

## **Expression Profiling and Immunohistochemical Analysis of Squamous Cell Carcinoma of Head and Neck (Tumor, Transition Zone, Normal) by Whole Genome Scale Sequencing**

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**Abstract :** The possibility to determine genome-wide expression profiles of cells and tissues opens a new level of analysis in the quest to define dysregulation in malignancy and thus identify new tumor markers. Toward this long-term aim, we here address two issues on this level for head and neck cancer specimen: i) defining profiles in different regions, i.e. the tumor, the transition zone and normal control and ii) comparing complete data sets for seven individual patients. Special focus in the flanking immunohistochemical part is given to adhesion/growth-regulatory galectins that upregulate chemo- and cytokine expression in an NF- $\kappa$ B-dependent manner, to these regulators and to markers of differentiation, i.e. keratins. The detailed listing of up- and down-regulations, also available in printed form (1), not only served to unveil new candidates for testing as marker but also let the impact of the tumor in the transition zone become apparent. The extent of interindividual variation raises a strong cautionary note on assuming uniformity of regulatory events, to be noted when considering therapeutic implications. Thus, a combination of test targets (and a network analysis for galectins and their downstream effectors) is (are) advised prior to reaching conclusions on further perspectives.

**Keywords :** galectins, genome scale sequencing, squamous cell carcinoma, transition zone

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