

# GENOMIC SURVEILLANCE OF THE RIFT VALLEY FEVER: FROM SEQUENCING TO LINEAGE ASSIGNMENT

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## Introduction

Rift Valley fever (RVF) virus is a re-emerging zoonotic disease of arboviral origin, and belonging to the *Bunyaviridae* family [1]. The evolutionary history of Rift Valley fever virus (RVFV) is complex and has been greatly influenced by dramatic changes to environment throughout Africa in the past 150 years. Over this time period, RVFV gene flow has been impacted on various levels such as geographic dispersal and reassortment events. Overall, there are 15 lineages, designated from A to O [2]. On numerous occasions, viruses from these lineages have been transported outside enzootic regions through movement of infected animals and/or mosquitoes. This has led to large outbreaks in countries where the disease had not been previously reported. Genomic surveillance of the virus diversity is crucial in developing intervention strategies. To undertake genomic surveillance of the virus, we sought:

1. To reliably classify and assign Rift Valley fever virus (RVFV) sequences to lineages.
2. To genetically characterize RVFV isolates through whole genome sequencing.

## Methods

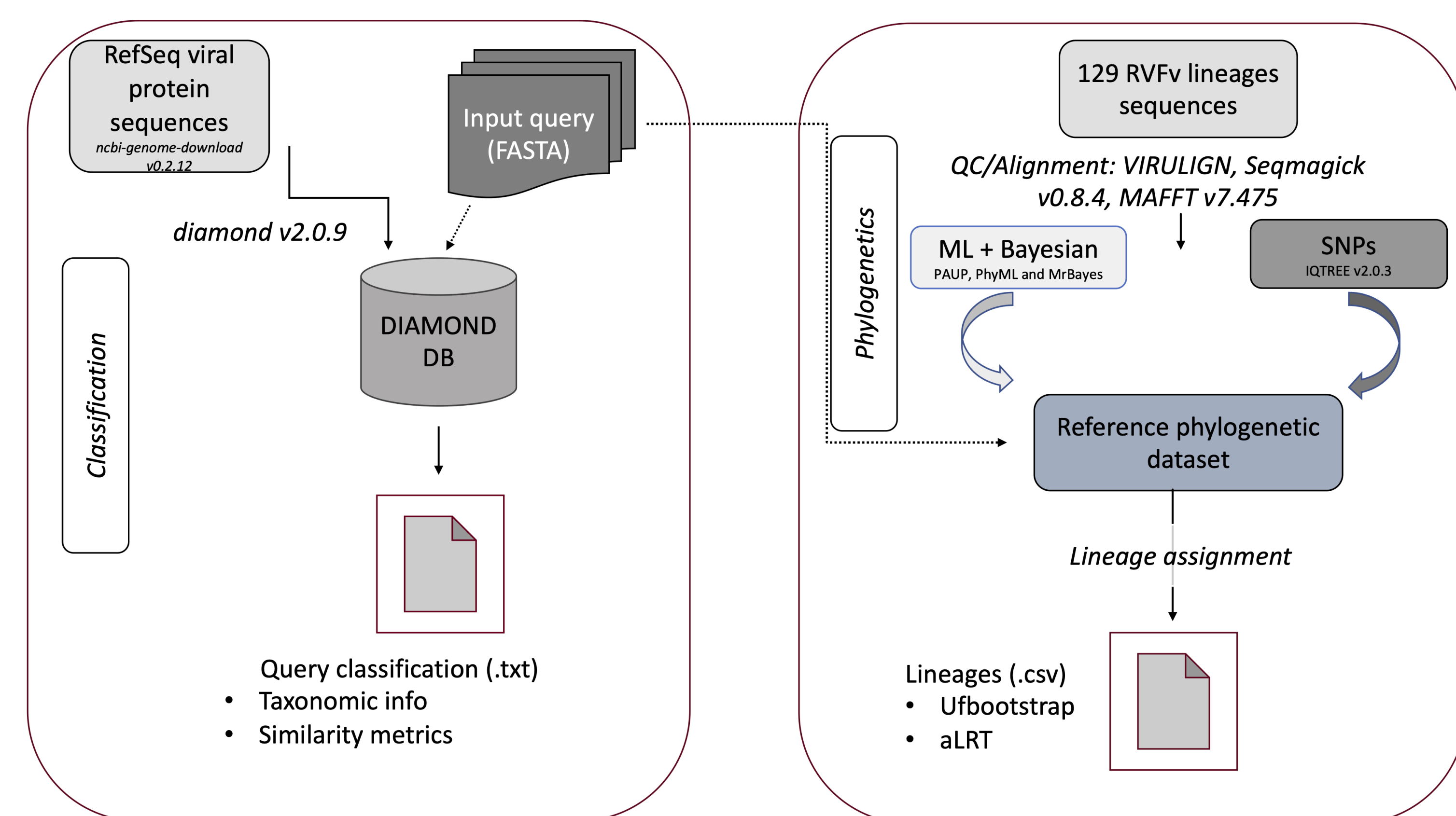


Figure 1: Lineage assignment process.

## Results

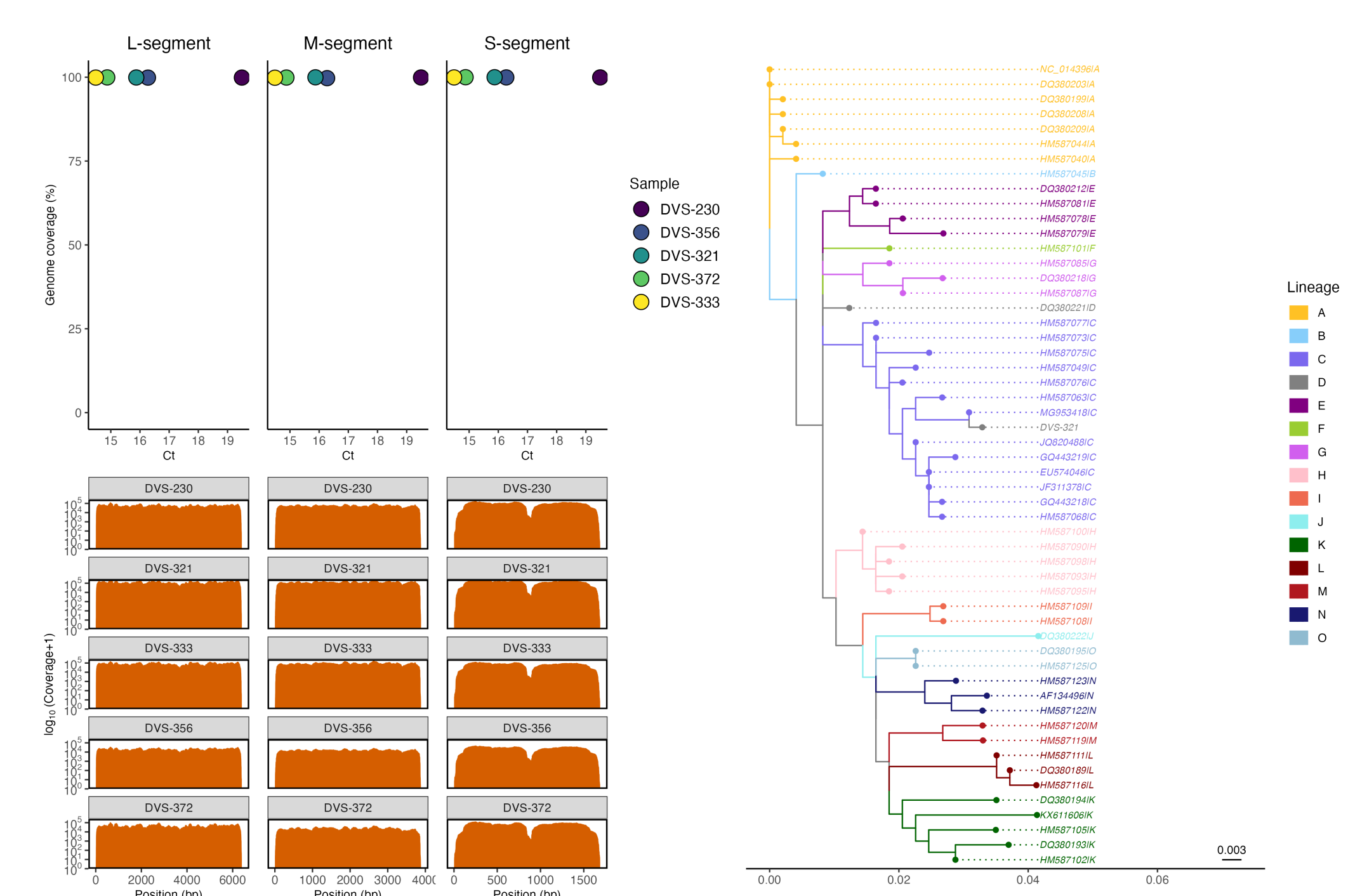


Figure 3: RVFV genome coverage versus cycle threshold values, Reads coverage and Maximum likelihood phylogenetic tree. Successfully recovered 99% viral consensus sequences. Query sequence, DVS-321, clusters in lineage C clade.

Query	Lineage	aLRT	UFboot	Segment	Length	Identity(%)
DVS-230	C	89	84	M	3885	99.3
DVS-321	C	86	95	M	3885	99.3
DVS-333	C	88	90	M	3885	99.4
DVS-356	C	88	89	M	3885	99.3
DVS-372	C	87	92	M	3885	99.4

## One Health Relevance

We generated complete genomic sequences of 5 Rift valley fever virus isolates from outbreak samples in Kenya. The isolates used were all vertebrate host (*Bos taurus*). These sequences will enrich genetic characterization of the virus by allowing phylogenetic inference between known and newly sequenced strains. We developed a command line pipeline and a user-friendly Rift Valley fever virus typing tool with the aim of rapidly characterizing RVF genomic sequences. This is useful in tracing the origin of outbreaks and supporting surveillance efforts.

## References

1. Michel Pepin, Michèle Bouloy, Brian H. Bird, Alan Kemp, Janusz Paweska. Rift Valley fever virus (*Bunyaviridae: Phlebovirus*): an update on pathogenesis, molecular epidemiology, vectors, diagnostics and prevention. *Veterinary Research* **41**, 1–40 (May 2010).
2. Grobbelaar A. A., Weyer J, Leman P. A., Kemp, A., Paweska, J. T., Swanepoel, R. Molecular Epidemiology of Rift Valley Fever Virus. *Emerging Infectious Diseases* **17** (2011).

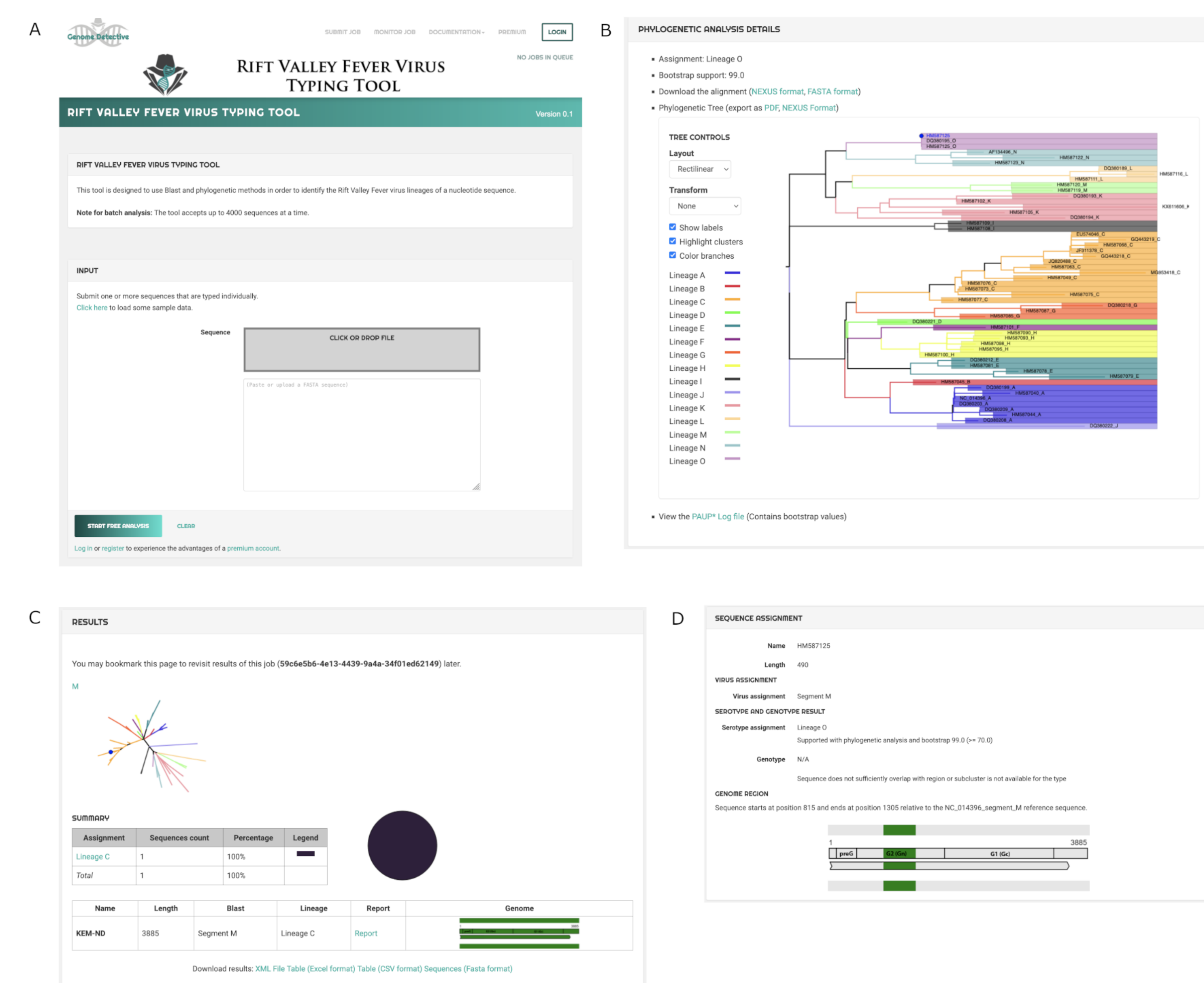


Figure 2: The web interface offers a portal for users to perform classification and visualize the results

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