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Emergence of a Bundibugyo virus variant in the 2026 outbreak in the Democratic Republic of the Congo and Uganda

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Editor summary:
A phylogenetic analysis of 22 genomes from the recent Bundibugyo virus outbreak in the Democratic Republic of the Congo and Uganda suggests the outbreak was caused by a new zoonotic spillover event

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1. Extended Data

Figure or Table # Please group Extended Data items by type, in sequential order. Total number of items (Figs. + Tables) must not exceed 10.	Figure/Table title One sentence only	Filename Whole original file name including extension. i.e.: Smith_ED_Fig1.jpg	Figure/Table Legend If you are citing a reference for the first time in these legends, please include all new references in the main text Methods References section, and carry on the numbering from the main References section of the paper. If your paper does not have a Methods section, include all new references at the end of the main Reference list.
Extended Data Fig. 1	Uncollapsed phylogenetic tree of Bundibugyo virus genomes showing the complete phylogenetic context.	Supplementary_Figure_Tree_Uncollapsed.pdf	
Extended Data Table. 1	Summary of sequencing data	Extended Data Table 1. Number of reads.docx	

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	output, complete BDBV genomes.		
Extended Data Table. 2	Previously published BDBV genome sequences used in this study with NCBI GenBank accession (Accession), date of sample collection (Date), country of origin (Country), associated BVD outbreak (Outbreak), Authors, and submitting institution (Institution).	Extended Data Table 2. Previous BDBV genomes.docx	
Extended Data Table. 3	Mutational profile of the 2026 BDBV genomes with nucleotide coordinates relative to BDBV	Extended Data Table 3. Mutational profil.docx	

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	reference genome (GenBank accession KC545393.1)		

1. Supplementary Information:

A. PDF Files

Item	Present?	Filename Whole original file name including extension. i.e.: Smith_SI.pdf. The extension must be .pdf	A brief, numerical description of file contents. i.e.: *Supplementary Figures 1-4, Supplementary Discussion, and Supplementary Tables 1-4.*
Supplementary Information	No		
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Emergence of a Bundibugyo virus variant in the 2026 outbreak in the Democratic Republic of the Congo and Uganda

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Abstract

In May 2026, an outbreak of Ebola disease caused by Bundibugyo virus (BDBV, species *Orthoebolavirus bundibugyoense*) was declared in the Democratic Republic of the Congo (DRC), with cases originating from DRC and locally transmitted cases reported in Uganda. Bundibugyo virus disease (BVD) outbreaks were previously recorded in 2007-2008 in Bundibugyo District, Uganda, and in 2012 in Isiro, DRC. Here, we generated 22 genomes from samples obtained from individuals with BVD in DRC and Uganda. These genomes form a well-supported phylogenetic cluster separate from BDBV variants associated with the 2007 and 2012 outbreaks, together with evidence for sustained human transmission. This is consistent with the emergence of a new zoonotic spillover event rather than resurgence from previously reported variants. Besides ongoing efforts in strengthening surveillance systems, community engagement, establishing Ebola treatment centers, and developing targeted medical countermeasures; our report advocates to specifically increase decentralized laboratory diagnostics capacity, with pan-*Orthoebolavirus* assays, including genomic sequencing capacity, for limiting further outbreak expansion, timely detection and control of future outbreaks.

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Main

Ebola disease is a severe and often fatal illness caused by viruses that belong to the genus *Orthoebolavirus*. Among the known orthoebolaviruses, three species are known as highly pathogenic in humans and have been responsible for multiple outbreaks with high case fatality rates in sub-Saharan Africa: *Orthoebolavirus zairense* (EBOV), *Orthoebolavirus sudanense* (SUDV), and *Orthoebolavirus bundibugyoense* (BDBV) [1]. The Democratic Republic of the Congo (DRC) has recorded the highest number (n=17) of Ebola disease outbreaks since the first recorded outbreak in 1976 in Yambuku, DRC [2], while in Uganda eight outbreaks have been recorded to date [3]. These recurrent epidemics underscore the persistent threat posed by orthoebolaviruses in sub-Saharan Africa. The 2013–2016 West Africa Ebola virus disease (EVD) outbreak, which resulted in 28,646 cases and 11,323 deaths, demonstrated that a high-consequence pathogen can overwhelm fragile health systems, disrupt essential services, and rapidly expand to neighboring regions, in the absence of field-deployable molecular point-of-care (POC) testing and targeted medical countermeasures [4].

On 13 May 2026, local health authorities in Bunia health zone, Ituri province, DRC, notified national authorities of a cluster of suspected EVD cases (based on the DRC Ministry of Health case definition for EVD) who were admitted to the Centre Medical Evangélique (CME) Bunia Hospital, Rwampara health zone in Ituri province. Clinical specimens, mainly blood and oropharyngeal swabs, were collected from 19 suspected and probable cases, and all tested negative for EBOV by GeneXpert Ebola assay at the provincial public health laboratory in Bunia, Ituri province. These samples were sent to the Institut National de Recherche Biomédicale (INRB), the national reference laboratory for emerging and re-emerging pathogens), in Kinshasa, for PCR-based testing. Rapid identification of *Orthoebolavirus* (non-EBOV) with species confirmation resulting from viral-enriched metagenomic sequencing at INRB provided evidence and confirmation of BDBV infection (Table 1).

Based on these results, the Ministry of Public Health, Hygiene and Social Welfare, DRC, officially declared a Bundibugyo virus disease (BVD) outbreak in Ituri province on 15 May 2026 [5]. This represents the 17th Ebola disease epidemic documented in the DRC, and the third documented BVD outbreak overall [3].

Concurrently, a BVD outbreak was declared on the same day by the Ugandan Ministry of Health following a post-mortem diagnostic confirmation of the disease at the Central Public Health Laboratories (CPHL), Kampala in a patient who traveled from Bunia, DRC, over Hoima to Kampala in Uganda (Table 1) [5, 6]. Additional BDBV infections were confirmed in Uganda,

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involving individuals mostly linked to the initial patient and including contacts involved in transportation and health care. A Public Health Emergency of International Concern [7] and a Public Health Emergency of Continental Security [8] were declared by the World Health Organization and Africa Centres for Disease Control and Prevention (Africa CDC) on 17 May 2026 and 18 May 2026, respectively. As of 09 July 2026, 20 PCR-confirmed cases (15 cases originating from DRC and 5 locally acquired cases) of BVD have been reported in Uganda; and 1,830 PCR-confirmed cases, including 648 deaths, in the DRC (https://insp.cd/sitrep-n32-mvb_15-06-2026/).

We generated viral genomes from this new outbreak to reconstruct the early events of the outbreak and to determine whether it resulted from a new zoonotic spillover event or represented a resurgence linked to previous Bundibugyo outbreaks in the region.

While all samples tested negative by GeneXpert Ebola assay (Cepheid, Sunnyvale, CA, USA), the pan-*Orthoebolavirus* diagnostic assays (POC RADIONE Ebola detection kit RP017 [KH Medical, Pyeongtaek-si, Republic of Korea] and Altona Filovirus Screen RT-PCR kit v1.0 [Altona Diagnostics GmbH, Hamburg, Germany]) tested positive. Interestingly, the Altona Filovirus Screen RT-PCR test failed to detect *Orthoebolavirus* in five samples (regarded as invalid results), while whole-genome sequencing with a viral probe-based enrichment approach did still successfully recover complete or partial BDBV genomes, ultimately confirming BVD for these five patients (Table 1).

High-quality viral genomes from 21 patients (14 from DRC and seven from Uganda), with a minimum mean depth coverage of 45x and genome coverage >80% (Extended Data Table 1), were used to infer the phylogenetic tree. Phylogenetic analysis, including contextual BDBV full genomes from previous outbreaks (Fig. 1a, Extended Data Table 2), demonstrated that the 2026 viral genome sequences form a distinct (Extended Data Fig. 1), well-supported cluster separate from viruses associated with the 2007 and 2012 outbreaks (Fig. 1b). Given the distinct phylogenetic placement these findings are consistent with a zoonotic spillover event rather than a resurgence from previously known BDBV variants.

Within the 2026 outbreak, phylogenetic analysis confirms cross-border transmission between DRC and Uganda (Fig. 1c). Importantly, available epidemiological investigations indicate that all included Ugandan cases belong to a single transmission chain, highlighting that the apparent separation of sequences in the phylogeny should not be overinterpreted as evidence for independent introductions. Additional genome data may help resolve these relationships in the future. Mutational analysis identified 25 mutations in total within the 2026 BDBV genome

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cluster, of which 9/25 (36%) showed patterns consistent with Adenosine Deaminase Acting on RNA (ADAR)-mediated editing [9]. ADAR mutations are a signature of ebolavirus transmission into the human population [10]. Of these 25 mutations, five resulted in non-synonymous substitutions (further detailed in Extended Data Table 3).

The ongoing 2026 Ebola outbreak in DRC and Uganda is of particular concern due to the absence of approved Bundibugyo-specific or pan-ebola vaccines or therapeutics. Bundibugyo virus disease is also associated with a high fatality rate [11]. The risk of regional and international spread is further increased by high population mobility and insecurity in affected mining regions. In addition, weakened health systems and community resilience hamper outbreak control efforts. Important diagnostic gaps remain, including the limited availability of POC tests [5, 12]. This outbreak highlights the continued vulnerability of Central and East Africa to recurrent zoonotic emergence of filoviruses and underscores the importance of sustained regional diagnostic and genomic surveillance capacity. While centralized laboratory molecular diagnostic testing and genomic sequencing enabled case confirmation and virus characterization, increasing similar de-centralized capacity might help to detect outbreaks at even earlier stages. Thus, rapid deployment of sustainable decentralized molecular diagnostic testing and genomic sequencing capacity should further decrease turn-around times for pathogen detection, patient management, outbreaks containment, and better prepare for future outbreaks. A key limitation of this study is the limited number of genomes, which precluded a robust estimation of the time to the most recent common ancestor. Decentralized sequencing capacity will enable the generation of additional genomes to accurately estimate the date of the most recent common ancestor of the 2026 BVD outbreak. In addition, near-real-time genomic surveillance will assist in early identification of viral spread dynamics and viral evolution affecting outbreak measures.

Together, rapid genomic data generation strengthened cross-border situational awareness and supported real-time epidemiologic investigations during the evolving outbreak response [13, 14]. These findings emphasize that sustained regional preparedness, molecular diagnostic capacity, real-time genomic sequencing capacity to support molecular epidemiology [15], and open international data sharing are critical components of filovirus outbreak response and global health security. Timely release of sequences of BDBV variant causing the 2026 epidemic in DRC and Uganda is relevant to public health, providing an important resource for the design or adaptation of specific medical countermeasures (vaccines and therapeutics) as well as molecular diagnostic tests.

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232 **Table 1.** Socio-demographic, clinical symptoms, molecular testing results of confirmed BDV patients, as well as BDBV genome coverage.

Sample ID	Sex	Health Zone	Clinical symptoms	Sample type	Sampling date	Status on collection	POC RADIONE Ebola (Ct value)	Altona RT-PCR (Ct value)	Genome coverage of BDBV	Pathoplexus accession
26FHV044	F	Rwampara	Fever, headache, pruritus, skin lesion, and conjunctival injection.	Blood	2026-05-03	Alive	Insufficient volume	Invalid	98.4%	PP_00712Q8.2
26FHV045	M	Bunia	Fever, nausea, vomiting, abdominal pain, asthenia, jaundice hematemesis, epistaxis, muscle pain, gingival bleeding, respiratory distress, and sore throat.	Oropharyngeal swab	2026-05-03	Deceased	Positive (27.36)	Positive (25.78)	99.09%	PP_006XHKB.2
26FHV046	F	Rwampara	Fever, headache, pruritus, nausea, vomiting, sore throat, asthenia, and muscle pain.	Blood	2026-05-03	Alive	Insufficient volume	Positive (31.74)	98.6%	PP_00711R7.2
26FHV047	F	Bunia	Fever, pruritus, headache, and conjunctival injection.	Blood	2026-05-02	Alive	Insufficient volume	Invalid	98.6%	PP_00711S5.2
26FHV051	F	Rwampara	Fever, skin lesions, pruritus, nausea, vomiting, headache, sore throat, abdominal pain, and muscle pain.	Blood	2026-05-03	Alive	Insufficient volume	Invalid	83%	PP_00711T3.2
26FHV053	F	Rwampara	Fever, nausea/vomiting, asthenia, bloody diarrhea, and anuria	Oropharyngeal swab	2026-05-07	Deceased	Positive (32.13)	Positive (24.53)	99.4%	PP_00711U1.2
26FHV054	F	Rwampara	Fever, nausea/vomiting, diarrhea, and asthenia.	Oropharyngeal swab	2026-05-07	Deceased	Positive (21.97)	Positive (17.27)	99.6%	PP_006XHL9.3
26FHV056	F	Rwampara	Fever, abdominal pain, diarrhea, and asthenia	Blood	2026-05-07	Alive	Positive (26.56)	Positive (27.33)	99.5%	PP_00711VZ.2
26FHV058	F	Katwa	Fever, nausea/vomiting, asthenia, bloody diarrhea, and anuria	Blood	2026-05-06	Alive	Positive (26.26)	Positive (23.28)	25%	*PP_006Y8ME.1
26FHV061	M	Bunia	Fever, headache, asthenia, and diarrhea	Blood	2026-05-15	Alive	Positive (33.04)	Positive (17.45)	99.4%	PP_006Y8NC.3
26FHV062	M	Bunia	Headache, general malaise, vomiting, asthenia	Blood	2026-05-15	Alive	Positive (27.35)	Positive (22.57)	98.6%	PP_006Y8PA.3

26FHV063	F	Bunia	Fever, vomiting, asthenia, bloody diarrhea, and arthralgia	Blood	2026-05-15	Alive	Positive (26.22)	Positive (21.44)	99.6%	PP_006Y8Q8.3
26FHV064	M	Bunia	Fever, nausea/vomiting, asthenia, abdominal pain, muscle pain, jaundice, respiratory distress, epistaxis, sore throat, and Coma/loss of consciousness	Oropharyngeal swab	2026-05-16	Deceased	Positive (31.78)	Positive (25.29)	99.7%	PP_006Y8R6.2
26FHV065	M	Bunia	Fever, diarrhea, vomiting, arthralgia, and asthenia	Oropharyngeal swab	2026-05-16	Deceased	Positive (34.23)	Positive (26.61)	99.59%	PP_006Y8S4.2
CL023114	M	Hoima	Fever, vomiting, diarrhea, epigastric pain, asthenia, and hiccups	Blood	2026-05-14	Deceased	NA	Positive (26.04)	99.79%	PP_006XCJJ.1
CL023370	M	Wakiso	Fever, headache, body weakness, and abdominal pain	Blood	2026-05-21	Alive	NA	Positive (29.67)	81.86%	PP_0076RJM.1
CL023421	M	Ntoroko	Diarrhea, headache, general malaise, myalgia	Blood	2026-05-22	Alive	NA	Positive (26.86)	95.21%	PP_0076RHP.1
CL023559	M	Wakiso	Fever, headache, body weakness, arthralgia	Blood	2026-05-24	Alive	NA	Positive (24.24)	99.73%	PP_0076REW.1
CL023560	M	Wakiso	Abdominal pain, diarrhea, difficulty breathing, and headache	Blood	2026-05-24	Alive	NA	Positive (25.64)	98.01%	PP_0076RFU.1
CL023824	M	Kampala	Fever, nausea, abdominal pain, cough, and asthenia	Blood	2026-05-29	Alive	NA	Positive (26.19)	90.85%	PP_0076RND.1
CL023976	M	Bunia, DRC	Headache, asthenia, vomiting, diarrhea, and arthralgia	Blood	2026-06-01	Alive	NA	Positive (21.2)	84.99%	PP_0076RS5.1
CL024040	F	Kampala	Fever, cough, asthenia, body weakness, and myalgia	Blood	2026-06-02	Alive	NA	Positive (11.8)	98.37%	PP_0076RT3.1

233 POC, Point-Of-Care; BDBV, Bundibugyo virus; *Sequence excluded from the phylogenetic analysis; NA, Not Applicable.

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Fig. 1| Geographic distribution and phylogenetic analyses of Bundibugyo virus (BDBV) genomes. a, Map of eastern DRC and Uganda showing all known BVD outbreak hotspot locations. **b,** Maximum-likelihood phylogeny of all known BVD outbreaks inferred using the +gamma model in IQTree2. Ultrafast bootstrap support values are shown for each branch. The scale is given in units of substitutions per site. The current outbreak is highlighted in dark green, previous outbreaks in orange (Uganda, 2007) and blue (DRC, 2012). **c,** Maximum-likelihood phylogeny of 21 high-quality 2026 BDBV genomes using the same parameters as described above. Mutations identified on each branch are indicated (ADAR-like and other), and branch IDs (i.e., 1-13) correspond to those listed in Extended Data Table 3 (Mutational analysis), providing a high-resolution view of the evolutionary relationships and mutations acquired during the 2026 outbreak. PP_006Y8R6 and PP_006Y8S4 represent two samples collected from the same patient.

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METHODS

Ethics Committee Approval

Specimens were collected as part of a routine country-wide surveillance of emerging and re-emerging infectious diseases and were therefore exempt from ethical approval. However, in DRC, permission to use anonymous data for publication was granted by the Ethics Committee of the Kinshasa School of Public Health (ESP-UNIKIN, Number ESP/CE/81/2026). In Uganda, for public health surveillance and outbreak response activities, a waiver of informed consent was granted through the Uganda National Health Laboratory Services Research and Ethics Committee (UNHLS-2025-133).

Methods

Direct molecular testing of clinical specimens

In this study, blood samples were collected by venipuncture into EDTA tubes, except for one case from Uganda, for which posthumous EDTA whole blood was available. Oral swab specimens were collected among deceased individuals by gently rubbing sterile dry swabs against the buccal mucosa (the inner surfaces of the cheeks) to collect oral fluids and cellular material. We analyzed clinical samples that were shipped to INRB, Kinshasa in two separate batches (n=21) on 14 and 17 May 2026, and to CPHL, Kampala on 15 and 26 May 2026. At INRB, clinical specimens were tested for the presence of EBOV RNA using the GeneXpert Ebola assay (Cepheid, Sunnyvale, CA, USA) and the RADIONE Ebola detection kit RP017 (KH Medical, Pyeongtaek-si, Republic of Korea). Direct molecular testing was not performed at CPHL.

Viral RNA extraction and Real-time qPCR amplification

Briefly, both at INRB and CPHL, viral RNA was extracted from 140 µL of inactivated blood using the QIAamp viral RNA Mini kit (QIAGEN), according to the manufacturer's instructions. Real-time PCR was performed using the RealStar Filovirus Screen RT-PCR Kit 1.0 (Altona Diagnostics GmbH, Hamburg, Germany) at INRB and the RealStar Filovirus Type RT-PCR assay (Altona Diagnostics GmbH, Hamburg, Germany) at CPHL, following the manufacturer's protocol. Additional negative and positive controls were included to ensure the absence of carryover contamination and efficiency of the assay.

Whole-genome sequencing (WGS)

At INRB, RNA extracts were reverse transcribed into complementary DNA (cDNA) using LunaScript RT SuperMix kit (New England Biolabs, Ipswich, MA, USA). The resulting cDNAs were subsequently used for sequencing library preparation with either the Illumina DNA Prep

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with enrichment (Illumina, San Diego, CA, USA) or the Twist Comprehensive Viral Research Panel probe-enrichment (Twist Bioscience, USA), following the manufacturer's instructions. Sequencing libraries were loaded on Oxford Nanopore Technologies (ONT) GridION and on the Illumina NextSeq 1000/2000 sequencer. At CPHL, whole-genome sequencing was performed using a targeted viral metagenomics approach on an Illumina NextSeq 2000 platform (Illumina, San Diego, CA, USA) with the Illumina Viral Surveillance Panel (Illumina, San Diego, CA, USA), following the manufacturer's instructions.

Phylogenetic inference

We generated consensus genomes using the Metatropics v0.1.0 (https://doi.org/10.5281/zenodo.20430617) for ONT Long-reads and Viralrecon 2.6.0 (https://github.com/nf-core/viralrecon) for Illumina short-reads. Both are Nextflow-driven pipelines that include trimming steps to generate high-quality sequencing data, which are subsequently used to construct consensus BDBV genomes (reference: KC545393.1) using default settings. The reference genome was selected based on two criteria: (i) the availability of a complete genome sequence from the 2012 Bundibugyo outbreak, and (ii) its close genetic similarity to the initial dataset, making KC545393.1 the appropriate reference genome. At CPHL, BDBV consensus genomes from patient samples were generated as previously described by Nsawotebba et al. [6]. The newly generated BDBV genome sequences from Uganda and DRC were analysed in the context of 34 BDBV genomes from the previous outbreaks in 2007 and 2012 downloaded from Pathoplexus (Extended Data Table 1). Refseq genomes from other orthoebolaviruses were used as outgroup to confirm the position of the root. Sequence alignment and phylogenetic were performed using RACCOON pipeline (https://github.com/artic-network/raccoon), which utilizes MAFFT to generate a multiple sequence alignment and IQTree2 to construct a maximum likelihood tree under the +gamma substitution model, and 1000 ultra-fast bootstrap iterations. The alignment was trimmed from position 18903 (coordinates relative to the reference genome used) due to evident sequencing noise in one genome (26FHV054; Pathoplexus accession: PP_006XHL9).

Statistics and reproducibility

This descriptive study included individuals with PCR-confirmed Bundibugyo virus infection. No statistical method was used to predetermine sample size. The sample size was determined by the number of samples received and tested on a first-come, first-served basis during the early phase of the 2026 Bundibugyo virus disease outbreak. One newly generated genome was excluded from the phylogenetic analysis because its genome coverage did not meet the

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predefined threshold. Reproducibility of the phylogenetic analyses was ensured through the use of common bioinformatics tools. All genome sequences are publicly available in the Pathoplexus database to enable independent reproduction of the phylogenetic analyses. The experiments were not randomized because the study did not involve treatment allocation or experimental groups. The investigators were not blinded to allocation during experiments and outcome assessment because there were no intervention groups.

Ethics and Inclusion statement

In this study, sex was determined based on physical examination and extracted from the national viral hemorrhagic fever case investigation form; information on gender was not collected. This research was conducted in close collaboration with local partners throughout all stages of the study, including conceptualization and study design, intellectual property, data ownership, and authorship of resulting publications. The inclusion of the national, provincial, and local researchers was central to the study, ensuring that their expertise and contextual knowledge guided the multidisciplinary investigation team and supported the implementation of medical countermeasures.

The study addressed a public health problem of regional and international significance, extending beyond the DRC and Uganda. Contributions of partners and collaborators were clearly defined. In addition, capacity-building activities were implemented, including open real-time PCR and sequencing activities at the Laboratoire Provincial de Santé Publique (Provincial Public Health Laboratory) in Bunia, Ituri, the epicenter of the 2026 Bundibugyo virus disease outbreak.

Ethical approval was obtained in both countries, ensuring adherence to ethical requirements. All laboratory activities were performed in compliance with recommended standards of biosafety and environmental protection. The research posed no risk of stigmatization, discrimination or incrimination of participants, and appropriate measures were in place to safeguard their confidentiality and well-being.

No transfer of biological materials or related knowledge out of the country involved benefit-sharing considerations. Finally, the findings were shared with the national health authorities, and all relevant contributors were appropriately acknowledged to recognize the existing body of work and strengthen the contextual understanding of our results.

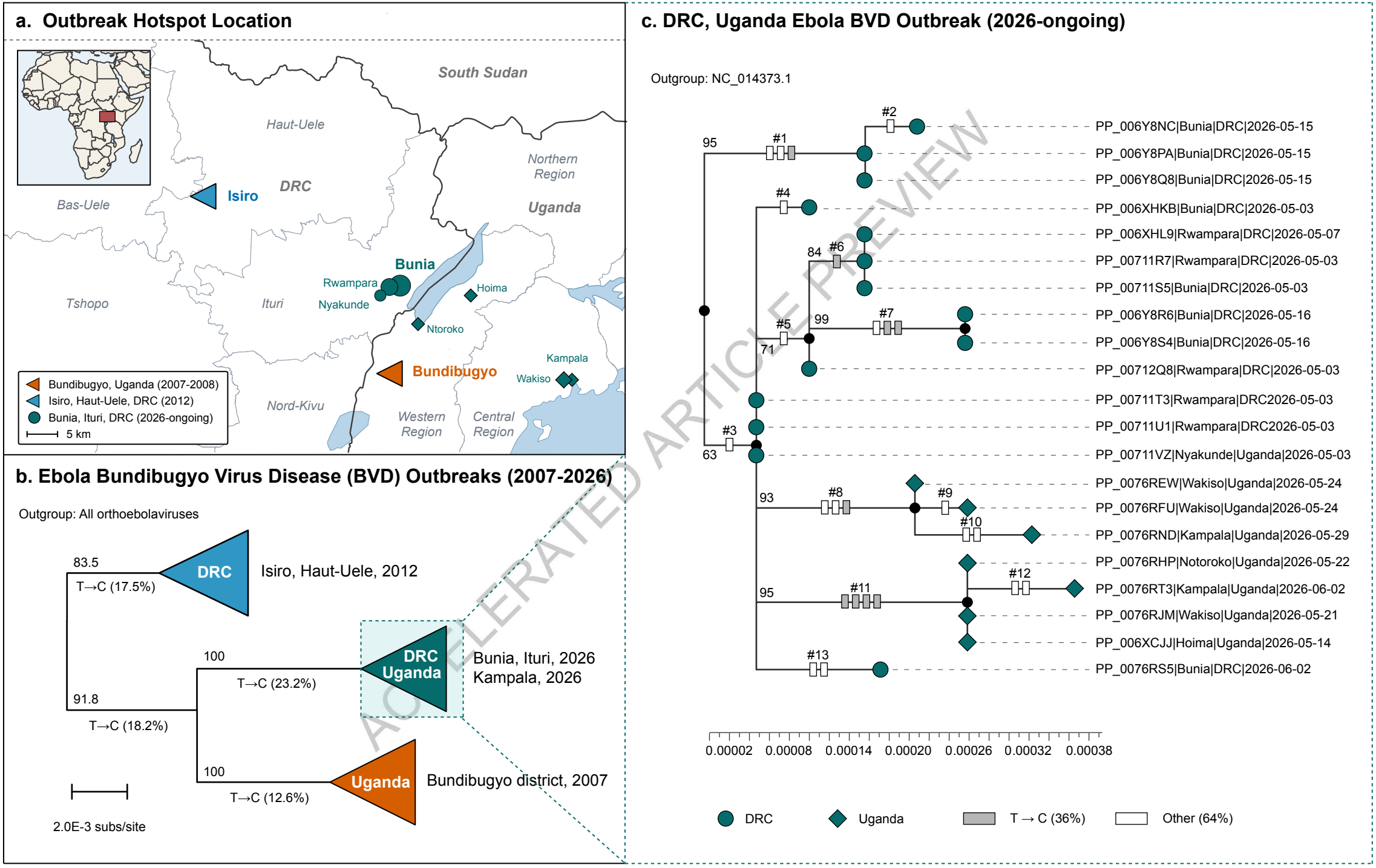
Data availability statement

The full-length genome sequences from this work are available in the Pathoplexus SeqSet (https://doi.org/10.62599/PP_SS_2905.1). The use of these sequences requires a transparent,

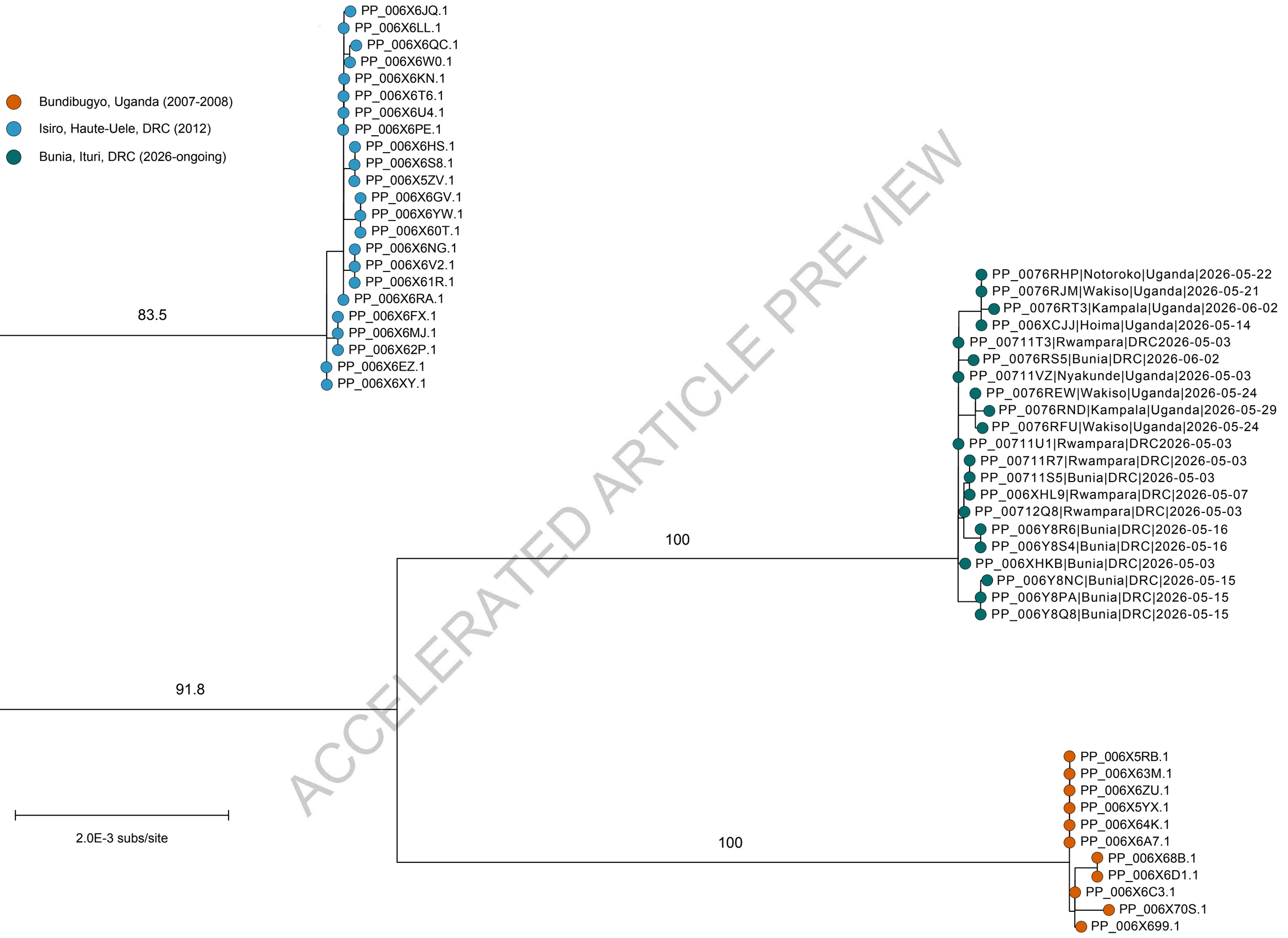
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formal request to the General Director of Institut National de Recherche Biomédicale (INRB), DRC and the Uganda's Ministry of Health.

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Lab ID	Total number of reads	Coverage	Mean depth coverage	GC content	Pathoplexus accession
26FHV044	779927	98.4%	118.14X	41.9%	PP_00712Q8.2
26FHV045	111467	99.09%	274.9X	42.0%	PP_006XHKB.2
26FHV046	742875	98.6%	142.45X	41.9%	PP_00711R7.2
26FHV047	861419	98.6%	131.65X	41.9%	PP_00711S5.2
26FHV051	224907	83%	48.58X	40.9%	PP_00711T3.2
26FHV053	160104	99.4%	141.48X	42.2%	PP_00711U1.2
26FHV054	298783	99.6%	45.5X	42.1%	PP_006XHL9.3
26FHV056	199775	99.5%	195.44X	42.2%	PP_00711VZ.2
26FHV058	378616	25%	15.7511X	40.1%	PP_006Y8ME.1
26FHV061	520623	99.4%	404.1X	41.8%	PP_006Y8NC.3
26FHV062	465301	98.6%	155.006X	41.3%	PP_006Y8PA.3
26FHV063	455301	99.6%	366.129X	41.9%	PP_006Y8Q8.3
26FHV064	300668	99.7%	131.392X	41.9%	PP_006Y8R6.2
26FHV065	379414	99.59%	161.903X	41.9%	PP_006Y8S4.2
CL023114	1147494	99.79%	4471X	41.16	PP_006XCJJ.1
CL023370	11148426	81.86%	104X	35.53	PP_0076RJM.1
CL023421	7186848	95.21%	202X	40.35	PP_0076RHP.1
CL0023559	2875458	99.73%	6812X	41.84	PP_0076REW.1
CL0023560	6353732	98.01%	278X	41.37	PP_0076RFU.1
CL023824	36770	90.85%	109X	38.24	PP_0076RND.1
CL023976	54435	84.99%	81X	35.65	PP_0076RS5.1
CL024040	107284	98.37%	131X	41.45	PP_0076RT3.1

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Accession	Date	Country	Outbreak	Authors	Institution
FJ217161.1	Nov. 2007	Uganda	BDBV-2007	Towner, J. S. et al.	Centers for Disease Control and Prevention, Special Pathogens Branch
JA489018.1	xx-xx-xx	Uganda	BDBV-2007	Towner, J. S. et al.	Centers for Disease Control and Prevention, Special Pathogens Branch
KR063673.1	01 Oct. 2007	Uganda	BDBV-2007	Das, S. R. et al.	J. Craig Venter Institute, Rockville, MD, USA
KU182911.1	14 Nov. 2007	Uganda	BDBV-2007	Das, S. R. et al.	J. Craig Venter Institute, Rockville, MD, USA
MK028834.1	2007	Uganda	BDBV-2007	Minogue, T. et al.	US Food and Drug Administration, Center for Devices and Radiological Health
MK028835.1	2007	Uganda	BDBV-2007	Bruce, C. B. et al.	US Food and Drug Administration, Center for Devices and Radiological Health
MK028856.1	2007	Uganda	BDBV-2007	Bruce, C. B. et al.	US Food and Drug Administration, Center for Devices and Radiological Health
MT583343.1	2007	Uganda	BDBV-2007	Lopera, J. G. et al.	ATCC/BEI Resources, Sequencing and Bioinformatics Center
MT583344.1	2007	Uganda	BDBV-2007	Lopera, J. G. et al.	ATCC/BEI Resources, Sequencing and Bioinformatics Center
NC_014373.1	Nov. 2007	Uganda	BDBV-2007	Towner, J. S. et al.	National Center for Biotechnology Information, NIH
OK573002.1	xx-xx-xx	Uganda	BDBV-2007	Bennett, R. et al.	US Food and Drug Administration, Center for Devices and Radiological Health
KC545393.1	2012	DRC	BDBV-2012	Albarino, C. G. et al.	Centers for Disease Control and Prevention, Viral Special Pathogens Branch
KC545394.1	2012	DRC	BDBV-2012	Albarino, C. G. et al.	Centers for Disease Control and Prevention, Viral Special Pathogens Branch
KC545395.1	2012	DRC	BDBV-2012	Albarino, C. G. et al.	Centers for Disease Control and Prevention, Viral Special Pathogens Branch
KC545396.1	2012	DRC	BDBV-2012	Albarino, C. G. et al.	Centers for Disease Control and Prevention, Viral Special Pathogens Branch
MT680245.1	20 Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680246.1	21 Sept. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680247.1	21 Sept. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680248.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680249.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680250.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680251.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680252.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680253.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680254.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680255.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680256.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680257.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680258.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680259.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680260.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680261.1	Aug. 2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT680262.1	8/20/2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences
MT742157.1	9/9/2012	DRC	BDBV-2012	Hulseberg, C. E. et al.	United States Army Research Institute of Infectious Diseases, Genome Sciences

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Branch identifier	Position	Nucleotide change	ADAR-like mutation (T→C)	Type of mutation	Amino acid change	Protein
B01	5606	G>A	no	intergenic		
B01	6657	T>C	yes	non-synonymous	Y213H	spike glycoprotein
B02	18640	C>T	no	intergenic		
B02	15587	C>T	no	non-synonymous	H1341Y	RNA-dependent RNA-polymerase
B03	10319	G>A	no	intergenic		
B04	17509	A>G	no	synonymous		
B05	5727	G>A	no	intergenic		
B06	16608	T>C	yes	non-synonymous	I1681T	RNA-dependent RNA-polymerase
B07	7049	C>T	no	synonymous		
B07	7405	T>C	yes	synonymous		
B07	7447	T>C	yes	non-synonymous	L476P	spike glycoprotein
B08	9552	A>C	no	intergenic		
B08	13024	T>C	yes	synonymous		
B08	18648	C>T	no	intergenic		
B09	13396	G>A	no	synonymous		
B10	2844	T>G	no	intergenic		
B10	2845	G>C	no	intergenic		
B11	4165	T>C	yes	intergenic		
B11	4167	T>C	yes	intergenic		
B11	4177	T>C	yes	intergenic		
B11	4191	T>C	yes	intergenic		
B12	3370	T>A	no	non-synonymous	V88E	polymerase cofactor
B12	5522	A>C	no	intergenic		
B13	1630	G>A	no	synonymous		
B13	5596	G>A	no	intergenic		

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nature portfolio

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Last updated by author(s): Aug 4, 2026

Reporting Summary

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For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☒	☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☒	☐ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	We did not use software to collect data.
Data analysis	RT-qPCR results were analyzed using the BIO-RAD CFX Maestro sotware version 2.3. Genome sequences were analyzed using using the Metatropics v0.1.0 (https://doi.org/10.5281/zenodo.20430617) for oxford nanopore long-reads and Viralrecon 2.6.0 (https://github.com/nf-core/viralrecon) for Illumina short-reads.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The full-length genome sequences from this work are available in the Pathoplexus SeqSet (https://doi.org/10.62599/PP_SS_2905.1).

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Sex was determined based on physical examination and extracted from the national viral hemorrhagic fever case investigation form; information on gender was not collected.
Reporting on race, ethnicity, or other socially relevant groupings	Race and ethnicity were not collected.
Population characteristics	This study involved individuals suspected of having Ebola disease and later tested PCR positive for Ebola virus.
Recruitment	Samples were collected from suspected cases of Ebola disease.
Ethics oversight	Specimens were collected as part of a routine country-wide surveillance of emerging and re-emerging infectious diseases and were therefore exempt from ethical approval. However, in DRC, permission to use anonymous data for publication was granted by the Ethics Committee of the Kinshasa School of Public Health (ESP-UNIKIN, Number ESP/CE/81/2026). In Uganda, for public health surveillance and outbreak response activities, a waiver of informed consent was granted through the Uganda National Health Laboratory Services Research and Ethics Committee (UNHLS-2025-133).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We used samples (n=22) collected during the 2026 Bundibugyo virus disease outbreak in DRC and Uganda.
Data exclusions	None
Replication	Real-time PCR was performed in duplicate. Repeat testing was limited by the public health response priorities during the outbreak.
Randomization	The study did not involve intervention groups.
Blinding	Investigators were not blinded because there were no experimental groups.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	This study was not a clinical trial.
Study protocol	This was an outbreak investigation.
Data collection	Data was collected by the outbreak investigation team.
Outcomes	Performed phylogenetic analysis of Bundibugyo virus samples from 2026 outbreak in DRC and Uganda.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*