WEEKLY RESPIRATORY PATHOGENS SURVEILLANCE REPORT

SOUTH AFRICA WEEK **2** 2022

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

CONTENTS

CUMULATIVE DATA FROM

02 MARCH 2020 ► **19 JANUARY 2022**

HIGHLIGHTS: WEEK 2

- In 2022 to date, four influenza cases have been detected, two each from Western Cape and Mpumalanga sentinel surveillance sites. Two new cases of influenza from Western Cape (n=1) and Mpumalanga (n=1) surveillance sites were detected in week2.

- RSV activity remains below seasonal threshold in both ILI and pneumonia surveillance programmes.

- In 2022 to date, a total of 82 COVID-19 cases were detected from all surveillance programmes. A decrease in detection rate of COVID-19 cases has been noted in both pneumonia surveillance and ILI in week2. Of the 34 hospitalised COVID-19 cases reported with available data on outcome, 3 (9%) died.

PROGRAMME DESCRIPTIONS

Programme	**Influenza-like illness (ILI)**	**Viral Watch**	**National syndromic surveillance for pneumonia**
Start year	2012	1984	2009
Provinces*	KZ NW WC** MP***	EC FS GP LP MP NC NW WC	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 **Suspected SARS-CoV-2** Any person presenting with an acute (≤14 days) respiratory tract infection or other clinical illness compatible with COVID-19[β]	**ILI:** An acute respiratory illness with a temperature (≥38°C) and cough, & onset ≤10 days **Suspected SARS-CoV-2** Any person presenting with an acute (≤14 days) respiratory tract infection or other clinical illness compatible with COVID-19[β]	**SRI:** Acute (symptom onset≤10 days) or chronic (symptom onset >10) lower respiratory tract infection **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. **Suspected SARS-CoV-2** Any person admitted with a physician-diagnosis of suspected COVID-19 and not meeting SRI case definition.
Specimens collected	Oropharyngeal & nasopharyngeal swabs	Throat and/or nasal swabs or Nasopharyngeal swabs	Oropharyngeal & nasopharyngeal swabs
Main pathogens tested****	INF RSV BP SARS-CoV-2	INF RSV BP SARS-CoV-2	INF RSV BP SARS-CoV-2
Testing Methods	**INF and RSV** - Fast-Track Diagnostics multiplex real-time reverse transcription polymerase chain reaction (until 31 March 2021) ***B. pertussis*** Multiplex real-time PCR (Tatti *et al., J Clin Microbiol* 2011) and culture (if PCR cycle threshold ≤25) **SARS-CoV-2** 1 April 2020 – 31 March 2021: Roche E gene real-time PCR essay (Corman *et al., Euro Surv* 2020) 1 April 2021 to date: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit • positivity assigned if PCR cycle threshold is <40 for ≥1 gene targets (N, S, OR RdRp)	**INF and RSV** - Fast-Track Diagnostics multiplex real-time reverse transcription polymerase chain reaction (until 31 March 2021) ***B. pertussis*** Multiplex real-time PCR (Tatti *et al., J Clin Microbiol* 2011) and culture (if PCR cycle threshold ≤25) **SARS-CoV-2** 1 April 2020 – 31 March 2021: Roche E gene real-time PCR essay Corman *et al., Euro Surv* 2020) 1 April 2021 to date: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit • positivity assigned if PCR cycle threshold is <40 for ≥1 gene targets (N, S, OR RdRp)	**INF and RSV** - Fast Track Diagnostics multiplex real-time reverse transcription polymerase chain reaction (until 31 March 2021) ***B. pertussis*** Multiplex real-time PCR (Tatti *et al., J Clin Microbiol* 2011) and culture (if PCR cycle threshold ≤25) **SARS-CoV-2** 1 April 2020 – 31 March 2021: Roche E gene real-time PCR essay (Corman *et al., Euro Surv* 2020) 1 April 2021 to date: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit • positivity assigned if PCR cycle threshold is <40 for ≥1 gene targets (N, S, OR RdRp)

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 (Viral Watch Programme) 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.

* EC: Eastern Cape; FS: Free State; GP: Gauteng; KZ: KwaZulu-Natal; LP: Limpopo; MP: Mpumalanga: NC: Northern Cape; NW: North West; WC: Western Cape

**Started in 2019

***Started in November 2020

****INF: influenza virus; RSV: respiratory syncytial virus; BP: *Bordetella pertussis*; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2

βSymptoms include ANY of the following respiratory symptoms: cough, sore throat, shortness of breath, anosmia (loss of sense of smell) or dysgeusia (alteration of the sense of taste), with or without other symptoms (which may include fever, weakness, myalgia, or diarrhoea). Testing for SARS-CoV-2 was initiated in all three surveillance programmes in week 10 of 2020 (week starting 2 March 2020).

COMMENTS

Influenza

In 2022 to date, a total of 4 influenza cases have been reported. In week2, transmission and impact are below threshold.

ILI programme: In 2022 to date, specimens from 51 patients meeting ILI case definition were tested from 4 ILI sites. Influenza was detected in two (4%) patients, of which one (50%) was influenza A(H1N1)pdm09-and another one (50%) was influenza A(pending subtype results). (Fig1, Table1).

Viral Watch programme: In 2022 to date, a specimen from one patient from one of the 8 Viral Watch sites participating in surveillance was tested. Influenza was not detected. (Fig7, Table5)

Pneumonia surveillance: Since the beginning of 2022, specimens from 158 patients with severe respiratory illness (SRI) were tested from the 6 sentinel sites. Influenza A was detected in two (1%) patients, both pending influenza A subtype results. (Fig12, Table9)

Respiratory syncytial virus

RSV activity remains below seasonal threshold in all programmes.

ILI programme: In 2022 to date, 51 specimens from patients meeting the ILI case definition were tested and RSV was not detected. (Fig4, Table2)

Viral Watch programme: In 2022 to date, one specimen from viral watch patient was tested and RSV was not detected. (Fig9, Table6)

Pneumonia surveillance: Since the beginning of 2022, 158 specimens were tested and RSV was detected in specimens of four (3%) patients. Of which, one (25%) was RSV subgroup B and three (75%) RSV (subgroup pending results). (Fig14, Table10)

SARS-CoV-2 (Severe acute respiratory syndrome coronavirus 2)

ILI programme: From 3 January 2022 to date, 51 patients were tested and SARS-CoV-2 was detected in 12 (24%) patients. SARS-CoV-2 variant results pending for 17 SARS-CoV-2 positive patients. (Fig6, Table4)

Viral Watch programme: From 3 January 2022 to date, one patients presenting with ILI was tested and SARS-CoV-2 was detected (100%). SARS-CoV-2 variant results pending for one SARS-CoV-2 positive patient. (Fig11, Table8)

Pneumonia surveillance: From 3 January 2022 to date, 158 patients with severe respiratory illness (SRI) were tested and SARS-CoV-2 was detected in 61 (39%) patients. SARS-CoV-2 variant results were pending for 64 patients with COVID-19. (Fig17, Table12)

In addition, SARS-CoV-2 was detected in 8 of 12 (67%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet the pneumonia/ILI surveillance case definitions.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

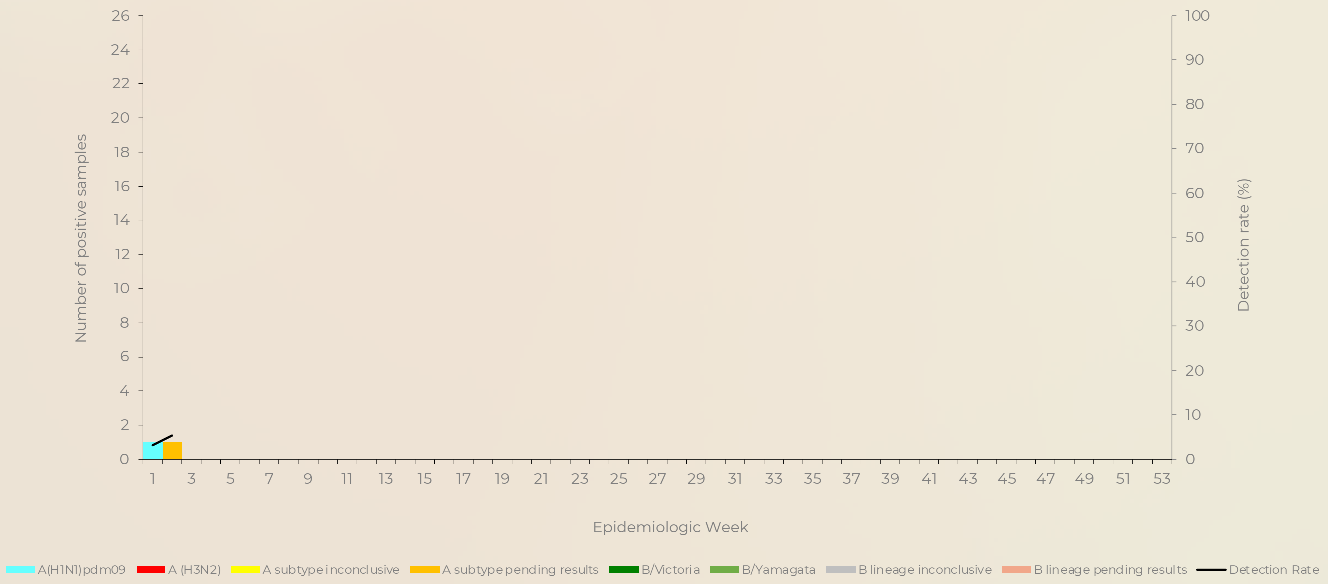

Figure 1. Number of influenza positive cases* by influenza subtype and lineage** and detection rate*** by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

Specimens from patients with influenza-like illnesses at 5 sentinel sites in 4 provinces
***Only reported for weeks with >10 specimens submitted
Inconclusive: insufficient viral load in sample and unable to characterise further

Table 1. Number of laboratory confirmed influenza cases by subtype and lineage** and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

Clinic (Province)	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending results^{β}	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending results^{β}	Total samples
Agincourt (MP)	0	0	0	1	0	0	0	0	6
Eastridge (WC)	1	0	0	0	0	0	0	0	7
Edendale Gateway (KZ)	0	0	0	0	0	0	0	0	16
Jouberton (NW)	0	0	0	0	0	0	0	0	17
Mitchell's Plain (WC)	0	0	0	0	0	0	0	0	5
Total:	**1**	**0**	**0**	**1**	**0**	**0**	**0**	**0**	**51**

KZ: KwaZulu-Natal; NW: North West; WC: Western Cape; MP: Mpumalanga

Inconclusive: insufficient viral load in sample and unable to characterise further
*^{β}influenza A subtype or B lineage results are pending

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

Figure 2. Influenza percentage detections and epidemic thresholds*, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

*Thresholds based on 2012-2019 data

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

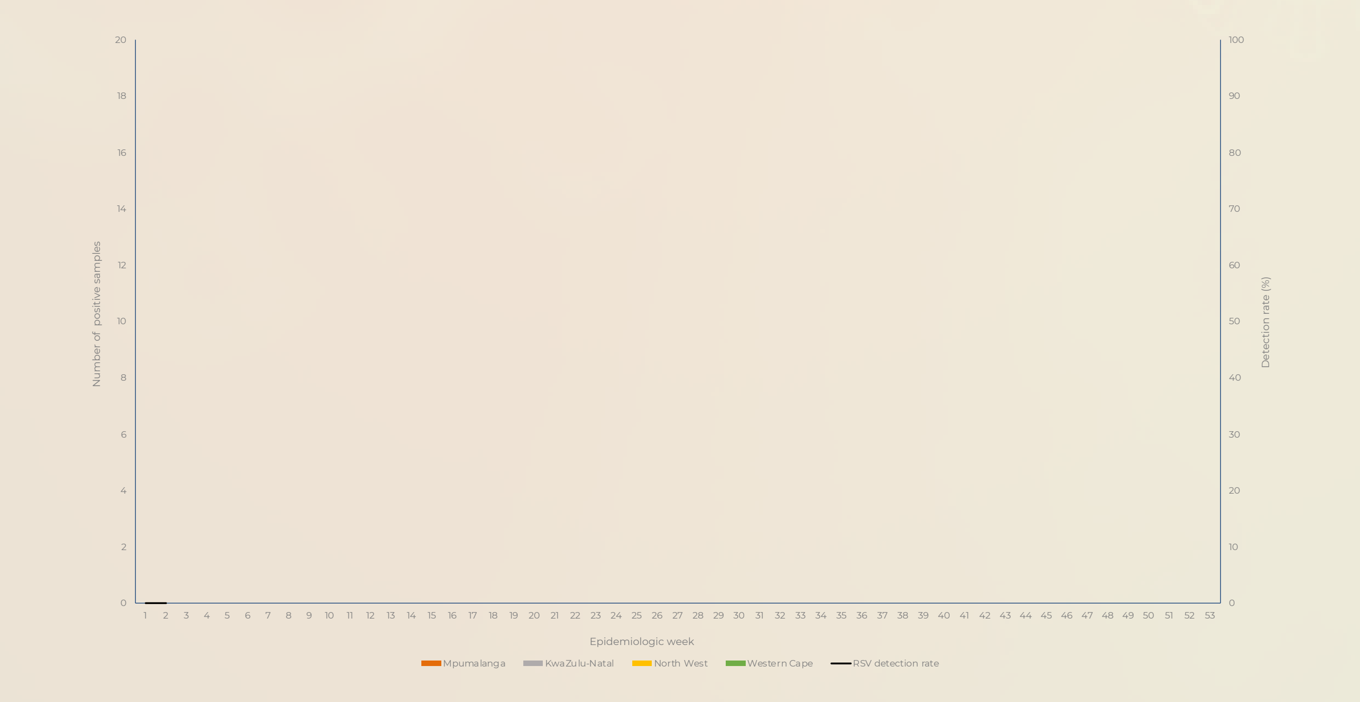

Figure 3. Number of patients testing positive for respiratory syncytial virus* by province and detection rate** by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

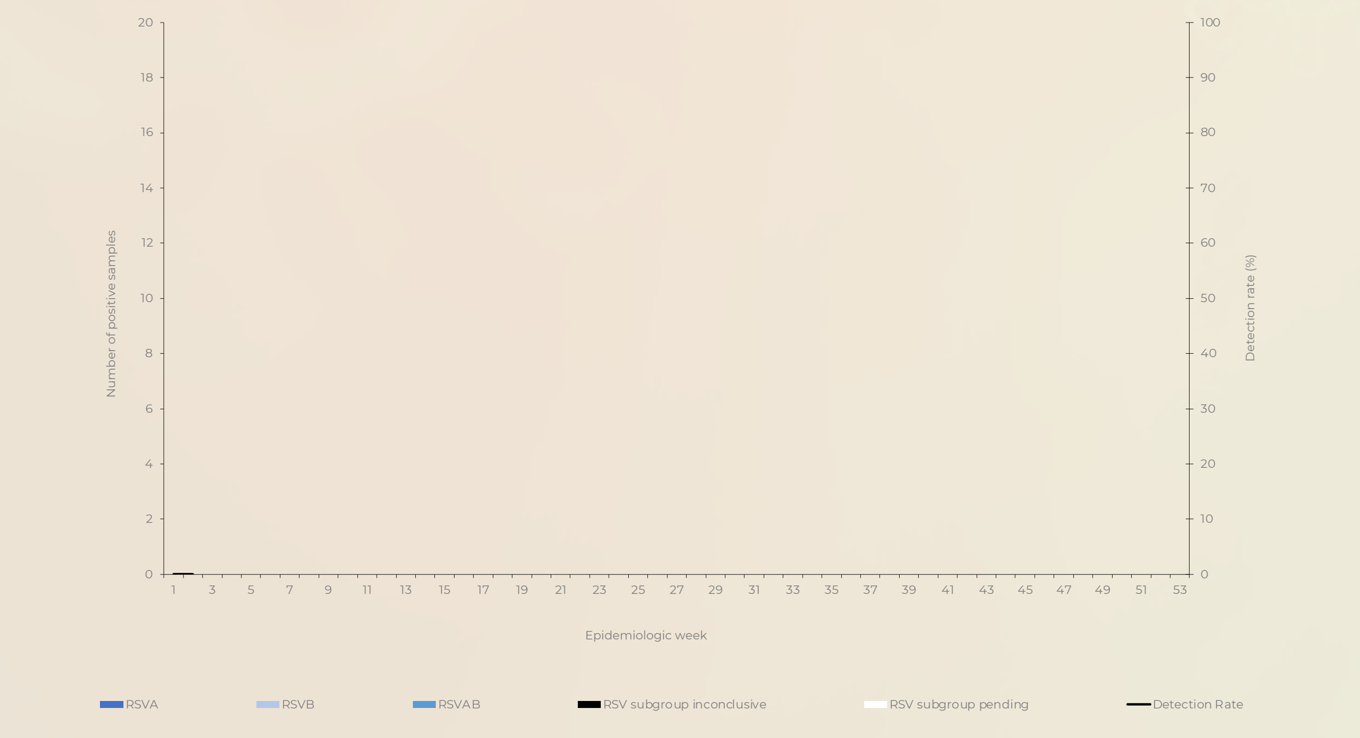

Figure 4. Number of patients testing positive for respiratory syncytial virus** by subgroup and detection rate by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified

Table 2. Number oof patients testing positive for respiratory syncytial virus (RSV) by subgroups identified and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

Clinic (Province)	**RSVA**	**RSVB**	**RSVAB**	**RSV subgroup inconclusive**	**RSV subgroup pending***	**Total samples**
Agincourt (MP)	0	0	0	0	0	6
Eastridge (WC)	0	0	0	0	0	7
Edendale Gateway (KZ)	0	0	0	0	0	16
Jouberton (NW)	0	0	0	0	0	17
Mitchell’s Plain (WC)	0	0	0	0	0	5
Total	**0**	**0**	**0**	**0**	**0**	**51**

KZ: KwaZulu-Natal; NW: North West; WC: Western Cape; MP: Mpumalanga
Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified
*RSV results for subgroups are pending

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

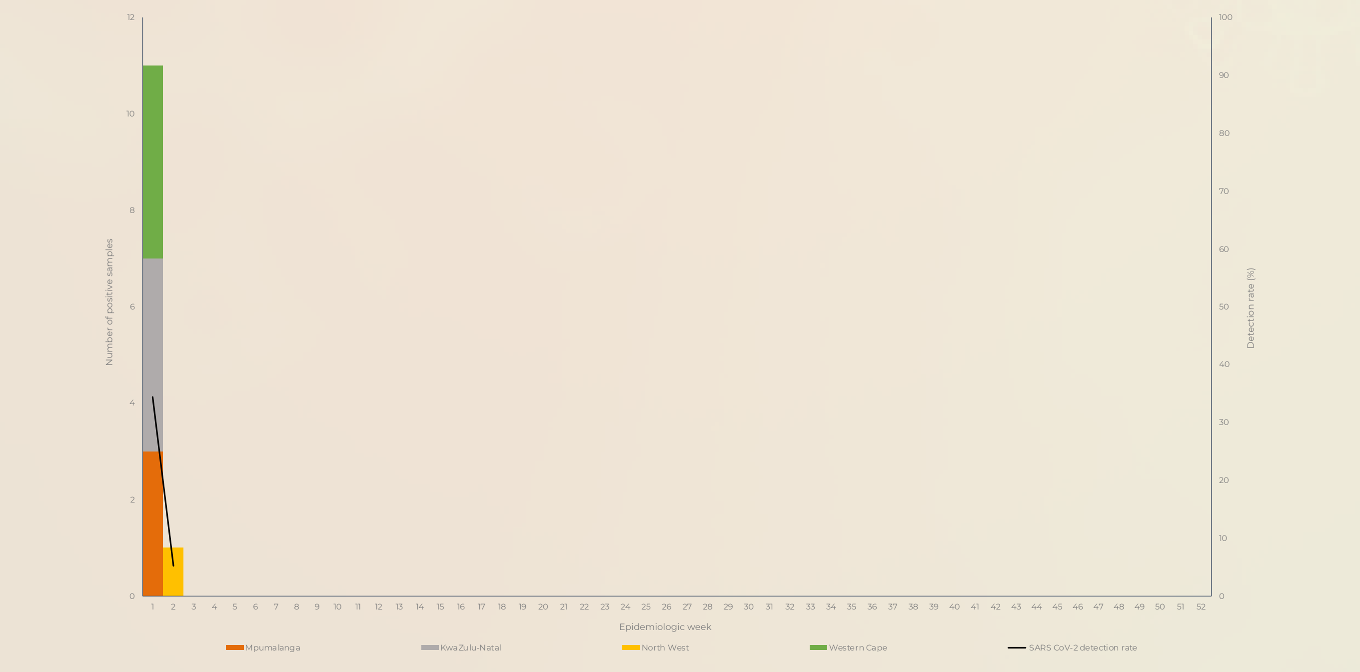

Figure 5. Number of patients testing positive for SARS-CoV-2* by province and detection rate by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

*Specimens from patients with influenza-like illnesses at 5 sentinel sites in 4 provinces
**SARS-CoV-2 was detected in 5 of 7 (71%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the epidemiological curve.

Table 3. Number of patients positive for SARS-CoV-2 identified and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance primary health care clinics, 03/01/2022 – 16/01/2022

Clinic (Province)	SARS-CoV-2 positive	Total samples tested
Agincourt (MP)	3	6
Eastridge (WC)	1	7
Edendale Gateway (KZ)	4	16
Jouberton (NW)	1	17
Mitchell's Plain (WC)	3	5
Total:	**12**	**51**

KZ: KwaZulu-Natal; NW: North West; WCP: Western Cape; MP: Mpumalanga

**SARS-CoV-2 was detected in 5 of 7 (71%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the table.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

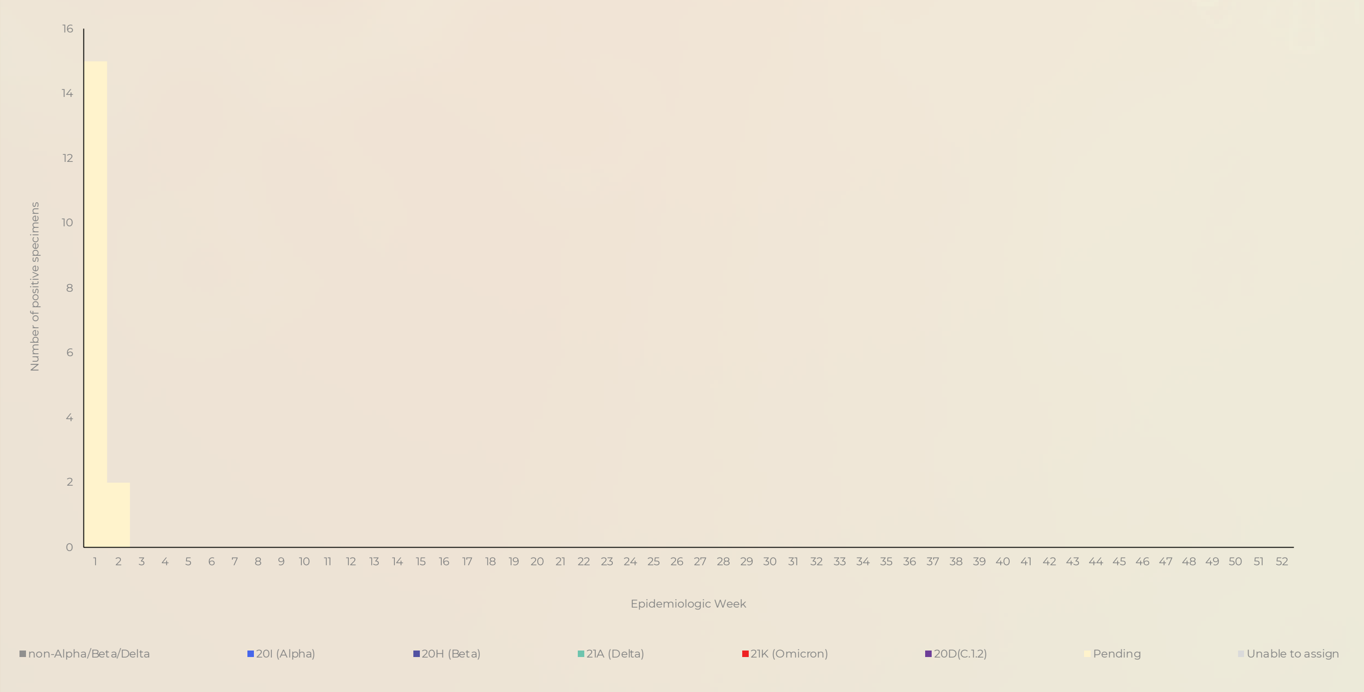

Figure 6. Number aand detection rate of laboratory confirmed SARS-CoV-2* cases by variant type (variant PCR/sequencing) and week, Influenza-like illness (ILI) surveillance in primary health care clinics, 03/01/2022 – 16/01/2022

*Specimens are from patients with influenza-like illness at 5 sentinel sites in 4 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the ILI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

Table 4. Number of SARS-CoV-2* positive cases by variant (variant PCR and/or sequencing) identified and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance primary health care clinics, 03/01/2022 – 16/01/2022

Clinic (Province)	Non-Alpha/ Beta/ Delta	20I (Alpha)	20H (Beta)	21A (Delta)	20D (C.1.2)	21K (Omicron)	Pending	Unable to assign	Total SARS-CoV-2 positive
Agincourt (MP)	0	0	0	0	0	0	5	0	5
Eastridge (WC)	0	0	0	0	0	0	1	0	1
Edendale Gateway (KZ)	0	0	0	0	0	0	6	0	6
Jouberton (NW)	0	0	0	0	0	0	2	0	2
Mitchell's Plain (WC)	0	0	0	0	0	0	3	0	3
Total:	**0**	**0**	**0**	**0**	**0**	**0**	**17**	**0**	**17**

KZ: KwaZulu-Natal; NW: North West; WCP: Western Cape; MP: Mpumalanga (started enrolling on the 10th November 2020)
*Specimens are from patients with influenza-like illness at 5 sentinel sites in 4 provinces who met suspected SARS-CoV-2 case definition or met ILI case definition

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

Figure 7. Number of positive patients* by influenza subtype and lineage and detection rate** by week, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

*Specimens from patients with Influenza-like illnesses at 90 sentinel sites in 8 provinces
** Only reported for weeks with >10 specimens submitted.
Inconclusive: insufficient viral load in sample and unable to characterise further

Table 5. Number of laboratory confirmed influenza cases by influenza subtype and lineage and total number of samples tested by province, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

Province	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending results*	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending results*	Total samples
Eastern Cape	0	0	0	0	0	0	0	0	0
Free State	0	0	0	0	0	0	0	0	0
Gauteng	0	0	0	0	0	0	0	0	1
Limpopo	0	0	0	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	0	0	0	0
North West	0	0	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	0	0	0
Western Cape	0	0	0	0	0	0	0	0	0
Total:	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1**

Inconclusive: insufficient viral load in sample and unable to characterise further
*Influenza A subtype or B lineage results are pending

From 04 January 2021 to date, no patients were tested for influenza at the time of entry into South Africa following travel abroad.

Patients known to have acquired influenza abroad are not included in the table or epidemiological curve.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

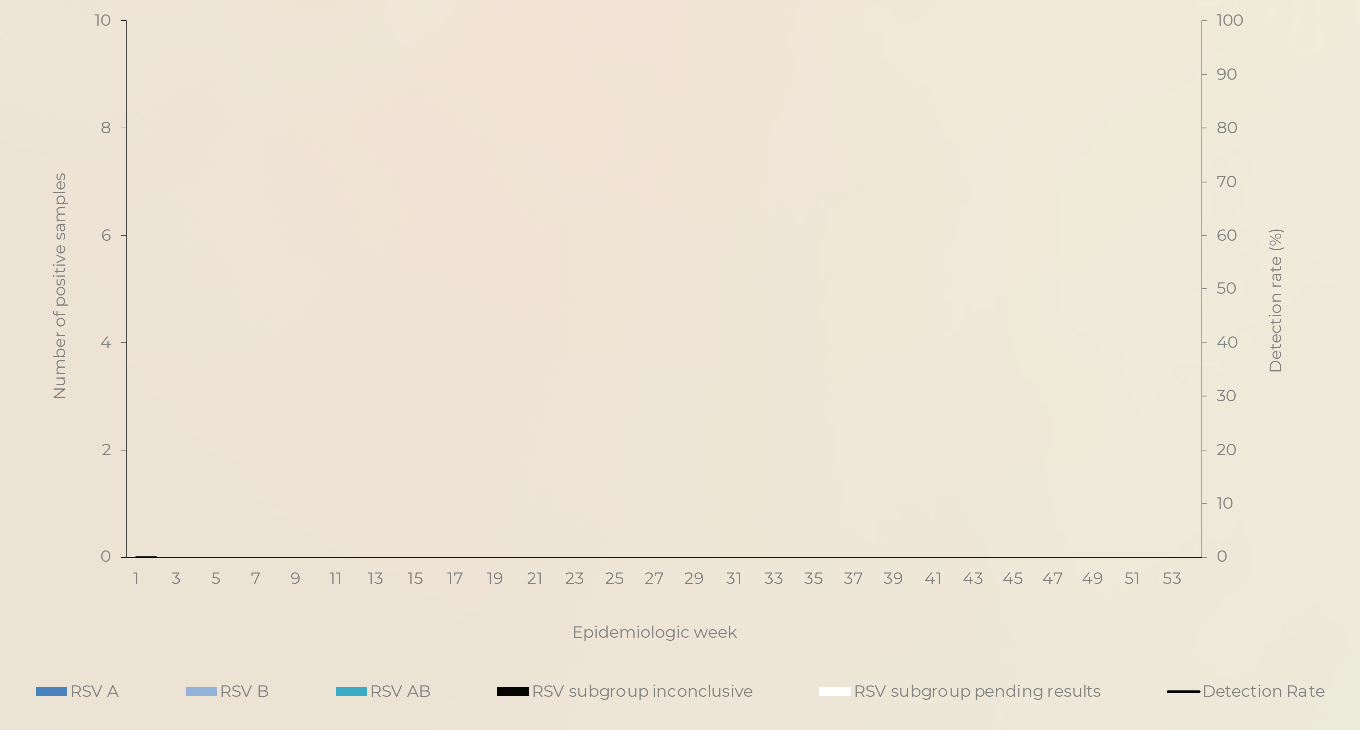

Figure 8. Number of RSV positive cases testing positive for respiratory syncytial virus (RSV)* by subgroup and detection rate by week, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

*RSV results for subgroups are pending

Table 6. Number of RSV positive cases identified and total number of samples tested by province, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

Province	RSV A	RSV B	RSV AB	RSV subgroup inconclusive**	RSV subgroup pending results*	Total samples tested
Eastern Cape	0	0	0	0	0	0
Free State	0	0	0	0	0	0
Gauteng	0	0	0	0	0	1
Limpopo	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	0
North West	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0
Western Cape	0	0	0	0	0	0
Total:	**0**	**0**	**0**	**0**	**0**	**1**

*RSV results for subgroups are pending

**Inconclusive: insufficient viral load in sample and unable to characterise further

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

Figure 9. Number of patients testing positive for SARS-CoV-2*, by site and detection rate by week, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

Table 7. Number of SARS-CoV-2 positive cases identified and total number tested by province, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

Province	SARS-CoV-2 positive	Total samples tested
Eastern Cape	0	0
Free State	0	0
Gauteng	1	1
Limpopo	0	0
Mpumalanga	0	0
North West	0	0
Northern Cape	0	0
Western Cape	0	0
Total:	**1**	**1**

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

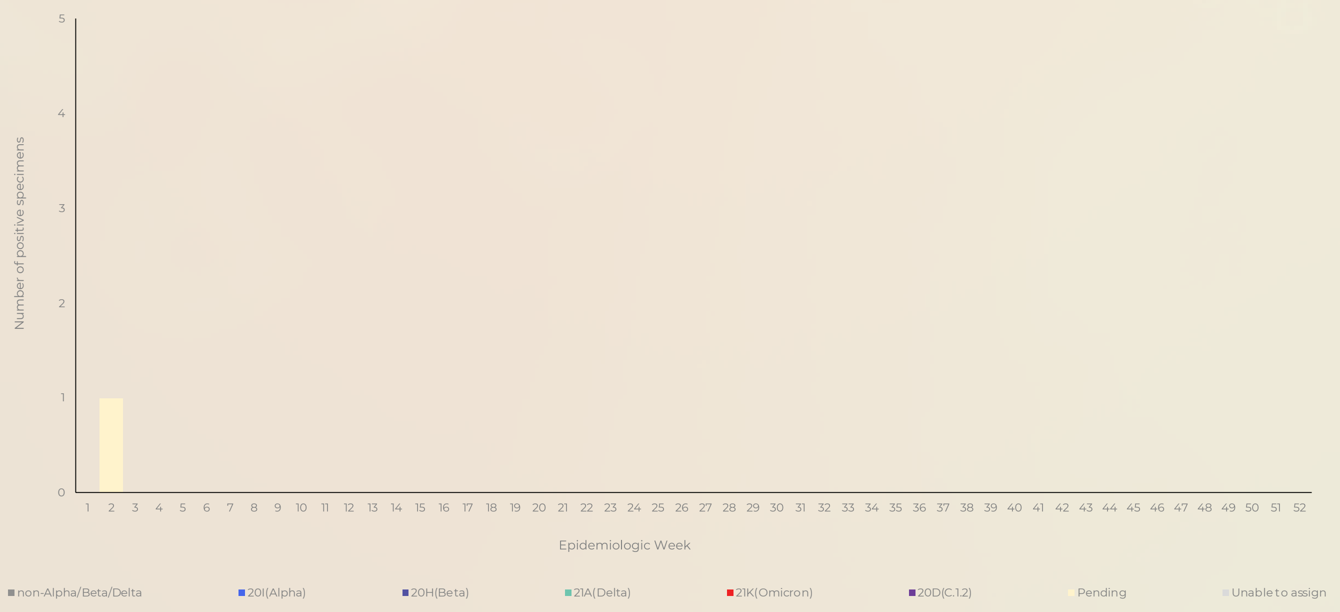

Figure 10. Number and detection rate of laboratory confirmed SARS-CoV-2* cases by variant type (variant PCR/sequencing) and week, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

Table 8. Number of SARS-CoV-2* positive cases by variant (variant PCR and/or sequencing) identified and total number of samples tested by province, ILI surveillance - Viral Watch, 03/01/2022 – 16/01/2022

Clinic (Province)	Non-Alpha/ Beta/Delta	20I (Alpha)	20H (Beta)	21A (Delta)	20D (C.1.2)	20K (Omicron)	Pending	Unable to assign	Total SARS-CoV-2 positive
Eastern Cape	0	0	0	0	0	0	0	0	0
Free State	0	0	0	0	0	0	0	0	0
Gauteng	0	0	0	0	0	0	1	0	1
Limpopo	0	0	0	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	0	0	0	0
North West	0	0	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	0	0	0
Western Cape	0	0	0	0	0	0	0	0	0
Total:	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**1**

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

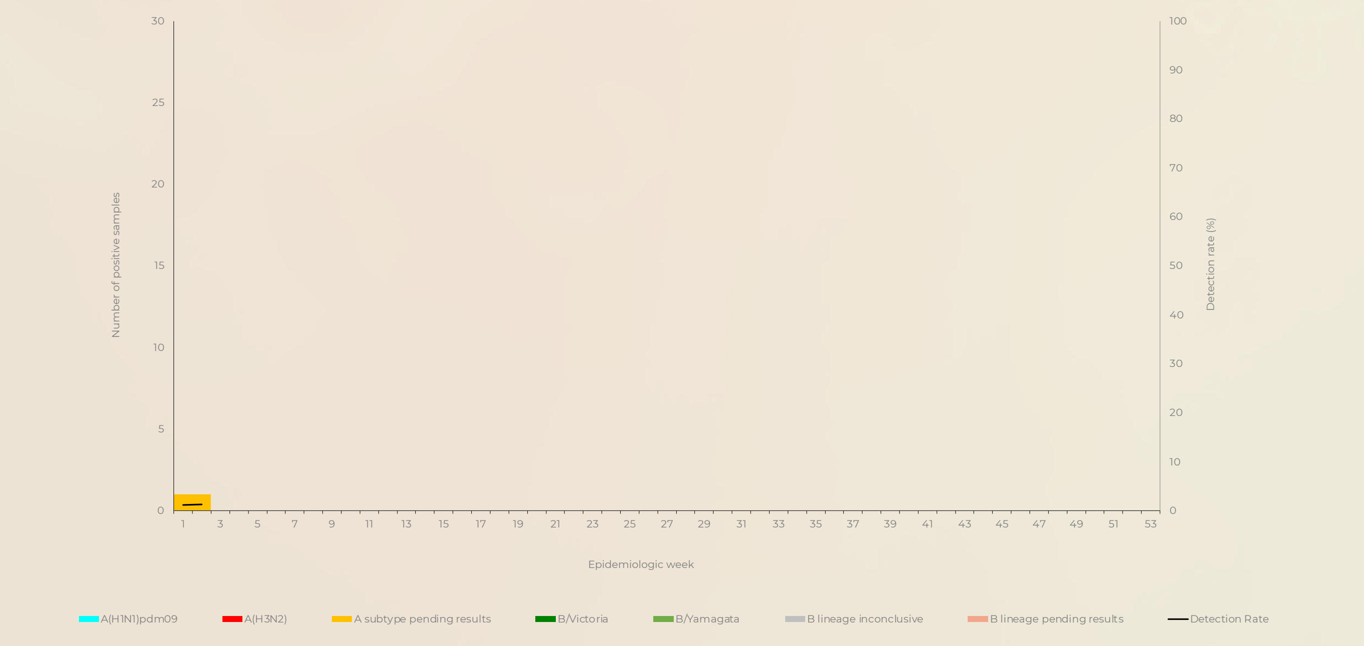

Figure 11. Number of positive influenza positive cases* by influenza subtype and lineage** and detection rate*** by week, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

*Specimens from patients hospitalised with pneumonia at 7 sentinel sites in 5 provinces
**Influenza was detected in one (25%) of four specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.
***Only reported for weeks with >10 specimens submitted
Inconclusive: insufficient viral load in sample and unable to characterise further

Table 9. Number of laboratory confirmed influenza cases by subtype and lineage** and total number of samples tested by hospital, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

Hospital (Province)	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending results***	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending results***	Total samples
Edendale (KZ)	0	0	0	0	0	0	0	0	32
Helen Joseph-Rahima Moosa (GP)	0	0	0	0	0	0	0	0	40
Klerksdorp-Tshepong (NW)	0	0	0	0	0	0	0	0	22
Mapulaneng-Matikwana (MP)	0	0	0	0	0	0	0	0	8
Red Cross (WC)	0	0	0	0	0	0	0	0	21
Mitchell's Plain (WC)	0	0	0	1	0	0	0	0	29
Tintswalo (MP)	0	0	0	1	0	0	0	0	6
Total:	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**	**158**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga (Tintswalo started enrolling on the 10th Feb 2021); WC: Western Cape
Inconclusive: insufficient viral load in sample and unable to characterise further
***influenza A subtype or B lineage results are pending

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

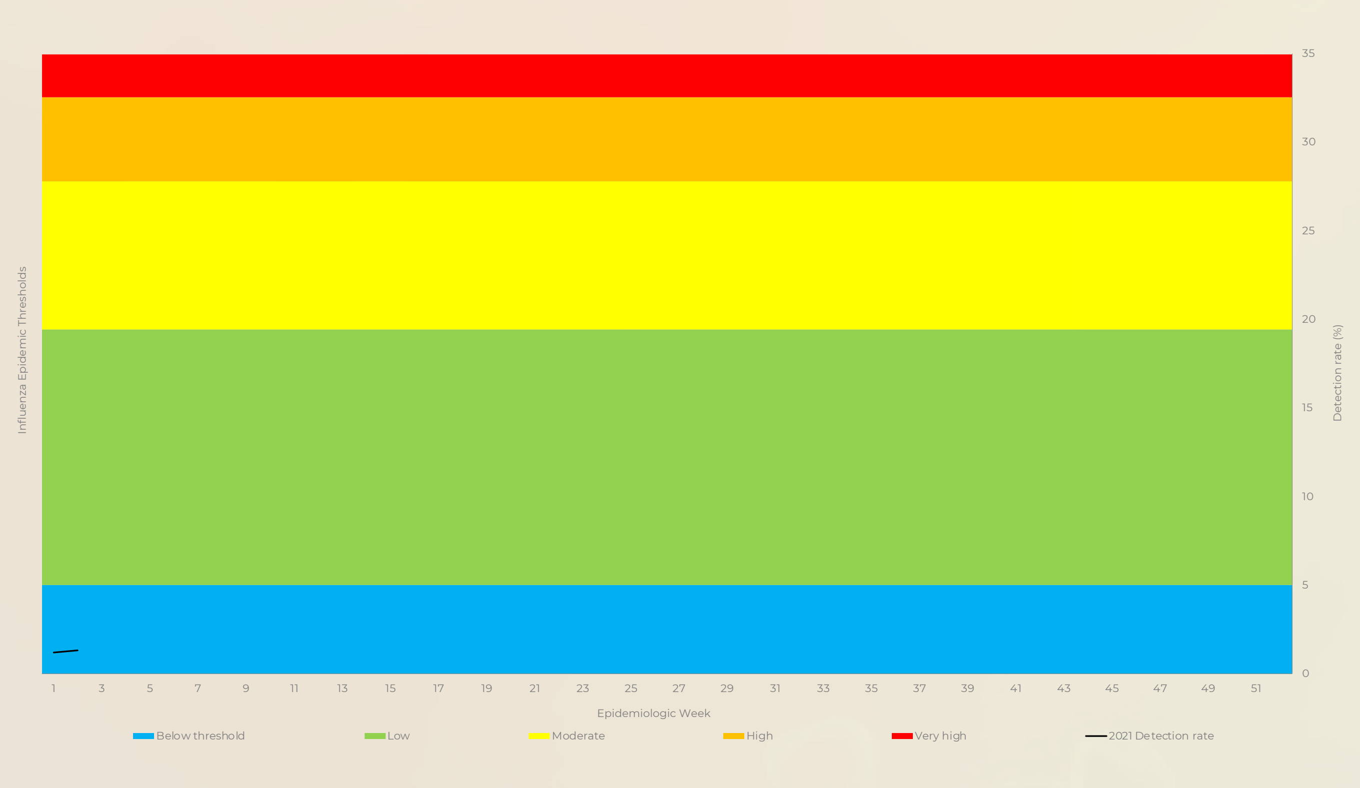

Figure 12. Influenza percentage detections and epidemic thresholds*, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

*Thresholds based on 2010-2019 data

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

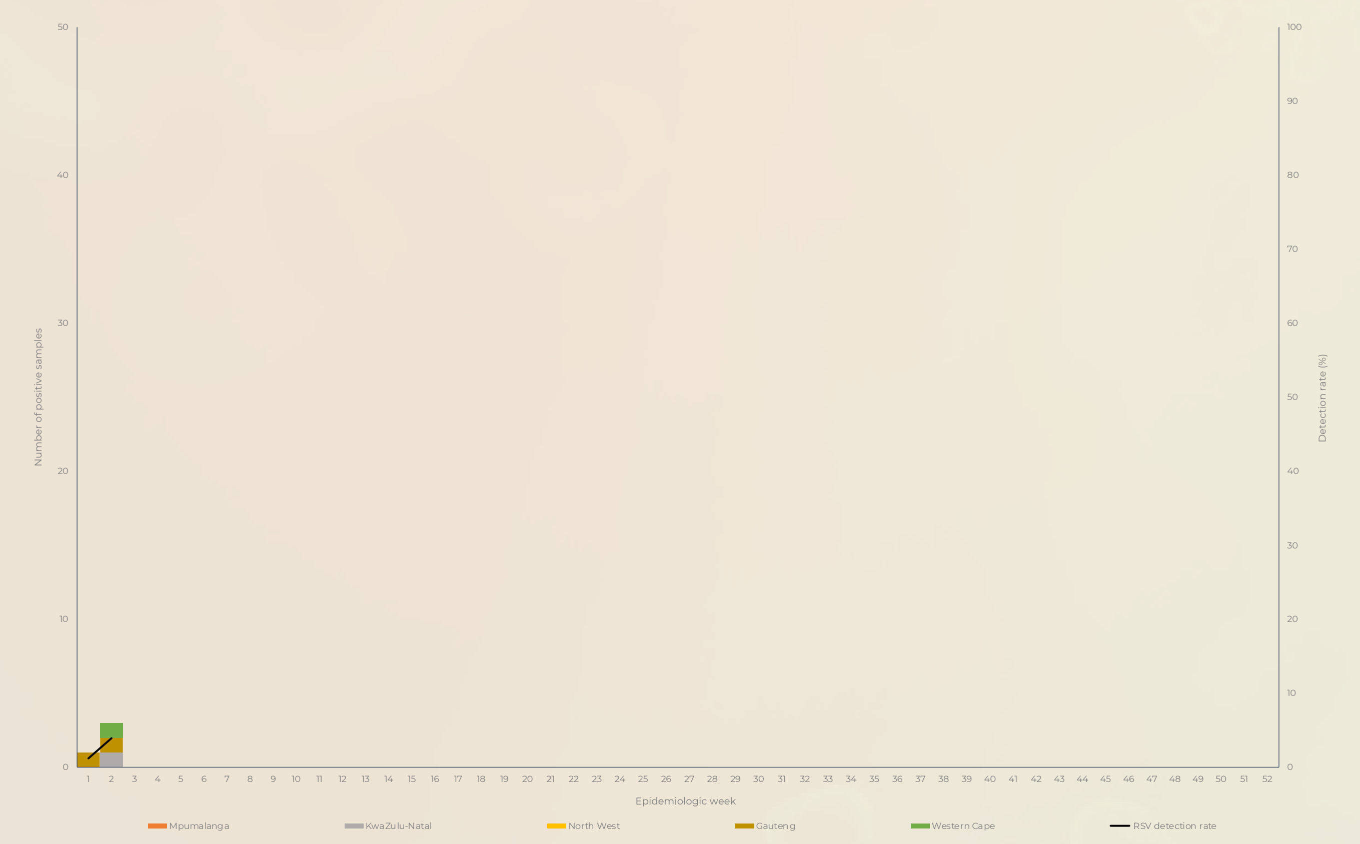

Figure 13. Number of patients testing positive for respiratory syncytial virus* by province and detection rate by week, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

*RSV was not detected in four specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

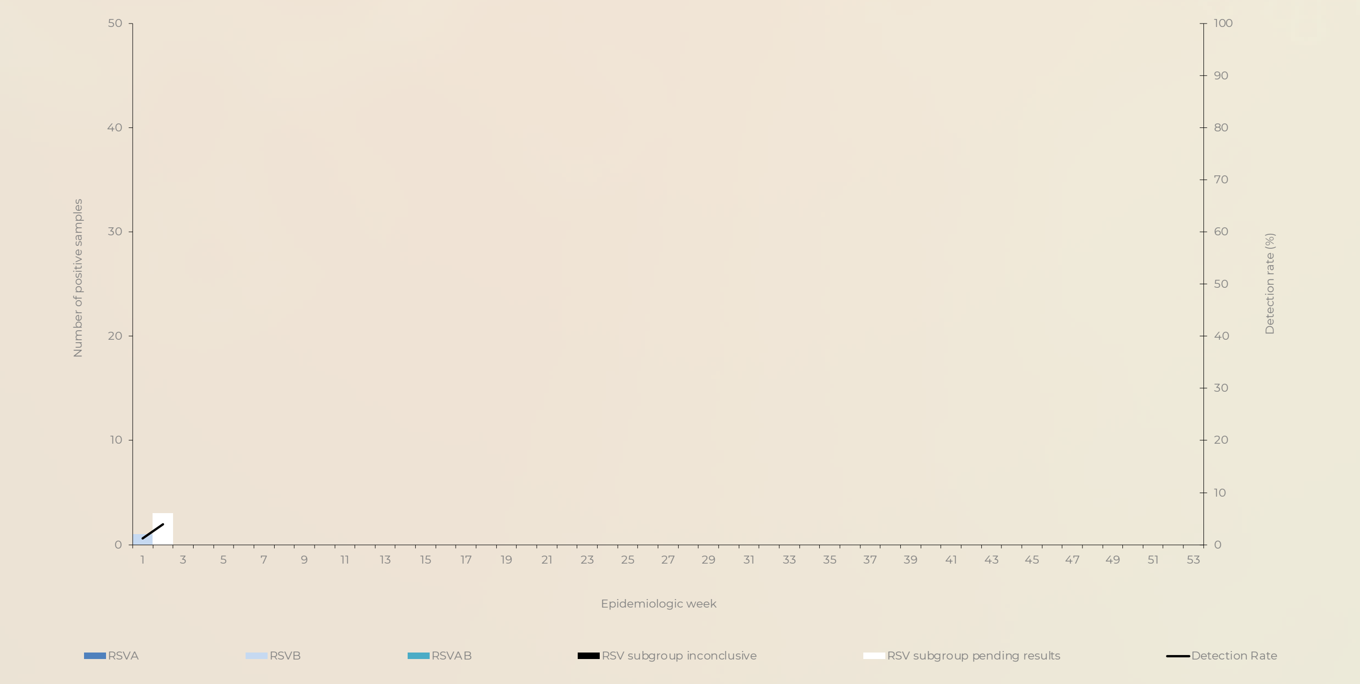

Figure 14. Number of patients testing positive for respiratory syncytial virus* by subgroup and detection rate by week, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified
RSV subgroup pending: RSV results for subgroups are pending

Table 10: Number of patients positive for respiratory syncytial virus subgroups** by subgroups identified and total number of samples tested by hospital, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

Hospital (Province)	RSVA	RSVB	RSVAB	RSV subgroup inconclusive	RSV subgroup pending*	Total samples
Edendale (KZ)	0	0	0	0	1	32
Helen Joseph-Rahima Moosa (GP)	0	0	0	0	1	40
Klerksdorp-Tshepong (NW)	0	0	0	0	0	22
Mapulaneng-Matikwana (MP)	0	0	0	0	0	8
Red Cross (WC)	0	0	0		1	21
Mitchell's Plain (WC)	0	0	0	0	0	29
Tintswalo (MP)	0	0	0	0	0	6
Total:	**0**	**0**	**0**	**0**	**3**	**158**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga (Tintswalo started enrolling on the 10th Feb 2021); WC: Western Cape
Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified
*RSV results for subgroups are pending

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

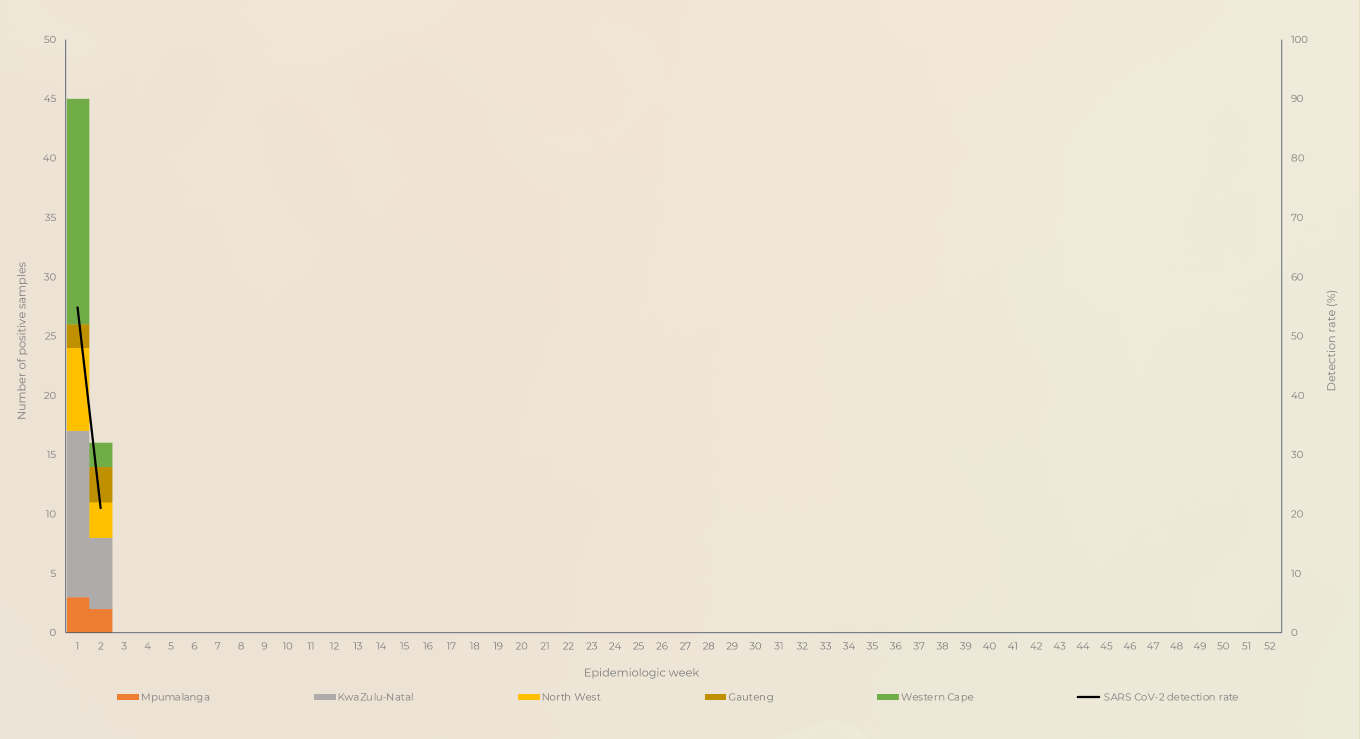

Figure 15. Number of patients testing positive for SARS-CoV-2*ᵝ by province and detection rate by week, pneumonia surveillance public hospitals, 01/01/2021 – 16/01/2022

*Specimens from patients hospitalized with pneumonia at 6 sentinel sites in 5 provinces

*ᵝSARS-CoV-2 was detected in 3 of 5 (60%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.

Table 11. Number of patients positive for SARS-CoV-2** and total number of samples tested by hospital, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

Hospital (Province)	SARS-CoV-2 positive	Total samples tested
Edendale (KZ)	20	32
Helen Joseph-Rahima Moosa (GP)	5	40
Klerksdorp-Tshepong (NW)	10	22
Mapulaneng-Matikwana (MP)	2	8
Red Cross (WC)	6	21
Mitchell's Plain (WC)	15	29
Tintswalo (MP)	3	6
Total:	**61**	**158**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga; WC: Western Cape

**SARS-CoV-2 was detected in 3 of 5 (60%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the table.

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

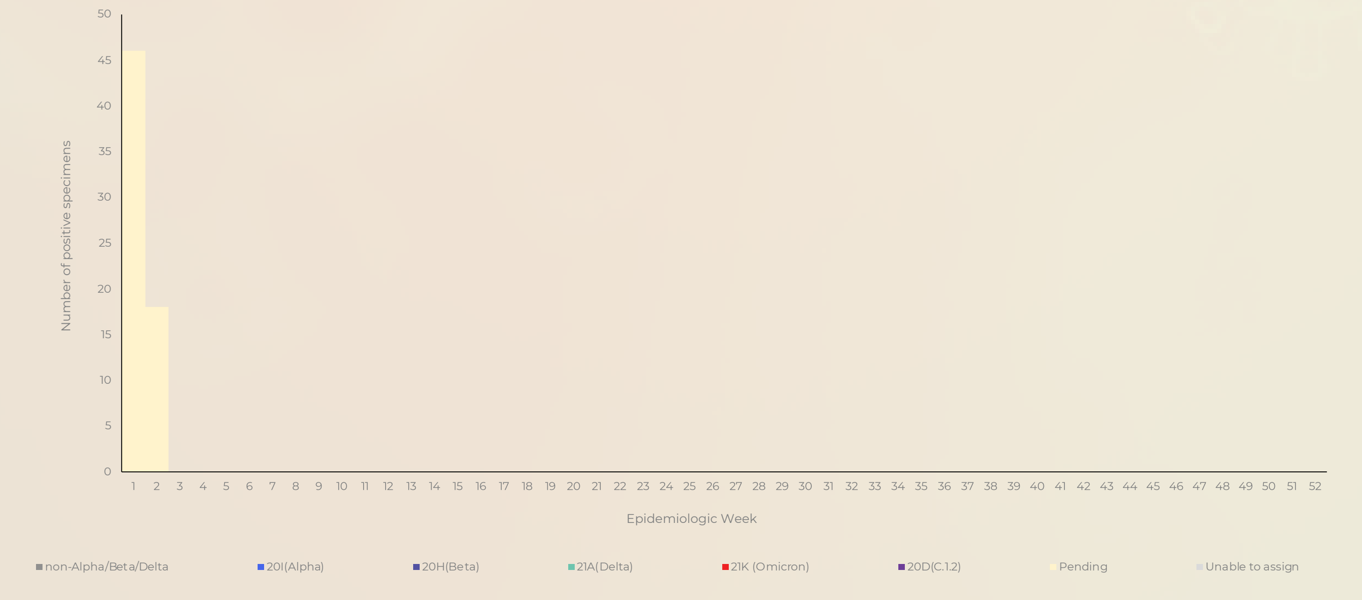

Figure 16. Number and detection rate of laboratory confirmed SARS-CoV-2 cases* by variant type (variant PCR/sequencing), pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

Specimens are from hospitalized patients at 7 sentinel sites in 5 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the SRI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result

Pending: outstanding variant results

Table 12. Number of SARS-CoV-2 positive cases* by variant (variant PCR and/or sequencing) identified and total number of samples tested by hospital, pneumonia surveillance public hospitals, 03/01/2022 – 16/01/2022

Hospital (Province)	Non-Alpha/ Beta/Delta	20I (Alpha)	20H (Beta)	21A (Delta)	20D (C.1.2)	21K (Omicron)	Pending	Unable to assign	SARS-CoV-2 positive
Edendale (KZ)	0	0	0	0	0	0	23	0	23
Helen Joseph-Rahima Moosa (GP)	0	0	0	0	0	0	5	0	5
Klerksdorp-Tshepong (NW)	0	0	0	0	0	0	10	0	10
Mapulaneng-Matikwana (MP)	0	0	0	0	0	0	2	0	2
Red Cross (WC)	0	0	0	0	0	0	6	0	6
Mitchell's Plain (WC)	0	0	0	0	0	0	15	0	15
Tintswalo (MP)	0	0	0	0	0	0	3	0	3
Total:	**0**	**0**	**0**	**0**	**0**	**0**	**64**	**0**	**64**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga (Tintswalo started enrolling on the 10th Feb 2021); WC: Western Cape
*Specimens are from hospitalized patients at 7 sentinel sites in 5 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the SRI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

SUMMARY OF LABORATORY CONFIRMED SARS-COV-2 CASES

Table 13. Characteristics of individuals with laboratory-confirmed SARS-CoV-2, enrolled in influenza-like illness (ILI) and pneumonia surveillance programmes, South Africa, 3 January 2022 – 16 January 2022

Characteristic	Influenza–like illness (ILI), public-sector, n=17 (%)	Pneumonia, n=64 (%)
Age group		
0-9	3/17 (18)	16/64 (25)
10-19	0/17 (0)	2/64 (3)
20-39	2/17 (12)	16/64 (25)
40-59	10/17 (59)	17/64 (27)
60-79	1/17 (6)	11/64 (17)
≥80	1/17 (6)	2/64 (3)
Sex-female	14/17 (82)	38/64 (59)
Province*		
Gauteng	N/A	5/64 (8)
KwaZulu-Natal	6/17 (35)	23/64 (36)
Mpumalanga**	5/17 (29)	5/64 (8)
North West	2/17 (12)	10/64 (16)
Western Cape	11/17 (24)	21/64 (33)
Race		
Black	8/12 (67)	37/53 (70)
Coloured	3/12 (25)	15/53 (28)
Asian/Indian	0/12 (0)	0/53 (0)
White	0/12 (0)	0/53 (0)
Other	1/12 (8)	1/53 (2)
Variant$$		
Non-Alpha/Beta/Delta	0/17 (0)	0/64 (0)
20I(Alpha)	0/17 (0)	0/64 (0)
20H(Beta)	0/17 (0)	0/64 (0)
21A(Delta)	0/17 (0)	0/64 (0)
20D(C.1.2)	0/17 (0)	0/64 (0)
21K(Omicron)	0/17 (0)	0/64 (0)
Pending results	17/17 (100)	64/64 (100)

Characteristic	Influenza–like illness (ILI), public-sector, n=17 (%)	Pneumonia, n=64 (%)
Presentation		
Fever	6/12 (50)	26/53 (49)
Cough	12/12 (100)	49/53 (92)
Shortness of breath	7/12 (58)	30/53 (57)
Chest pain	3/12 (25)	23/53 (43)
Diarrhoea	0/12 (0)	7/53 (13)
Underlying conditions		
Hypertension$	3/12 (25)	12/53 (23)
Cardiac	0/12 (0)	1/53 (2)
Lung disease	12/12 (100)	52/53 (98)
Diabetes	0/12 (0)	8/53 (15)
Cancer	0/12 (0)	0/53 (0)
Tuberculosis	0/12 (0)	1/53 (2)
HIV-infection	3/12 (25)	15/53 (28)
Other ***	0/12 (0)	0/53 (0)
SARS-CoV-2 Vaccine		
Pfizer-BioNTech (1st dose)	2/10 (20)	7/48 (15)
Pfizer-BioNTech (2nd dose)	2/10 (20)	6/48 (13)
Johnson & Johnson	2/10 (20)	2/48 (4)
Management		
Oxygen therapy	0/12 (0)	17/53 (32)
ICU admission	N/A	0/53 (0)
Ventilation	N/A	0/53 (0)
Outcome* **		
Died	0/12 (0)	3/34 (9)

*ILI surveillance not conducted in Gauteng province

**Mpumalanga (ILI site started enrolling on the 10th November 2020 and an additional SARI site started enrolling on the 10th February 2021)

***Chronic lung, liver and kidney disease, organ transplant, pregnancy, malnutrition, obesity, tracheostomy, prematurity, seizure, stroke, anaemia, asplenia, burns, Systemic lupus erythematosus, seizures

****Outcome includes patients who are still hospitalised, have been discharged or referred, and those who died

[$] Data on hypertension was not collected on all cases.

[$$] These individuals with unassigned sequence are not included, ILI (n=181) and SRI (n=594)

Note: Children may be over-represented amongst hospitalised patients due to the inclusion of a large paediatric hospital in Cape Town. Of the 3 patients who died, one was in the 20-39 year age group and two were ≥60 years; 2/3 (67%) were female.

METHODS

SARS-CoV-2 Testing

March 2020 – March 2021: SARS-CoV-2 was detected using the Roche E gene real-time PCR assay (Corman et al. Euro Surveillance 2020) with cycle threshold (Ct) <40 interpreted as positive for SARS-CoV-2. From April 2021 to date the laboratory canged to the Allplex™ SARS-CoV-2/FluA/FluB/RSV kit (Seegene Inc., Seoul, South Korea), with positivity assigned if the PCR cycle threshold (Ct) was <40 for ≥1 gene targets (N, S or RdRp).

A confirmed SARS-CoV-2 case is a person of any age enrolled in surveillance with laboratory confirmation of SARS-CoV-2 infection by PCR. Only positive SARS-CoV-2 specimens on PCR are further tested to determine variant/lineage type by variant PCR or genomic sequencing.

Variant PCR

Allplex™ SARS-CoV-2 Variants I PCR detects Alpha and Beta/Gamma variants. The assay was conducted on all SARS-CoV-2-positive samples from 1 March 2020 – 30 June 2021.

Allplex™ SARS-CoV-2 Variants II PCR detects Delta variant and distinguishes Beta from Gamma. The assay was conducted on SARS-CoV-2-positive samples from 1 Jan to 30 June 2021.

Extraction: Total nucleic acids were extracted from 200µl NP/OP samples in universal or viral transport medium using a MagNA Pure 96 automated extractor and DNA/Viral NA Small Volume v2.0 extraction kit (Roche Diagnostics, Mannheim, Germany).

SARS-CoV-2 genomic surveillance

SARS-CoV-2 Whole-Genome Sequencing and Genome Assembly

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 cleanup 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).