778	42.22222		60	40			
	N2+	26	29	47.27273	39	16	70.90909	34	19	64.15094	30	23	35.84906	56.60377	43.39623
		47.27273	52.72727		70.90909	29.09091		64.15094	35.84906		56.60377	43.39623			
Stage	I	7	4	0.426	9	2	0.319	5	5	0.816	7	3	0.477		
		63.63636364	36.36363636		81.81818	18.18182		50	50		70	30			
	II	17	11	60.71428571	19	9	67.85714	14	8	63.63636	14	8	36.36364	63.63636	36.36364
		60.71428571	39.28571429		67.85714	32.14286		63.63636	36.36364		63.63636	36.36364			
	III	10	15	53.48837209	21	4	65.11628	14	10	65.11628	15	9	34.88372	48.83721	51.16279
		53.48837209	46.51162791		65.11628	34.88372		65.11628	34.88372		48.83721	51.16279			
IV	40	60	57.14285714	84	16	71.42857	58.33333	41.66667	62.7907	62.5	37.5	37.2093	62.7907	37.2093	
	57.14285714	42.85714286		71.42857	28.57143		62.7907	37.2093		62.7907	37.2093				
T	1	10	8	0.624	15	3	0.599	9	7	0.915	11	5	0.399		
		55.55555556	44.44444444		83.33333	16.66667		56.25	43.75		68.75	31.25			
	2	28	21	57.14285714	35	14	71.42857	27	16	62.7907	27	16	37.2093	62.7907	37.2093
		57.14285714	42.85714286		71.42857	28.57143		62.7907	37.2093		62.7907	37.2093			
	3	7	11	38.88888889	13	5	72.22222	11	8	57.89474	9	10	42.10526	47.36842	52.63158
		38.88888889	61.11111111		72.22222	27.77778		57.89474	42.10526		47.36842	52.63158			
4	12	10	54.54545455	14	8	63.63636	14	7	66.66667	10	11	33.33333	47.61905	52.38095	
	54.54545455	45.45454545		63.63636	36.36364		66.66667	33.33333		47.61905	52.38095				
Gender	F	18	13	0.67	24	7	0.484	19	10	0.656	15	14	0.506		
		58.06451613	41.93548387		77.41935	22.58065		65.51724	34.48276		51.72414	48.27586			
	M	39	37	51.31578947	53	23	69.73684	42	28	60	42	28	30.26316	60	40
		51.31578947	48.68421053		69.73684	30.26316		60	40		60	40			

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Age	<68	35	22	0.84	43	14	0.549	36	15	0.066	28	23	0.685
		61.40350877	38.59649123		75.4386	24.5614		70.58824	29.41176		54.90196	45.09804	
	>68	22	28		34	16		25	23		29	19	
		44	56		68	32		52.08333	47.91667		60.41667	39.58333	
Chemotherapy	No	31	21	0.473	38	14	0.5	25	19	0.458	27	17	0.234
		59.61538462	40.38461538		73.07692308	26.92307692		56.81818	43.18182		61.36364	38.63636	
	Yes	13	13		17	9		19	9		13	15	
		50	50		65.38461538	34.61538462		67.85714	32.14286		46.42857	53.57143	
Radiotherapy	No	8	8	0.584	11	5	0.599	4	9	0.025	6	7	0.543
		50	50		68.75	31.25		30.76923	69.23077		46.15385	53.84615	
	Yes	36	26		44	18		40	19		34	25	
		58.06451613	41.93548387		70.96774194	29.03225806		67.79661	32.20339		57.62712	42.37288	
Anatomic site	Lip	2	2	0.608	2	2	0.277	1	3	0.258	2	2	0.157
		50	50		50	50		25	75		50	50	
	Toungue	32	33		50	15		35	23		38	20	
		49.23076923	50.76923077		76.92307692	23.07692308		60.34483	39.65517		65.51724	34.48276	
	Other	23	15		25	13		25	12		17	20	
		60.52631579	39.47368421		65.78947368	34.21052632		67.56757	32.43243		45.94595	54.05405	

HOX genes and oral squamous cell carcinoma

Supplementary Table 3. Correlation between nuclear or cytoplasmic HOXC13 expression and main clinical features in deep and superficial margin of the lesion

Crosstabs		HOXC13 Deep nuclear expression		P value	HOXC13 Deep cytoplasmic expression		P value	HOXC13 Superficial nuclear expression		P value	HOXC13 Superficial cytoplasmic expression		P value
		≤10	11+		≤10	11+		≤10	11+		≤10	11+	
Grading	G1	11	9	0.892	15	5	0.896	9	10	0.738	13	6	0.67
		55	45		75	25		47.36842	52.63158		68.42105	31.57895	
	G2	34	23	59.64912	40.35088	78.94737	21.05263	55.31915	44.68085	78.7234	21.2766		
		56	44		80	20	46.42857	53.57143	71.42857	28.57143			
Lymphnode metastasis	N0	24	24	0.164	37	11	0.814	23	20	0.679	30	13	0.477
		50	50		77.08333	22.91667		53.48837	46.51163		69.76744	30.23256	
	N+	34	19	64.15094	35.84906	79.24528	20.75472	48	52	78	22		
		56	44		80	20	46.42857	53.57143	71.42857		28.57143		
STAGE	I	5	5	0.408	8	2	0.132	7	4	0.833	8	3	0.553
		50	50		80	20		63.63636	36.36364		72.72727	27.27273	
	II	14	12	53.84615	46.15385	65.38462	34.61538	50	50	63.63636	36.36364		
		50	50		92.30769	7.692308	45.45455	54.54545	81.81818		18.18182		
	III	13	13	68.29268	31.70732	78.04878	21.95122	52.5	47.5	77.5	22.5		
		50	50		92.30769	7.692308	45.45455	54.54545	81.81818		18.18182		
	IV	28	13	64.70588	35.29412	82.35294	17.64706	72.22222	27.77778	77.77778	22.22222		
		26	19		33	12	18	22	29		11		
T	1	11	6	0.357	14	3	0.738	13	5	0.161	14	4	0.974
		57.77778	42.22222		73.33333	26.66667		45	55		72.5	27.5	
	2	8	11	42.10526	57.89474	84.21053	15.78947	38.88889	61.11111	77.77778	22.22222		
		15	7		18	4	11	8	14		5		
	3	8	11	68.18182	31.81818	81.81818	18.18182	57.89474	42.10526	73.68421	26.31579		
		42.10526	57.89474		84.21053	15.78947	38.88889	61.11111	77.77778		22.22222		
Gender	F	17	12	1	23	6	1	16	9	0.168	20	5	0.597
		58.62069	41.37931		79.31034	20.68966		64	36		80	20	
	M	43	31	58.10811	41.89189	78.37838	21.62162	33	37	72.85714	27.14286		
		58.10811	41.89189		78.37838	21.62162	47.14286	52.85714	72.85714		27.14286		
Age	<68	39	16	0.009	45	10	0.473	31	22	0.151	45	8	0.017
		70.90909	29.09091		81.81818	18.18182		58.49057	41.50943		84.90566	15.09434	
	>68	21	27	43.75	56.25	75	25	42.85714	57.14286	61.90476	38.09524		
		43.75	56.25		75	25	42.85714	57.14286	61.90476		38.09524		

HOX genes and oral squamous cell carcinoma

Chemotherapy	No	27	23	1	37	13	1	24	22	0.806	32	14	0.791
		54	46		74	26		52.17391	47.82609		69.56522	30.43478	
	Yes	14	11		18	7		12	13		16	9	
		56	44		72	28		48	52		64	36	
Radiotherapy	No	7	7	0.771	9	5	0.504	7	6	1	7	6	0.327
		50	50		64.28571	35.71429		53.84615	46.15385		53.84615	46.15385	
	yes	34	27		46	15		29	29		41	17	
		55.7377	44.2623		75.40984	24.59016		50	50		70.68966	29.31034	
Anatomic site	Lip	1	3	0.373	2	2	0.374	2	2	1	1	3	0.071
		25	75		50	50		50	50		25	75	
	Toungue	38	24		50	12		29	28		44	13	
		61.29032	38.70968		80.64516	19.35484		50.87719	49.12281		77.19298	22.80702	
	Other	21	16		29	8		18	16		26	8	
		56.75676	43.24324		78.37838	21.62162		52.94118	47.05882		76.47059	23.52941	

HOX genes and oral squamous cell carcinoma

Supplementary Table 4. Correlation between nuclear or cytoplasmic HOXD13 expression and main clinical features in deep and superficial margin of the lesion

Crosstabs	HOXD13 Deep nuclear expression		P value	HOXD13 Deep cytoplasmic expression		P value	HOXD13 Superficial nuclear expression		P value	HOXD13 Superficial cytoplasmic expression		P value			
	≤15	16+		≤0	1+		≤15	16+		≤0	1+				
Grading	G1	7	1	15	1	0.163	7	8	0.869	13	2	0.216			
		43.75			93.75		6.25			46.66667	53.33333			86.66667	13.33333
	G2	24			37		16			20	20			25	15
		45.28302		69.81132	30.18868		50	50		62.5	37.5				
	G3	10		16	6		13	10		16	7				
		45.45455		72.72727	27.27273		56.52174	43.47826		69.56522	30.43478				
Lymphonode metastasis	N0	20	0.525	32	9	0.633	17	18	0.651	25	10	1			
		48.78049			78.04878		21.95122			48.57143	51.42857			71.42857	28.57143
	N+	20			36		13			23	19			29	13
		40.81633		73.46939	26.53061		54.7619	45.2381		69.04762	30.95238				
STAGE	I	6	0.26	8	1	0.038	5	4	0.962	7	2	0.369			
		66.66667			88.88889		11.11111			55.55556	44.44444			77.77778	22.22222
	II	7			18		4			9	7			13	3
		31.81818			81.81818		18.18182			56.25	43.75			81.25	18.75
	III	13			21		3			9	10			14	5
	54.16667		87.5	12.5		47.36842	52.63158		73.68421	26.31579					
	IV	16		22	15		17	17		20	14				
		43.24324		59.45946	40.54054		50	50		58.82353	41.17647				
T	1	7	0.709	14	2	0.001	8	6	0.477	9	5	0.01			
		43.75			87.5		12.5			57.14286	42.85714			64.28571	35.71429
	2	16			32		8			19	13			27	5
		40			80		20			59.375	40.625			84.375	15.625
	3	10			16		2			8	10			13	5
	55.55556		88.88889	11.11111		44.44444	55.55556		72.22222	27.77778					
	4	9		7	11		5	9		5	9				
		50		38.88889	61.11111		35.71429	64.28571		35.71429	64.28571				
Gender	F	10	0.487	15	11	0.03	10	9	1	10	9	0.09			
		38.46154			57.69231		42.30769			52.63158	47.36842			52.63158	47.36842
	M	32			54		12			30	29			44	15
		48.48485		81.81818	18.18182		50.84746	49.15254		74.57627	25.42373				

HOX genes and oral squamous cell carcinoma

Age	<68	24	0.304	34	13	0.633	15	26	0.007	26	15	0.327
		51.06383		72.34043			27.65957			36.58537		
	>68	18		35	10		25	12		28	9	
		40		77.77778			22.22222			67.56757		
Chemotherapy	No	18	0.613	35	9	0.027	23	16	0.092	27	12	0.557
		40.90909		79.54545			20.45455			58.97436		
	Yes	11		12	11		6	13		11	8	
		47.82609		52.17391			47.82609			31.57895		
Radiotherapy	No	6	0.75	10	2	0.324	4	6	0.73	9	1	0.141
		50		83.33333			16.66667			40		
	Yes	23		37	18		25	23		29	19	
		41.81818		67.27273			32.72727			52.08333		
Anatomic site	Lip	2	0.383	3	1	0.915	2	2	0.862	3	1	0.915
		50		75			25			50		
	Tongue	27		40	12		22	23		32	13	
		51.92308		76.92308			23.07692			48.88889		
	Other	13		26	10		16	13		19	10	
		36.11111		72.22222			27.77778			55.17241		