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Viralign: A tool for uncovering functional viral elements

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Abstract

The availability of broad epigenomic profiles of human tissues provides an opportunity to uncover viral sequences and their corresponding functional regulatory elements in otherwise overlooked datasets. We developed Viralign, a throughput screening method to discover and interpret viral functional information in existing short read archive data. Using a comprehensive reference database, Viralign scans sequence data for known viral sequences and generates an alignment report with read information and genome coverage. Viralign analyzes functional datasets for regulatory elements and provides coordinate and visualization files that can be viewed in a genome browser. Additionally, this method searches for potential integration sites and variants by genome assembly. In a pilot study, we performed H3K27me3 ChIP-seq in monocytes of an HHV6 infected individual and compared this to U2OS cells infected with HHV6A and HHV6B and use Viralign to detect HHV6 insertion loci and H3K27me3 enriched regions.

Keywords:

The source code as well as additional data for Viralign will be made publicly available