Inventory of Supporting Information

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| Please complete each of the Inventory Tables below to outline your Extended Data and Supplementary Information items.  There are four sections:   * *Extended Data* * *Supplementary Information: Flat Files* * *Supplementary Information: Additional Files* * *Source Data*   Each section includes specific instructions. Please complete these tables as fully as possible. We ask that you avoid using spaces in your file names, and instead use underscores, i.e.: Smith\_ED\_Fig1.jpg not Smith ED Fig1.jpg  Please note that titles and descriptive captions will only be lightly edited, so please ensure that you are satisfied with these prior to submission.  If you have any questions about any of the information contained in this inventory, please contact the journal. |
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1. **Extended Data**

**Complete the Inventory below for all Extended Data figures.**

* Keep Figure Titles to one sentence only
* Upload your files as ‘Figure Files’ in our Manuscript Tracking system
* File names should include the Figure Number. i.e.: *Smith\_ED\_Fig1.jpg*
* Please be sure to include the file extension in the Filename. Note that Extended Data files must be submitted as .jpg, .tif or .eps files *only*, and should be approximately 10MB
* All Extended Data figure legends must be provided in the Inventory below and should not exceed 300 words each *(if possible)*
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| Figure # | Figure title  One sentence only | Filename  This should be the name the file is saved as when it is uploaded to our system. Please include the file extension. i.e.: *Smith\_ED\_Fig1.jpg* | Figure Legend  If you are citing a reference for the first time in these legends, please include all new references in the main text Methods References section, and carry on the numbering from the main References section of the paper. If your paper does not have a Methods section, include all new references at the end of the main Reference list. |
| Extended Data Fig. 1 | **Impact of SARS-CoV-2 Ag-RDT testing rates and daily proportion of positive specimens to sample for sequencing on observed Omicron variant proportions**. | GS\_ED\_Fig1.jpg | Different genomic surveillance strategies (i.e. all specimens collected from all healthcare facilities sent to onefacility to be sampled for sequencing (*population-wide* strategy); only *one*, 10%, 25%, 50% or 100% of all tertiary facilities acting as sentinel sites that would sample the specimens they collected for sequencing) were simulated. (**A**) Maximum absolute difference between observed and circulating variant proportions. (**B**) Proportion of timepoints when sequencing was performed that the absolute difference between observed and circulating variant proportions is greater than 20%. All results were computed from 1,000 random independent simulations for each surveillance strategy. |
| Extended Data Fig. 2 | **Sensitivity analyses on variant detection operating curve for different relative transmissibility factor**. | GS\_ED\_Fig2.jpg | For each Ag-RDT availability (differently colored), the expected day (points and line) and the standard deviation (shaded region) when the first Omicron variant specimen (in the background of extant Delta variant) is sampled for sequencing since its introduction is plotted against the proportion of positive specimens to be sampled for sequencing daily. All specimens collected from the population from all healthcare facilities were sent to onefacility to be sampled for sequencing (population-wide genomic surveillance strategy). Different transmissibility factor of Omicron relative to Delta () were assumed. (**A**) 10% and (**B**) 40% of the population had immunity against Omicron initially. The plotted results were computed from 1,000 random independent simulations for each surveillance strategy. |
| Extended Data Fig. 3 | **Sensitivity analyses on accuracy of observed variant proportions for different relative transmissibility factor**. | GS\_ED\_Fig3.jpg | Omicron-like virus properties assumed for variant and initial proportion of population with some degree of protection against the variant virus assumed at 10%. All specimens collected from the population from all healthcare facilities were sent to onefacility to be sampled for sequencing (population-wide genomic surveillance strategy). Different transmissibility factor of Omicron relative to Delta () were assumed. (**A**) Maximum absolute difference between observed and circulating variant proportions. (**B**) Proportion of timepoints when sequencing was performed that the absolute difference between observed and circulating variant proportions is greater than 20%. All results were computed from 1,000 random independent simulations for each surveillance strategy. |
| Extended Data Fig. 4 | **Sensitivity analyses on accuracy of observed variant proportions for different relative transmissibility factor**. | GS\_ED\_Fig4.jpg | Omicron-like virus properties assumed for variant and initial proportion of population with some degree of protection against the variant virus assumed at 40%. All specimens collected from the population from all healthcare facilities were sent to onefacility to be sampled for sequencing (population-wide genomic surveillance strategy). Different transmissibility factor of Omicron relative to Delta () were assumed. (**A**) Maximum absolute difference between observed and circulating variant proportions. (**B**) Proportion of timepoints when sequencing was performed that the absolute difference between observed and circulating variant proportions is greater than 20%. All results were computed from 1,000 random independent simulations for each surveillance strategy. |
| Extended Data Fig. 5 | **Impact of prevalence of extant variant of concern () at the time of new variant introduction**. | GS\_ED\_Fig5.jpg | For each Ag-RDT availability (differently colored), the expected day (points and line) and the standard deviation (shaded region) when the first Omicron variant specimen (in the background of Delta) is sampled for sequencing since its introduction is plotted against the proportion of positive specimens to be sampled for sequencing daily. Each panel shows a different prevalence of the Delta variant () at the point of Omicron introduction. Sampling for sequencing was drawn from the population-wide scenario. The plotted results were computed from 1,000 random independent simulations for each surveillance strategy. |
| Extended Data Fig. 6 | **Recommended approach to enhance genomic surveillance robustness**. | GS\_ED\_Fig6.jpg | In each plot, the operating curves of the expected day when the first Omicron BA.1 variant sequence is generated are plotted for different proportion of specimens to sample for sequencing per day and turnaround times. We assumed that the Omicron BA.1 variant was circulating at 1% initially with Delta variant in the background. We also assumed that positive specimens sampled within each week for sequencing are consolidated into a batch before they are referred for sequencing. Turnaround time refers to the time between collection of each weekly consolidated batch of positive specimens to the acquisition of its corresponding sequencing data. The vertical axes denote the number of days passed since the introduction of the Omicron variant (left) and its corresponding circulating proportion (right). The horizontal axes denote the proportion of positive specimens to sample for sequencing per day (bottom) and the corresponding mean number of sequences to be generated per week per 1,000,000 people over a 90-day epidemic period. (**A**) Specimen pools for sequencing from *one* tertiary facility with testing rate at 27 tests per 100,000 persons per day (tests/100k/day). (**B**) Specimen pools for sequencing from *one* tertiary sentinel facility with testing rate at 100 tests/100k/day. (**C**) Specimen pools for sequencing from 25% of all tertiary facilities acting as sentinel sites with testing rate at 100 tests/100k/day. (**D**) Zoomed-in plot of (C) for sequencing proportions varying between 1-25%. Sequencing 5-10% of positive specimens (blue shaded region) would ensure that we would expectedly detect Omicron within 30 days if turnaround time is kept within one week. All results were computed from 1,000 random independent simulations for each surveillance strategy. The shaded region depicts the standard deviation across simulations. |
| Extended Data Fig. 7 | **Transmissions attributed to infectors of different disease status**. | GS\_ED\_Fig7.jpg | Proportion of transmissions events (data points) attributed to different disease status of infectors across all independent epidemic simulations (n = 280). Bar plots show the mean proportion with error bars denoting standard deviation. |
| Extended Data Fig. 8 | **Model validation**. | GS\_ED\_Fig8.jpg | We compared the mean number of reported cases (blue line, top panel) and deaths (red line, bottom panel) estimated by our simulations (10 simulations in total; see Supplementary Text) against the actual case and death counts (black lines) in Lusaka, Zambia during the second wave of infections between 25 December 2020 and 24 March 2021. Actual case and death counts were retrieved from the Zambia COVID-19 Dashboard (<https://www.arcgis.com/apps/dashboards/3b3a01c1d8444932ba075fb44b119b63>). The blue and red shaded regions in each plot denotes the standard deviation of reported cases (top panel) and deaths (bottom panel) respectively. |

***Delete rows as needed to accommodate the number of figures (10 is the maximum allowed).***

1. **Supplementary Information:**
2. **Flat Files**

**Complete the Inventory below for all additional textual information and any additional Supplementary Figures, which should be supplied in one combined PDF file.**

* **Row 1:** A combined, flat PDF containing any Supplementary Text, Discussion, Notes, Additional Supplementary Figures, Supplementary Protocols, simple tables, and all associated legends. Only one such file is permitted.
* **Row 2:** Nature Research’s Reporting Summary; if previously requested by the editor, please provide an updated Summary, fully completed, without any mark-ups or comments. **(Reporting Summaries are not required for all manuscripts.)**

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| Supplementary Information | Yes | GS\_supplementary\_information.pdf | Supplementary Notes, and Supplementary Table 1 |
| Reporting Summary | Yes | nr-reporting-summary\_GS.pdf |
| Peer Review Information | Choose an item. | *OFFICE USE ONLY* |

1. **Additional Supplementary Files**

**Complete the Inventory below for all additional Supplementary Files that cannot be submitted as part of the Combined PDF.**

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* Where possible, include the title and description within the file itself
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* Compressed files are acceptable where necessary. ZIP files are preferred.
* Please note that the *ONLY* allowable types of additional Supplementary Files are:

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| * Supplementary Tables | * Supplementary Audio | * Supplementary Videos | * Supplementary Software |
| * Supplementary Data, for example: raw NMR Data, Cryo-EM Data, Computational Data, Crystallographic Data, etc. | | | |

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1. **Source Data**

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* Acceptable types of Source Data for Main Figures and Extended Data Figures are:
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    - One file for each relevant Figure, containing all source data
  + Full-length, unprocessed Gels or Blots
    - JPG, TIF, or PDF formats only
    - One file for each relevant Figure, containing all supporting blots and/or gels
* ‘Source Data’ is only allowed for Main Figures and Extended Data Figures.
  + Include Unprocessed Gels or Blots for Supplementary Figures as additional Supplementary Figures.
  + Include Statistical Source Data for Supplementary Figures as ‘Supplementary Data’ files and list them in section 2B.
  + Please see [this example of Source Data](https://www.nature.com/articles/s41591-019-0505-4) in a publication.

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