# EXPLORING GENE AND PROTEIN EXPRESSION IN THE TUMOUR AND TUMOUR MICROENVIRONMENT OF NASOPHARYNGEAL CARCINOMA

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Nasopharyngeal carcinoma (NPC) is an Epstein-Barr virus (EBV)-associated malignancy with high incidence in southeast China and southeast Asia [1,2]. EBV is consistently associated with these tumours and is reported to be expressed in all tumour cells [3]. While we know that the pattern of viral expression in NPC is Latency II [4], we lack an understanding of 1) if and which viral proteins are co-expressed in individual virally infected cells, 2) the impact of this viral protein expression on the phenotype of nearby cells and 3) the spatial composition of the tumour microenvironment (TME). In order to explore these unknowns, we are currently using multiplex IHC (40-plex, CODEX) to spatially examine the viral and cellular protein expression in the tumour and TME. This data will be complimented by 100-plex RNA-ISH to spatially examine the viral and cellular gene expression in the same malignancy. Both techniques will interrogate immune cell subsets including B cells, T cells and macrophages to identify their distribution and phenotype within the tumour. Together, these projects aim to identify spatial features of the tumour/TME which can advance our understanding of NPC and hence improve treatment of this malignancy.

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