Human papillomaviruses (HPVs) are the small circular double-stranded DNA onco-viruses known to play a crucial role in the progression and etiology of cervical cancer, head and neck squamous cell carcinomas (HNSCCs), and many more. Viral integration is a key incident in HPV-mediated carcinogenesis, which leads to the disruption of various key cellular genes. Thus, contributes in aberrant proliferation, genomic instability i.e. structural alterations, translocations, large deletions etc., cellular immortalization and enhance malignant progression.

In this study, we have performed a systematic meta-analysis of 463 disrupted genes due to integration events that might be expedient to support cancer biomarker discovery.

Our integrative functional and biological network analysis identify distinct pattern or modules associated with various biological processes, protein classes, pathways, molecular functions in the context of gene ontology, co-expression, co-localization, protein-protein interactions etc.

Most of the genes are interrelated with tumor development and various regulatory processes mainly binding, cell differentiation, DNA repair mechanisms, apoptosis, signaling and so on, that could jointly become involved in viral induced oncogenesis.

In this study, we have performed a systematic meta-analysis of 463 disrupted genes due to integration events that might be expedient to support cancer biomarker discovery.

These findings may be helpful to accelerate clinical biomarker discovery for HPV mediated carcinomas.