Centre for Respiratory Diseases and Meningitis Sentinel Surveillance in South Africa Respiratory Pathogens Report

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

Report week: 52
Reporting period: 1 January 2024 to 29 December 2024
Date of data extraction: 8 January 2025

Data are provisional as on date data extracted. Number of consultations/specimens are reported/analysed by date of consultation/specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports. Refer to end of report for methodology and definitions.

Highlights

- The influenza season started in week 17 (week starting 22 April 2024), peaked in week 23 (week starting 3 June 2024) and ended in week 41 (week starting 7 October 2024). The first peak of the season was predominated by A(H1N1)pdm09, with influenza transmission and impact reaching a high level. A second lower peak was observed in week 35 (week starting 26 August 2024) and was predominated by B/Victoria.
- The RSV season started in week 6 (week starting 5 February 2024), peaked in week 16 (week starting 15 April 2024) at the moderate level, and ended in week 28 (week starting 8 July 2024).
- In week 52 (23 December 2024 to 29 December 2024), we detected no cases of influenza (0%, 0/7) and RSV (0%, 0/7) and 1 (14.3%, 1/7) case of SARS-CoV-2. In the month of December, we detected 8 (3.4%, 8/232) cases of *B. pertussis*.
- From 01 January 2024 to 29 December 2024, from 7690 samples tested we detected 1001 (13%) cases of influenza, 856 (11.1%) cases of respiratory syncytial virus (RSV), 324 (4.2%) cases of SARS-CoV-2 and 79 (1.3%) cases of *Bordetella pertussis*.
- SARS-CoV-2 continues to circulate at low levels with fluctuations. There have been small increases in detections over the recent weeks, but not very different from fluctuations seen throughout the year.
- An increase in pertussis cases among inpatients from the Pneumonia Surveillance Programme (since week 42, week starting 14 October 2024) has been observed initially in the Western Cape but in more recent weeks cases have been observed in KwaZulu-Natal and Mpumalanga. Monitoring of this is ongoing.
- Since week 12 (week starting 18 March 2024), Omicron 24A/JN.1 was the most common SARS-CoV-2 lineage detected in all surveillance programmes. KP.3 lineages have also been detected more recently.

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Epidemic thresholds

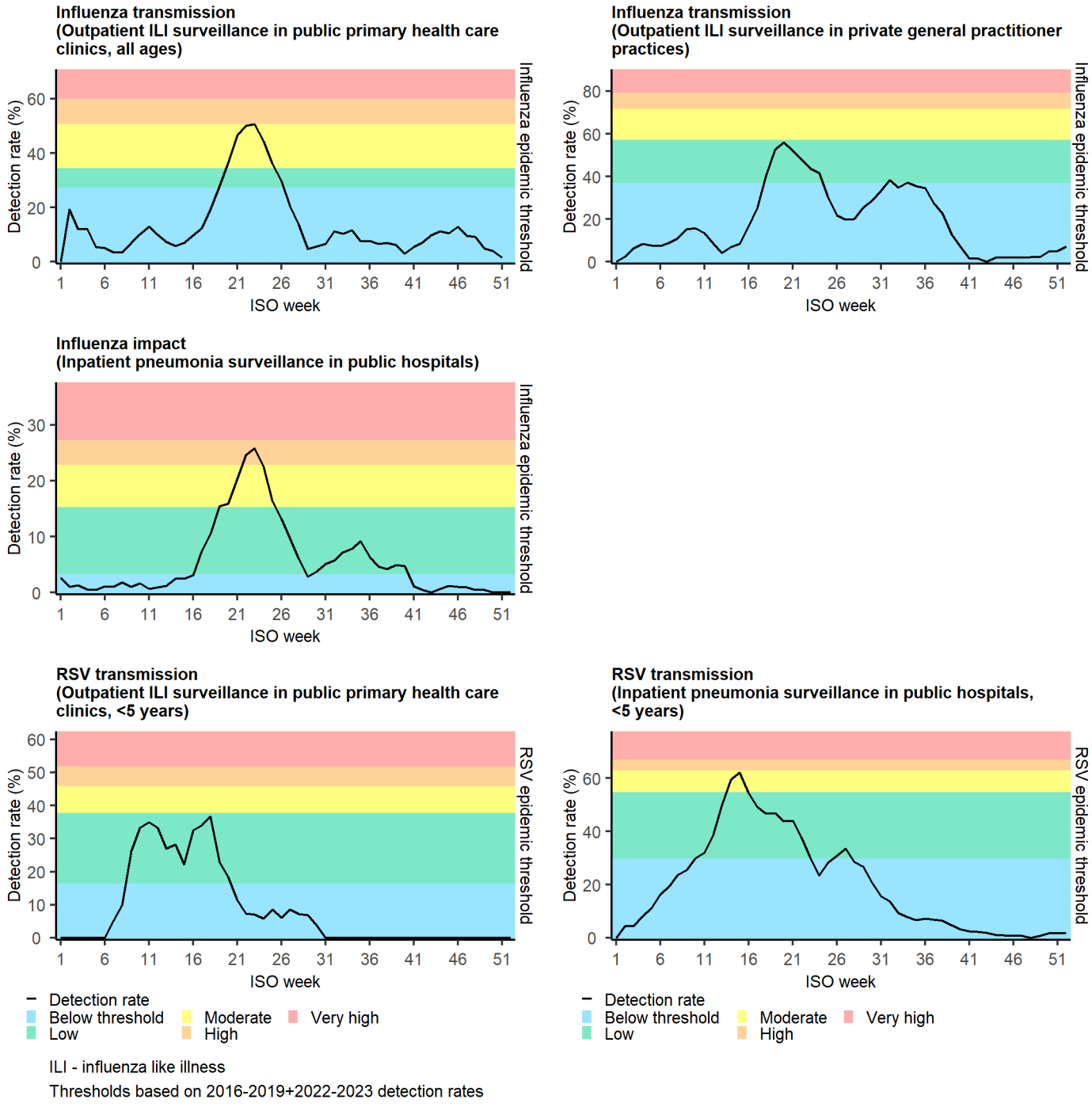

Figure 1: Influenza and respiratory syncytial virus (RSV) surveillance epidemic threshold summary, sentinel surveillance, South Africa, 01 January 2024 to 29 December 2024.

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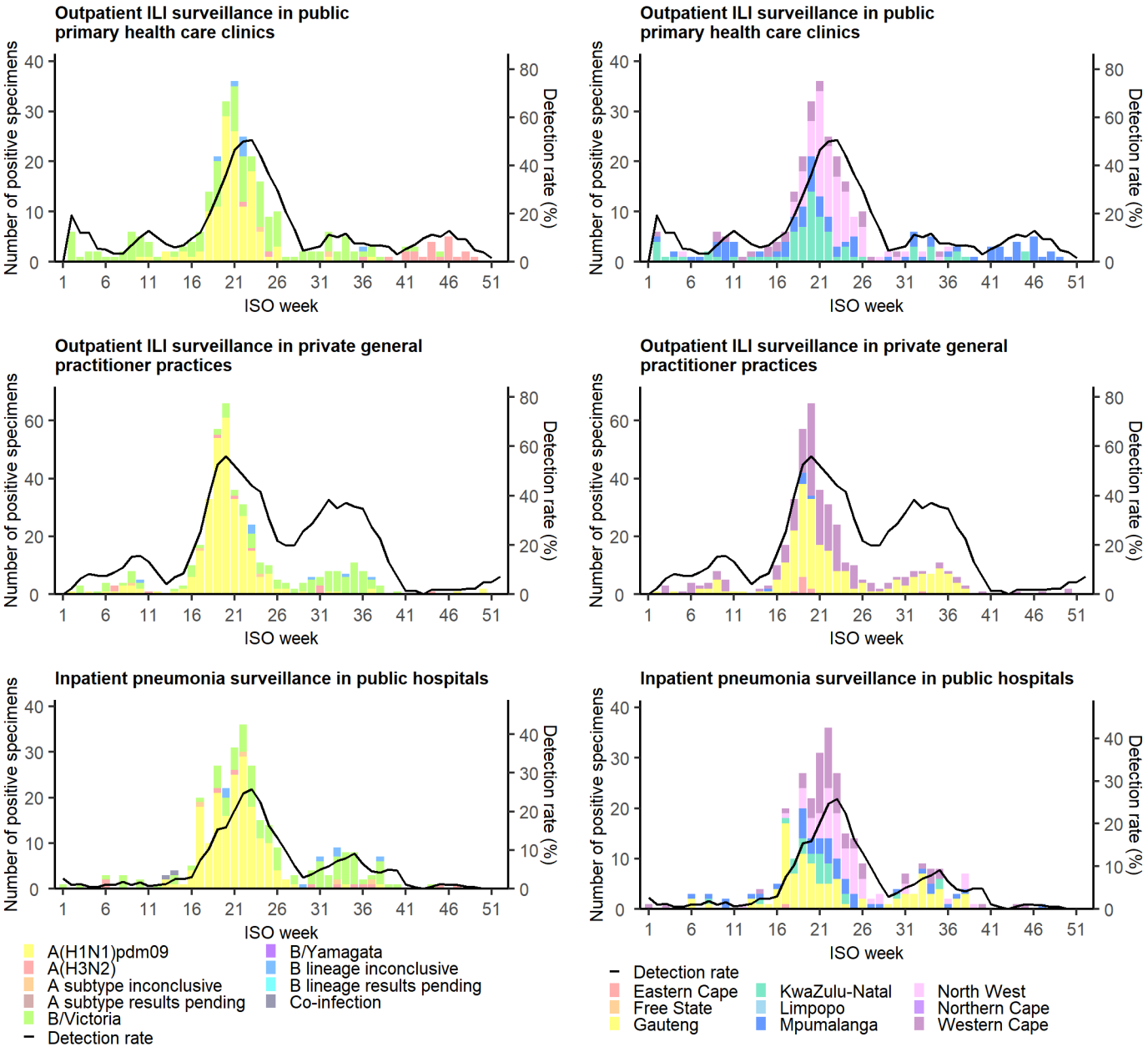
Influenza



ILI - influenza like illness, ISO - International Organization for Standardization

Detection rate presented as three-week moving average

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital

Figure 2: Number of laboratory-confirmed influenza cases and detection rate by subtype and lineage (left) and province (right) in all ages, sentinel surveillance, South Africa, 01 January 2024 to 29 December 2024.

Data are provisional as on date data extracted. Number of consultations/specimens are reported/analysed by date of consultation/specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Table 1: Number of laboratory-confirmed influenza cases by subtype and lineage and total number of samples tested by clinic and province in all ages, outpatient ILI surveillance in public primary health care clinics, South Africa, 01 January 2024 to 29 December 2024.

Clinic (Province)	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending	Co-infection	Total influenza	Total specimens
Edendale Gateway (KZ)	47	1	0	0	28	0	0	0	0	78	514
Agincourt (MP)	18	22	1	0	36	0	1	0	0	80	286
Jouberton (NW)	41	0	1	0	46	0	6	0	0	94	544
Eastridge (WC)	17	0	0	0	16	0	0	0	0	33	281
Mitchell's Plain (WC)	4	0	0	0	0	0	0	0	0	4	125
Total	127	23	2	0	126	0	7	0	0	289	1750

Specimens where more than one influenza subtype or lineage was detected denoted as co-infection, and included in the counts for each separate type as well. Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Table 2: Number of laboratory-confirmed influenza cases by subtype and lineage and total number of samples tested by province in all ages, outpatient ILI surveillance in private general practitioner practices, South Africa, 01 January 2024 to 29 December 2024.

Province	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending	Co-infection	Total influenza	Total specimens
Eastern Cape	8	1	0	0	1	0	0	0	0	10	22
Free State	0	0	0	0	0	0	0	0	0	0	0
Gauteng	155	4	3	0	58	0	3	0	0	223	1066
Limpopo	0	0	0	0	0	0	0	0	0	0	0
Mpumalanga	6	0	0	0	0	0	0	0	0	6	12
North West	0	0	0	0	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	0	0	0	0	2
Western Cape	116	5	0	0	51	0	4	0	0	176	438
Total	285	10	3	0	110	0	7	0	0	415	1540

Specimens where more than one influenza subtype or lineage was detected denoted as co-infection, and included in the counts for each separate type as well. Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Table 3: Number of laboratory-confirmed influenza cases by subtype and lineage and total number of samples tested by hospital and province in all ages, inpatient pneumonia surveillance in public hospitals, South Africa, 01 January 2024 to 29 December 2024.

Hospital (Province)	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending	Co-infection	Total influenza	Total specimens
Livingstone (EC)	1	0	0	0	0	0	0	0	0	1	41
Helen Joseph-Rahima Moosa (GP)	66	4	1	0	24	0	4	0	0	99	1057
Tambo Memorial (GP)	0	0	0	0	0	0	0	0	0	0	28
Tembisa (GP)	2	0	0	0	0	0	0	0	0	2	113
Harry Gwala (KZ)	20	0	0	0	6	0	0	0	0	26	504
Mapulaneng-Matikwana (MP)	13	4	1	0	11	0	1	0	1	29	416
Tintswalo (MP)	8	1	0	0	6	0	0	0	0	15	162
Klerksdorp-Tshepong (NW)	38	0	1	0	23	0	1	0	0	63	527
Khayelitsha (WC)	0	0	0	0	0	0	0	0	0	0	106
Mitchell's Plain (WC)	10	1	0	0	6	0	1	0	0	18	317
Red Cross (WC)	19	1	1	0	23	0	1	0	1	44	1129
Tygerberg (WC)	0	0	0	0	0	0	0	0	0	0	0
Total	177	11	4	0	99	0	8	0	2	297	4400

Specimens where more than one influenza subtype or lineage was detected denoted as co-infection, and included in the counts for each separate type as well. Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Table 4: Description of cases with more than one influenza subtype or lineage detected (denoted as co-infection in plots and tables), by surveillance programme

Infection description	Outpatient ILI surveillance in public primary health care clinics	Outpatient ILI surveillance in private general practitioner practices	Inpatient pneumonia surveillance in public hospitals
A(H1N1)pdm09 + B lineage inconclusive	0	0	1
A(H1N1)pdm09 + B/Victoria	0	0	1

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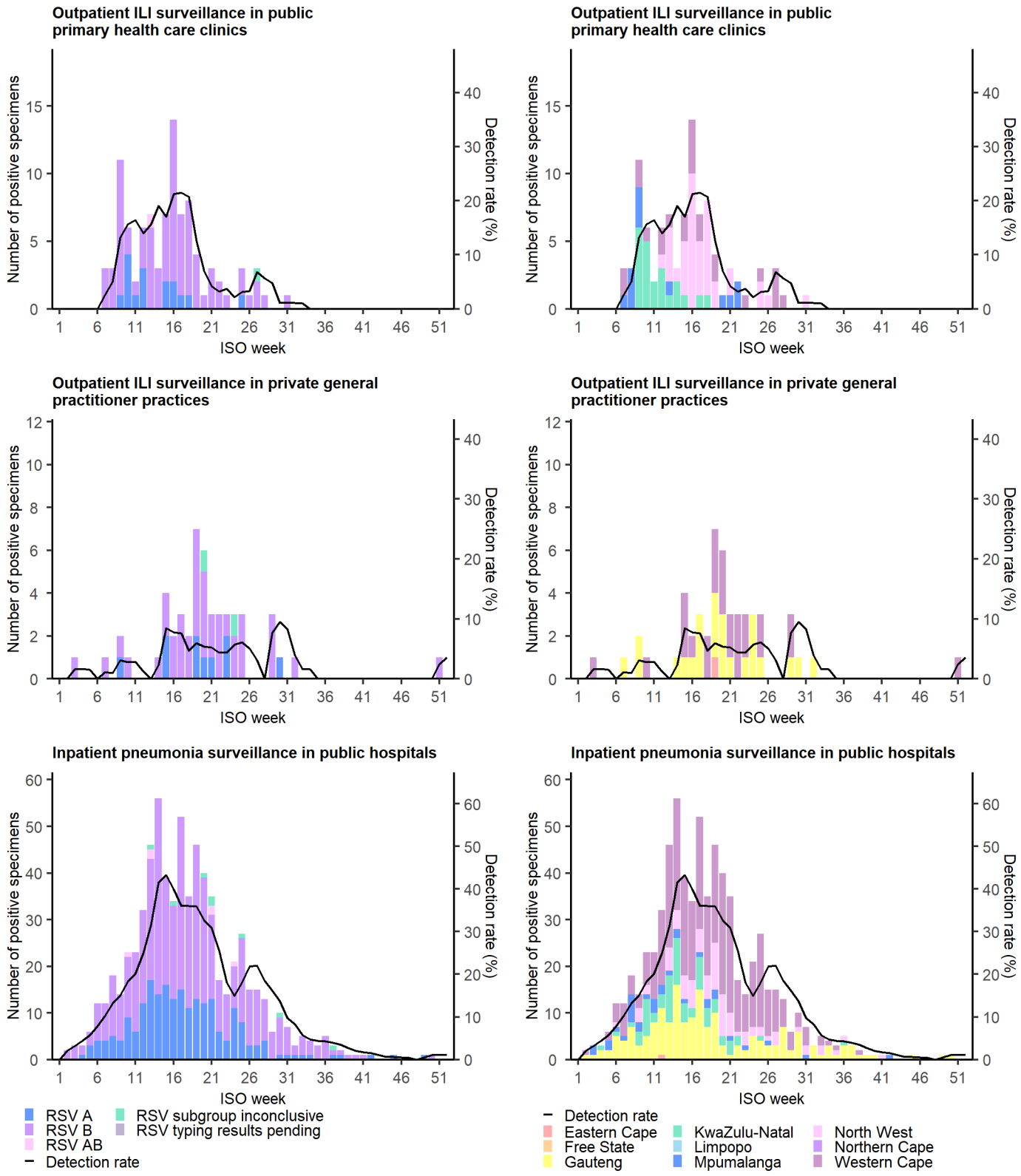
Respiratory syncytial virus (RSV)



ILI - influenza like illness, ISO - International Organization for Standardization

Detection rate presented as three-week moving average

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital

Figure 3: Number of laboratory-confirmed respiratory syncytial virus (RSV) cases and detection rate by type (left) and province (right) in all ages, sentinel surveillance, South Africa, 01 January 2024 to 29 December 2024.

Data are provisional as on date data extracted. Number of consultations/specimens are reported/analysed by date of consultation/specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Table 5: Number of laboratory-confirmed respiratory syncytial virus (RSV) cases by type and total number of samples tested by clinic and province in all ages, outpatient ILI surveillance in public primary health care clinics, South Africa, 01 January 2024 to 29 December 2024.

Clinic (Province)	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV typing results pending	Total RSV	Total specimens
Edendale Gateway (KZ)	9	13	0	0	0	22	514
Agincourt (MP)	0	12	0	0	0	12	286
Jouberton (NW)	0	39	0	0	0	39	544
Eastridge (WC)	7	14	1	1	0	23	281
Mitchell's Plain (WC)	0	1	0	0	0	1	125
Total	16	79	1	1	0	97	1750

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Table 6: Number of laboratory-confirmed respiratory syncytial virus (RSV) cases by type and total number of samples tested by province in all ages, outpatient ILI surveillance in private general practitioner practices, South Africa, 01 January 2024 to 29 December 2024.

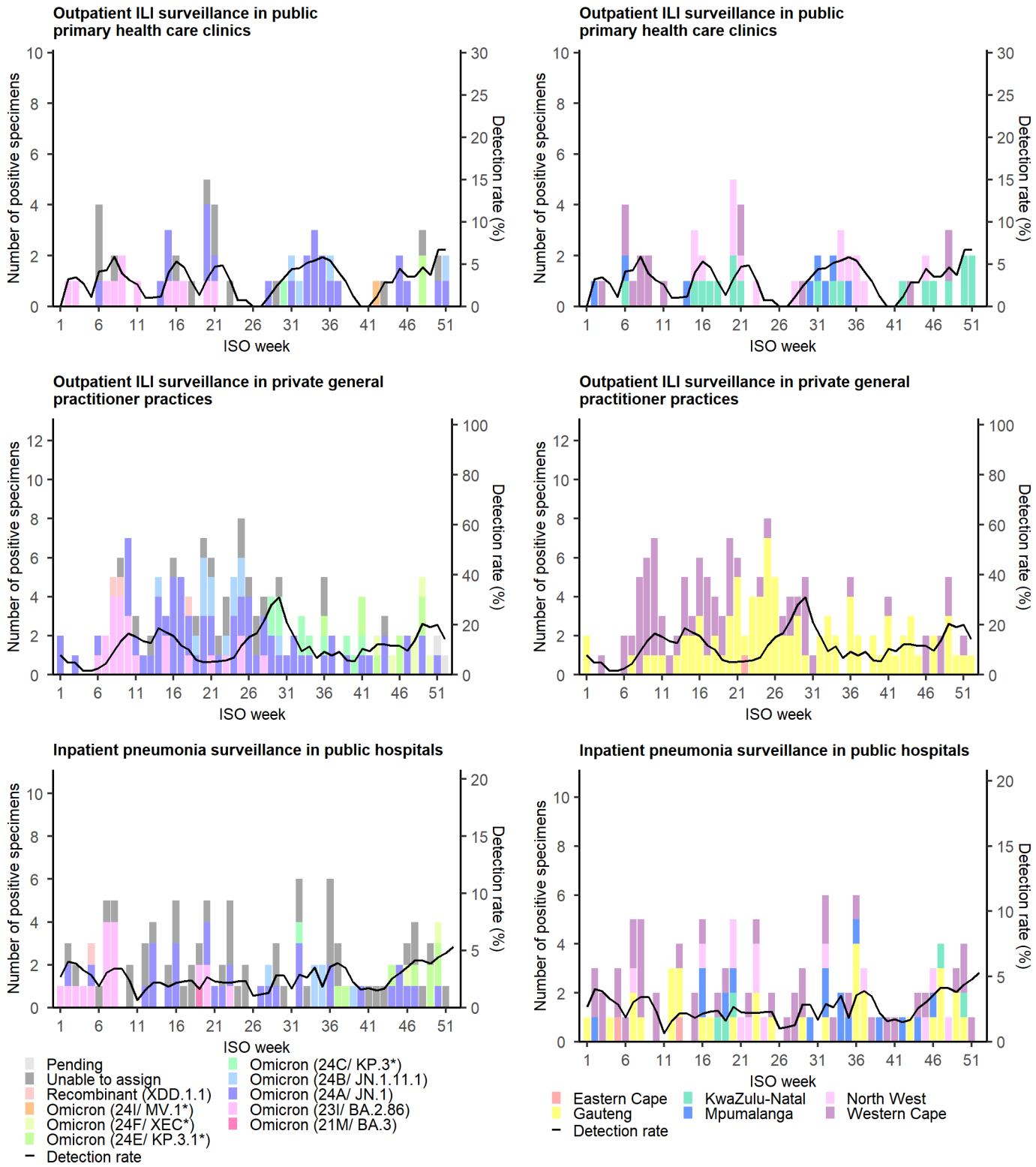
Province	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV typing results pending	Total RSV	Total specimens
Eastern Cape	0	1	0	0	0	1	22
Free State	0	0	0	0	0	0	0
Gauteng	2	21	0	1	0	24	1066
Limpopo	0	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	0	12
North West	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	2
Western Cape	8	17	0	1	0	26	438
Total	10	39	0	2	0	51	1540

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Table 7: Number of laboratory-confirmed respiratory syncytial virus (RSV) cases by type and total number of samples tested by hospital and province in all ages, inpatient pneumonia surveillance in public hospitals, South Africa, 01 January 2024 to 29 December 2024.

Hospital (Province)	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV typing results pending	Total RSV	Total specimens
Livingstone (EC)	0	1	0	0	0	1	41
Helen Joseph-Rahima Moosa (GP)	33	142	0	3	0	178	1057
Tambo Memorial (GP)	0	0	0	0	0	0	28
Tembisa (GP)	0	2	0	0	0	2	113
Harry Gwala (KZ)	40	26	1	1	0	68	504
Mapulaneng-Matikwana (MP)	1	23	0	0	0	24	416
Tintswalo (MP)	1	9	0	0	0	10	162
Klerksdorp-Tshepong (NW)	11	67	0	2	0	80	527
Khayelitsha (WC)	2	3	0	0	0	5	106
Mitchell's Plain (WC)	21	21	1	0	0	43	317
Red Cross (WC)	112	179	4	2	0	297	1129
Tygerberg (WC)	0	0	0	0	0	0	0
Total	221	473	6	8	0	708	4400

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.



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Detection rate presented as three-week moving average

*Including sub-lineages

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital

Figure 4: Number of laboratory-confirmed SARS-CoV-2 cases and detection rate by variant type (left) and province (right) in all ages, sentinel surveillance, South Africa, 01 January 2024 to 29 December 2024.

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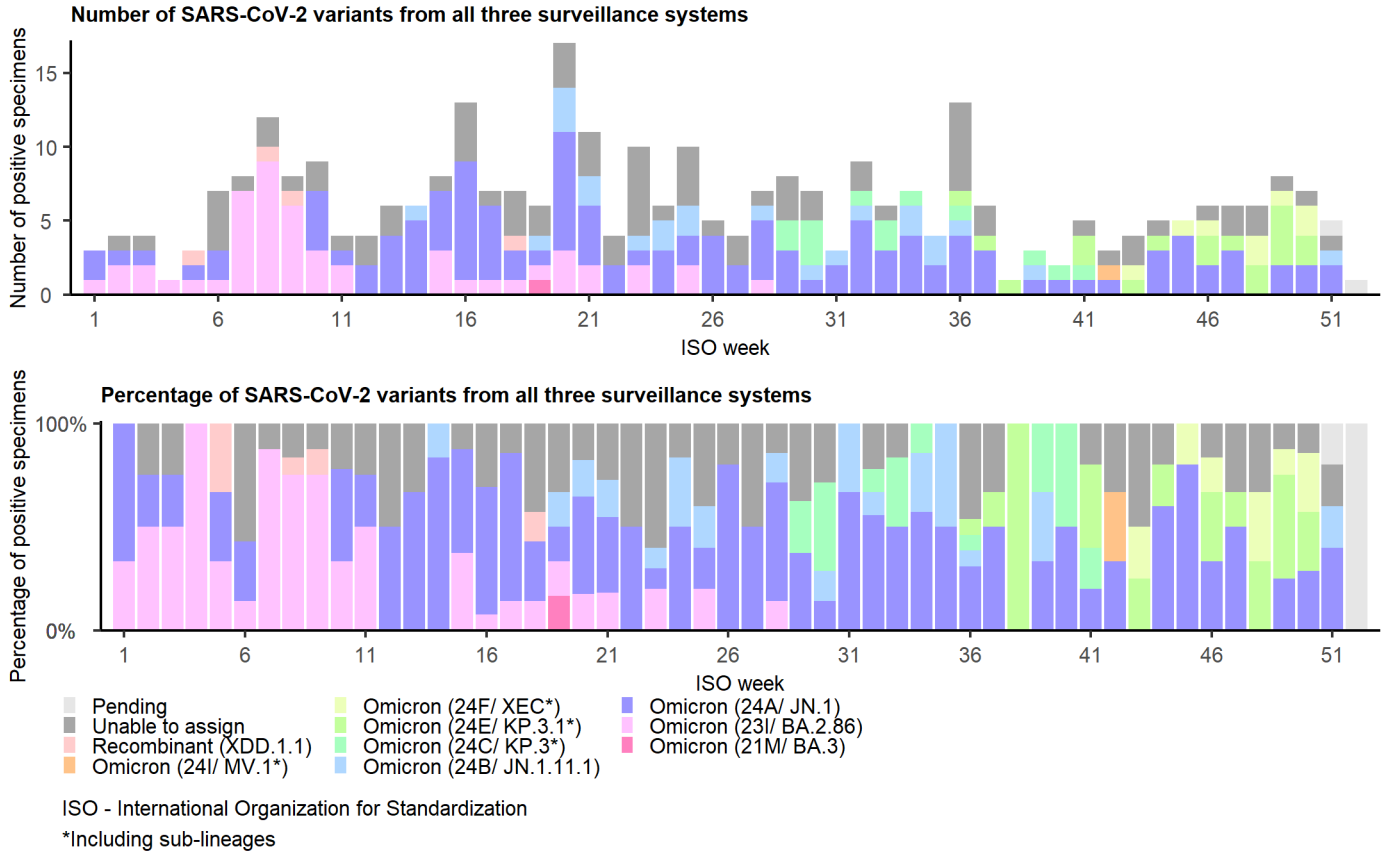

Figure 5: Combined number and percentage of SARS-CoV-2 variants in all ages from three sentinel surveillance systems: outpatient influenza like illness (ILI) surveillance in public primary health care clinics, outpatient ILI surveillance in private general practitioner practices, and inpatient pneumonia surveillance in public hospitals, South Africa, 01 January 2024 to 29 December 2024.

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Table 8: Number of laboratory-confirmed SARS-CoV-2 cases by variant type and total number of samples tested by clinic and province in all ages, outpatient ILI surveillance in public primary health care clinics, South Africa, 01 January 2024 to 29 December 2024.

Clinic (Province)	Omicron (21M/ BA.3)	Omicron (23I/ BA.2.86)	Omicron (24A/ JN.1)	Omicron (24B/ JN.1.11.1)	Omicron (24C/ KP.3*)	Omicron (24E/ KP.3.1*)	Omicron (24F/ XEC*)	Omicron (24I/ MV.1*)	Recombinant (XDD.1.1)	Pending	Unable to assign	Total SARS-CoV-2	Total specimens
Edendale Gateway (KZ)	0	5	6	2	0	0	0	1	0	0	5	19	514
Agincourt (MP)	0	1	4	1	1	0	0	0	0	0	1	8	286
Jouberton (NW)	0	0	12	1	0	0	0	0	0	0	3	16	544
Eastridge (WC)	0	2	1	0	0	2	0	0	0	0	4	9	281
Mitchell's Plain (WC)	0	4	1	0	0	0	0	0	0	0	1	6	125
Total	0	12	24	4	1	2	0	1	0	0	14	58	1750

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital. *Including sub-lineages

Table 9: Number of laboratory-confirmed SARS-CoV-2 cases by variant type and total number of samples tested by province in all ages, outpatient ILI surveillance in private general practitioner practices, South Africa, 01 January 2024 to 29 December 2024.

Province	Omicron (21M/ BA.3)	Omicron (23I/ BA.2.86)	Omicron (24A/ JN.1)	Omicron (24B/ JN.1.11.1)	Omicron (24C/ KP.3*)	Omicron (24E/ KP.3.1*)	Omicron (24F/ XEC*)	Omicron (24I/ MV.1*)	Recombinant (XDD.1.1)	Pending	Unable to assign	Total SARS-CoV-2	Total specimens
Eastern Cape	0	0	1	0	0	0	0	0	0	0	0	1	22
Free State	0	0	0	0	0	0	0	0	0	0	0	0	0
Gauteng	0	11	42	6	7	4	3	0	0	1	15	89	1066
Limpopo	0	0	0	0	0	0	0	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	0	0	0	0	0	0	0	12
North West	0	0	0	0	0	0	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	0	0	0	0	0	0	2
Western Cape	0	12	25	7	4	4	3	0	3	1	5	64	438
Total	0	23	68	13	11	8	6	0	3	2	20	154	1540

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital. *Including sub-lineages

Table 10: Number of laboratory-confirmed SARS-CoV-2 cases by variant type and total number of samples tested by hospital and province in all ages, inpatient pneumonia surveillance in public hospitals, South Africa, 01 January 2024 to 29 December 2024.

Hospital (Province)	Omicron (21M/ BA.3)	Omicron (23I/ BA.2.86)	Omicron (24A/ JN.1)	Omicron (24B/ JN.1.11.1)	Omicron (24C/ KP.3*)	Omicron (24E/ KP.3.1*)	Omicron (24F/ XEC*)	Omicron (24I/ MV.1*)	Recombinant (XDD.1.1)	Pending	Unable to assign	Total SARS-CoV-2	Total specimens
Livingstone (EC)	0	1	0	0	0	0	0	0	0	0	1	2	41
Helen Joseph-Rahima Moosa (GP)	0	4	7	0	0	3	1	0	0	0	14	29	1057
Tambo Memorial (GP)	0	2	0	0	0	0	0	0	0	0	0	2	28
Tembisa (GP)	0	0	1	0	0	0	0	0	0	0	0	1	113
Harry Gwala (KZ)	0	2	1	0	0	0	0	0	0	0	2	5	504
Mapulaneng-Matikwana (MP)	1	1	5	2	0	0	0	0	0	0	3	12	416
Tintswalo (MP)	0	0	0	2	0	0	1	0	0	0	1	4	162
Klerksdorp-Tshepong (NW)	0	0	7	0	0	0	0	0	0	0	7	14	527
Khayelitsha (WC)	0	1	2	0	0	0	0	0	0	0	3	6	106
Mitchell's Plain (WC)	0	1	2	1	1	0	0	0	0	0	7	12	317
Red Cross (WC)	0	5	5	1	0	5	0	0	1	0	8	25	1129
Tygerberg (WC)	0	0	0	0	0	0	0	0	0	0	0	0	0
Total	1	17	30	6	1	8	2	0	1	0	46	112	4400

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital. *Including sub-lineages

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Bordetella pertussis

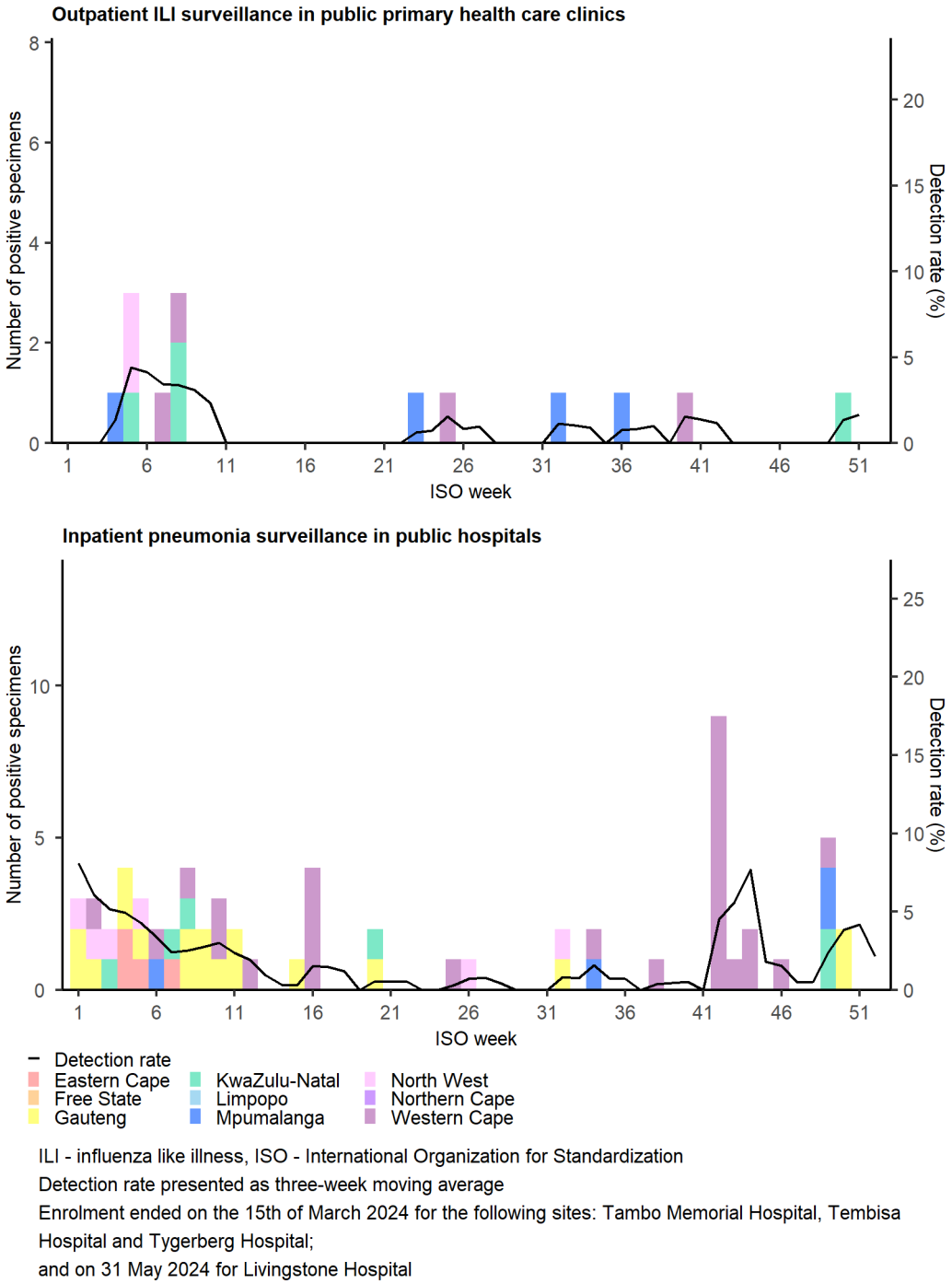

Figure 6: Number of laboratory-confirmed *Bordetella pertussis* cases and detection rate by province in all ages, sentinel surveillance, South Africa, 01 January 2024 to 29 December 2024.

Table 11: Number of laboratory-confirmed *Bordetella pertussis* cases and total number of samples tested by province in all ages, outpatient ILI surveillance in public primary health care clinics, South Africa, 01 January 2024 to 29 December 2024.

Province	Positive	Pending testing	Total specimens
KwaZulu-Natal	4	0	514
Mpumalanga	4	0	286
North West	2	0	544
Western Cape	4	0	406
Total	14	0	1750

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Table 12: Number of laboratory-confirmed *Bordetella pertussis* cases and total number of samples tested by province in all ages, inpatient pneumonia surveillance in public hospitals, South Africa, 01 January 2024 to 29 December 2024.

Province	Positive	Pending testing	Total specimens
Eastern Cape	4	0	41
Gauteng	18	0	1198
KwaZulu-Natal	6	0	504
Mpumalanga	4	0	578
North West	6	0	527
Western Cape	27	0	1552
Total	65	0	4400

Enrolment ended on the 15th of March 2024 for the following sites: Tambo Memorial Hospital, Tembisa Hospital and Tygerberg Hospital; and on 31 May 2024 for Livingstone Hospital.

Methods

Table 13: Programme descriptions for sentinel surveillance in South Africa

Programme	Influenza-like illness (ILI)	Viral Watch	National Syndromic Surveillance for Pneumonia
Description	Outpatient ILI surveillance in public primary health care clinics	Outpatient ILI surveillance in private general practitioner practices	Inpatient pneumonia surveillance in public hospitals
Start year	2012	1984	2009
Provinces	KZ, NW, WC, MP.	EC, FS, GP, LP, MP, NC, NW, WC.	EC, GP, KZ, MP, NW, WC.
Type of site	Primary health care clinics.	General practitioners.	Public hospitals.
Case definition	ILI: An acute respiratory illness with a temperature (≥38°C) and cough, & onset ≤10 days. Suspected pertussis: Any person with an acute cough illness lasting ≥14 days (or cough illness of any duration for children <1 year), without a more likely diagnosis AND one or more of the following signs or symptoms: paroxysms of coughing, or inspiratory "whoop", or post-tussive vomiting or apnoea in children <1 year; OR Any person in whom a clinician suspects pertussis.	ILI: An acute respiratory illness with a temperature (≥38°C) and cough, & onset ≤10 days.	SRI: Patients aged 2 days to <3 months: Diagnosis of sepsis or suspected sepsis, or physician diagnosed LRTI AND symptoms of any duration. Patients aged 3 months to <5years: Physician diagnosed LRTI, symptoms of any duration. Patients aged ≥5 years with fever (≥38) or history of fever AND cough AND symptoms of any duration. Suspected pertussis: Any person with an acute cough illness lasting ≥14 days (or cough illness of any duration for children <1 year), without a more likely diagnosis AND one or more of the following signs or symptoms: paroxysms of coughing, or inspiratory "whoop", or post-tussive vomiting or apnoea in children <1 year; OR Any person in whom a clinician suspects pertussis.
Specimens collected	Mid-turbinate nasal swabs.	Throat and/or nasal swabs or Nasopharyngeal swabs.	Mid-turbinate nasal swabs.
Main pathogens tested	Influenza virus, RSV, SARS-CoV-2, *B. pertussis*.	Influenza virus, RSV, SARS-CoV-2.	Influenza virus, RSV, SARS-CoV-2, *B. pertussis*.
Testing Methods	Influenza virus, RSV, SARS-CoV-2: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit. *B. pertussis*: Multiplex real-time PCR (Tatti et al., J Clin Microbiol 2011) and culture.	Influenza virus, RSV, SARS-CoV-2: Allplex™ SARS-CoV-2/ FluA/FluB/RSV PCR kit.	Influenza virus, RSV, SARS-CoV-2: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit. *B. pertussis*: Multiplex real-time PCR (Tatti et al., J Clin Microbiol 2011) and culture.

Abbreviations and definitions:

- ILI: Influenza-like illness
- SRI: Severe respiratory infection
- EC: Eastern Cape
- FS: Free State
- GP: Gauteng
- KZ: KwaZulu-Natal
- LP: Limpopo Province
- MP: Mpumalanga
- NW: North West
- NC: Northern Cape
- WC: Western Cape
- Subtype/lineage/subgroup inconclusive: Insufficient viral load in sample and unable to characterize further
- Subtype/lineage/subgroup pending: Further characterization in progress
- Unable to assign SARS-CoV-2 lineage: No lineage assigned due to poor sequence quality OR low viral load (Ct≥35)
- Epidemic threshold: Thresholds are calculated using the Moving Epidemic Method (MEM), a sequential analysis using the R Language, available from: http://CRAN.R-project.org/web/package=mem) designed to calculate the duration, start and end of the annual influenza epidemic. MEM uses the 40th, 90th and 97.5th percentiles established from available years of historical data to calculate thresholds of activity. Thresholds of activity for influenza and RSV are defined as follows: Below seasonal threshold, low activity, moderate activity, high activity, very high activity. For influenza, thresholds from outpatient influenza like illness (ILI in primary health care clinics) are used as an indicator of disease transmission in the community and thresholds from pneumonia surveillance are used as an indicator of impact of disease. For influenza the start and end of the season is defined as once the three week moving average of the detection rate remains above or below the seasonal threshold for two consecutive weeks, respectively. For RSV, thresholds from outpatient influenza like illness (ILI in primary health care clinics) from children aged < 5 years are used as an indicator of disease transmission in the community and thresholds from pneumonia surveillance from children aged < 5 years are used as an indicator of impact of disease. For RSV the start and end of the season is defined as once the three week moving average of the detection rate in children <5 years from inpatient pneumonia surveillance in public hospitals remains above or below 15% for two consecutive weeks, respectively.

Laboratory testing for influenza, RSV, SARS-CoV-2 and *B. pertussis*:

Influenza A and B viruses, RSV and SARS-CoV-2 were tested using a commercial multiplex RT-PCR assay (Allpex SARS-CoV-2/FluA/FluB/RSV PCR kit, Seegene Inc., Seoul, South Korea). A specimen was considered positive for influenza A, B or RSV if the PCR cycle threshold (Ct) was <40 for the respective target, and considered positive for SARS-CoV-2 when the Ct was <40 for ≥1 of the S, N or RdRp gene targets. *B.pertussis* was tested using a previously described RT-PCR method (Tatti KM, et al. Journal of Clinical Microbiology. 2011;49(12):4059-4066). A specimen was considered positive when the IS481 and/or ptxS1 gene targets are detected with a Ct <45.

Further characterization of influenza, RSV, and SARS-CoV-2:

Influenza A and B positive specimens were subtyped using the US Centres for Disease Control and Prevention (CDC) RT-PCR protocol and reagents (International Reagent Resource (IRR) [Available from: https://www.internationalreagentresource.org/). RSV positive specimens were subgrouped using an in-house assay (Pretorius M, et al. Journal of Infectious Diseases. 2012(1537-6613)). SARS-CoV-2 positive specimens were sequenced using the Illumina COVIDSeq protocol

(Illumina, CA, USA).

SARS-CoV-2 whole-genome sequencing and genome assembly for SARS-CoV-2 genomic surveillance:

RNA extraction: RNA was extracted either manually or automatically in batches, using the QIAamp viral RNA mini kit (QIAGEN, CA, USA) or the Chemagic 360 using the CMG-1049 kit (PerkinElmer, MA, USA). A modification was done on the manual extractions by adding 280 µl per sample, in order to increase yields. 300 µl of each sample was used for automated magnetic bead-based extraction using the Chemagic 360. RNA was eluted in 60 µl of the elution buffer. Isolated RNA was stored at -80 °C prior to use.

PCR and library preparation:

Sequencing was performed using the Illumina COVIDSeq protocol (Illumina Inc., CA, USA) or nCoV-2019 ARTIC network sequencing protocol v3 (https://artic.network/ncov-2019). These are amplicon-based next-generation sequencing approaches. Briefly, for the nCoV-2019 ARTIC network sequencing protocol, the first strand synthesis was carried out on extracted RNA samples using random hexamer primers from the SuperScript IV reverse transcriptase synthesis kit (Life Technologies, CA, USA) or LunaScript RT SuperMix Kit (New England Biolabs (NEB), MA , USA). The synthesized cDNA was amplified using multiplex polymerase chain reactions (PCRs) using ARTIC nCoV-2019 v3 primers. For the COVIDSeq protocol, the first strand synthesis was carried out using random hexamer primers from Illumina and the synthesized cDNA underwent two separate multiplex PCR reactions. For Illumina sequencing using the nCoV-2019 ARTIC network sequencing protocol, the pooled PCR products underwent bead-based tagmentation using the Nextera Flex DNA library preparation kit (Illumina Inc., CA, USA). The adapter-tagged amplicons were cleaned up using AmpureXP purification beads (Beckman Coulter, High Wycombe, UK) and amplified using one round of PCR. The PCRs were indexed using the Nextera CD indexes (Illumina Inc., CA, USA) according to the manufacturer's instructions. For COVIDSeq sequencing protocol, pooled PCR amplified products were processed for tagmentation and adapter ligation using IDT for Illumina Nextera UD Indexes. Further enrichment and clean-up was performed as per protocols provided by the manufacturer (Illumina Inc., CA, USA). Pooled samples from both COVIDSeq protocol and nCoV-2019 ARTIC network protocol were quantified using Qubit 3.0 or 4.0 fluorometer (Invitrogen Inc., MA, USA) using the Qubit dsDNA High Sensitivity assay according to manufacturer's instructions. The fragment sizes were analyzed using TapeStation 4200 (Invitrogen Inc., MA, USA). The pooled libraries were further normalized to 4nM concentration and 25 µl of each normalized pool containing unique index adapter sets were combined in a new tube. The final library pool was denatured and neutralized with 0.2 N sodium hydroxide and 200 mM Tris-HCL (pH7), respectively. 1.5 pM sample library was spiked with 2% PhiX. Libraries were loaded onto a 300-cycle NextSeq 500/550 HighOutput Kit v2 and run on the Illumina NextSeq 550 instrument (Illumina Inc., CA, USA).

Assembly, processing and quality control of genomic sequences:

Raw reads from Illumina sequencing were assembled using the Exatype NGS SARS-CoV-2 pipeline v1.6.1, (https://sars-cov-2.exatype.com/). The resulting consensus sequence was further manually polished by considering and correcting indels in homopolymer regions that break the open reading frame (probably sequencing errors) using Aliview v1.27, (http://ormbunkar.se/aliview/) (Larsson, 2014). Mutations resulting in mid-gene stop codons and frameshifts were reverted to wild type. All assemblies determined to have acceptable quality (defined as having at least 1 000 000 reads and at least 40 % 10 X coverage) were deposited on GISAID (https://www.gisaid.org/) (Elbe & Buckland-Merrett, 2017; Shu & McCauley, 2017).

Classification of lineage, clade and associated mutations:

Assembled genomes were assigned lineages using the 'Phylogenetic Assignment of Named Global Outbreak Lineages' (PANGOLIN) software suite (https://github.com/hCoV-2019/pangolin) (Rambaut et al., 2020), a tool used for dynamic SARS-CoV-2 lineage classification. The SARS-CoV-2 genomes in our dataset were also classified using the clade classification proposed by NextStrain (https://nextstrain.org/), a tool built for real-time tracking of the pathogen evolution (Hadfield et al., 2018).