



Supplementary Materials for

The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance

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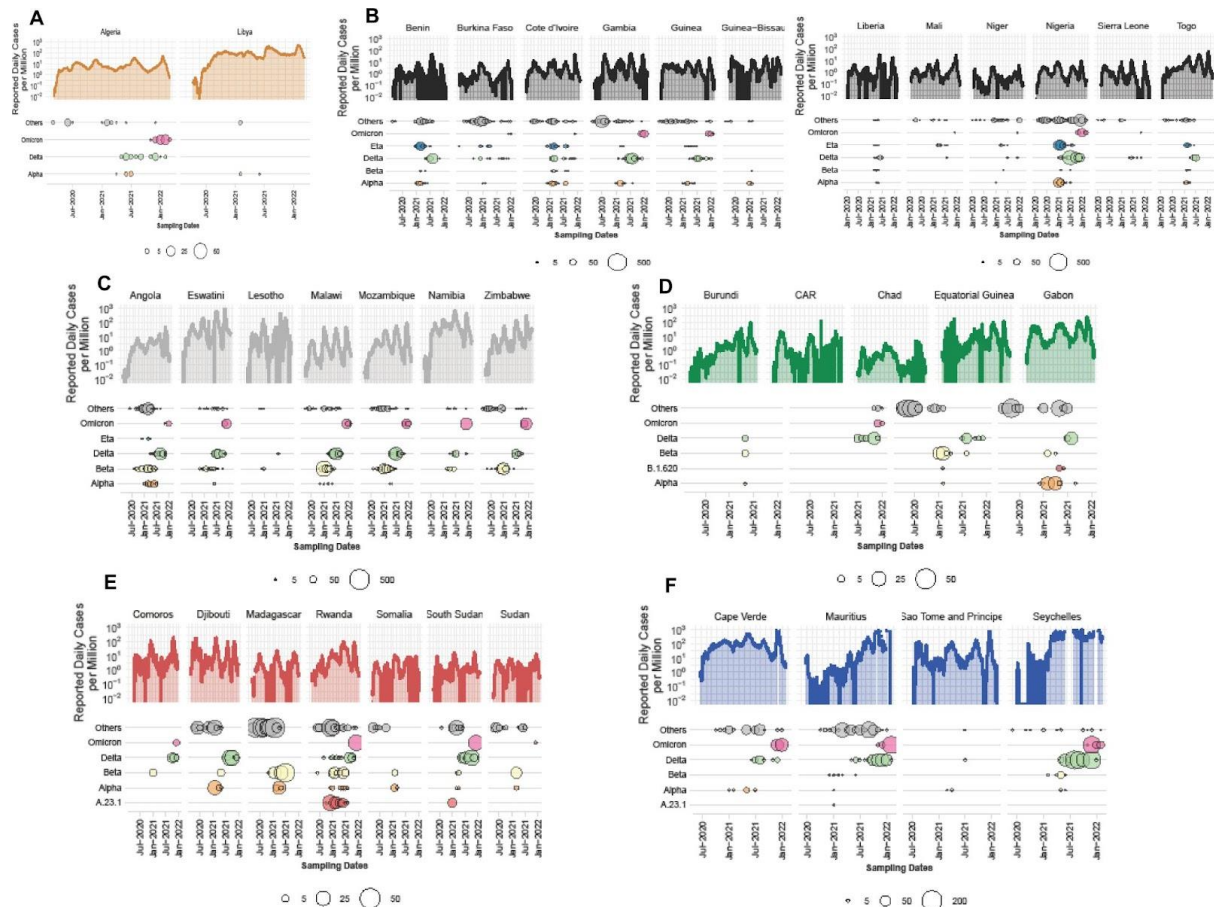
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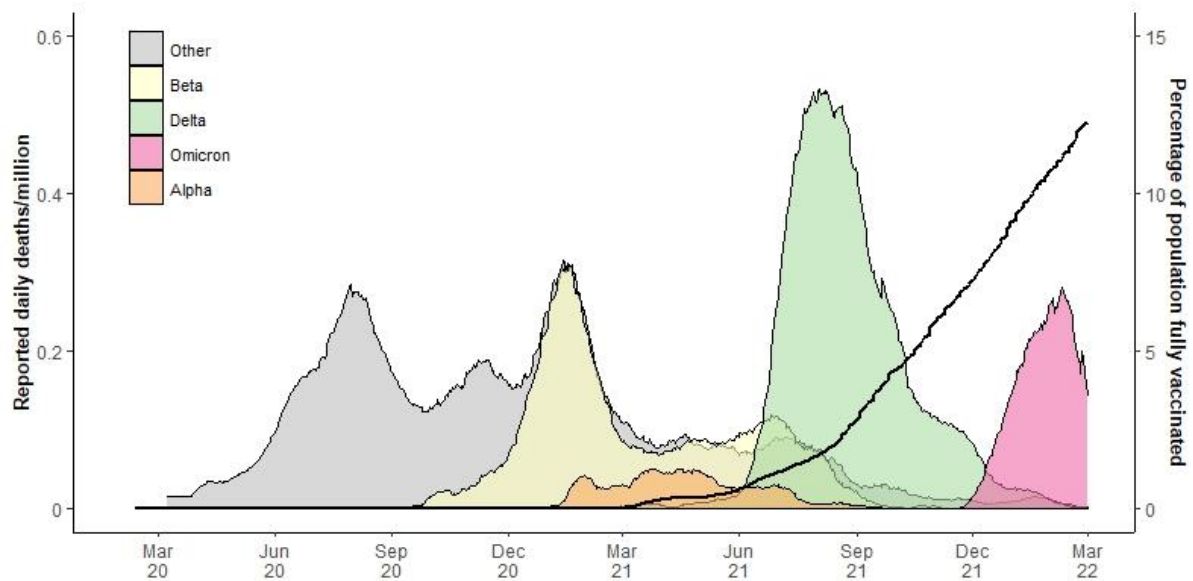
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Supplementary Materials

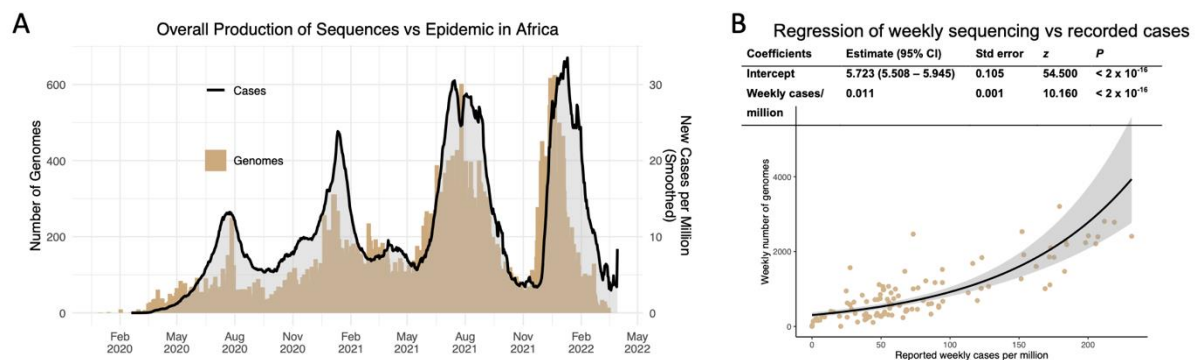
Supplementary Figures



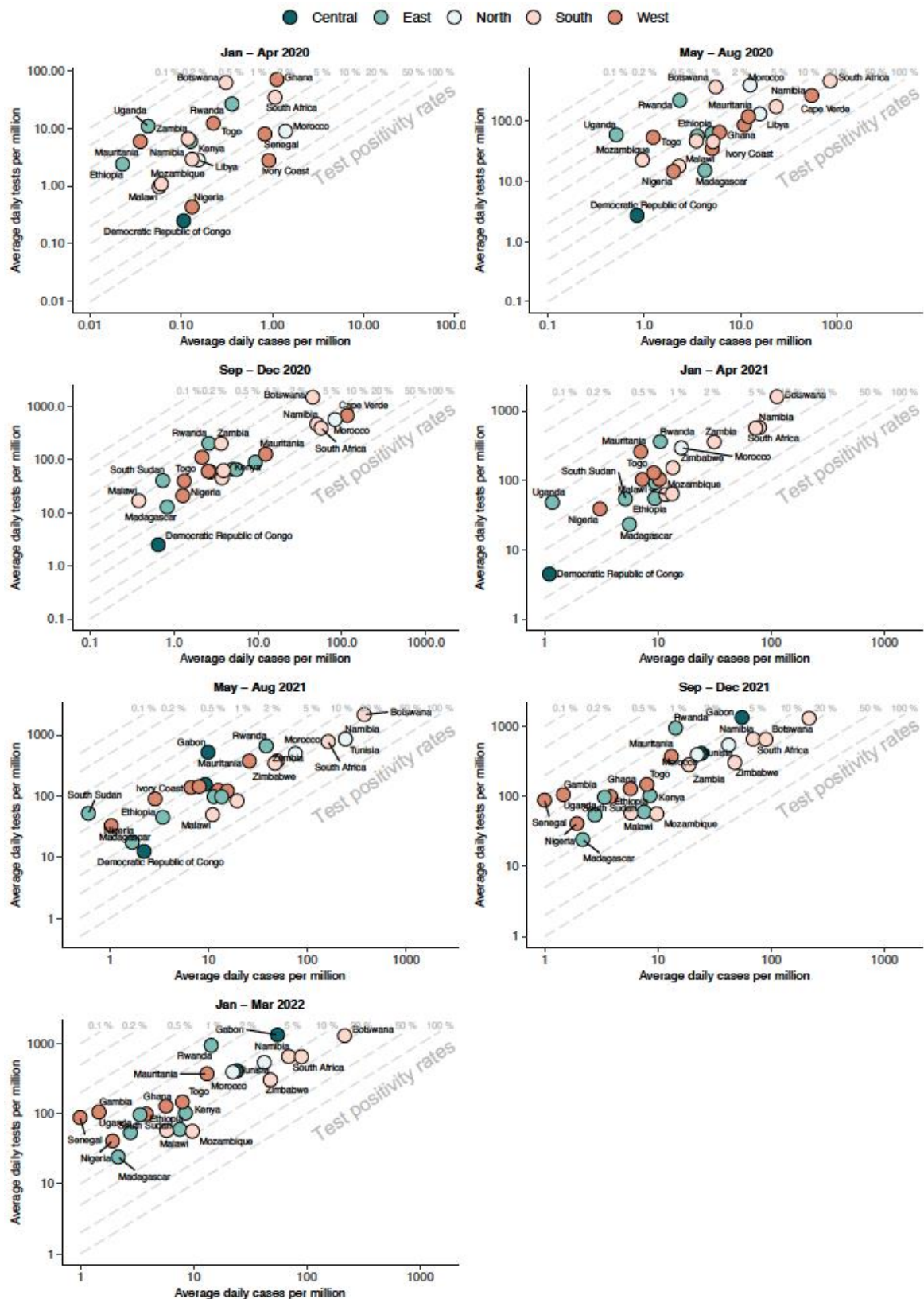
Supplementary Figure S1: Epidemiological progression of the COVID-19 pandemic in all African countries overlaid with the distribution of VOCs, the Eta VOI and other lineages through time (size of circles proportional to the number of genomes sampled per month for each category). The graphs show a breakdown of new cases per million and monthly sampling of VOCs, regional variant or lineage of interest and other lineages for all African countries not shown in Figure 1, grouped by region: A) North Africa, B) West Africa, C) Southern Africa, D) Central Africa, E) East Africa, F) Cape Verde, Mauritius, Sao Tome and Principe and Seychelles, from the beginning of the pandemic to February 2022.



Supplementary Figure S2: Daily reported deaths per million people attributed to each variant of concern with vaccination coverage across Africa. The daily reported deaths were calculated to be attributed to each variant of concern based on the proportion of the variants in genomic surveillance data available from GISAID. We applied an assumption of a 20 day time lag from infection to death (77). Alpha caused the lowest peak in reported mortality in Africa, while the largest is attributed to Delta which coincided with the beginning of vaccinations on the continent. The impact of Omicron on mortality is to a much lesser extent than Delta, the peak of Omicron mortality occurred when approximately 12% of the African population was fully vaccinated (completed the initial vaccination protocol of 2 doses for most vaccines, 1 or 3 for some manufacturers).

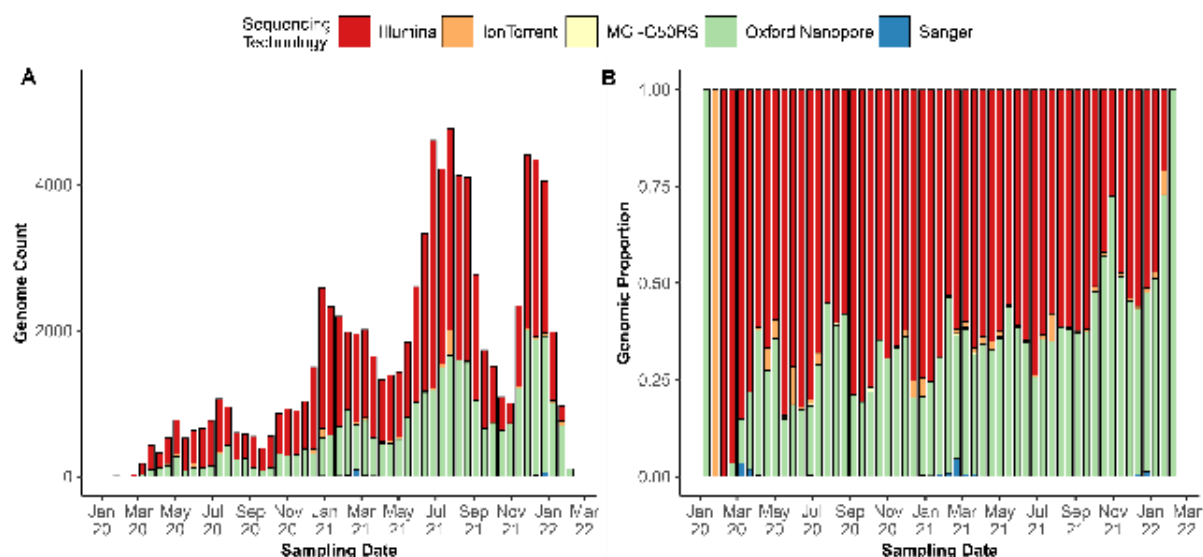


Supplementary Figure S3: Trends of genomic sequencing and epidemic size in Africa. A) Corresponding daily progression of genomic sequence production and epidemic size in Africa. B) Regression of weekly sequencing against recorded cases in Africa. We used a negative binomial regression, with a log link function and maximum likelihood estimation of theta, to investigate the relationship between the number of SARS-CoV-2 genomes produced per week and the weekly number of reported COVID-19 cases in Africa. The regression results indicated a significant positive effect of case numbers on the number of genomes produced, with each one-unit increase in reported weekly cases per million, the expected log count of genomes produced increased by 0.011 ($\theta = 2.23$).

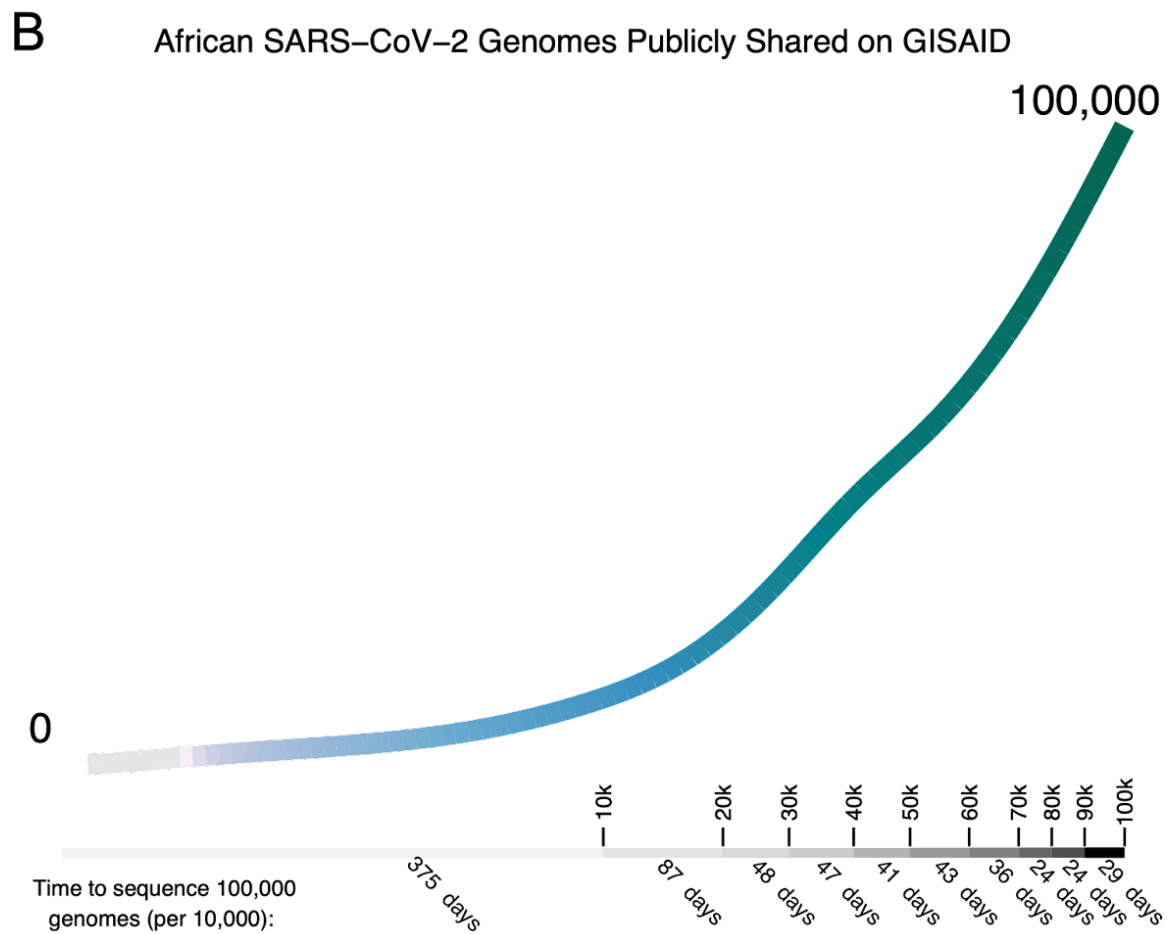
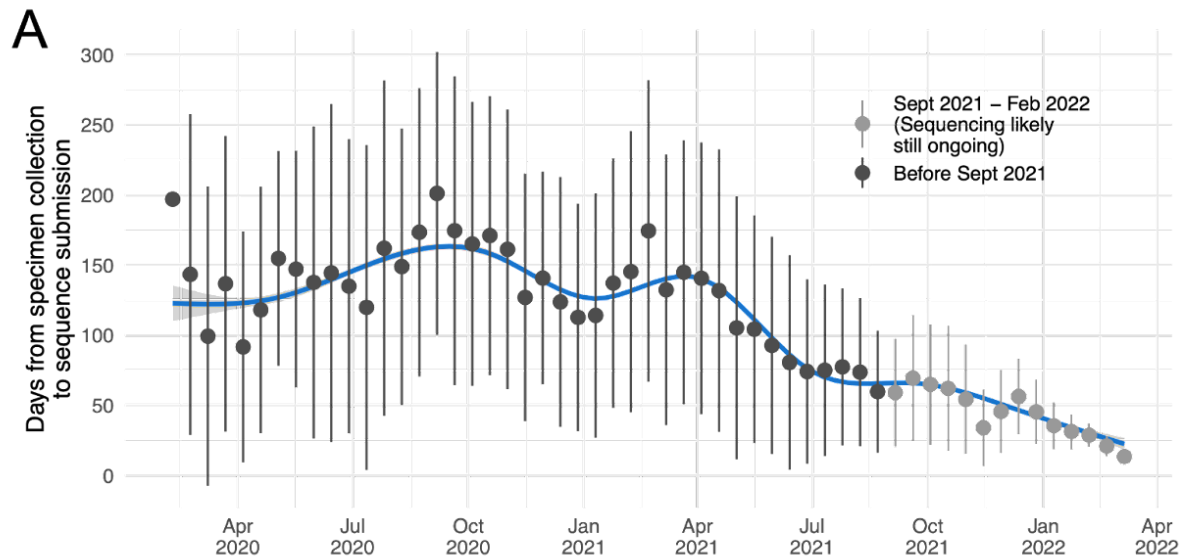


Supplementary Figure S4: COVID-19 testing rates in Africa against recorded cases per million for countries with available data. The extent of testing (average daily number of tests) is shown relative to the size of outbreaks (average daily number of reported cases) per million people per country in Africa. Data is obtained from Our World in Data (OWID). Panels span four-month intervals over the first two years of the epidemic. Test positive rates are displayed in gray segmented lines (0.02 – 100%). Testing efforts of most countries varied considerably

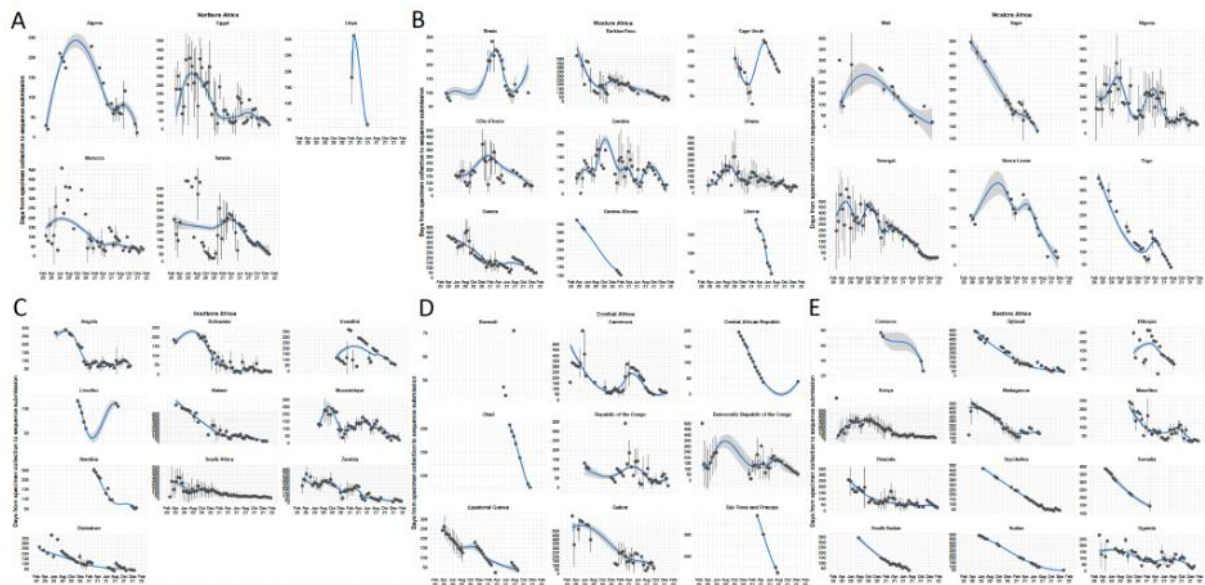
over the course of the epidemic with several southern African countries demonstrating generally the highest positive rate (highest testing rate per case) over the last year of the epidemic. Additionally, the spread of points mostly reduced to between 1 and 20% positive rate from January 2021 to March 2022. Points are shown for countries reporting the relevant data and with an average daily number of tests greater than zero for the relevant period. Axes are log scaled.



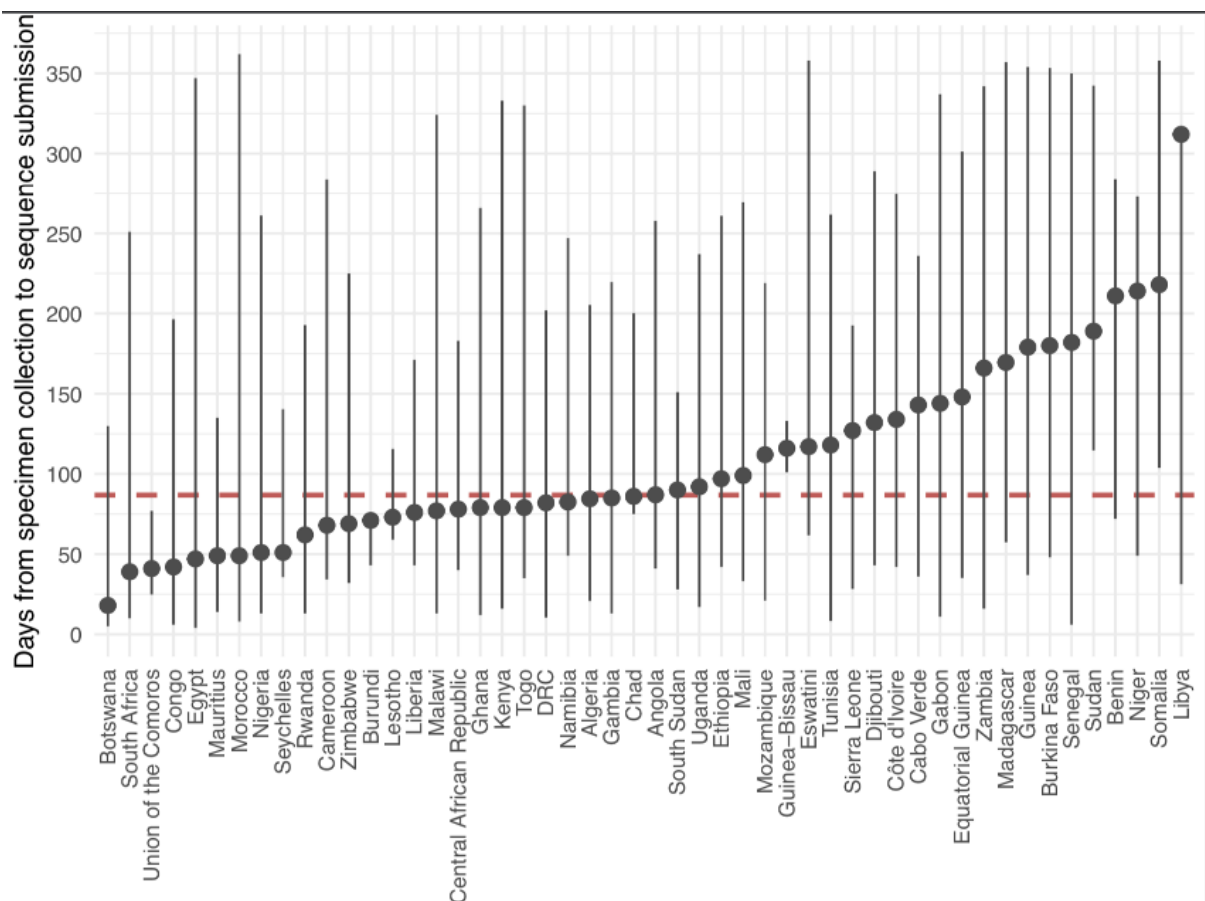
Supplementary Figure S5: The progression of sequencing technologies used for SARS-CoV-2 sequencing in Africa. Sequences are aggregated by associated sequencing technologies as reported on GISAID. Panel A represent the raw number of sequence generated using the five different technologies, while panel B represent the proportion of sequences generated by technology over time.



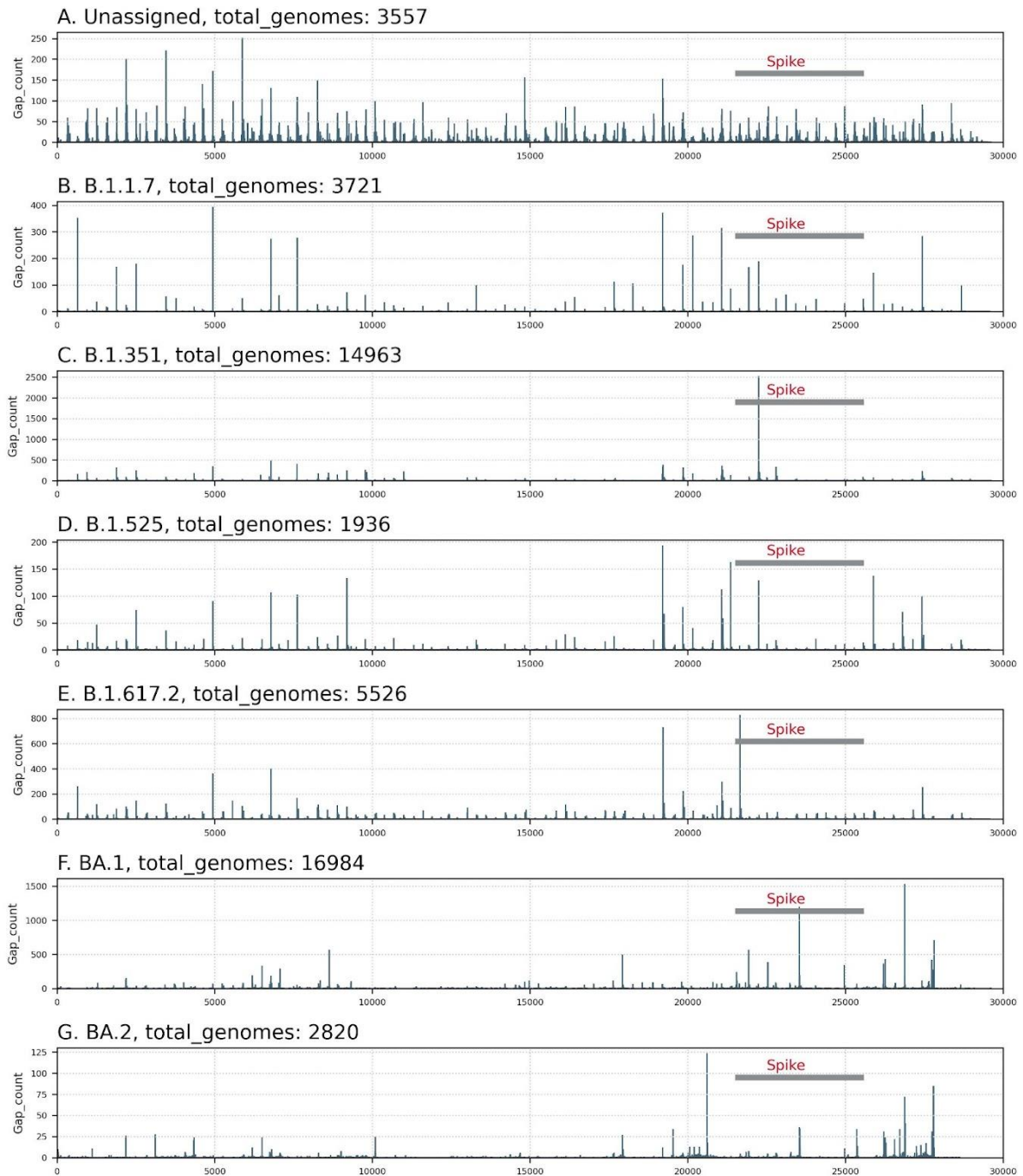
Supplementary Figure S6: Trends of sequencing turnaround time in Africa. A) Overall decreasing trend in sequencing turnaround time in Africa, with the caveat that sequencing for recent samples may not be completed. B) Number of days taken to sequence 10 000 sequences increment in Africa, until the 100 000 sequences milestone.



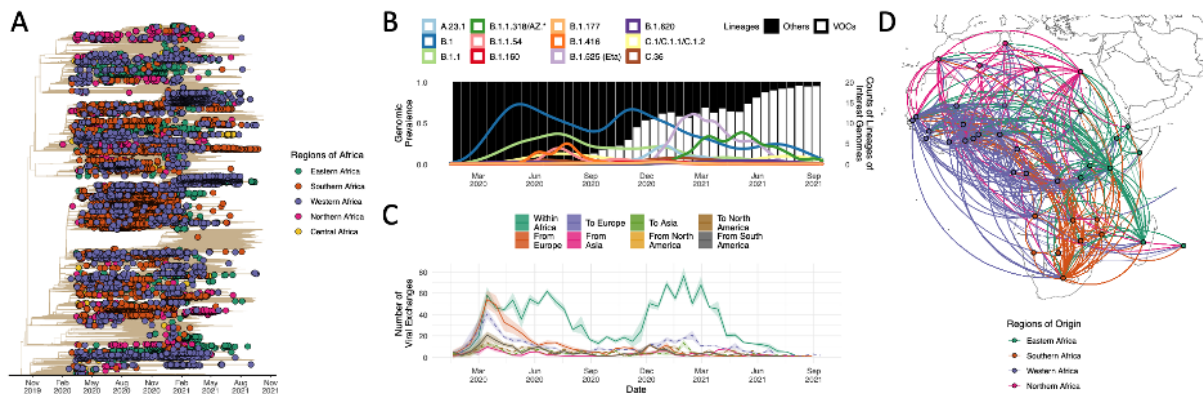
Supplementary Figure S7: Sequencing turnaround time progression per country in each region of Africa. Trends are shown for A) North Africa, B) West Africa, C) Southern Africa, D) Central Africa, and E) East Africa



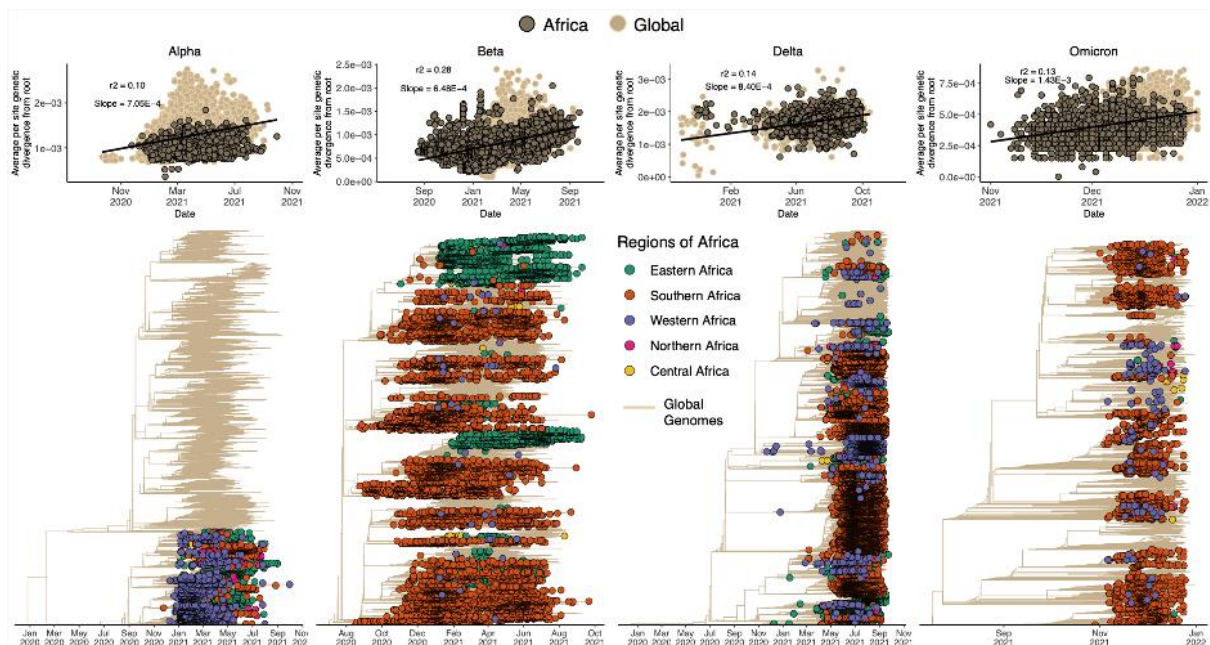
Supplementary Figure S8: Sequencing turnaround time average by country. The circles indicate the mean number of days between specimen collection and sequence submission to GISAID and the bars indicate the distribution of values for each country.



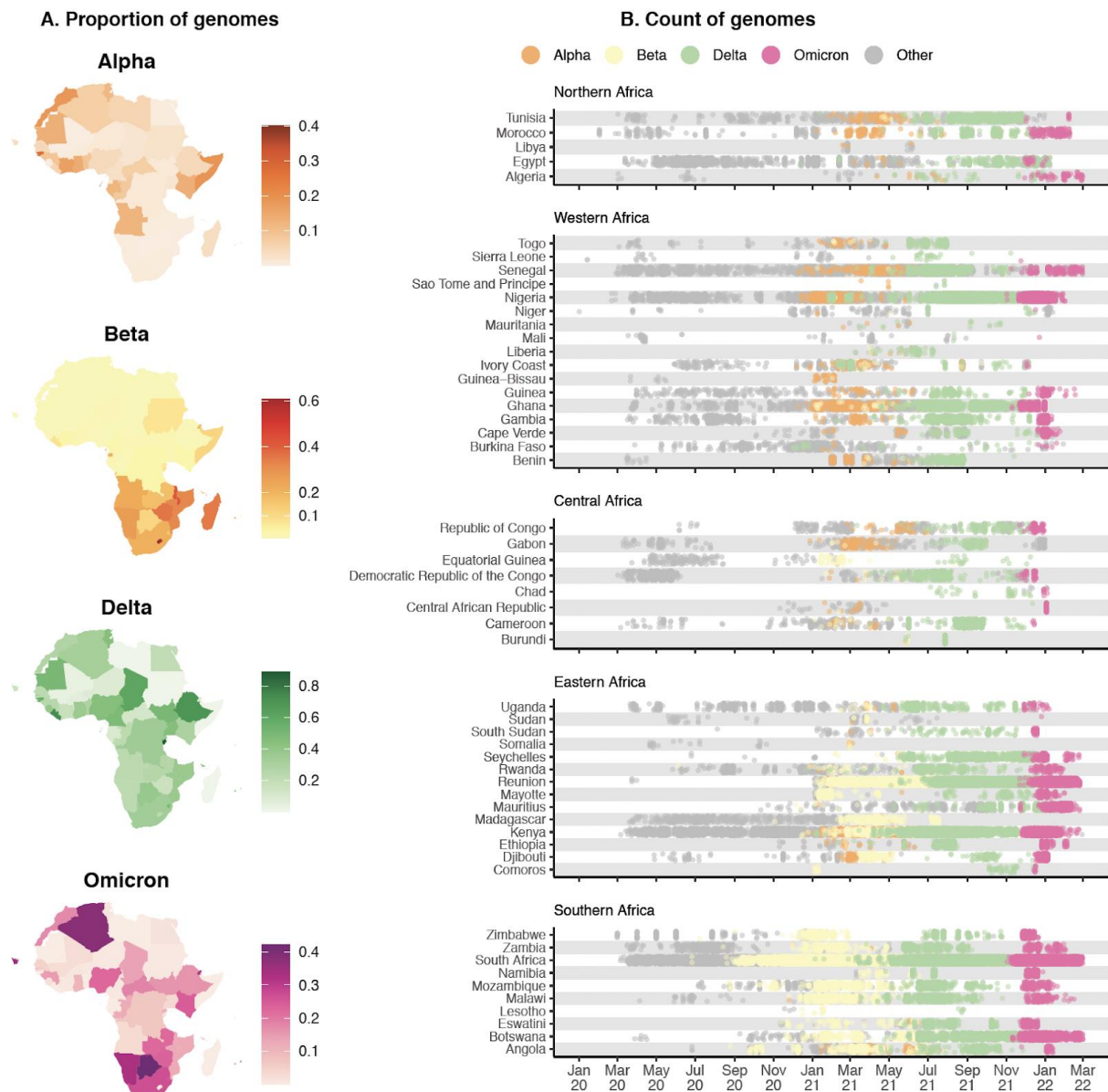
Supplementary Figure S9. Gapped positions in genomes by lineage. The positions of 200 nt N gaps in the 6 major SARS-CoV-2 lineages (plus unassigned entries) were plotted to document lineage-specific patterns in the genome entries. For each lineage (or unassigned entries) the number of 200nt N motifs was plotted by position. The lineage and the total number of genomes classified in the lineage are indicated above each panel. The position of the Spike coding region is indicated with a grey bar. A) Unassigned, B) B.1.1.7 (Alpha), C) B.1.351 (Beta), D) B.1.525 (Eta), E) B.1.617.2 (Delta), F) BA.1 (Omicron), G) BA.2 (Omicron).



Supplementary Figure S10: Phylogenetic inference of non-VOC lineages in Africa. A) Maximum-Likelihood timetrees of non-VOC genomes in Africa from the beginning of the pandemic till March 2022 against a global reference with African genomes denoted by tippoint circles coloured by regions of Africa. B) Genomic prevalence of non-VOC (black) vs VOC (white) lineages in Africa overlaid by frequency progressions of some lineages of interest in Africa. C) Inferred viral dissemination patterns of non-VOC lineages to, from and within the Africa continent from the beginning of the pandemic to October 2021. Introductions and viral transitions within Africa are shown in solid lines and exports from Africa are shown in dotted lines and these are coloured by continent. The shaded areas around the lines represent uncertainty of this analysis from ten replicates. D) Dissemination patterns of the non-VOC lineages within Africa, from inferred ancestral state reconstructions, annotated and coloured by region in Africa. The countries of origin of viral exchange routes are also shown with dots and the curves go from country of origin to destination country in an anti-clockwise direction.



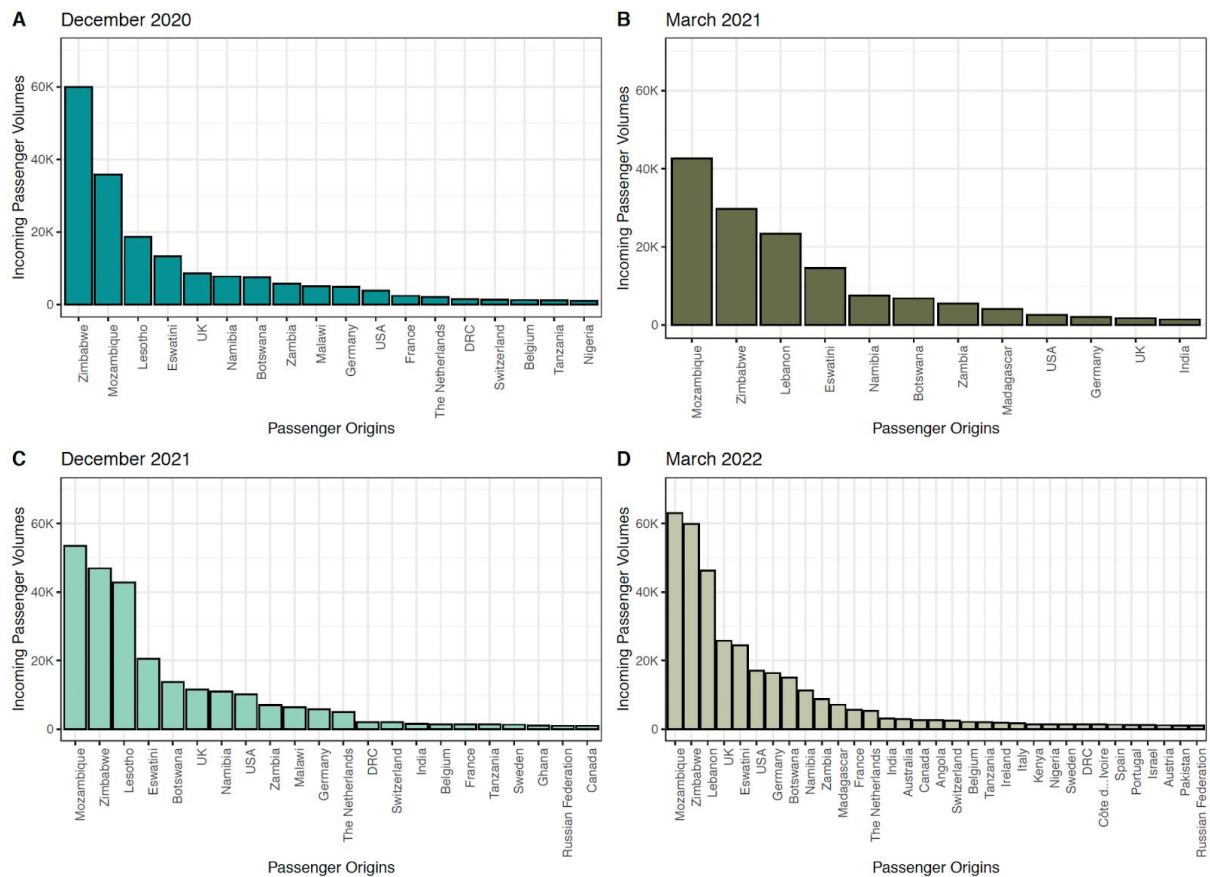
Supplementary Figure S11: Phylogenetic inference of VOCs in Africa using Africa-focused sampling. Top - Molecular clock evolution. Bottom - VOC-specific Maximum-Likelihood timetrees with African genomes denoted by tippoints coloured by regions of Africa.



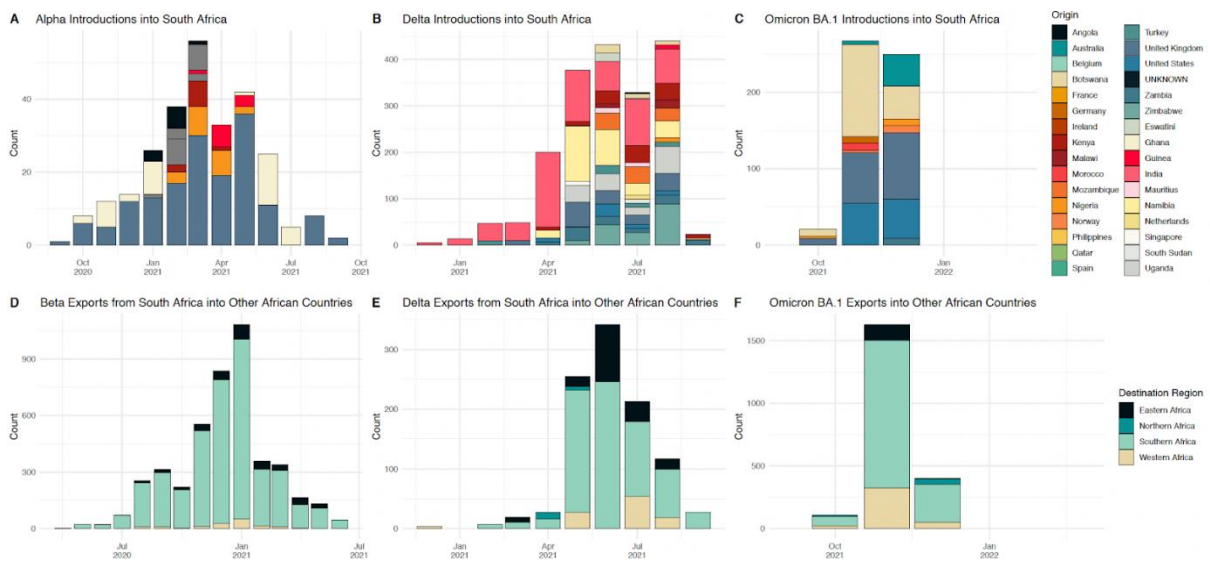
Supplementary Figure S12: Spatial and temporal circulation of four variants of concern (VOC) across Africa. A) The proportion of genomes of each VOC (of all genomes produced) sequenced per country. B) Scatterplot displaying the total number of genomes sequenced per VOC per country from January 2020 to March 2022. Alpha and Beta variants circulated within Africa at similar times in the epidemic however, a greater number of Alpha genomes were sequenced in Northern and Western African countries whereas Beta was more prevalent in Eastern and Southern African countries. Certain Central and Eastern African countries, such as Cameroon and Uganda, display a similar level of co-circulation of both variants. Thereafter, Delta and then Omicron, mostly dominated the landscape in isolation.



Supplementary Figure S13: Patterns of viral importations into different regions of Africa under an African-focused sampling strategy. Proportions of introductions into East, Northern, southern and West Africa attributed to specified origins for A) non-VOC lineages, B) Alpha VOC, C) Beta VOC, D) Delta VOC, and E) Omicron VOC during the relevant time periods are shown.

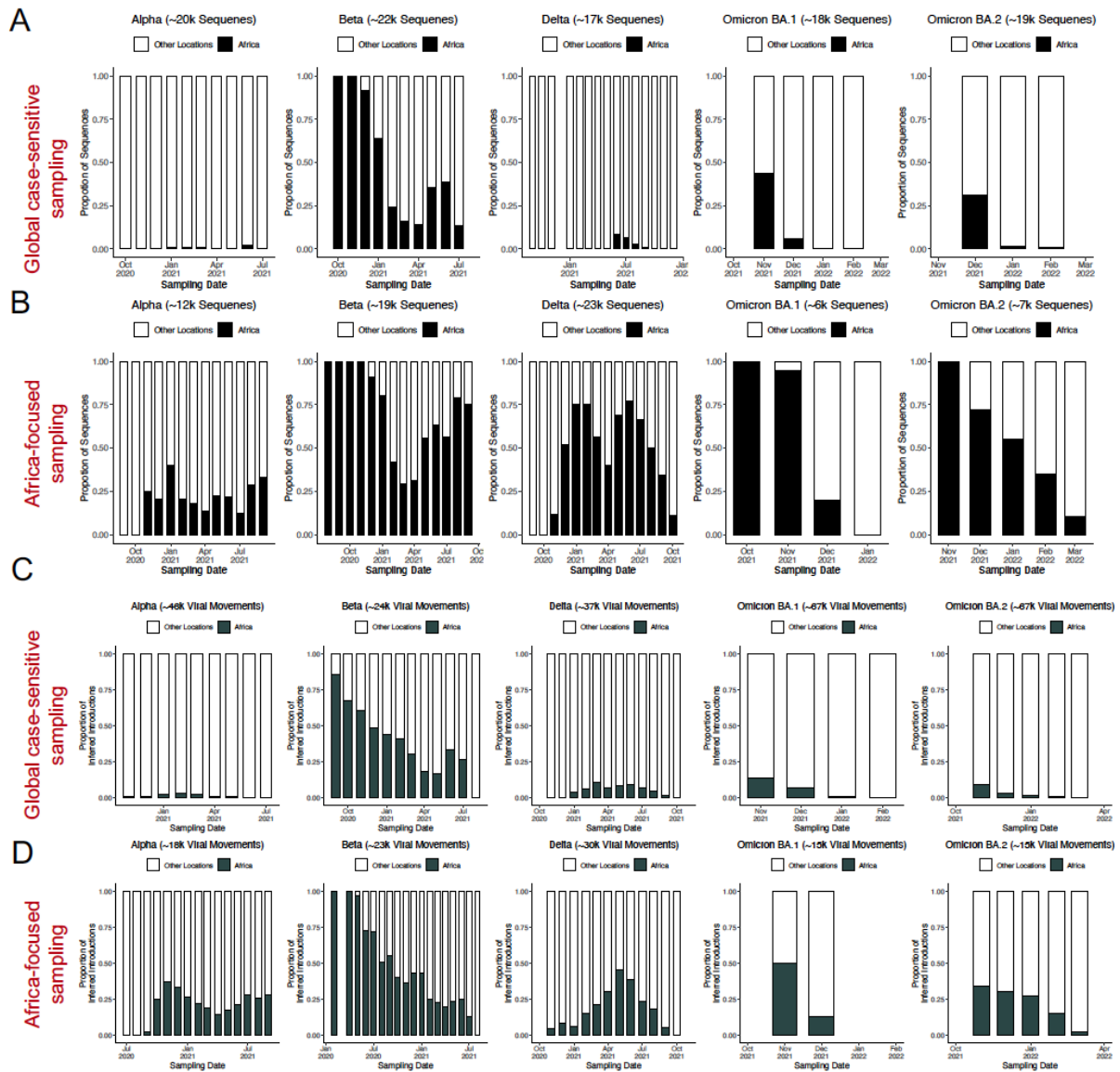


Supplementary Figure S14: Statistics of incoming passenger volume into South Africa by country of origin. Periods shown are December 2020 (A), March 2021 (B), December 2021 (C), and March 2022 (D). Data is obtained from Statistics South Africa Statistical Release P0351 - Tourism and Migration.



Supplementary Figure S15: Inferred introductions into and out of South Africa specified by country of inferred origin. (A) Alpha introductions into South Africa from Africa-focused phylogeography, (B) Delta introductions into South Africa from global case-sensitive phylogeography, (C) Omicron BA.1 introductions into South Africa from global case-sensitive

phylogeography, (D-E) Beta, Delta and Omicron BA.1 exports from South Africa into regions of Africa from Africa-focused phylogeography.



Supplementary Figure S16: Sensitivity analysis for phylogeography from ancestral state reconstruction. (A-B) Sampling proportions of African sequences in two strategies. (C-D) Proportion of inferred introductions into Africa in corresponding two strategies

Supplementary Table S1: NextStrain builds of the five major geographical regions in Africa. Each build focuses on a specific region within Africa and includes sequences from outside the region and the continent to place the regional sequences into context of the global pandemic. All the data used in the builds are publicly available on GISAID and are maintained and updated by the Africa CDC in collaboration with the NextStrain team on a weekly basis.

Region	Regional Builds
Central African Region	https://nextstrain.org/groups/africa-cdc/ncov/central-africa
Eastern African Region	https://nextstrain.org/groups/africa-cdc/ncov/eastern-africa
Northern African Region	https://nextstrain.org/groups/africa-cdc/ncov/northern-africa
Southern African Region	https://nextstrain.org/groups/africa-cdc/ncov/southern-africa
Western African Region	https://nextstrain.org/groups/africa-cdc/ncov/western-africa

Supplementary Table S2: Individual country specific NextStrain builds from the African continent. Each build focuses on a specific country within Africa and includes sequences from the rest of the world in order to place the country's sequences into context of the global pandemic. All the data used in the builds are publicly available on GISAID and are maintained and updated by the Africa CDC in collaboration with the NextStrain team on a weekly basis.

Region	Country	Build
Central African Region	Burundi	https://nextstrain.org/groups/africa-cdc/ncov/burundi
	Cameroon	https://nextstrain.org/groups/africa-cdc/ncov/cameroon
	Central African Republic	https://nextstrain.org/groups/africa-cdc/ncov/central-african-republic
	Chad	https://nextstrain.org/groups/africa-cdc/ncov/chad
	Republic of Congo	https://nextstrain.org/groups/africa-cdc/ncov/republic-of-the-congo
	Democratic Republic of Congo	https://nextstrain.org/groups/africa-cdc/ncov/democratic-republic-of-the-congo
	Equatorial Guinea	https://nextstrain.org/groups/africa-cdc/ncov/equatorial-guinea
	Gabon	https://nextstrain.org/groups/africa-cdc/ncov/gabon
Eastern African Region	Comoros	https://nextstrain.org/groups/africa-cdc/ncov/comoros
	Djibouti	https://nextstrain.org/groups/africa-cdc/ncov/djibouti
	Ethiopia	https://nextstrain.org/groups/africa-cdc/ncov/ethiopia
	Kenya	https://nextstrain.org/groups/africa-cdc/ncov/kenya
	Madagascar	https://nextstrain.org/groups/africa-cdc/ncov/madagascar
	Mauritius	https://nextstrain.org/groups/africa-cdc/ncov/mauritius
	Rwanda	https://nextstrain.org/groups/africa-cdc/ncov/rwanda

	Seychelles	https://nextstrain.org/groups/africa-cdc/ncov/seychelles
	Somalia	https://nextstrain.org/groups/africa-cdc/ncov/somalia
	South Sudan	https://nextstrain.org/groups/africa-cdc/ncov/south-sudan
	Sudan	https://nextstrain.org/groups/africa-cdc/ncov/sudan
	Uganda	https://nextstrain.org/groups/africa-cdc/ncov/uganda
Northern African Region	Algeria	https://nextstrain.org/groups/africa-cdc/ncov/algeria
	Egypt	https://nextstrain.org/groups/africa-cdc/ncov/egypt
	Libya	https://nextstrain.org/groups/africa-cdc/ncov/libya
	Morocco	https://nextstrain.org/groups/africa-cdc/ncov/morocco
	Tunisia	https://nextstrain.org/groups/africa-cdc/ncov/tunisia
Southern African Region	Angola	https://nextstrain.org/groups/africa-cdc/ncov/angola
	Botswana	https://nextstrain.org/groups/africa-cdc/ncov/botswana
	Eswatini	https://nextstrain.org/groups/africa-cdc/ncov/eswatini
	Lesotho	https://nextstrain.org/groups/africa-cdc/ncov/lesotho
	Malawi	https://nextstrain.org/groups/africa-cdc/ncov/malawi
	Mozambique	https://nextstrain.org/groups/africa-cdc/ncov/mozambique
	Namibia	https://nextstrain.org/groups/africa-cdc/ncov/namibia
	South Africa	https://nextstrain.org/groups/africa-cdc/ncov/south-africa
	Zambia	https://nextstrain.org/groups/africa-cdc/ncov/zambia

	Zimbabwe	https://nextstrain.org/groups/africa-cdc/ncov/zimbabwe
Western African Region	Benin	https://nextstrain.org/groups/africa-cdc/ncov/benin
	Burkina Faso	https://nextstrain.org/groups/africa-cdc/ncov/burkina-faso
	Cabo Verde	https://nextstrain.org/groups/africa-cdc/ncov/cabo-verde
	Côte d'Ivoire	https://nextstrain.org/groups/africa-cdc/ncov/cote-divoire
	Gambia	https://nextstrain.org/groups/africa-cdc/ncov/gambia
	Ghana	https://nextstrain.org/groups/africa-cdc/ncov/ghana
	Guinea	https://nextstrain.org/groups/africa-cdc/ncov/guinea
	Guinea-Bissau	https://nextstrain.org/groups/africa-cdc/ncov/guinea-bissau
	Liberia	https://nextstrain.org/groups/africa-cdc/ncov/liberia
	Mali	https://nextstrain.org/groups/africa-cdc/ncov/mali
	Niger	https://nextstrain.org/groups/africa-cdc/ncov/niger
	Nigeria	https://nextstrain.org/groups/africa-cdc/ncov/nigeria
	Senegal	https://nextstrain.org/groups/africa-cdc/ncov/senegal
	Sierra Leone	https://nextstrain.org/groups/africa-cdc/ncov/sierra-leone
	Togo	https://nextstrain.org/groups/africa-cdc/ncov/togo

Supplementary Table S3 (excel file): Sequencing and epidemiological reporting survey results. S3.1) Aggregate results of the survey with responses from 25 countries across the continent. S3.2) frequency of epidemiological reporting (i.e. of new cases and deaths) in the different countries. S3.3) Sequencing strategies employed by different countries as the pandemic progressed. S3.4) The proportion of sequences from the major administrative regions of each country (i.e. provinces, districts or regions). The table can also be found at the github repository (<https://github.com/CERI-KRISP/SARS-CoV-2-epidemic-in-Africa>).

Supplementary Table S4 (excel file): GISAID acknowledgment table. The table can also be found at the github repository (<https://github.com/CERI-KRISP/SARS-CoV-2-epidemic-in-Africa>).

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