

Report week: 37

Reporting period: 30 December 2024 to 14 September 2025

Date of data extraction: 2025-09-18

Data are provisional as of the date of extraction. The number of consultations/specimens is reported/analysed by date of consultation/specimen collection. Data cleaning is ongoing, and this may result in some changes in subsequent reports. Refer to the end of the report for methodology and definitions.

Highlights

- In week 37 (08 September 2025 to 14 September 2025), from 156 samples tested, we detected 4 (2.6%) cases of influenza, 2 (1.3%) cases of RSV and 9 (5.8%) cases of SARS-CoV-2.
- The influenza season started in week 13 (week starting 24 March 2025), peaked in week 20 (week starting 12 May 2025) and ended in week 30 (week starting 21 July 2025). The season began earlier than in the previous years, and throughout the season, the detection rate remained within the low threshold.
- The RSV season started in week 11 (week starting 10 March 2025), peaked in week 16 (week starting 15 April 2025) at the moderate level, and ended in week 31 (week starting 28 July 2025).
- An increase in SARS-CoV-2 detections has been observed since week 29 (week starting 14 July 2025). The detection rate among hospitalised patients in public hospitals has reached the low threshold, while the detection rate among outpatients in public clinics and private general-practitioner practices remains below the epidemic threshold. Among cases with sequencing data available since week 29, 19 (54%, 19/35) were identified as the XFG recombinant variant.
- In August, we detected 2 (0.4%, 2/515) cases of *Bordetella pertussis*.
- From 30 December 2024 to 14 September 2025, from 5667 samples tested, we detected 561 (9.9%) cases of influenza, 757 (13.4%) cases of respiratory syncytial virus (RSV), 182 (3.2%) cases of SARS-CoV-2 and 37 (0.9%) cases of *B. pertussis*.

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Monitoring potentially imported cases of respiratory viruses

No specimens were received from the OR Tambo International Airport clinic in week 37 (week starting 8 September 2025). Since 30 December 2024, one specimen has been received and tested, which was positive for influenza. This case was excluded from subsequent tables and figures, as it was likely not acquired in South Africa.

Influenza & respiratory syncytial virus (RSV) epidemic thresholds

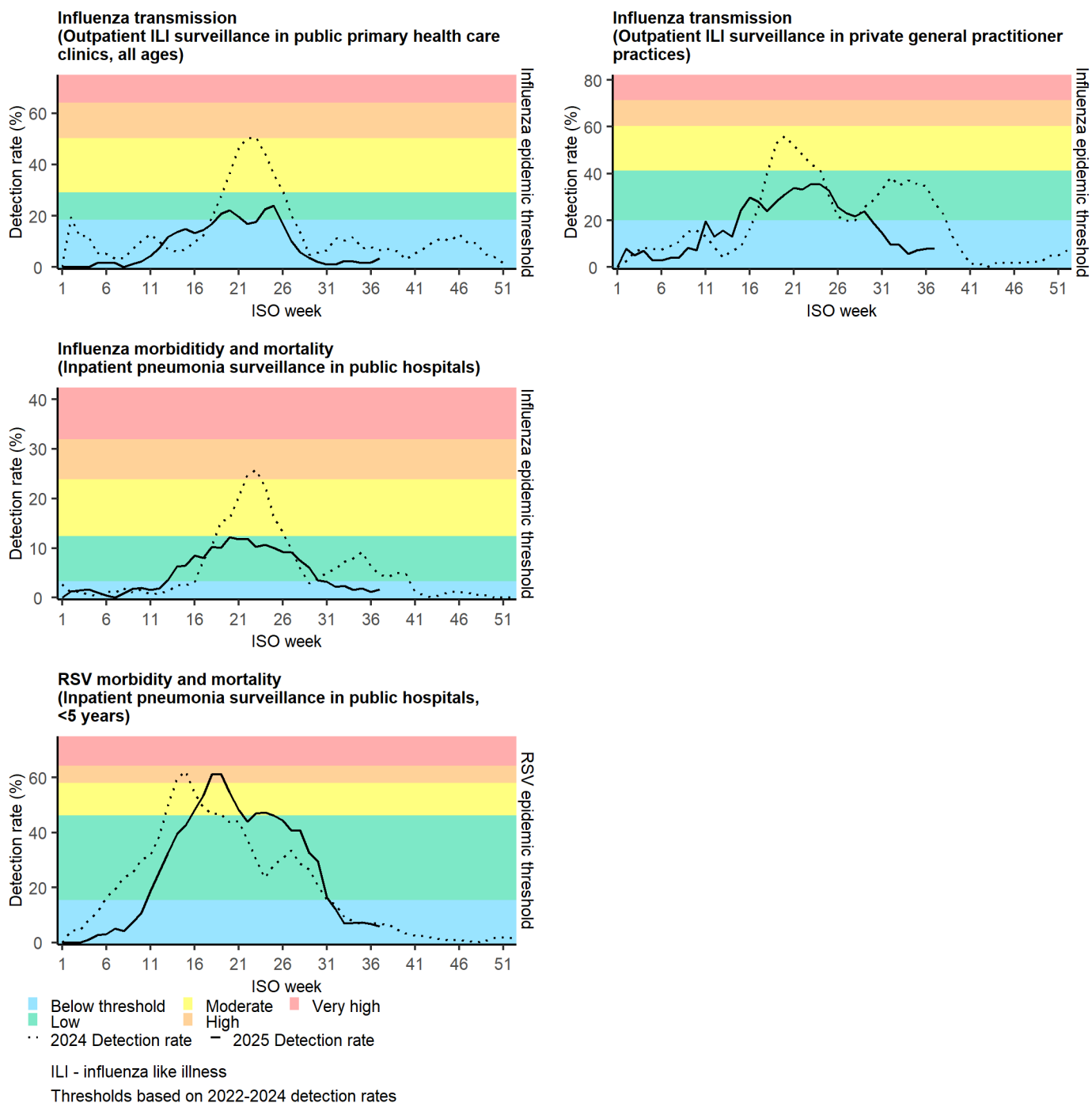


Figure 1: Influenza and Respiratory Syncytial Virus (RSV) surveillance epidemic threshold summary, Sentinel Surveillance, South Africa, 30 December 2024 to 14 September 2025.

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SARS-CoV-2 epidemic thresholds

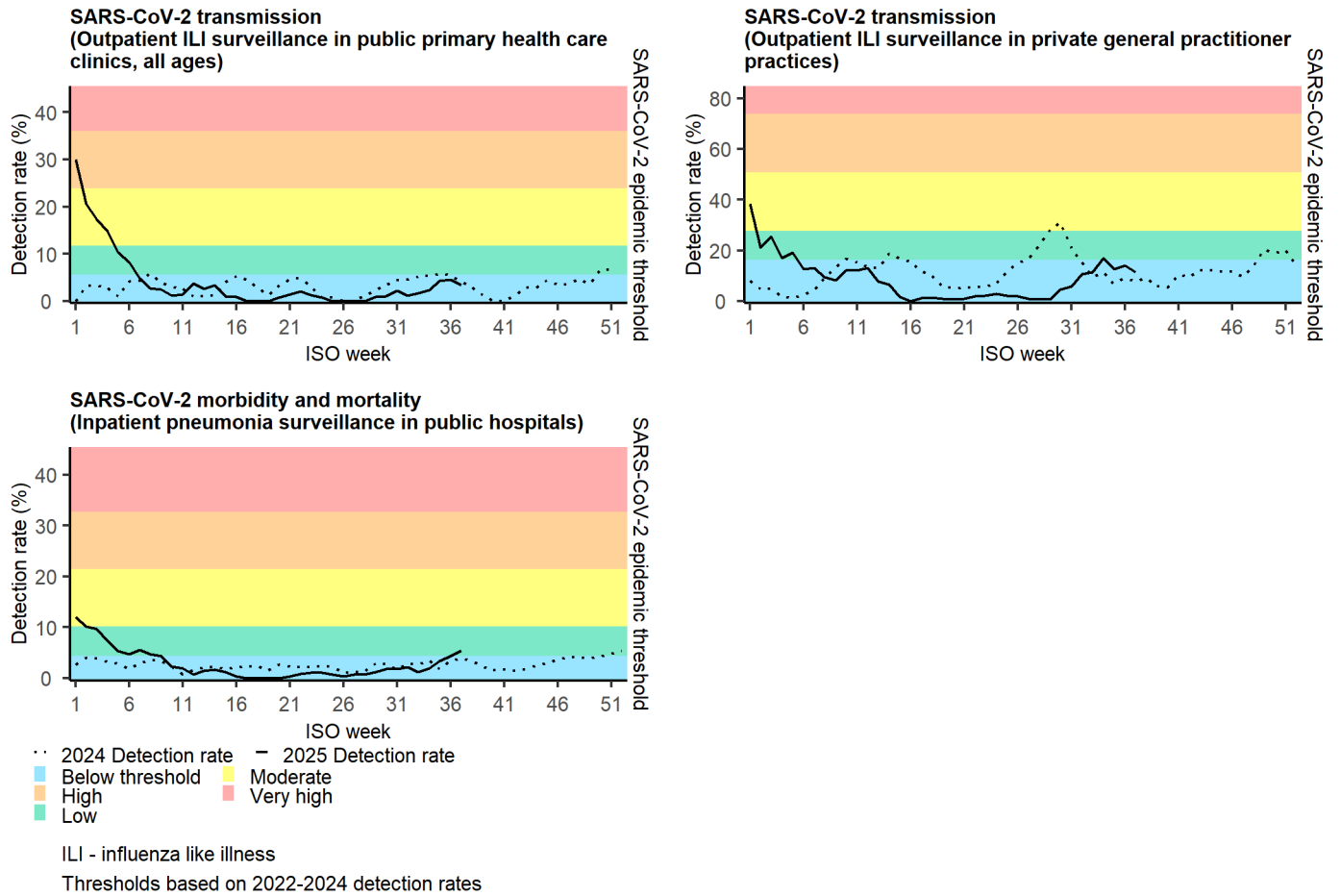


Figure 2: Severe acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) surveillance epidemic threshold summary, sentinel surveillance, South Africa, 30 December 2024 to 14 September 2025.

Influenza

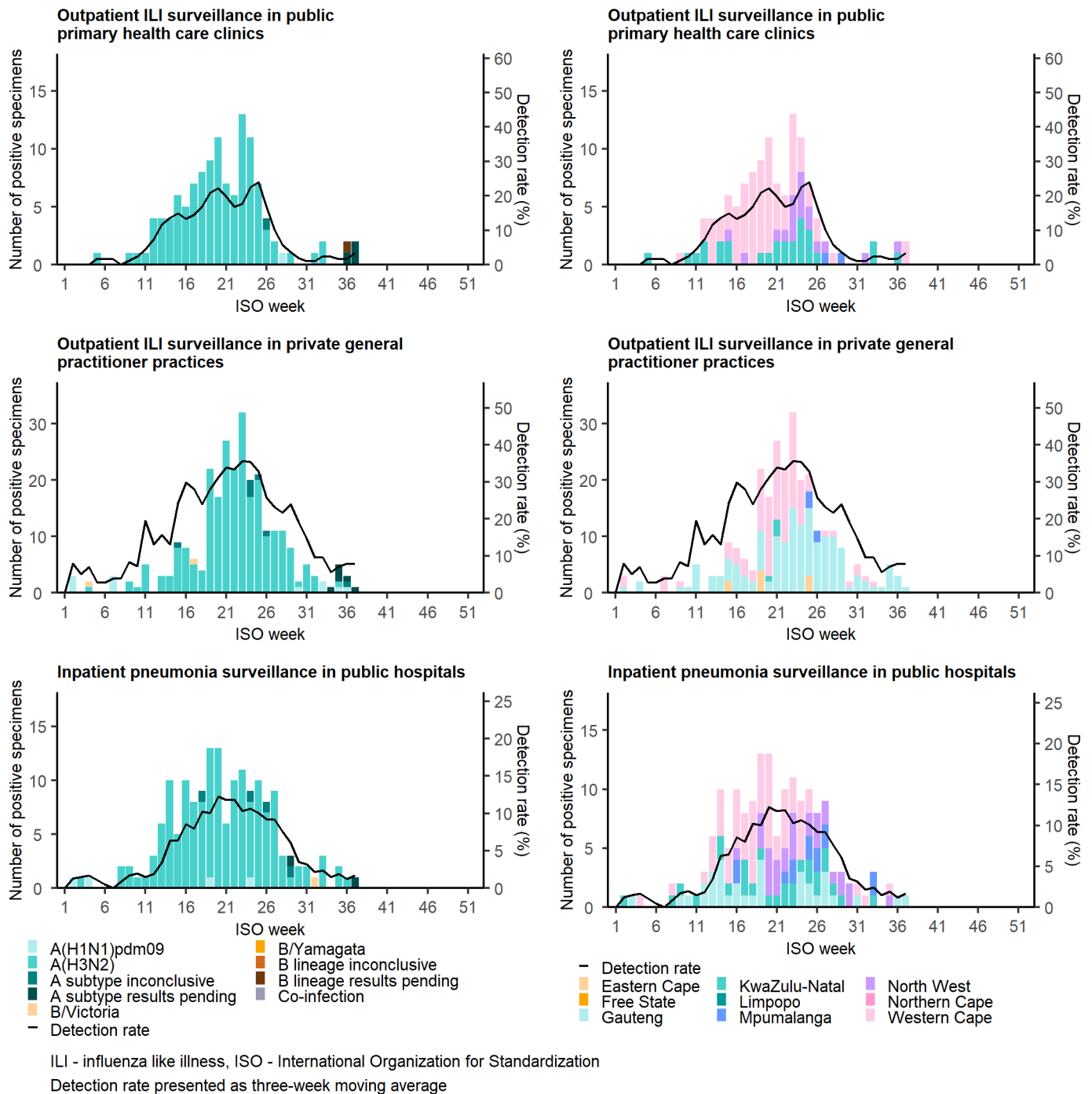


Figure 3: Number of laboratory-confirmed influenza cases and detection rate by subtype and lineage (left) and province (right) in all ages, sentinel surveillance, South Africa, 30 December 2024 to 14 September 2025.

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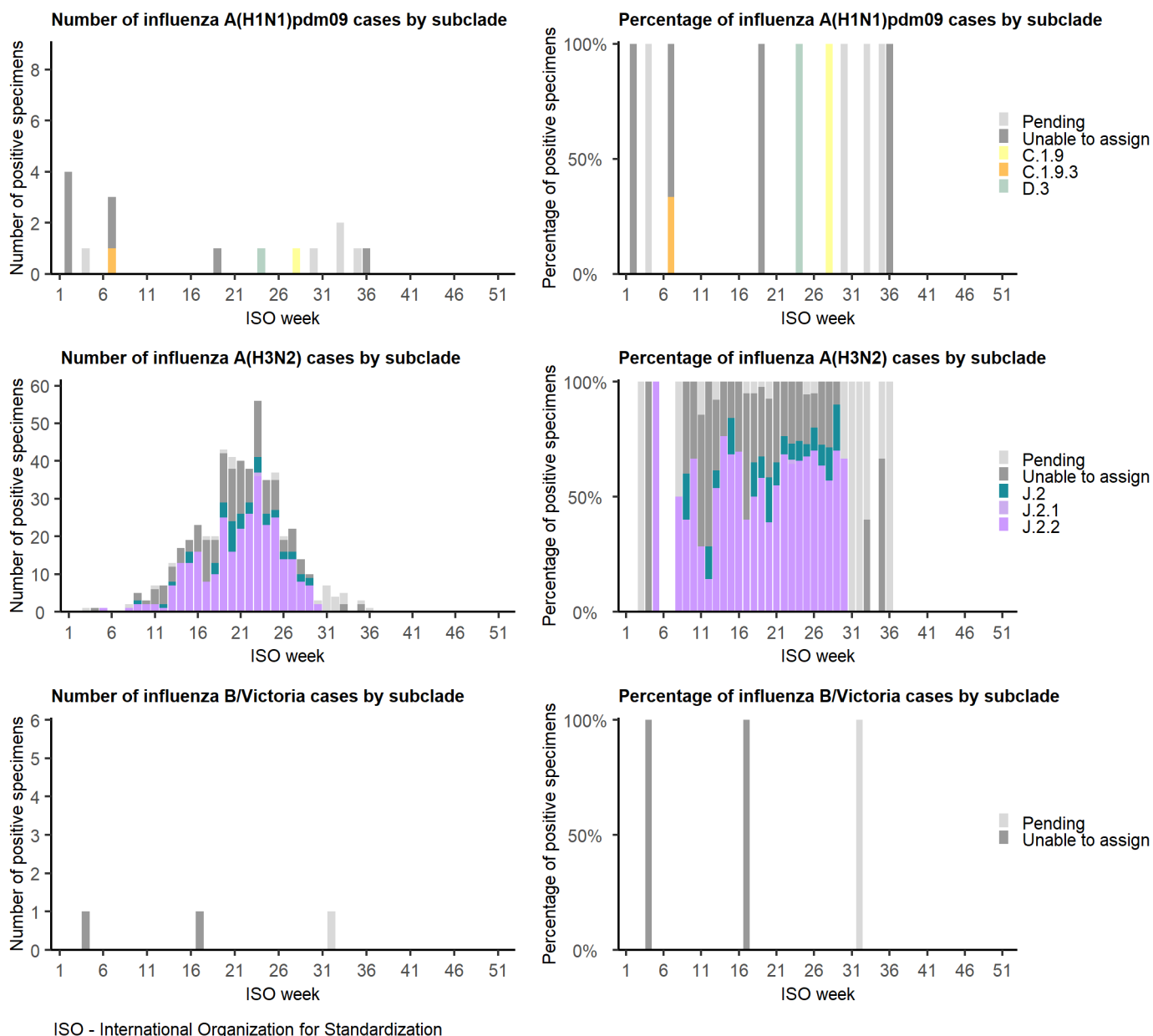


Figure 4: Combined number and percentage of influenza cases by subclade in all ages from three sentinel surveillance systems: outpatient influenza-like illness (ILI) surveillance in public primary health care clinics, outpatient ILI surveillance in private general practitioner practices, and inpatient pneumonia surveillance in public hospitals, South Africa, 30 December 2024 to 14 September 2025.

Table 1: Combined number of influenza cases by subclade and clade 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, 30 December 2024 to 14 September 2025.

Subtype/Lineage	Clade	Subclade	Count
A(H1N1)pdm09	6B.1A.5a.2a	C.1.9	1
A(H1N1)pdm09	6B.1A.5a.2a	C.1.9.3	1
A(H1N1)pdm09	6B.1A.5a.2a.1	D.3	1
A(H3N2)	3C.2a1b.2a.2a.3a.1	J.2	45
A(H3N2)	3C.2a1b.2a.2a.3a.1	J.2.1	1
A(H3N2)	3C.2a1b.2a.2a.3a.1	J.2.2	294

Table 2: 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, 30 December 2024 to 14 September 2025.

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 (KZN)	0	27	0	0	0	0	0	1	0	28	423
Agincourt (MP)	0	2	0	0	0	0	0	0	0	2	56
Jouberton (NW)	0	17	0	1	0	0	0	0	0	18	265
Eastridge (WC)	1	69	1	2	0	0	0	0	0	73	456
Mitchell's Plain (WC)	0	0	0	0	0	0	0	0	0	0	53
Total	1	115	1	3	0	0	0	1	0	121	1253

Specimens where more than one influenza subtype or lineage was detected were denoted as co-infection, and included in the counts for each separate type as well. The Agincourt clinic was not active from February – June 2025.

Table 3: 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, 30 December 2024 to 14 September 2025.

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	0	9	0	0	0	0	0	0	0	9	17
Free State	0	0	0	0	0	0	0	0	0	0	1
Gauteng	4	136	4	6	1	0	0	0	0	151	975
KwaZulu-Natal	0	4	0	0	0	0	0	0	0	4	15
Limpopo	0	0	0	0	0	0	0	0	0	0	0
Mpumalanga	0	4	1	0	0	0	0	0	0	5	35
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	0
Western Cape	7	94	2	0	1	0	0	0	0	104	287
Total	11	247	7	6	2	0	0	0	0	273	1330

Specimens where more than one influenza subtype or lineage was detected were denoted as co-infection, and included in the counts for each separate type as well.

Table 4: 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, 30 December 2024 to 14 September 2025.

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
Helen Joseph-Rahima Moosa (GP)	0	33	0	1	0	0	0	0	0	34	550
Harry Gwala (KZN)	1	25	2	0	0	0	0	0	0	28	457
Mapulaneng-Matikwana (MP)	0	7	0	0	0	0	0	0	0	7	175
Tintswalo (MP)	0	6	0	0	0	0	0	0	0	6	179
Klerksdorp-Tshepong (NW)	1	28	0	1	0	0	0	0	0	30	442
Mitchell's Plain (WC)	0	31	1	0	0	0	0	0	0	32	524
Red Cross (WC)	2	26	1	0	1	0	0	0	0	30	757
Total	4	156	4	2	1	0	0	0	0	167	3084

Specimens where more than one influenza subtype or lineage was detected were denoted as co-infection, and included in the counts for each separate type as well. Enrolment ended on the 31st of January 2025 at Matikwana Hospital.

Respiratory syncytial virus (RSV)

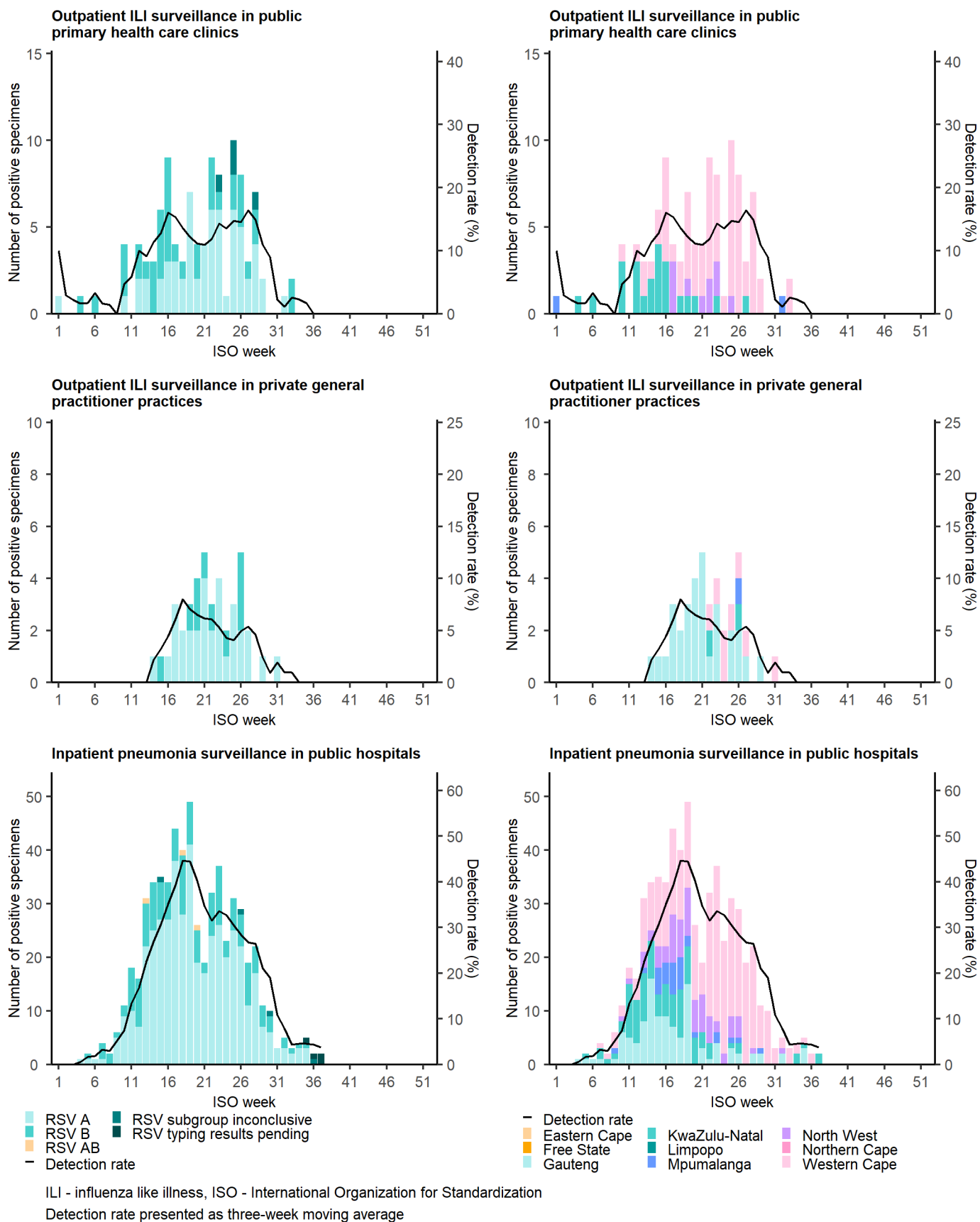


Figure 5: Number of laboratory-confirmed respiratory syncytial virus (RSV) cases and detection rate by type (left) and province (right) in all ages, sentinel surveillance, South Africa, 30 December 2024 to 14 September 2025.

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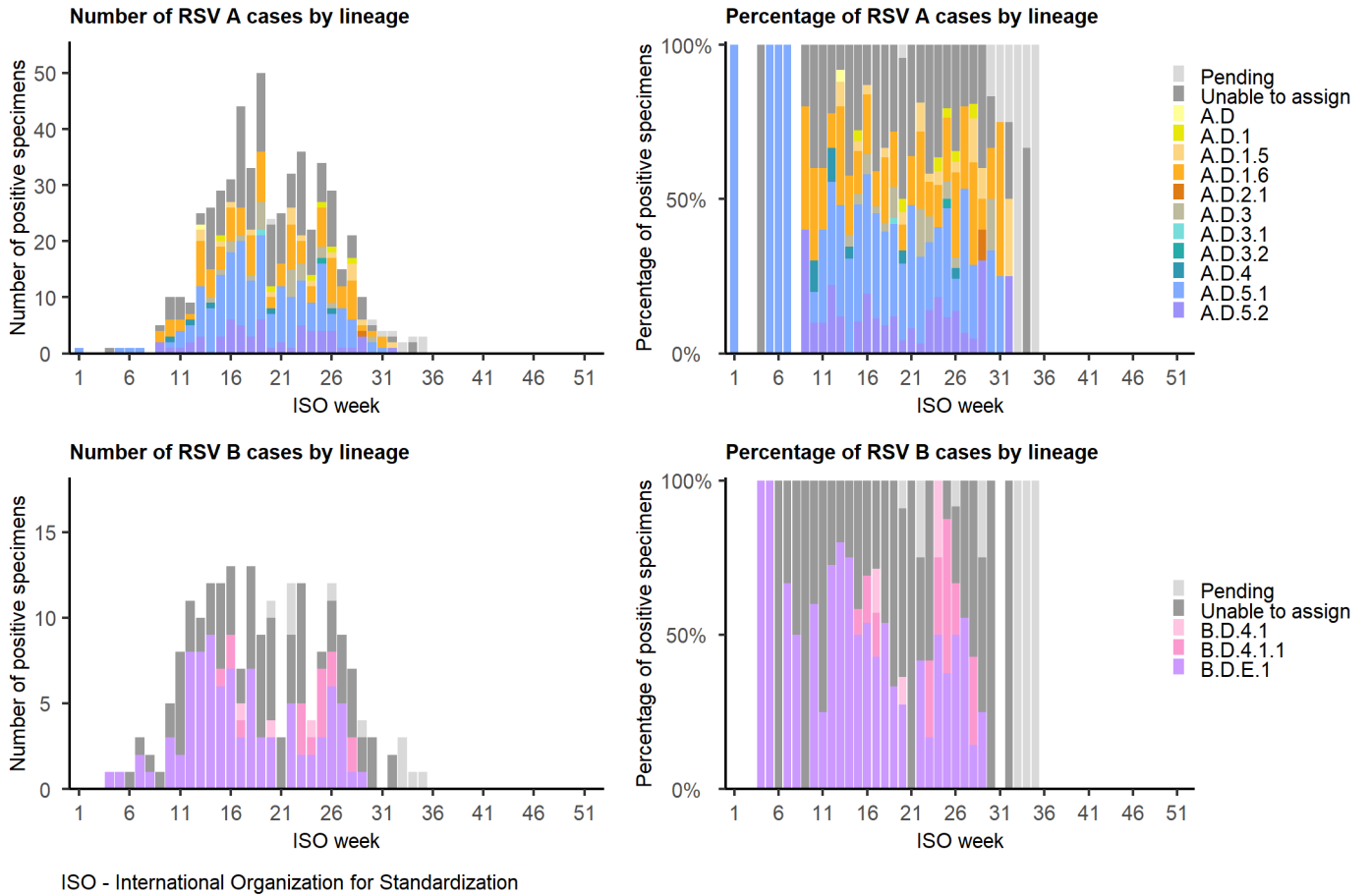


Figure 6: Combined number and percentage of RSV cases by lineage in all ages from three sentinel surveillance systems: outpatient influenza-like illness (ILI) surveillance in public primary health care clinics, outpatient ILI surveillance in private general practitioner practices, and inpatient pneumonia surveillance in public hospitals, South Africa, 30 December 2024 to 14 September 2025.

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, 30 December 2024 to 14 September 2025.

Clinic (Province)	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV typing results pending	Total RSV	Total specimens
Edendale Gateway (KZN)	3	19	0	1	0	23	423
Agincourt (MP)	2	0	0	0	0	2	56
Jouberton (NW)	9	0	0	1	0	10	265
Eastridge (WC)	46	20	0	2	0	68	456
Mitchell's Plain (WC)	2	0	0	0	0	2	53
Total	62	39	0	4	0	105	1253

The Agincourt clinic was not active from February – June 2025.

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, 30 December 2024 to 14 September 2025.

Province	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV typing results pending	Total RSV	Total specimens
Eastern Cape	0	0	0	0	0	0	17
Free State	0	0	0	0	0	0	1
Gauteng	24	6	0	0	0	30	975
KwaZulu-Natal	0	2	0	0	0	2	15
Limpopo	0	0	0	0	0	0	0
Mpumalanga	0	1	0	0	0	1	35
North West	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	0
Western Cape	7	1	0	0	0	8	287
Total	31	10	0	0	0	41	1330

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, 30 December 2024 to 14 September 2025.

Hospital (Province)	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV typing results pending	Total RSV	Total specimens
Helen Joseph-Rahima Moosa (GP)	107	4	0	0	0	111	550
Harry Gwala (KZN)	26	64	0	0	2	92	457
Mapulaneng-Matikwana (MP)	14	1	0	0	0	15	175
Tintswalo (MP)	9	7	0	0	0	16	179
Klerksdorp-Tshepong (NW)	65	6	0	0	0	71	442
Mitchell's Plain (WC)	67	23	0	3	1	94	524
Red Cross (WC)	163	44	3	1	1	212	757
Total	451	149	3	4	4	611	3084

SARS-CoV-2

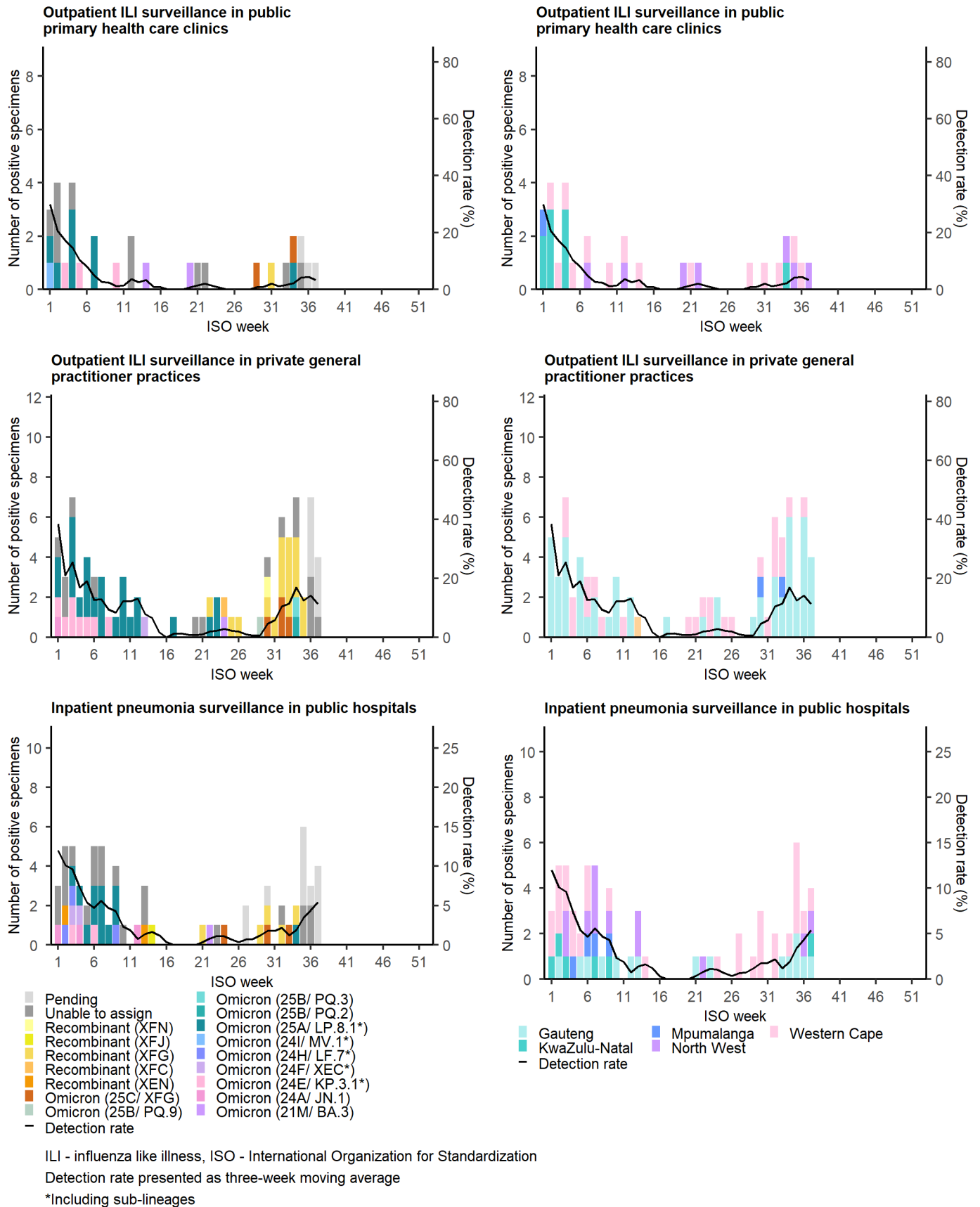


Figure 7: Number of laboratory-confirmed SARS-CoV-2 cases and detection rate by variant type (left) and province (right) in all ages, sentinel surveillance, South Africa, 30 December 2024 to 14 September 2025.

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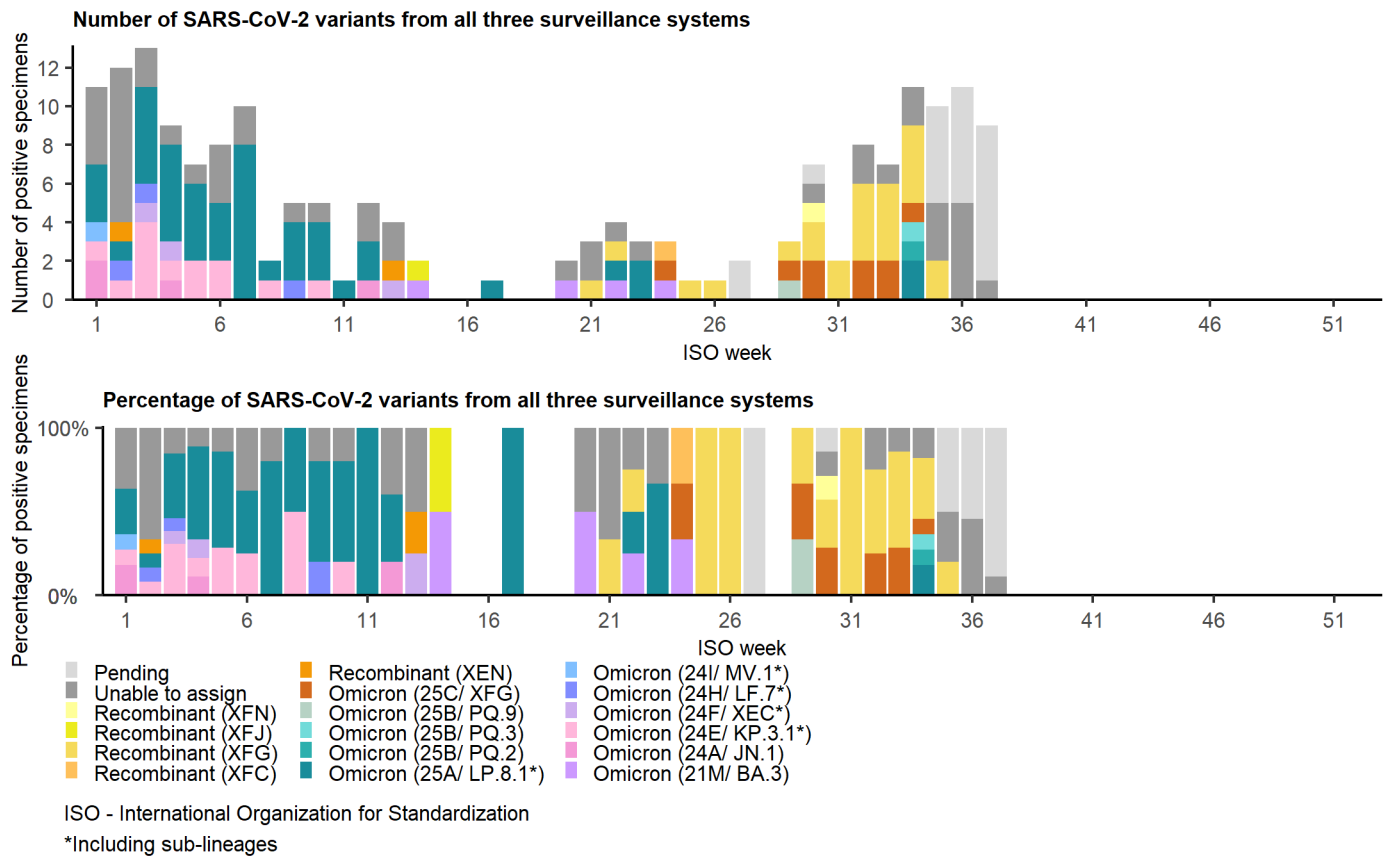


Figure 8: Combined number and percentage of SARS-CoV-2 variants in all ages from three sentinel surveillance systems: outpatient influenza-like illness (ILI) surveillance in public primary health care clinics, outpatient ILI surveillance in private general practitioner practices, and inpatient pneumonia surveillance in public hospitals, South Africa, 30 December 2024 to 14 September 2025.

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, 30 December 2024 to 14 September 2025.

Clinic (Province)	Om (21M/BA.3)	Om (24A/JN.1)	Om (24E/KP.3.1*)	Om (24F/XEC*)	Om (24H/LF.7*)	Om (24I/MV.1*)	Om (25A/LP.8.1*)	Om (25B/PQ.2)	Om (25B/PQ.3)	Om (25B/PQ.9)	Om (25C/XFG)	Rcb (XEN/XFC/XFG/XFJ/XFN)	Pending	Unable to assign	Total SARS-CoV-2	Total specimens
Edendale Gateway (KZN)	0	0	0	0	0	1	4	0	0	0	1	0	0	3	9	423
Agincourt (MP)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	56
Jouberton (NW)	1	0	0	0	0	0	2	0	0	0	0	0	1	3	7	265
Eastridge (WC)	0	0	3	0	0	0	1	0	0	0	1	0	2	3	10	456
Mitchell's Plain (WC)	1	0	0	0	0	0	0	0	0	0	0	1	0	2	4	53
Total	2	0	3	0	0	1	8	0	0	0	2	1	3	11	31	1253

The Agincourt clinic was not active from February – June 2025. Om = Omicron; Rcb = Recombinant. *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, 30 December 2024 to 14 September 2025.

Clinic (Province)	Om (21M/BA.3)	Om (24A/JN.1)	Om (24E/KP.3.1*)	Om (24F/XEC*)	Om (24H/LF.7*)	Om (24I/MV.1*)	Om (25A/LP.8.1*)	Om (25B/PQ.2)	Om (25B/PQ.3)	Om (25B/PQ.9)	Om (25C/XFG)	Rcb (XEN/XFC/XFG/XFJ/XFN)	Pending	Unable to assign	Total SARS-CoV-2	Total specimens
Eastern Cape	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	17
Free State	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Gauteng	1	1	4	0	0	0	17	1	1	1	4	8	6	12	56	975
KwaZulu-Natal	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15
Limpopo	0	0	0	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	2	0	0	2	35
North West	0	0	0	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	0	0	0	0
Western Cape	0	0	4	0	0	0	8	0	0	0	0	9	1	3	25	287
Total	1	1	8	1	0	0	25	1	1	1	4	19	7	15	84	1330

Om = Omicron; Rcb = Recombinant. *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, 30 December 2024 to 14 September 2025.

Hospital (Province)	Om (21M/BA.3)	Om (24A/JN.1)	Om (24E/KP.3.1*)	Om (24F/XEC*)	Om (24H/LF.7*)	Om (24I/MV.1*)	Om (25A/LP.8.1*)	Om (25B/PQ.2)	Om (25B/PQ.3)	Om (25B/PQ.9)	Om (25C/XFG)	Rcb (XEN/XFC/XFG/XFJ/XFN)	Pending	Unable to assign	Total SARS-CoV-2	Total specimens
Helen Joseph-Rahima Moosa (GP)	0	1	0	0	0	0	3	0	0	0	1	2	2	6	15	550
Harry Gwala (KZN)	0	0	0	1	0	0	2	0	0	0	0	0	1	2	6	457
Mapulaneng-Matikwana (MP)	0	0	0	0	0	0	1	0	0	0	0	0	0	1	2	175
Tintswalo (MP)	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	179
Klerksdorp-Tshepong (NW)	1	0	1	0	0	0	3	0	0	0	0	0	2	5	12	442
Mitchell's Plain (WC)	0	1	1	0	0	0	0	0	0	0	1	3	4	4	14	524
Red Cross (WC)	0	1	0	1	3	0	3	0	0	0	1	3	3	1	16	757
Total	1	3	2	2	3	0	12	0	0	0	3	8	12	21	67	3084

Om = Omicron; Rcb = Recombinant. *Including sub-lineages

Bordetella pertussis

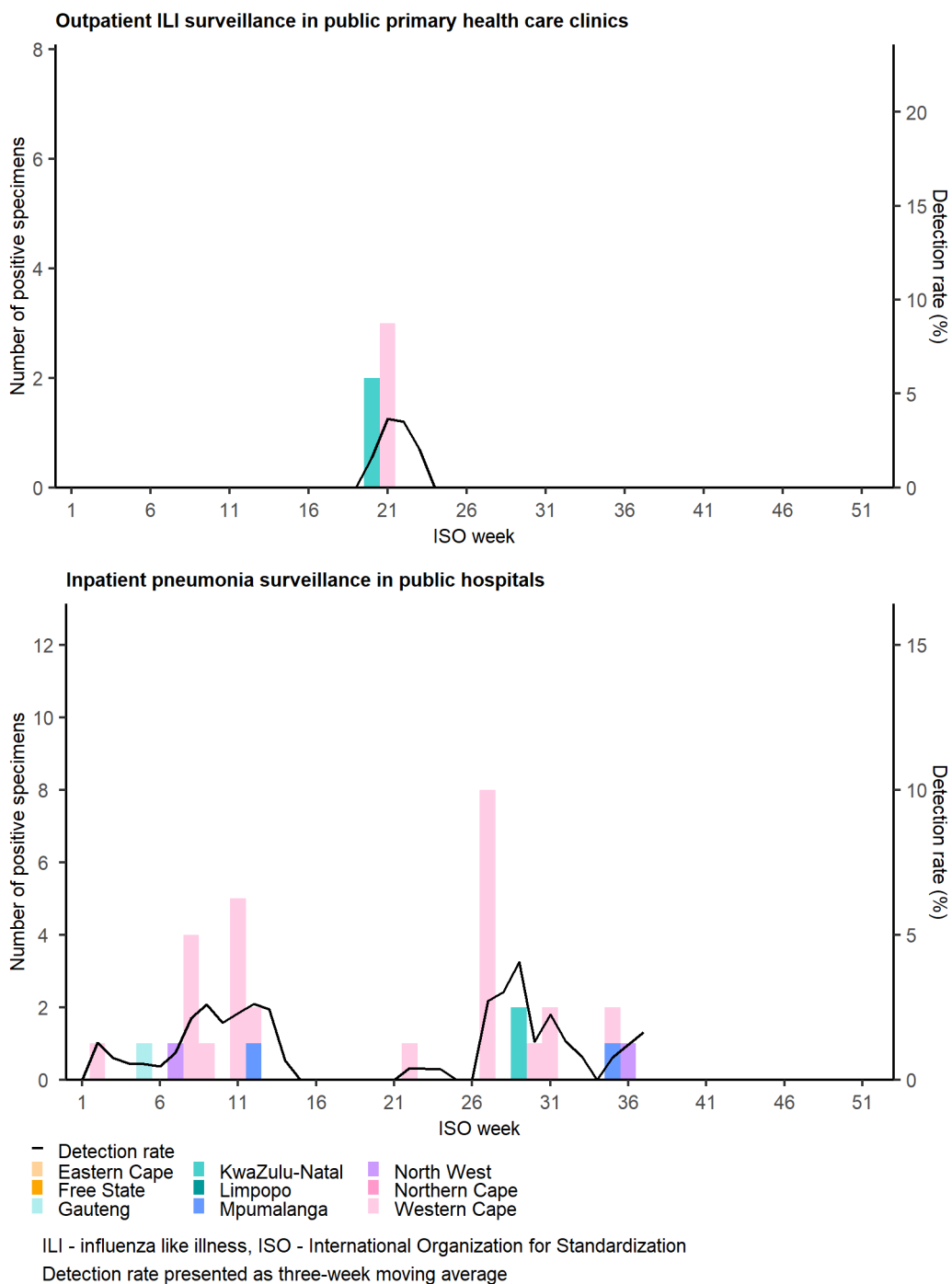


Figure 9: Number of laboratory-confirmed *Bordetella pertussis* cases and detection rate by province in all ages, sentinel surveillance, South Africa, 30 December 2024 to 14 September 2025.

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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, 30 December 2024 to 14 September 2025.

Province	Positive	Pending testing	Total specimens
KwaZulu-Natal	2	5	423
Mpumalanga	0	7	56
North West	0	18	265
Western Cape	3	24	509
Total	5	54	1253

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, 30 December 2024 to 14 September 2025.

Province	Positive	Pending testing	Total specimens
Gauteng	1	12	550
KwaZulu-Natal	2	7	457
Mpumalanga	2	8	354
North West	2	7	442
Western Cape	25	25	1281
Total	32	59	3084

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	KZN, NW, WC, MP	EC, FS, GP, KZN, LP, MP, NC, NW, WC	EC, GP, KZN, MP, NW, WC
Type of site	Primary health care clinics	General practitioners.	Public hospitals.
Case definition	ILI: An acute respiratory illness with a temperature ($\geq 38^{\circ}\text{C}$) or history of fever 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 ($\geq 38^{\circ}\text{C}$) or history of fever 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 < 5 years: 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	Before 8 September 2025: Influenza virus, RSV, SARS-CoV-2, and B. pertussis. From 8 September 2025: Influenza virus, RSV, SARS-CoV-2, human metapneumovirus, human adenovirus, human rhinovirus, human parainfluenza virus and B. pertussis	Before 8 September 2025: Influenza virus, RSV and SARS-CoV-2 From 8 September 2025: Influenza virus, RSV, SARS-CoV-2, human metapneumovirus, human adenovirus, human rhinovirus and human parainfluenza virus	Before 8 September 2025: Influenza virus, RSV, SARS-CoV-2, and B. pertussis. From 8 September 2025: Influenza virus, RSV, SARS-CoV-2, human metapneumovirus, human adenovirus, human rhinovirus, human parainfluenza virus and B. pertussis
Testing Methods	Respiratory viruses: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit before 8 September 2025 and Allplex™ RV Master Assay from 8 September 2025. B. pertussis: Multiplex real-time PCR (Tatti et al., 2011)	Respiratory viruses: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit before 8 September 2025 and Allplex™ RV Master Assay from 8 September 2025	Respiratory viruses: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit before 8 September 2025 and Allplex™ RV Master Assay from 8 September 2025. B. pertussis: Multiplex real-time PCR (Tatti et al., 2011)

Abbreviations and definitions:

- ILI: Influenza-like illness
- SRI: Severe respiratory infection
- EC: Eastern Cape
- FS: Free State
- GP: Gauteng
- KZN: KwaZulu-Natal
- LP: Limpopo
- MP: Mpumalanga
- NW: North West
- NC: Northern Cape
- WC: Western Cape
- Subtype/lineage/subgroup inconclusive: Insufficient viral load in sample and unable to characterise further
- Subtype/lineage/subgroup pending: Further characterisation in progress
- Unable to assign (lineage/subclade): No lineage/subclade assigned due to poor sequence quality OR low viral load ($\text{Ct} \geq 35$ for SARS-CoV-2 and $\text{Ct} \geq 30$ for influenza/RSV)
- Epidemic threshold: Flu and RSV 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. We used the "original method" included in the package to determine the start of the season. 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, and 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 influenza-associated morbidity and mortality. For influenza, the start and end of the season are 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 RSV-associated morbidity and mortality. For RSV, the start and end of the season are 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. SARS-CoV-2 thresholds were calculated using the mean standard deviation (MSD) method, where the seasonal threshold level is determined using the mean three-week moving average of the detection rate of the selected historical years and severity levels are based on the

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mean plus one, three, or five standard deviations for moderate, high and very high thresholds, respectively. The MSD method has been detailed by Sinnathamby et al.2024.

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

Before 8 September 2025: Influenza A and B viruses, RSV and SARS-CoV-2 were identified using a commercial multiplex RT-PCR assay (Allplex 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. From 8 September 2025: Influenza A, influenza B, RSV (detects subgroup A and B), SARS-CoV-2, human metapneumovirus, human adenovirus (detects species A-F), human rhinovirus (detects species A-C) and human parainfluenza virus (detects types 1-4) were identified using a commercial multiplex RT-PCR assay (Allplex™ RV Master Assay, Seegene Inc., Seoul, South Korea). A specimen was considered positive for human metapneumovirus if the Ct was ≤39 for the respective target; RSV at Ct ≤38, and for the remaining respiratory pathogens (adenovirus, SARS-CoV-2, influenza A, influenza B, rhinovirus, and parainfluenza) at Ct ≤42.

B. pertussis was tested throughout the period using a previously described RT-PCR method (Tatti et al., 2011). A specimen was considered positive when the IS481 and/or ptxS1 gene targets were detected with a Ct <45.

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

Influenza A, B and RSV positive specimens were subtyped using the US Centers for Disease Control and Prevention (CDC) RT-PCR protocol and reagents (International Reagent Resource (IRR) [Available from: <https://www.internationalreagentresource.org/>]). All influenza-positive and RSV-positive specimens with Ct<30, and all SARS-CoV-2 positive specimens with Ct≤35 were characterised by whole genome sequencing.

RNA extraction for influenza, RSV and SARS-CoV-2 whole genome sequencing: RNA was extracted from 300µl of specimen using the Chemagic360 automated extractor and the CMG-1049 kit (Revitiiy, Massachusetts, USA) and eluted in 60µl elution buffer.

SARS-CoV-2 whole-genome sequencing and analysis:

PCR and library preparation: SARS-CoV-2 was sequenced using the Illumina COVIDSeq Kit (Illumina Inc., CA, USA) with nCoV-2019 ARTIC network tiling primers v5.4.2 (<https://artic.network/ncov-2019>). Complementary DNA (cDNA) was synthesised using random hexamers from the kit. Using tiling PCR, two amplicon pools of SARS-CoV-2 (400bp) were multiplexed and processed for libraries. The pooled amplicons underwent bead-based tagmentation and the adapter-tagged amplicons were purified and amplified using one round of PCR. Amplicons were indexed using the Illumina UDI indexes (Illumina) according to the manufacturer's instructions. Further enrichment and clean-up were performed as per the manufacturer's instructions. Purified libraries were quantified using the Qubit 4.0 fluorimeter (Invitrogen Inc., MA, USA) using the Qubit dsDNA High Sensitivity assay according to the manufacturer's instructions. The fragment sizes were analysed using TapeStation 4200 (Agilent Technologies, California, USA). Pooled libraries were normalised to 4nM concentration, and spiked with 1% PhiX (PhiX Control v3 adaptor-ligated library used as a control). Libraries were sequenced at 0.65pM using the NextSeq1000/2000 instruments with the P1 reagent cartridge (300 cycles) and the P1 Flow Cell (Illumina).

Assembly, processing and quality control of genomic sequences: Raw reads from Illumina sequencing were assembled using the CZID SARS-CoV-2 pipeline v1.6.1 (<https://github.com/chanzuckerberg/czid-workflows/tree/main/workflows/consensus-genome/>). 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/>). All assemblies determined to have acceptable quality (defined as having at least 1,000,000 reads and at least 50% 10x coverage) were deposited on GISAID (<https://www.gisaid.org/>).

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. SARS-CoV-2 genomes 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).

Influenza whole-genome sequencing and analysis:

PCR and library preparation: cDNA synthesis was performed using Invitrogen™ SuperScript™ III One-Step RT-PCR System with Platinum™ Taq High Fidelity DNA Polymerase (ThermoFischer Scientific, Massachusetts, USA) and three universal primer sets namely; Uni13/Inf-1, Uni12/Inf-1 and MBTuni-12.4 for influenza A (Zhou et al., 2009), and eight universal primer sets for influenza B viruses (Zhou et al., 2014). Before library preparation, amplicons underwent quality verification and quantification using the Qubit 4.0 fluorometer (ThermoFischer Scientific) and the Qubit dsDNA High Sensitivity assay kit. Fragment sizes were analysed using the TapeStation 4200 (Agilent Technologies, California, USA). Libraries were prepared using the Illumina DNA Library Preparation kit as per the manufacturer's protocol (Illumina, San Diego, CA, USA). Amplicons were fragmented and tagmented, then indexed using different sets of UDI indexes by IDT for Illumina DNA library preparation kit (Illumina). The indexed libraries were cleaned and normalised to 4nM for pooling. The pooled library was spiked with 1% PhiX (PhiX Control v3 adaptor-ligated library used as a control). Libraries were sequenced at 0.65pM using the NextSeq1000/2000 instrument with the P1 reagent cartridge (300 cycles) and the P1 Flow Cell (Illumina).

Assembly, processing and quality control of genomic sequences: Sequencing reads were analysed using the IRMA/MIRA pipeline (<https://wonder.cdc.gov/amd/flu/irma/irma.html>) with default parameters (Shepard et al., 2016). The quality of the mapping was assessed using QualiMap (García-Alcalde et al., 2012). Consensus sequences were uploaded to the GISAID EpiFlu database if they met the quality criteria of >1000 reads and 90% coverage at ≥50x depth for the HA and NA segments. Sequences were assigned to clades and subclades using Nextclade (<https://clades.nextstrain.org/>).

RSV whole-genome sequencing and analysis:

PCR and library preparation: cDNA synthesis was performed using LunaScript® RT SuperMix (New England Biolabs, Massachusetts, USA) according to the manufacturer's instructions, followed by amplification with Q5® Hot Start High-Fidelity 2X Master Mix (New England Biolabs, Massachusetts, USA) and eight pooled primer sets targeting RSV-A and RSV-B genome regions (Talts et al., 2024). Amplicons were quantified using the Qubit 4.0 fluorometer (ThermoFisher Scientific, Massachusetts, USA) and the Qubit 1X dsDNA High Sensitivity assay kit. Primer pools were normalised to equimolar concentrations prior to library preparation. Libraries were prepared using the Illumina CovidSeqLibrary Prep kits (Illumina, San Diego, CA, USA) following the manufacturer's protocol, indexed with unique dual indexes (IDT for Illumina), normalised, and pooled with 1% PhiX Control v3. Sequencing was performed using NextSeq 1000/2000 instruments with the P1 reagent cartridge (300 cycles) and the P1 Flow Cell (Illumina).

Assembly, processing and quality control of genomic sequences: RSV-GenoScan (<https://github.com/AlexandreD-bio/RSV-GenoScan>) was used for the assembly of RSV reads, which included trimming and quality control of raw reads, and then mapping reads to the RSV-A and RSV-B references (GenBank accession: NC_001803.1 and AY353550.1 for RSV-A and RSV-B, respectively). The minimum depth for consensus sequence generation was set at 50x. A sequence was considered high quality if the whole-genome coverage was ≥90%, and the coverage of the G and F genes was 100%. A whole-genome coverage of at least 70% was accepted for lineage determination. Nextclade (<https://clades.nextstrain.org/>) was used for lineage assignment based on the Goya et. al. 2023 classifications.

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Data are provisional as on the 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.

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