The foremost aim of this study was to evaluate the relation amongst the clinical history and histo-pathology of OSCC and OPC patients with Human Papilloma Virus (HPV) infection and to correlate the molecular expression between the HPV positive and negative tumours.
A total of 211 patients were obtained from University College London Hospital (UCLH) data base and information on various clinicopathological parameters. In addition, FFPE samples from 8 tonsillar SCC patients and 16 sites i.e. two sites each from 8 cancer patients (n=8, HPV positive=4×2; HPV negative= 4×2) were micro-dissected, RNA was extracted and expression assay was developed using qRT-PCR. The assay was used to assess various HPV and other genes. The expression assay tested for the following HPV related genes; HPV 16-E6, HPV 16-E7, HPV 18, HPV 33, p16 and exons from two genes implicated in oral cancers; TP53 and PIK3CA. Statistical significance was found when comparing between progression of disease with medical history (p=0.014), HPV positive tumours and invasion (TNM classification) in the tissues (p=0.014), HPV infected tumours and progression of the cancer (p=0.037). Analysis of the data from the in house expression assay showed significance when comparing immunohistochemistry HPV positive and negative cases for HPV 16-E6 (p=0.002) and p16 (p=0.009) respectively. The assay's flexibility make it a powerful diagnostic tool for screening multiple patients for virus specific and clinically specific biomarkers for oral cancers. Future study would use this assay to screen a larger cohort of patients with other viral genes and oral cancer related biomarkers.