High throughput mutational profiling of signaling molecules in oral cancer.

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Abstract:

It is well established that a plethora of mutations that occur in oncogenes and tumor-suppressor genes are the main drivers of tumorigenesis. The identification of these mutations provides important clues to the cellular processes of carcinogenesis and affords an opportunity for these genes to be used for diagnostic and therapeutic purposes. In comparison to cancers such as breast, lung and colorectal, there is a lack of systematic, large scale characterization of oncogenic mutations oral squamous cell carcinoma (OSCC).

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