

# SELECTION AND PLATFORM TRANSITION OF PROGNOSTIC GENE SIGNATURES OF ORAL CANCER

**Introduction:** Accurate predictions regarding the staging and prognosis of oral cancer patients remain challenging. Molecular profiling might be of assistance to predict the major relevant outcome parameters of oral cancer: N-staging of the clinically N0 neck, locoregional recurrence and survival.

**Purpose:** To identify a set of genes that can be assayed on an RT-qPCR platform to improve N-staging and outcome prediction of oral cancer.

**Methods:** Two independent microarray studies of HPV-negative oral cancer patients (n=150 and n=94) were used for gene selection. Univariate and multivariate tests were performed to select genes related to overall survival, locoregional recurrence and/or nodal metastasis. Validation of the selected gene sets is performed in 100 additional independent oral cancer patients by RT-qPCR.

**Results:** From the microarray data, 60 genes were chosen for further analysis, of which 20 were associated with overall survival, 20 with locoregional recurrence and 20 with the presence of nodal metastasis. These genes were transferred to an RT-qPCR platform that is more stable, user-friendly and widely applied, which will favour clinical implementation. For further gene selection on this platform, the genes were tested on 20 cases for which the microarray data were available, and 20 independent cases. In total 54 genes showed promising results, and 6 genes had to be substituted.

**Conclusion:** An oral cancer prognostic signature of 60 genes was selected from microarray analysis, transferred to an RT-qPCR platform, improved by interim analysis, and will now be retrained and validated on 100 independent oral cancers to improve N-staging and outcome prediction.

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