Diagnostics and spread of SARS-CoV-2 in Western Africa: An observational laboratory-based study from Benin

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Abstract

Information on severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) spread in Africa is limited by fragile surveillance systems and insufficient diagnostic capacity.

We assessed the coronavirus disease-19 (COVID-19)-related diagnostic workload in Benin, Western Africa, characterized SARS-CoV-2 genomes from 12 acute cases of COVID-19, used those together with public data to estimate SARS-CoV-2 transmission dynamics in a Bayesian framework, validated a widely used diagnostic dual target RT-PCR kit donated to African countries, and conducted serological analyses in 68 sera from confirmed COVID-19 cases and from febrile patients sampled before the predicted SARS-CoV-2 introduction.

We found a 15-fold increase in the monthly laboratory workload due to COVID-19. Genomic surveillance showed introductions of three distinct SARS-CoV-2 lineages. SARS-CoV-2 genome-based analyses yielded an R0 estimate of 4.4 (95% confidence interval: 2.0-7.7), suggesting intense spread of SARS-CoV-2 in Africa. RT-PCR-based tests were highly sensitive but showed variation of internal controls and between diagnostic targets. Commercially available SARS-CoV-2 ELISAs showed up to 25% false-positive results depending on antigen and antibody types, likely due to unspecific antibody responses elicited by acute malaria according to lack of SARS-CoV-2-specific neutralizing antibody responses and relatively higher parasitemia in those sera.

We confirm an overload of the diagnostic capacity in Benin and provide baseline information on the usability of genome-based surveillance in resource-limited settings. Sero-epidemiological studies needed to assess SARS-CoV-2 spread may be put at stake by low specificity of tests in tropical settings globally. The increasing diagnostic challenges demand continuous support of national and supranational African stakeholders.

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Introduction

Coronavirus infectious disease-19 (COVID-19) emerged in China late 2019 and has afforded over 5 million cases globally by early June 2020. The large numbers of cases cause pressure to health care systems worldwide including laboratory diagnostics of the causative severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). Africa may be particularly vulnerable to COVID-19. As shown in Figure 1A, Sub-Saharan Africa is the most underdeveloped region globally according to the United Nations Development Programme (UNDP). Weak health care and surveillance systems may fail to control SARS-CoV-2 spread and provide basic medical attention as evidenced by the low UNDP health indicators of quantity of physicians and hospital beds per 10,000 people (Figure 1B). Age is a major risk factor for severe COVID-19 globally, hence the relatively younger African population may be relatively more protected (Figure 1A). However, frequent cardiovascular and chronic respiratory diseases, malaria, HIV infection and tuberculosis combined with unhealthy diets may increase risks for severe courses of COVID-19 in Africa despite a relatively young population.

To date, over 70 thousand confirmed COVID-19 cases from all African countries have been reported. The reasons for the relatively lower numbers compared to other continents are unclear, but underreporting due to lack of diagnostic capacity is likely a major factor limiting surveillance and patient care in Africa. Therefore, the Chinese Jack Ma Foundation donated more than 1 million RT-PCR-based SARS-CoV-2 test kits to all African countries in March 2020 (https://edition.cnn.com/2020/03/16/africa/jack-ma-donate-masks-coronavirus-africa/index.html; accessed 9 June 2020).

Benin is a West-African country with 12 million inhabitants, representing one of the most densely populated African regions (Figure 1C), which may facilitate intense SARS-CoV-2 spread. The Laboratoire des Fièvres Hémorragiques Virales du Benin (LFHB) is Benin’s reference laboratory for respiratory diseases, testing all the country’s suspected COVID-19 cases. Here, we provide insight into all aspects of SARS-CoV-2 laboratory performance at LFHB, as an example for the challenges inferred by the COVID-19 pandemic in Western Africa.

Methods

Study design and participants

We assessed daily data on sample receipt and RT-PCR-based SARS-CoV-2 detections during January-April 2020. We characterized SARS-CoV-2 from 12 PCR-confirmed travelers entering Benin during March-April 2020.
We obtained early convalescent sera from eight PCR-confirmed patients sampled during March-April 2020, taken an average 8 days post SARS-CoV-2 RT-PCR confirmation (range: 1-10 days) (appendix p 4). We obtained 60 sera sampled from patients with acute febrile illness during hemorrhagic fever surveillance activities at LFHB during October-November 2019 (appendix p 5-6; p 47). Samples were taken by trained technicians and stored at –20°C until usage. This study was approved by the ethics committee of the Ministry of Health (Arrêté 2020 No. 030/MS/DC/SGM/DNSP/CJ/SA/027SGG2020) and followed the Declaration of Helsinki. Written consent was obtained from all the patients participating in the study. Anonymized datasets were used, and all analysis of personally identifiable data took place only in the LFHB.

Laboratory testing and in-silico analyses

RNA was extracted from oro-nasopharyngeal swabs suspended in 140 μl of viral transport medium using the viral RNA mini kit (Qiagen, Germany) following the manufacturer’s instructions. Diagnostics of SARS-CoV-2 was performed using the kit donated by the Jack Ma Foundation termed 2019 Novel Coronavirus RNA detection kit (Da An Gene Co., Ltd. Of SunYat-sen University, China) which targets the ORF1ab and N genes of SARS-CoV-2, the RealStar SARS-CoV-2 RT-PCR Kit 1.0 (Altona Diagnostics, Germany) which targets the E and S genes of SARS-CoV-2 as well as SarbecoV E-gene kit and SARS-CoV-2 RdRP kit (TIB Molbiol, Germany). Probit regression analyses to determine the lower limit of detection of real-time RT-PCR assays were done using full viral RNA extracted from supernatant of Vero cells infected with the strain 2019-nCoV/München-1.2/2020/985 quantified with a SARS-CoV-2-specific in-vitro RNA transcript and real-time-RT SARS-CoV-2 E-gene assay as described earlier. Analyses were done using SPSS V22 (IBM, Germany) using eight parallel test replicates. Whole genome amplification was done using the Artic Consortium PCR-based protocol (https://artic.network/ncov-2019). Library preparation and Illumina MiSeq sequencing was done using the KAPA Frag Kit and KAPA Hyper Prep kit (Roche Molecular Diagnostics, Switzerland) and MiSeq reagent v2 chemistry (Illumina, U.S.A) according to the manufacturers’ protocols. Genome assembly was done by mapping MiSeq reads to a representative African SARS-CoV-2 sequence (hCoV-19/Senegal/611/2020/EPI_ISL_420076). Genome annotations were made in analogy to a SARS-CoV-2 reference sequence (NC045512) using Geneious 9.1.8 (https://www.geneious.com).
Time-stamped Bayesian phylogenies based on sampling dates were performed in BEAST2 (appendix p 2). The phylogeny was annotated with TreeAnnotator and visualized in FigTree from the BEAST package. Bayesian birth-death skyline analyses were performed in BEAST2 using parameters described in the appendix on p 2.

Serology

Sera were tested using commercially available ELISAs relying on different antigens and antibody classes, namely SARS-CoV-2 N antigen (IgG), spike S1 subunit (both IgG and IgA) and Middle East respiratory syndrome coronavirus (MERS)-CoV S1 (IgG; all from Euroimmun, Germany). Additionally, sera were tested using commercially available ELISA kits (Euroimmun) against the Zika virus (ZIKV) NS1 antigen (IgG), the Epstein-Barr virus (EBV) EBNA1 antigen (IgG), the EBV VCA antigen (both IgM and IgG) and using real-time-PCR for Plasmodia (all human pathogenic species), EBV and cytomegalovirus (CMV) (all from TIB Molbiol). Plaque reduction neutralization tests (PRNT) for SARS-CoV-2 and ZIKV were performed as described in the appendix on p 2.

Antibody testing against common cold betacoronaviruses HCoV-OC43 and HCoV-HKU1 that belong to the same viral genus as SARS-CoV-2, and may thus elicit cross-reactive antibodies, relied on recombinant spike protein-based immunofluorescence assays as previously described (appendix p 2).

Data availability

The nucleotide sequences of the SARS-CoV-2 genomes used in this study are available at the GISAID database (https://www.gisaid.org/) under accession IDs EPI_ISL_476822- EPI_ISL_476831 and EPI_ISL_476833- EPI_ISL_476834.

Results

SARS-CoV-2 workload at LFHB

One of the major problems that health systems worldwide face during the COVID-19 pandemic is the overload of their diagnostic capacities. At the LFHB in Benin, oro-nasopharyngeal swabs for SARS-CoV-2 diagnostics were first received the 1st of March 2020 and the first case was detected in a traveler on the 14th of March. Until the 28th of April 2020, LFHB had received a total of 4,382 samples for SARS-CoV-2 molecular testing with up to 543 samples per day (Figure 2). The actual maximum testing capacity was up to 100 samples daily due to the limited availability of personnel, reagents and laboratory equipment, which was exceeded on 14 days during March-April, demonstrating
the immense workload that LFHB has compensated using night shifts and all its available workforce only for SARS-CoV-2 diagnostics, at the cost of viral hemorrhagic fever surveillance. Notably, the average number of positive samples detected per day was 1·4 (range 1-5), irrespective by the number of samples received per day, which may have resulted from imprecise country-level case definitions.10

Phylogenomic analyses of SARS-CoV-2 in Benin

By the 26th of May 2020, 29,290 SARS-CoV-2 full genomes have been fully or partially sequenced by the global scientific community and deposited in GISAID. Of those, only 1% (n=201) originated from Africa (Figure 3A). To investigate the SARS-CoV-2 diversity introduced into Benin, we amplified 12 SARS-CoV-2 genomes from Beninese citizens. One of these 12 individuals was a patient from a local hospital, whereas the other 11 were returning travelers from Europe or Central-West African countries who showed no symptoms of disease but had to be tested for SARS-CoV-2 infection during quarantine upon re-entering Benin (appendix p 3).

In a Bayesian phylogenetic analysis, the SARS-CoV-2 genomes clustered with the globally spreading SARS-CoV-2 lineages A and B11 (Figure 3B), which is in accordance with those individuals’ travel history. To further characterize the SARS-CoV-2 genomic diversity in Africa, we analyzed nucleotide differences in a dataset comprising the Beninese and another 42 full African SARS-CoV-2 genomes available in GISAID until the 13th of May. Within the Benin-derived sequences, 12 variable nucleotide positions were observed, resulting in seven amino acid exchanges, all of which were corresponding to previously published variable positions12 (Figure 3C). According to distinct genomic signatures, seven different clades were identified for SARS-CoV-2 in Africa (appendix p 7-9). The SARS-CoV-2 genomes from Benin belonged to three of those seven clades (Figure 3C). Those three clades also included viruses from Algeria, the Democratic Republic of the Congo, Senegal and South Africa, as well as France and Italy, hinting either at transmission across different African countries or parallel introduction of diverse SARS-CoV-2 lineages into African countries. In sum, genomic analyses suggest several independent introductions of globally circulating SARS-CoV-2 lineages into Africa due to returning travelers, resulting in a high SARS-CoV-2 genetic diversity in Africa.

Bayesian skyline analyses to determine $R_0$
Phylogenetic data can be used to estimate changes in the basic reproduction number ($R_0$) over time. We inferred $R_0$ using all SARS-CoV-2 genomes found in the GISAID databases from Africa until the 13th of May and the novel SARS-CoV-2 genomes from this study (Figure 3D). The calculated median $R_0$ increased from 2.4 (95% confidence interval (CI): 1.04-3.7) to 4.4 (95% CI: 2.0-7.7) from February to March 2020, consistent with the first SARS-CoV-2 detection in Africa on February 14th in Egypt (https://www.egypttoday.com/Article/1/81641/Egypt-announces-first-Coronavirus-infection), the first detection in Benin in mid-March 2020 and consistent with rapidly increasing number of cases from the African continent thereafter.

Evaluation of diagnostic tests donated to Africa

Diagnostics of acute SARS-CoV-2 infections rely on molecular testing. However, access to state-of-the-art reagents and external quality control remain unresolved key issues of outbreak response in resource-limited regions. In March 2020, Jack Ma, co-founder and head of the Alibaba Group in China, kindly donated and distributed more than 1 million RT-PCR kits produced in China to Africa. No external validation of the kit has been performed to date, hindering assessments of diagnostic performance. Using serial dilutions of quantified SARS-CoV-2 cell culture-derived RNA, we determined a very high analytical sensitivity with a 95% limit of detection of 0.7-7.8 copies per reaction of both assays included in this dual-target kit (Figure 4A). Notably, one of those two assays targeting the genomic ORF1ab region showed a 10-fold lower sensitivity than the other assay targeting the N genomic region (Figure 4A). This may lead to inconclusive results during testing of patient specimens containing low amounts of viral RNA sampled late during the course of infection.

Nucleotide mutations in binding regions of PCR oligonucleotides are known to affect the diagnostic sensitivity of an assay, potentially leading to false-negative results. The exact target sites of the assays donated by the Jack Ma foundation are unknown. Therefore, we tested the donated kit on six clinical swab samples representing the genetic variation of SARS-CoV-2 in Benin (Clades 1-3). The donated kit detected SARS-CoV-2 RNA in all six clinical samples identical or superior to commercially available assays (Figure 4B), suggesting robust diagnostic sensitivity. However, in 29.6% (21/71) of the tested clinical sample replicates, the assay’s internal control was not detected, which according to the manufacturer’s instructions invalidates the test. No further information about the internal control is given in the manufacturer’s protocol. In sum, the donated kit can be used confidently for diagnostics in Africa, but
laboratories need to be alert about variations between the two different genomic targets and variations of the assay’s internal controls, which may have to be ignored to ensure diagnostic testing.

Serological assessment in the West-African setting

Serological assays detecting antibodies against SARS-CoV-2 suggestive of past infection are required for accurate estimates of viral spread and of the time of SARS-CoV-2 introduction into Africa, potentially facilitated by more than 200,000 Chinese workers on the African continent (https://sais-cari.org/data-chinese-workers-in-africa). Serological studies in European and Asian countries indicate high sensitivity and specificity of widely used SARS-CoV-2 serological tests such as ELISAs, but no assessment has been performed in African populations. In eight RT-PCR-confirmed patients from Benin, SARS-CoV-2 seroconversion ranged from 62.5 to 87.5% (7/8; 95% CI: 30.8-99.1%), depending on the ELISA that was used and confirmed a higher sensitivity of the IgA-based compared to the IgG-based SARS-CoV-2 ELISAs (Figure 5A). As shown in Figure 5B, 87.5% (7/8) of those ELISA results were confirmed by a highly specific SARS-CoV-2 PRNT. In 60 samples taken during October-November 2019 from febrile patients, 23.3% positive or borderline ELISA results potentially representing true positives were observed (14/60; 95% CI: 14.3-35.5%). Different from PCR-confirmed cases, ELISA reactivity contrasted with the complete lack of SARS-CoV-2-specific neutralizing antibodies in those samples (Figure 5A and 5B). Likely unspecific SARS-CoV-2 ELISA reactivity may be consistent with three scenarios. First, antibodies elicited by common infections with endemic human coronaviruses may cross-react with SARS-CoV-2 antigens. However, sera that yielded positive SARS-CoV-2 ELISA results did not differ significantly from sera that yielded negative SARS-CoV-2 ELISA results in their reactivity with common cold coronaviruses (45.7-63.6% versus 70.4-74.0%; p=0.1 and p=0.7, Fisher’s exact test) (appendix p 47). Similarly, the magnitude of antibody responses against common cold coronaviruses did not differ significantly between those groups (p=0.09 and p=0.8, t-test) (appendix p 47). Second, polyclonal B-cell activation can occur in infections or reactivations with herpesviruses such as CMV and EBV and elicit false-positive results in serological tests. However, only two patients were positive in a CMV PCR and one in an EBV PCR, and SARS-CoV-2 ELISA-positive versus ELISA-negative individuals did not differ in their past exposure to those human herpesviruses according to detailed serological analyses (appendix p 48). Lastly, polyclonal B-cell activation can also be caused by acute malaria, which is widespread in Africa. As shown in Figure 5C, a higher proportion of those individuals that yielded positive SARS-CoV-2 ELISA results than those that yielded negative ELISA results were
positive for Plasmodia in a highly sensitive PCR test (71.4% versus 54.3%), albeit this difference was not statistically
significant (p=0.35, Fisher’s exact test). In contrast, significantly higher parasite loads occurred within SARS-CoV-2
ELISA-positive compared to ELISA-negative individuals (Figure 5C) (p=0.035; t-test). Higher parasite loads that
decrease overtime have been observed in acute malaria, suggesting a higher proportion of acute malaria in SARS-
CoV-2 ELISA-positive patients compared to sub-acute or chronic malaria in SARS-CoV-2 ELISA-negative patients.21
To assess the breadth of potentially unspecific reactivity, we tested the sera from febrile patients using a Zika virus
(ZIKV) IgG-ELISA for which unspecific reactivity in cases of acute malaria has been reported previously.20 As shown
in Figure 5D, sera that elicited potentially unspecific SARS-CoV-2 ELISA results also elicited significantly more
frequently positive ZIKV ELISA results (57.1 versus 23.9%; p=0.019, Fisher’s exact test). None of the sera yielding
positive ZIKV ELISA results showed ZIKV-specific neutralizing antibodies, suggesting unspecific reactivity of those
sera in the ZIKV ELISA. Additionally, sera that yielded potentially false-positive results in the SARS-CoV-2 ELISA
were also significantly more likely to show potentially false-positive results in in the ZIKV ELISA (p=0.04; Chi-
Square test) (appendix p 49). Notably, no serum reacted with MERS-CoV antigens, suggesting that unspecific
reactivity may not automatically apply to all coronavirus antigens and tests (appendix p 47). In sum, close to 25% of
the febrile patients showed unspecific reactivity in SARS-CoV-2 ELISAs, possibly due to acute malaria.

Discussion

We performed an observational study investigating COVID-19-related diagnostics in a West-African reference
laboratory. Our genome-based R₀ estimates, although preliminary, provide a blueprint to support notoriously weak
surveillance in resource-limited African settings and support increased efforts to characterize SARS-CoV-2 genomes
over time across geographic regions, similar to the large genomic dataset generated by multiple groups during the
2013-2016 West African Ebola outbreak.22 Our relatively high R₀ estimate compared to other regions suggests intense
spread of SARS-CoV-2 on the African continent.23 The relatively higher R₀ compared to the initially low number of
reported cases from Africa likely results from weak surveillance systems, albeit a high number of asymptomatic
infections limiting accurate estimates of disease spread24 or an insufficient genomic dataset to infer robust R₀ estimates
cannot be ruled out. Nevertheless, Even an R₀ in the range of 2, which corresponds to the lower end of the 95%
confidence intervals of our R₀ estimate, may imply more than 80 million cases in Africa if no intervention is
established according to a recent modeling study\textsuperscript{25}, highlighting the need of non-pharmaceutical and other medical
interventions in densely populated African settings.

Serological testing presenting up to 25\% unspecific reactivity might affect public health interventions in tropical
regions, leading to an overestimate of SARS-CoV-2 circulation in regions where malaria is endemic and to
misidentification of real SARS-CoV-2 hotspots. Additionally, target populations for vaccine campaigns once those
become available might be missed, and co-circulating diseases such as malaria might be overlooked based on false-
positive SARS-CoV-2 results, leading to higher mortality from those endemic diseases.\textsuperscript{26, 27} The robustness of SARS-
CoV-2 serological tests should be further assessed by multi-centric sero-epidemiological studies from different
tropical regions affected by multiple infections potentially affecting accurate serology-based SARS-CoV-2
diagnostics.\textsuperscript{28}

Limitations of our study include the small number of patients as well as limited patient metadata. Furthermore, due to
the small number of available SARS-CoV-2 genomic sequences from Africa and the short time span of the pandemic,
our $R_0$ estimates are preliminary and should be considered with caution. However, the calculated $R_0$ estimates are in
concordance with estimates from Asian regions during the time of intense SARS-CoV-2 spread, suggesting robustness
of our data.\textsuperscript{29} Additionally, testing of sera for CMV and EBV by PCR may not have been sensitive due to lack of cell-
associated viral nucleic acid, so that a potential impact of herpesvirus reactivation in serologic testing cannot be fully
excluded.

Despite those limitations, we provide an assessment of COVID-19-related diagnostics from Sub-Saharan Africa that
highlights how urgently African laboratories need support to deal with the increasing diagnostic burden. Our detailed
investigation of the limitations of widely used serological test and the underlying mechanism contributes to accurate
epidemiological studies aiming at studying SARS-CoV-2 spread. Strengthening of African national and supranational
stakeholders coordinating the continent’s response such as the Africa Center for Disease Control and Prevention
(Africa CDC) and the African Union (AU) are needed to accelerate evidence-based public health responses to the
pandemic on the continent.\textsuperscript{30}

\section*{Contributors}

AY, ALS, AMS, CT, GH, YB, CF, NK, EFOF and SB carried out the experiments; AY, ALS, AMS, MN and JFD
wrote the manuscript; AY, AMS, PA, AD, MAJA, MHD, BH, MN and JFD supervised the project; AY, PA, AD,
MAJA, MHD and BH obtained samples; PA, AD, MAJA, MHD, BH, MN and JFD conceptualized the project. All authors read and approved the final manuscript.

Declaration of interests

The authors declare no conflict of interests.

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Figure 1. Ranking of world regions and population density of the African continent. 

A) Regional human development indexes. Longevity (orange), income (red) and education (gray) indexes, and the human development index (HDI) (blue) as the geometric mean of the three aforementioned indices is shown. 

B) Regional quality of health indicators. Quantity of physicians (blue) and quantity of hospital beds (grey) per 10,000 people are shown. Data retrieved from The Human Development Reports from the United Nations Development Programme (http://hdr.undp.org/en/content/human-development-index-hdi; June 9 2020) 

C) Population density map constructed using freely available data from (https://www.worldpop.org/doi/10.5258/SOTON/WP00004; 9 June, 2020). Benin (BJ) is shown below. The red arrow denotes the location of the the Laboratoire des Fièvres Hémorragiques Virales du Benin (LFHB) in Cotonou.

Figure 2. COVID-19 workload at the Laboratoire des Fièvres Hémorragiques Virales du Benin (LFHB).

Overall SARS-CoV-2 daily diagnostic requests received at the LFHB since late January until 28.04.2020 (black) and positive cases confirmed per day at the LFHB (red). Dotted lines denote the range of maximal daily diagnostic capacity of LFHB. Marked is the 14.03.2020, day of the first confirmed SARS-CoV-2 case in Benin.
Figure 3. Phylogenetic analyses of SARS-CoV-2 in Africa.

A) SARS-CoV-2 sequence entries per geographic region in GISAID on the 27th of May, 2020. B) Phylogenetic tree inferred using BEAST2 showing 24 complete SARS-CoV-2 genomes globally sampled from humans. A codon position-specific general time reversible (GTR) substitution model with $\gamma$-distributed rates among sites was used. SARS-CoV-2 MT019529 from Wuhan was used as an outgroup. Displayed is the majority consensus of 10,000 trees sampled from the posterior distribution with mean branch lengths. Posterior support is shown for nodes >0.90 as filled circles. Benin-derived sequences are shown in bold. Colored circles represent global lineage circulation, colors according to regions given in panel A. C) Alignment showing all variable sites across Benin SARS-CoV-2 genomes from this study. Empty characters indicate lack of sequence information. Red boxes denote variable nucleotide positions in the Benin SARS-CoV-2 sequences within the complete analyzed African dataset (appendix p 7-9). Grey boxes denote groups belonging to Lineage A or B according to Rambaut et. al.11 Asterisks indicate nonsynonymous substitutions. BEL, Belgium; BFA, Burkina Faso; COD, Democratic Republic of the Congo; FRA, France; ITA, Italy; TOG, Togo; NSP, non-structural protein; ORF, open-reading frame. D) $R_0$ estimation for Africa with Benin-derived SARS-CoV-2 genomes. Black line denotes median $R_0$ with greyish shaded standard deviation.
Figure 4. Molecular diagnostic test sensitivity. A) Analytical sensitivity of the DAAN real-time RT-PCR assay for both targets of the assay. The solid line shows predicted proportion of positive results at a given input; colored lines show the 95% CI. The genome illustration highlights the two target genes of the assay, ORF1ab and N. CI: confidence interval; LOD: lower limit of detection. B) SARS-CoV-2 assay comparison using clinical samples. LOD in a representative subset of samples using commercially available and the DAAN RT-PCR assay for both targets.
Figure 5. Serological investigation of SARS-CoV-2 in Benin.  
A) SARS-CoV-2 ELISA reactivity in febrile patients from 2019 and SARS-CoV-2 RT-PCR-confirmed patients from 2020.  
B) SARS-CoV-2 plaque reduction neutralization test from the same patients.  
C) Parasitemia in febrile patients that were SARS-CoV-2 ELISA-positive versus SARS-CoV-2 ELISA-negative febrile patients. Right: plasmodium copies per ml. Asterisk denotes p<0.05.  
D) ZIKV seropositivity between febrile patients that were SARS-CoV-2 ELISA-positive versus SARS-CoV-2 ELISA-negative patients. Asterisk denotes p<0.05. Right: ZIKV IgG ELISA reactivity within both groups. N.s. not significant.
Supplemental Material:

1. Supplementary methods
2. Supplementary Table 1: Characteristics of SARS-CoV-2 positive patients for which SARS-CoV-2 full genomes were generated for this study taken from March-April 2020.
3. Supplementary Table 2: Characteristics of confirmed SARS-CoV-2 positive patients for which serum samples were available taken from March-April 2020.
4. Supplementary Table 3: Characteristics of patients with febrile illnesses of unknown origin taken from October-November 2019.
5. Supplementary Table 4: Variable positions in a dataset comprising the Beninese and another 42 full African SARS-CoV-2 genomes.
6. Supplementary Table 5: SARS-CoV-2 sequences found in the GISAID database that were used in this study.
7. Supplementary Figure 1. Origin of the samples of febrile patients from 2019 and serological diagnostics of other betacoronaviruses in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020.
8. Supplementary Figure 2. Molecular and serological diagnostics of Epstein-Barr virus (EBV) and cytomegalovirus (CMV) in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020.
9. Supplementary Figure 3. Molecular and serological diagnostics of malaria and Zika virus (ZIKV) infections in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020.
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Supplementary information to “Diagnostics and spread of SARS-CoV-2 in Western Africa: An observational laboratory-based study in Benin”

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Supplementary methods:

Nucleotide sequence data included in the study
The basis for all generated datasets used in this study was a search for African SARS-CoV-2 full genome information on the Global Initiative on Sharing All Influenza Data (GISAID) platform on the 13th of May 2020. To that date, 161 SARS-CoV-2 full genomes from African countries were available. Depending on the question behind the analysis, we generated three different datasets.

1. To analyze variable positions of all SARS-CoV-2 strains circulating in Africa, we generated a dataset discarding incomplete and identical sequences from the original GISAID search, resulting in 42 final sequences for analysis.
2. For the phylogenetic analysis we followed the nomenclature of Rambaut et. al. and included one representative sequence of each of the 13 identified lineages A.1-A.5 and B.1-B.8 where full-genome information was available in order to represent the global diversity of SARS-CoV-2 genomes. Finally, we completed this dataset by the full genomes we characterized from Benin.
3. For R0 estimates we generated a third dataset expanding the Benin-derived genomes with all African sequences from the original GISAID search.

Serology
Samples originated from three major health centers: Akkasato Health Center (AHC), Centre National Hospitalier Universitaire Hubert Koutoukou MAGA (CNHU) and the Clinique Boni (CB) inside or near of Cotonou.

Plaque reduction neutralization tests were performed using similar methods for SARS-CoV-2 and for Zika virus. Briefly, VeroE6 cells were seeded in 24-well plates and incubated overnight. Prior to PRNT, patient sera were heat-inactivated at 56°C for 30 minutes. Next, patient sera were serially diluted in 200 µl OptiPro and mixed 1:1 with 200 µl virus solution containing 100 plaque forming units. The 400 µl serum-virus solution was vortexed and incubated at 37°C for 1 hour. Each 24-well was incubated 1 hour at 37°C with 200 µl serum-virus solution after which the cells were washed with PBS and supplemented with 1.2% Avicel solution in DMEM. After 3 days at 37°C, the supernatants were removed, and the 24-well plates were fixed and inactivated using a 6% formaldehyde/PBS solution and stained with crystal violet.

Immunofluorescence-Assays
Briefly, open reading frames for full spike proteins were cloned from human coronaviruses (HCoV) HCoV-OC43 and HCoV-HKU1 as described previously. Vero cells were then seeded on chamber slides and transfected with equal amounts of the respective expression plasmids. Due to the limited quantity of serum available, samples were used at dilutions of 1:100, 1:1000, 1:10000.

Bayesian Skyline analysis
The following parameters and prior settings were chosen in BEAST2: SARS-CoV-2 was first detected late December of 2019, however, the earliest sequence from Africa in the GISAID database was sequenced in Nigeria on early February 2020 (hCoV-19/Nigeria/Lagos01/2020). As the origin date in BDSKY analysis has to be older than the root age, the lower bound was set to 114 days in the past from the last African sequence in the dataset, being end of April 2020 (Lognormal; M=0.8, S=1.0), to address a plausible earlier introduction to Africa in January 2020 assuming a month between introduction and detection, as suggested for SARS-CoV-2 first detection in China. The “become uninfectious” rate (the reciprocal of the duration of infection) was set to 10 days using a lognormal distribution (M= -0.6, S= 1.25), based on the assumption that no viable virus was isolated after 10 days post onset of symptoms. Priors for the sampling proportion followed the consideration that our alignment consists only of a tiny fraction of the circulating SARS-CoV-2 in Africa (alpha=1, beta=9999). All analyses were performed with a relaxed clock exponential using recent SARS-CoV-2 evolutionary rate estimates of 1E-4 substitutions per site per year.
Supplementary Tables:

**Supplementary Table 1: Characteristics of SARS-CoV-2 positive patients for which SARS-CoV-2 full genomes were generated for this study taken from March-April 2020.**

| Sample-ID | Location     | Travel history | Symptoms | Sampling date |
|-----------|--------------|----------------|----------|---------------|
| 197       | Oueme        | none           | None     | 15.03.2020    |
| 260       | Cotonou      | France         | None     | 17.03.2020    |
| 314       | Cotonou      | France         | None     | 17.03.2020    |
| 461       | Cotonou      | France         | None     | 17.03.2020    |
| 501       | Cotonou      | France         | None     | 17.03.2020    |
| 843       | Natitingou   | Burkina Faso   | None     | 19.03.2020    |
| 1022      | Cotonou      | Togo           | None     | 25.03.2020    |
| 1092      | Cotonou      | Belgium        | None     | 27.03.2020    |
| 1408      | Cotonou      | Italy          | None     | 04.04.2020    |
| 1409      | Cotonou      | DR Congo       | None     | 06.04.2020    |
| 1950      | Cotonou      | Belgium        | Fever    | 15.04.2020    |
| 2012      | Cotonou      | France         | None     | 15.04.2020    |
**Supplementary Table 2: Characteristics of confirmed SARS-CoV-2 positive patients for which serum samples were available taken from March-April 2020.**

| Sample-ID | Sampling date | Location  | Travel history | Symptoms | Day serum sample taken after PCR confirmation |
|-----------|---------------|-----------|----------------|----------|---------------------------------------------|
| 1         | March 2020    | Cotonou   | France         | Fever    | 8                                           |
| 2         | March 2020    | Cotonou   | Niger          | Fever    | 1                                           |
| 3         | March 2020    | Cotonou   | France         | Fever    | 8                                           |
| 4         | March 2020    | Cotonou   | France         | Fever    | 10                                          |
| 5         | April 2020    | Cotonou   | Germany        | Fever    | 10                                          |
| 6         | April 2020    | Cotonou   | France         | Fever    | 9                                           |
| 7         | April 2020    | Cotonou   | France         | Fever    | 8                                           |
| 8         | April 2020    | Cotonou   | Germany        | Fever    | 8                                           |
**Supplementary Table 3: Characteristics of patients with febrile illnesses of unknown origin taken from October-November 2019.**

| Sample- ID | Health Center* | Sampling date | Symptoms | Treatment                      |
|------------|----------------|---------------|----------|-------------------------------|
| 215        | CNHU           | October 2019  | Fever    | Drugs against febrile illness |
| 311        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 312        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 313        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 314        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 315        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 316        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 317        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 318        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 319        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 320        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 321        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 322        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 323        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 324        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 325        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 326        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 327        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 328        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 329        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 330        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 331        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 332        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 333        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 334        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 335        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 336        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 337        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 338        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 339        | CB             | October 2019  | Fever    | Drugs against febrile illness |
| 201        | CB             | November 2019 | Fever    | Drugs against febrile illness |
| 202        | CB             | November 2019 | Fever    | Drugs against febrile illness |
| 203        | CB             | November 2019 | Fever    | Drugs against febrile illness |
| 204        | CB             | November 2019 | Fever    | Drugs against febrile illness |
| 205        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 206        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 207        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 208        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 209        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 210        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 211        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 212        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| 213        | AHC            | November 2019 | Fever    | Drugs against febrile illness |
| Sample No. | Location     | Date       | Symptom | Diagnosis                          |
|------------|--------------|------------|---------|------------------------------------|
| 214        | AHC          | November 2019 | Fever | Drugs against febrile illness     |
| 216        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 217        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 218        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 219        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 220        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 221        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 222        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 223        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 224        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 225        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 226        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 227        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 228        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 229        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 230        | CNHU         | November 2019 | Fever | Drugs against febrile illness     |
| 291        | AHC          | November 2019 | Fever | Drugs against febrile illness     |

* Samples originated from three major health centers: Akkasato Health Center (AHC), Centre National Hospitalier Universitaire Hubert Koutoukou MAGA (CNHU) and the Clinique Boni (CB).
Supplementary Table 4: Variable positions in a dataset comprising the Beninese and another 42 full African SARS-CoV-2 genomes.

| Clade | Sample-ID | sampling date | Sample origin | Position in genome MT324062 |
|-------|-----------|---------------|---------------|-----------------------------|
|       |           |               | 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 | |
| 1     | 2012/Benin| 2020-04-15    | Benin         | 1,059 * 2,416 3,037 * 8,782 * 10,582 11,083 13,006 * 14,408 * 15,324 * 18,877 22,468 * 23,403 * 25,563 * 25,688 * 28,144 * 28,878 * 28,881 28,882 * |
|       | 1950/Benin| 2020-04-15    | Benin         | C C C T C G T C C C T A G C C A G G G |
|       | 461/Benin | 2020-03-17    | Benin         | C C C T C G T C C C G A G C C A G G G |
|       | 843/Benin | 2020-03-19    | Benin         | C C C Y C G T C C C G A G N:A C A G G |
|       | EPI_ISL_418216| 2020-03-13  | Senegal       | C C C T C G T C C C G A G C C A G G G |
|       | EPI_ISL_420077| 2020-03-20  | Senegal       | C C C T C G T C C C T A G C C A G G G |
| 2     | 1022/Benin| 2020-03-25    | Benin         | T N:A N:A C N:A G T T T T C G G G G C T G G G |
|       | 197/Benin  | 2020-03-15    | Benin         | T N:A N:A C N:A G T T T T C G G G G C T G G G |
|       | 1092/Benin | 2020-03-27    | Benin         | T N:A N:A C N:A G T T T T C G G G G C T G G G |
|       | EPI_ISL_417946| 2020-03-18  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_437337| 2020-04-15  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_437348| 2020-04-16  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_435032| 2020-04-09  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_417437| 2020-03-17  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_420030| 2020-03-21  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_420947| 2020-03-26  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_417947| 2020-03-19  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_437350| 2020-04-16  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_420032| 2020-03-22  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_417948| 2020-03-19  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
|       | EPI_ISL_437338| 2020-04-15  | DR Congo      | C C T C C G G T T T T C G G G G C T G G G |
| EPI_ISL_437352|2020-04-17 | EPI_ISL_437339|2020-04-15 | EPI_ISL_420070|2020-03-17 | Senegal | C C T C C C G T T T C C G G G C T G G G |
| EPI_ISL_418210|2020-03-10 | Senegal | C C T C C C G T T T C C G G G C T G G G |
| EPI_ISL_418213|2020-03-12 | EPI_ISL_420074|2020-03-20 | South Africa | C C T C C C G T T T C C G G G C T G G G |
| EPI_ISL_421574|2020-04-01 | EPI_ISL_417186|2020-03-07 (MT324062) | Senegal | T C T C C G C T C C G G T T T G G G |
| EPI_ISL_418207|2020-03-02 | Senegal | T C T C C C G C C T C C C G G T T T G G G |
| EPI_ISL_418209|2020-03-03 | Senegal | T C T C C C G C C T C C C G G T T T G G G |
| EPI_ISL_418241|2020-03-02 | Algeria | T C T C T G T T T C C C G G T C T G G G |
| EPI_ISL_418242|2020-03-08 | South Africa | T C T C T G T T T C C C G G T C T G G G |
| EPI_ISL_420037|2020-03-02 | EPI_ISL_418241|2020-03-02 | Benin | T C T C C C G T T T C C G G G T T T G G G |
| EPI_ISL_418207|2020-03-02 | Senegal | T C T C C C G C C T C C C G G T T T G G G |
| EPI_ISL_418242|2020-03-02 | South Africa | T C T C C C G T T T C C C G G T C T G G G |
| EPI_ISL_420037|2020-03-02 | South Africa | T C T C C C G T T T C C C G G T C T G G G |
| EPI_ISL_420849|2020-03-28 | DR Congo | C C T C C C G T T T C C C G G G C T G A A |
| Date       | EPI ISL | Country     | Sequence       |
|------------|---------|-------------|----------------|
| 2020-03-22 | EPI ISL | Gambia      | C C T C C G G T T C C G G G C T G A A |
| 2020-03-17 | EPI ISL | South Africa| C C T C C T T T C C G G G C T G A A |
| 2020-03-27 | EPI ISL | South Africa| C C T C C T T T C C G G G C T G A A |
| 2020-04-15 | EPI ISL | DR Congo    | C C T C C G G T T C T G G G T C T G G G |
| 2020-04-15 | EPI ISL | DR Congo    | C C T C C G G T T C T G G G T C T G G G |
| 2020-04-18 | EPI ISL | Egypt       | C C T C C T T C T G G G T C T G G G |
| 2020-04-18 | EPI ISL | Egypt       | C C T C C T T C T G G G T C T G G G |
| 2020-04-20 | EPI ISL | Gambia      | C T T C C G G T T C C G G G T C T G G G |

*Nucleotide positions that are also variable within Benin sequences.
### Supplementary Table 5: SARS-CoV-2 sequences found in the GISAID database that were used in this study

We gratefully acknowledge the following Authors from the Originating laboratories responsible for obtaining the specimens and the Submitting laboratories where genetic sequence data were generated and shared via the GISAID Initiative, on which this research is based. All submitters of data may be contacted directly via www.gisaid.org

| Accession ID | Virus name          | Collection date | Originating laboratory                                                                 | Submitting laboratory                                                                 | Authors                                                                 |
|-------------|---------------------|-----------------|----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|------------------------------------------------------------------------|
| EPI_ISL_413550 | hCoV-19/Nigeria/Lagos01/2020 | 2020-02-27      | Centre for Human and Zoonotic Virology (CHAVZV), College of Medicine University of Lagos/Lagos University Teaching Hospital (LUTH), part of the Laboratory Network of the Nigeria Centre for Disease Control (NCDC) | African Centre of Excellence for Genomics of Infectious Diseases (ACEGID), Redeemer's University, Ede, Osun State, Nigeria | Oluniyi P.E., Ajogbasile F.V., Kayode A., Oguzie J., Folarin O.A., Ihekweazu C., Happi C.T. |
| EPI_ISL_414647 | hCoV-19/DRC/KN-13/2020 | 2020-03-09      | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417186 | hCoV-19/South Africa/R03006/2020 | 2020-03-07 | National Institute for Communicable Diseases of the National Health Laboratory Service | National Institute for Communicable Diseases of the National Health Laboratory Service | Allam M, Kventh S, van Heusden P, Khumalo Z, Mohale T, Subramoney K, von Gottberg, A, Ismail A, Bhiman JN |
| EPI_ISL_417433 | hCoV-19/DRC/KN-0017/2020 | 2020-03-11      | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417434 | hCoV-19/DRC/KN-0038/2020 | 2020-03-14      | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417435 | hCoV-19/DRC/KN-0043/2020 | 2020-03-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417436 | hCoV-19/DRC/KN-0051/2020 | 2020-03-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417437 | hCoV-19/DRC/KN-0054/2020 | 2020-03-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417438 | hCoV-19/DRC/KN-0058/2020 | 2020-03-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417439 | hCoV-19/DRC/KN-0059/2020 | 2020-03-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417440 | hCoV-19/DRC/KN-0060/2020 | 2020-03-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417441 | hCoV-19/DRC/KN-0070/2020 | 2020-03-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417948 | hCoV-19/DRC/108/2020 | 2020-03-19 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
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| EPI_ISL_417950 | hCoV-19/DRC/158/2020 | 2020-03-20 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_417955 | hCoV-19/DRC/191/2020 | 2020-03-21 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_418206 | hCoV-19/Senegal/003/2020 | 2020-02-28 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418207 | hCoV-19/Senegal/016/2020 | 2020-03-02 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418208 | hCoV-19/Senegal/020/2020 | 2020-03-04 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418209 | hCoV-19/Senegal/026/2020 | 2020-03-03 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418210 | hCoV-19/Senegal/073/2020 | 2020-03-10 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418211 | hCoV-19/Senegal/082/2020 | 2020-03-11 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418212 | hCoV-19/Senegal/087/2020 | 2020-03-11 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha sall |
| EPI_ISL_418213 | hCoV-19/Senegal/094/2020 | 2020-03-12 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418214 | hCoV-19/Senegal/102/2020 | 2020-03-12 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418215 | hCoV-19/Senegal/119/2020 | 2020-03-12 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418216 | hCoV-19/Senegal/136/2020 | 2020-03-13 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418217 | hCoV-19/Senegal/139/2020 | 2020-03-13 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418218 | hCoV-19/Senegal/139/2020 | 2020-03-13 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_418219 | hCoV-19/Senegal/2264/2020 | 2020-03-02 | NIC Viral Respiratory Unit - Institut Pasteur de Algerie | National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris | Mélanie Albert, Marion Barbet, Sylvie Behillil, Mélène Bizard, Angela Brisebarre, Flora Donati, Etienne Simon-Lorière, Vincent Enouf, Maud Vanpeene, Sylvie van der Werf, Fawzi Derrar |
| EPI_ISL_418242 | hCoV-19/Algeria/G0640_2265/2020 | 2020-03-08 | NIC Viral Respiratory Unit - Institut Pasteur of Algeria | National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris | Mélanie Albert, Marion Barbet, Sylvie Behili, Méline Bizard, Angela Brisebarre, Flora Donati, Etienne Simon-Lorière, Vincent Enouf, Maud Vanpeene, Sylvie van der Werf, Fawzi Derrar |
| EPI_ISL_420030 | hCoV-19/DRC/214/2020 | 2020-03-21 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420031 | hCoV-19/DRC/215/2020 | 2020-03-21 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420032 | hCoV-19/DRC/236/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420033 | hCoV-19/DRC/241/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420034 | hCoV-19/DRC/243/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420035 | hCoV-19/DRC/248/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
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| EPI_ISL_420037 | hCoV-19/Algeria/G0860_2262/2020 | 2020-03-02 | NIC Viral Respiratory Unit - Institut Pasteur of Algeria | National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris | Mélanie Albert, Marion Barbet, Sylvie Behillil, Méline Bizard, Angela Brisebarre, Flora Donati, Etienne Simon-Lorière, Vincent Enouf, Maud Vanpeene, Sylvie van der Werf, Fawzi Derrar |
| EPI_ISL_420069 | hCoV-19/Senegal/306/2020 | 2020-03-17 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420070 | hCoV-19/Senegal/315/2020 | 2020-03-17 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420071 | hCoV-19/Senegal/328/2020 | 2020-03-17 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420072 | hCoV-19/Senegal/370/2020 | 2020-03-18 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420073 | hCoV-19/Senegal/382/2020 | 2020-03-19 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420074 | hCoV-19/Senegal/600/2020 | 2020-03-20 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420075 | hCoV-19/Senegal/610/2020 | 2020-03-20 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420076 | hCoV-19/Senegal/611/2020 | 2020-03-20 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Ndongo Dia |
| EPI_ISL_420077 | hCoV-19/Senegal/618/2020 | 2020-03-20 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420078 | hCoV-19/Senegal/620/2020 | 2020-03-20 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420079 | hCoV-19/Senegal/640/2020 | 2020-03-20 | Institut Pasteur Dakar | Institut Pasteur de Dakar | Ndongo Dia, Moussa Moise Diagne, Mamadou Diop, Ousmane Faye, Amadou Alpha Sall |
| EPI_ISL_420838 | hCoV-19/DRC/253/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420839 | hCoV-19/DRC/254/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420840 | hCoV-19/DRC/299/2020 | 2020-03-20 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420841 | hCoV-19/DRC/300/2020 | 2020-03-22 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420842 | hCoV-19/DRC/307/2020 | 2020-03 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420843 | hCoV-19/DRC/353/2020 | 2020-03 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420844 | hCoV-19/DRC/355/2020 | 2020-03 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420845 | hCoV-19/DRC/397/2020 | 2020-03-26 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
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| EPI_ISL_420846 | hCoV-19/DRC/400/2020 | 2020-03 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420847 | hCoV-19/DRC/431/2020 | 2020-03-26 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420848 | hCoV-19/DRC/445/2020 | 2020-03 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420853 | hCoV-19/DRC/402/2020 | 2020-03-26 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_420854 | hCoV-19/DRC/521/2020 | 2020-03-25 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_421572 | hCoV-19/South Africa/KRISP-02/2020 | 2020-03-23 | Molecular Diagnostic Services and FLowpath | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Ngcapu S, Samsunder N, Lessells R, Chimukangara B, Deforche K, Tegally H, Wilkinson E, de Oliveira T |
| EPI_ISL_421573 | hCoV-19/South Africa/KRISP-06/2020 | 2020-03-31 | Molecular Diagnostic Services | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Ngcapu S, Samsunder N, Lessells R, Chimukangara B, Deforche K, Tegally H, Wilkinson E, de Oliveira T |
| EPI_ISL_421574 | hCoV-19/South Africa/KRISP-07/2020 | 2020-04-01 | Molecular Diagnostic Services | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Ngcapu S, Samsunder N, Lessells R, Chimukangara B, Deforche K, Tegally H, Wilkinson E, de Oliveira T |
| EPI_ISL_421575 | hCoV-19/South Africa/KRISP-011/2020 | 2020-04-01 | Molecular Diagnostic Services | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Ngcapu S, Samsunder N, Lessells R, Chimukangara B, Deforche K, Tegally H, Wilkinson E, de Oliveira T |
| EPI_ISL_421576 | hCoV-19/South Africa/KRISP-012/2020 | 2020-04-01 | Molecular Diagnostic Services | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Ngcapu S, Samsunder N, Lessells R, Chimukangara B, Deforche K, Tegally H, Wilkinson E, de Oliveira T |
| EPI_ISL_422382 | hCoV-19/Ghana/1513_S1/2020 | 2020-03-24 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Misita, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Maya, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjaquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Gordon A. Awandare, William Ampofo |
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| EPI_ISL_422384 | hCoV-19/Ghana/1622_S2/2020  | 2020-03-24 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-May, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjaquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwabena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422387 | hCoV-19/Ghana/1651_S3/2020  | 2020-03-25 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-May, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjaquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwabena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422398 | hCoV-19/Ghana/2853_S7/2020 | 2020-03-29 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Mayaa, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwapena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422399 | hCoV-19/Ghana/2914_S8/2020 | 2020-03-30 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Mayaa, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwapena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422400 | hCoV-19/Ghana/2944_S9/2020 | 2020-03-30 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Mayaa, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwapena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422401 | hCoV-19/Ghana/2986_S10/2020 | 2020-03-31 | NMIMR, Department of Virology | WACCBIP, University of Ghana |
|----------------|-------------------------------|------------|-------------------------------|-----------------------------|
| EPI_ISL_422402 | hCoV-19/Ghana/3176_S11/2020  | 2020-03-30 | NMIMR, Department of Virology | WACCBIP, University of Ghana |
| EPI_ISL_422403 | hCoV-19/Ghana/3177_S12/2020  | 2020-03-30 | NMIMR, Department of Virology | WACCBIP, University of Ghana |

Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Maya, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwabena Anang, Gordon A. Awandare, William Ampofo
| EPI_ISL_422404 | hCoV-19/Ghana/1565_S13/2020 | 2020-03-24 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Maya, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwabena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422405 | hCoV-19/Ghana/1659_S14/2020 | 2020-03-25 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Maya, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwabena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_422406 | hCoV-19/Ghana/2850_S15/2020 | 2020-03-29 | NMIMR, Department of Virology | WACCBIP, University of Ghana | Joyce M. Ngoi, Bright Adu, Collins M. Morang’a, Selassie Kumordjie, Miriam Eshun, Linda Boatemaa, Vanessa Magnussen, Erasmus Kotey, Fred Tei-Maya, Dominic S. Y. Amuzu, Peter Quashie, Augustina Arjarquah, Ivy Asante, Evelyn Bonney, George B. Kyei, Kofi Bonney, Abraham Kwabena Anang, Gordon A. Awandare, William Ampofo |
| EPI_ISL_428855 | hCoV-19/Gambia/GC19-015/2020 | 2020-03-17 | MRCG at LSHTM Genomics lab | MRCG at LSHTM Genomics lab | Sesay et al |
| EPI_ISL_428856 | hCoV-19/Gambia/GC19-026/2020 | 2020-03-21 | MRCG at LSHTM Genomics Lab | MRCG at LSHTM Genomics lab | Sesay et al |
| EPI_ISL_428857 | hCoV-19/Gambia/GC19-029/2020 | 2020-04-20 | MRCG at LSHTM Genomics lab | MRCG at LSHTM Genomics lab | Sesay et al |
| EPI_ISL_429254 | hCoV-19/DRC/998/2020 | 2020-04-03 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
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| EPI_ISL_429255 | hCoV-19/DRC/1131/2020 | 2020-04-05 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_429258 | hCoV-19/DRC/1234/2020 | 2020-04-06 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_429259 | hCoV-19/DRC/1249/2020 | 2020-04-06 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_430297 | hCoV-19/South Africa/R02827/2020 | 2020-03-06 | National Institute for Communicable Diseases of the National Health Laboratory Service | Allam M, Kwenda S, van Heusden P, Khumalo Z, Mohale T, Subramoney K, von Gottberg, A, Ismail A, Bhiman JN |
|----------------|---------------------------------|------------|--------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------|
| EPI_ISL_430819 | hCoV-19/Egypt/NRC-03/2020        | 2020-03-18 | Center of Scientific Excellence for Influenza Viruses, National Research Centre (NRC), Egypt. | Mohamed Ahmed Ali, Ahmed Kandeil, Ahmed Mostafa, Rabeh El-Shesheny, Mahmoud Shehata, Wael Rosldy, Shymaa Showky Ahmed, Amal Naguib, Nancy M. El Guindy, Mokhtar Gomaa, Ahmed El-Taweel, Ahmed E Kayed, Yassmin Moatasim, Omnia Kutkat, Sara Mahmoud, Mina Kanel, Abo Shama, M Noura, Mohamed El Sayes |
| EPI_ISL_430820 | hCoV-19/Egypt/NRC-01/2020        | 2020-03-18 | Center of Scientific Excellence for Influenza Viruses, National Research Centre (NRC), Egypt. | Mohamed Ahmed Ali, Ahmed Kandeil, Ahmed Mostafa, Rabeh El-Shesheny, Mahmoud Shehata, Wael Rosldy, Shymaa Showky Ahmed, Amal Naguib, Mokhtar Gomaa, Ahmed El-Taweel, Ahmed E Kayed, Yassmin Moatasim, Omnia Kutkat, Sara Mahmoud, Mina Kanel, Abo Shama, M Noura, Mohamed El Sayes, Nancy M. El Guindy |
| EPI_ISL_431011 | hCoV-19/DRC/1319/2020           | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nbembe, Eddy Kinganda-Lusamaki, Amuri Azita, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pautner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfam |
| Study ID       | Sample ID          | Date       | Lab Information                                                                 |
|---------------|--------------------|------------|----------------------------------------------------------------------------------|
| EPI_ISL_431012| hCoV-19/DRC/1376/2020 | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB)          |
|               |                    |            | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB)       |
|               |                    |            | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_434678| hCoV-19/DRC/1377/2020 | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB)          |
|               |                    |            | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB)       |
|               |                    |            | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_434679| hCoV-19/DRC/1397/2020 | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB)          |
|               |                    |            | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB)       |
|               |                    |            | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_434680 | hCoV-19/DRC/1422/2020 | 2020-04-08 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni; Edith Nkwembe; Eddy Kinganda-Lusamaki; Amuri Aziza; Francisca Muyembe Mawete; Catherine Pratt; Matthias Pauthner; Josh Quick; Allison Black; James Hadfield; Trevor Bedford; Ian Goodfellow; Andrew Rambaut; Nick Loman; Kristian Andersen; Michael Wiley; Steve Ahuka-Mundeke; Jean-Jacques Muyembe Tamfum |
| EPI_ISL_434681 | hCoV-19/DRC/1565/2020 | 2020-04-09 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni; Edith Nkwembe; Eddy Kinganda-Lusamaki; Amuri Aziza; Francisca Muyembe Mawete; Catherine Pratt; Matthias Pauthner; Josh Quick; Allison Black; James Hadfield; Trevor Bedford; Ian Goodfellow; Andrew Rambaut; Nick Loman; Kristian Andersen; Michael Wiley; Steve Ahuka-Mundeke; Jean-Jacques Muyembe Tamfum |
| EPI_ISL_434710 | hCoV-19/DRC/1423/2020 | 2020-04-08 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_434711 | hCoV-19/DRC/1486/2020 | 2020-04-08 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435032 | hCoV-19/DRC/1516/2020 | 2020-04-09 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435033 | hCoV-19/DRC/1324/2020 | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435058 | hCoV-19/South Africa/R02606/2020 | 2020-03-11 | National Institute for Communicable Diseases of the National Health Laboratory Service | National Institute for Communicable Diseases of the National Health Laboratory Service | Allam M, Kwenda S, van Heusden P, Khumalo Z, Mohale T, Subramoney K, von Gottberg, A, Ismail A, Bhiman JN |
| EPI_ISL_435059 | hCoV-19/South Africa/R05475/2020 | 2020-03-20 | National Institute for Communicable Diseases of the National Health Laboratory Service | National Institute for Communicable Diseases of the National Health Laboratory Service | Allam M, Kwenda S, van Heusden P, Khumalo Z, Mohale T, Subramoney K, von Gottberg, A, Ismail A, Bhiman JN |
|----------------|---------------------------------|------------|---------------------------------------------------------------------------------|---------------------------------------------------------------------------------|---------------------------------------------------------------------------------|
| EPI_ISL_435113 | hCoV-19/DRC/1382/2020           | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB)        | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB)      | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435114 | hCoV-19/DRC/1398/2020           | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB)        | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB)      | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435116 | hCoV-19/DRC/1326/2020           | 2020-04-07 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB)        | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB)      | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| Accession Number | Sample Name          | Collection Date | Institution                  | Authors                                                                 |
|------------------|----------------------|-----------------|-----------------------------|-------------------------------------------------------------------------|
| EPI_ISL_435117   | hCoV-19/DRC/1375/2020| 2020-04-07      | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435118   | hCoV-19/DRC/1378/2020| 2020-04-07      | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Adrienne Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435156   | hCoV-19/DRC/1715/2020| 2020-04-10      | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435157 | hCoV-19/DRC/1767/2020 | 2020-04-10 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
|---|---|---|---|---|---|
| EPI_ISL_435158 | hCoV-19/DRC/1779/2020 | 2020-04-10 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435159 | hCoV-19/DRC/1952/2020 | 2020-04-11 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435160 | hCoV-19/DRC/1982/2020 | 2020-04-12 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
|----------------|-----------------------|------------|--------------------------------------------------------------------------------|--------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| EPI_ISL_435161 | hCoV-19/DRC/2047/2020 | 2020-04-12 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435162 | hCoV-19/DRC/2063/2020 | 2020-04-12 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435163 | hCoV-19/DRC/2120/2020 | 2020-04-12 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Franciscia Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
|----------------|----------------------|-----------|----------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------|
| EPI_ISL_435164 | hCoV-19/DRC/2121/2020 | 2020-04-12 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Franciscia Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435165 | hCoV-19/DRC/2122/2020 | 2020-04-13 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Franciscia Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435166 | hCoV-19/DRC/2125/2020 | 2020-04-13 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435167 | hCoV-19/DRC/2128/2020 | 2020-04-13 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_435168 | hCoV-19/DRC/2133/2020 | 2020-04-13 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_436194 | hCoV-19/DRC/2169/2020 | 2020-04-13 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_436412 | hCoV-19/DRC/2299/2020 | 2020-04-14 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_436684 | hCoV-19/South Africa/KRISP-04/2020 | 2020-03-31 | KRISP, KZN Research Innovation and Sequencing Platform | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Lessells R, Chimukangara B, Deforce K, Teghally H, Wilkinson E, de Oliveira T |
| EPI_ISL_436685 | hCoV-19/South Africa/KRISP-010/2020 | 2020-04-01 | KRISP, KZN Research Innovation and Sequencing Platform | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Lessells R, Chimukangara B, Deforce K, Teghally H, Wilkinson E, de Oliveira T |
| EPI_ISL_436686 | hCoV-19/South Africa/KRISP-045/2020 | 2020-03-27 | KRISP, KZN Research Innovation and Sequencing Platform | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Lessells R, Chimukangara B, Deforce K, Teghally H, Wilkinson E, de Oliveira T |
| EPI_ISL_436687 | hCoV-19/South Africa/KRISP-051/2020 | 2020-03-28 | KRISP, KZN Research Innovation and Sequencing Platform | KRISP, KZN Research Innovation and Sequencing Platform | Giandhari J, Pillay S, Lessells R, Chimukangara B, Deforce K, Teghally H, Wilkinson E, de Oliveira T |
| ID          | Sample ID          | Date       | Lab Name                                      | Authorship                                                                 |
|-------------|--------------------|------------|-----------------------------------------------|-----------------------------------------------------------------------------|
| EPI_ISL_437193 | hCoV-19/DRC/2364/2020 | 2020-04-14 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437194 | hCoV-19/DRC/2363/2020 | 2020-04-14 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437195 | hCoV-19/DRC/2369/2020 | 2020-04-14 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437196 | hCoV-19/DRC/2384/2020 | 2020-04-14 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437337 | hCoV-19/DRC/2496/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437338 | hCoV-19/DRC/2529/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437339 | hCoV-19/DRC/2536/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
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| EPI_ISL_437340 | hCoV-19/DRC/2563/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437341 | hCoV-19/DRC/2580/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| Entry | Sample Name | Date | Laboratory | Authors |
|-------|-------------|------|------------|---------|
| EPI.ISL.437342 | hCoV-19/DRC/2644/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI.ISL.437343 | hCoV-19/DRC/2670/2020 | 2020-04-15 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI.ISL.437344 | hCoV-19/DRC/2727/2020 | 2020-04-16 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437345 | hCoV-19/DRC/2728/2020 | 2020-04-16 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437346 | hCoV-19/DRC/2813/2020 | 2020-04-16 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437347 | hCoV-19/DRC/2819/2020 | 2020-04-16 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437352 | hCoV-19/DRC/2904/2020 | 2020-04-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437353 | hCoV-19/DRC/2938/2020 | 2020-04-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437354 | hCoV-19/DRC/2939/2020 | 2020-04-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437355 | hCoV-19/DRC/2942/2020 | 2020-04-17 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
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| EPI_ISL_437356 | hCoV-19/DRC/3041/2020 | 2020-04-18 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
| EPI_ISL_437357 | hCoV-19/DRC/3070/2020 | 2020-04-18 | Viral Respiratory Lab, National Institute for Biomedical Research (INRB) | Pathogen Sequencing Lab, National Institute for Biomedical Research (INRB) | Placide Mbala-Kingebeni, Edith Nkwembe, Eddy Kinganda-Lusamaki, Amuri Aziza, Francisca Muyembe Mawete, Catherine Pratt, Matthias Pauthner, Josh Quick, Allison Black, James Hadfield, Trevor Bedford, Ian Goodfellow, Andrew Rambaut, Nick Loman, Kristian Andersen, Michael Wiley, Steve Ahuka-Mundeke, Jean-Jacques Muyembe Tamfum |
Supplementary Figure 1. Origin of the samples of febrile patients from 2019 and serological diagnostics of other betacoronaviruses in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020. A) Sampling sites of the serum samples from patients with febrile illness of unknown origin. Akkasato Health Center (AHC), Centre National Hospitalier Universitaire Hubert Koutoukou MAGA (CNHU) and the Clinique Boni (CB). B) Individual reactivity of SARS-CoV-2 ELISA, SARS-CoV-2 plaque reduction neutralization test (PRNT) and Immunofluorescence (IFA) reactivity to common cold betacoronaviruses OC43 and HKU1 in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020. –, assay not performed. C) Common cold betacoronaviruses seropositivity between 2019 febrile patients that were SARS-CoV-2 ELISA positive versus SARS-CoV-2 ELISA negative. D) HKU1 and OC43 IFA log_{10} titers of SARS-CoV-2 ELISA positive versus SARS-CoV-2 ELISA negative patients. Samples that were negative are not shown for graphical reasons. N.s., not significant. E) MERS-CoV ELISA ratio in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020.
Supplementary Figure 2. Molecular and serological diagnostics of Epstein-Barr virus (EBV) and cytomegalovirus (CMV) in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020. A) Individual reactivity of SARS-CoV-2 ELISA, SARS-CoV-2 plaque reduction neutralization test (PRNT), EBV-PCR, CMV-PCR and three EBV ELISA: CA-IgM, CA-IgG and EBNA-1-IgG in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020. B) EBV-CA-IgM, EBV-CA-IgG and EBNA-1-IgG ELISA ratio between 2019 febrile patients that were SARS-CoV-2 ELISA positive versus SARS-CoV-2 ELISA negative. Line shows the median ELISA ratio. N.s.; not significant.
Supplementary Figure 3. Molecular and serological diagnostics of malaria and Zika virus (ZIKV) infection in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020. A) Individual reactivity of SARS-CoV-2 ELISA, SARS-CoV-2 plaque reduction neutralization test (PRNT), ZIKV-IgG ELISA, ZIKV-PRNT and Plasmodium PCR in febrile patients from 2019 and SARS-CoV-2 RT-PCR confirmed patients from 2020. B) ZIKV-PRNT50 log10 results of 2019 febrile patients that were SARS-CoV-2 ELISA positive versus SARS-CoV-2 ELISA negative. C) Relation of reactivity between SARS-CoV-2 S1-IgA, S1-IgG and N-IgG ELISA positive patients with ZIKV-IgG ELISA.
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