## TRANSCRIPTOME ANALYSIS OF HEAD AND NECK AND THYROIDTUMOURS BASED ON THE GENERATION AND ANALYSIS OF 200,000 ESTs

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In order to contribute to the understanding of the molecular basis of squamous cell carcinomas of head and neck and thyroid tumours (HNT), we have generated 213,636 EST sequences derived from normal and tumour tissues obtained from oral cavity. larynx, pharynx and thyroid. These sequences were clustered, mapped and classified according to putative function based on Gene Onthology (GO). Visual inspection of all clusters matching human genes indicated 748 putatively new alternative splicing isoforms and many new human transcripts. A subset of the new transcripts and new splicing isoforms was selected and experimentally confirmed by RT-PCR in tumour and non-tumour samples from diverse tissues. Transcriptome sharing analysis was performed for the mucosal tumours using different approaches, showed pharynx tumours to be more distantly related from oral cavity and larynx. An analysis of differential expression using selected sequences mapped to regions frequently amplified or deleted in these tumours enabled the identification of putative markers for these malignancies that were subsequently confirmed by guantitative PCR in a different set of samples. This is the largest dataset of ESTs derived from HNT tissues and it provides potential a list of malignancy markers in the form of new splicing variants, new transcripts or candidates for differential gene expression that can be used for the better understanding of these tumours. A website has been built and is available for a further analysis of these tissues and sequences. This approach should be valuable for gathering relevant biological information for a number of tumours such as colon, breast and prostate, which have been extensively studied by cDNA sequencing.