TESSy - The European Surveillance System

Coronavirus disease 2019 (COVID-19) data

Reporting Protocol

Version 5.11, 18 July 2022

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Summary of changes

18 July 2022

Updated coded value list for the variable VirusVariant (for both NCOV and NCOVVARIANT recordtypes) for reporting of BA.2.75 (Omicron BA.2 sub-lineage with mutations D339H, G446S, N460K, and R493Q in the RBD, and mutations K147E, W152R, F157L, I210V, and G257S in the N-terminal domain of the Spike protein)

10 June 2022

Updated coded value list for the variable VirusVariant (for both NCOV and NCOVVARIANT recordtypes) for reporting of BA.2+L452X (Omicron BA.2 and any of its sub-lineages with mutations at position 452 of the Spike protein)

13 May 2022 Removed variant "B.1.1.529" (Omicron) from the coded value list for variable VirusVariant (Omicron cases should be assigned to a specific sublineage)

07 April 2022 Added Omicron sublineages BA.4 and BA.5 to coded value list for variable VirusVariant in both NCOV and NCOVVARIANT recordtypes

18 February

- New variables in NCOV: VaccDose4, and BrandDose4
- Updated coded value list for variable NCOV VaccStatus to report fourth dose (4DOSE)
- Updated list of vaccine products to the coded value list for variables BrandDose1, BrandDose2, and BrandDose3: "Chumakov - Covi-Vac", "Novavax - Covovax", "Novavax - Nuvaxovid" and "Gamaleya - Sputnik-Light

27 January

Updated coded value list for the variable VirusVariant (for both NCOV and NCOVVARIANT recordtypes) for reporting of sublineages of B.1.1.529 (BA.1, BA.2, BA.3)

01 December

- Updated reporting instructions for sequenced cases.
- Updated list of mutations for B.1.1.529.
- New variables in NCOVVARIANT: NumberTargetedImported, NumberTargetedLocal

26 November 2021

Updated coded value list for reporting of variants of concern and variants of interest adding B.1.1.529. This variant can now be reported as part of the coded value list for the variable VirusVariant (for both NCOV and NCOVVARIANT recordtypes) and VariantEpisode1 (NCOV recordtype).

How to use this document

This Reporting Protocol provides information for data managers in reporting countries in two main sections:

- *Reporting to TESSy* – contains guidelines on how to prepare data for submission to TESSy, deadlines for reporting, subject-specific information (e.g. new changes to metadata), and links to further information.
- *Annex* – contains:
    - A history of metadata changes for the subject(s) covered by this Reporting Protocol.
    - The metadata set for the subject(s) covered by this Reporting Protocol.

Finding further information

Paragraphs denoted by the information icon tell where you can find further information.

Updated links to all the schedules, documentation and training materials mentioned in this Reporting Protocol are included in the *TESSy Technical Guidelines & Tools* (see the menu 'Technical Guidelines and Tools' when logged in TESSy), including:

- Metadata sets and history.
- Tutorials for data transformation using respectively Excel and Access.
- TESSy user documentation.
- *CSV* and *XML* transport protocols.

Copyright

Introduction

This Reporting Protocol describes surveillance of COVID-19 in the EU/EEA and wider WHO European region. It includes four record-types:

1. **Case-based reporting** of all probable and confirmed COVID-19 cases (recordtype: **NCOV**). When possible, please report case-based data.
2. **Aggregated reporting** of all probable and confirmed cases for countries not reporting case-based data (recordtype: **NCOVAGGR**)
3. **Aggregated reporting** of SARS-CoV-2 tests performed by method, age-group and subnational region (recordtype: **NCOVTEST**)
4. **Aggregated reporting** of SARS-CoV-2 variants of interest and of concern (recordtype: **NCOVVARIANT**)

Reporting of transmission status in the country (at NUTS2 level) based on WHO classification (recordtype: NCOVCLASSIFICATION) is no longer required and the record type was deactivated 26 July 2021.

For cases tested Monday to Sunday the previous week, data **should be reported every Tuesday by 23:59 and updated retrospectively**.

Please note that:

1. All data collected are shared with the World Health Organisation – Regional Office for Europe (WHO/Europe) on a daily basis to fulfil Member States reporting requirements to WHO. Duplicate reporting is therefore not required.
2. If data have not been uploaded in TESSy and approved by Tuesday 23:59 it will not be possible to include the data in weekly reports and the *maps* in support of the Council Recommendation on a coordinated approach to the restriction of free movement in response to the COVID-19 pandemic in the EU/EEA. If you are unable to meet this deadline, please contact the ECDC COVID surveillance team (*influenza@ecdc.europa.eu* and copy *tessy@ecdc.europa.eu*).

Definitions

Case definition: Probable and confirmed cases should be reported according to the current *EU case definition*. Data on possible cases are not collected.

Definition of a hospitalised case: A patient who has tested positive for COVID-19 (within 14 days prior to admission or during the current admission) presenting with severe symptoms/complications from COVID-19 that require admission to a hospital or ICU/HDU facility. Patients admitted to hospital for isolation purposes and not because of clinical need should not be counted as hospitalised cases where it is possible to make a distinction.

Definition of a case admitted to an intensive care unit (ICU) or a high dependency unit (HDU)[1]: A patient who has tested positive for COVID-19 (within 14 days prior to admission or during the current admission) presenting with severe symptoms/complications from COVID-19 that require admission to an ICU/HDU facility. For the purposes of reporting ICU occupancy data, COVID-19 cases in ICU/HDU should continue to be counted even after they test negative provided the current ICU/HDU stay is a consequence of the COVID-19 infection.

Number of tests: Total number of individuals tested during each epidemiological week. For individuals with multiple tests only the first test should be retained for that week.

[1] *High dependency unit: a unit with capabilities for more intensive observation, treatment and nursing care than can be provided on a regular ward*

Definition of *suspected* COVID-19 reinfection case: Positive PCR or rapid antigen test (RAT) sample ≥60 days following: previous positive PCR, previous positive RAT, previous positive serology (anti-spike IgG Ab).

Aim

To support the timely and complete reporting of key information on COVID-19 epidemiology in the EU/EEA.

Objectives

1. Monitor the intensity and geographical spread of the virus in the population;
2. Identify risk groups for severe disease;
3. Measure the impact on the population and the healthcare system;
4. Measure the impact of any mitigation measures;
5. Measure the prevalence of SARS-CoV-2 variants of concern;
6. Monitor the incidence of suspected COVID-19 reinfection cases.

Objective 1 will be addressed by all four recordtypes; objective 2 will be addressed by the case-based recordtype (NCOV); objectives 3, 4,5 and 6 will be addressed by all recordtypes together with the use of additional sources of data.

Reporting to TESSy

When, what and how to report

Deadline for reporting:

Tuesday 23:59 for all recordtypes. There is no requirement for daily reporting.

All countries should report:

- **Recordtype "NCOVTEST"**. This includes the number of tests by method, age and region.

Countries reporting case-based surveillance data should:

- **Report recordtype "NCOV",** preferably using recordtype version 5. Please report on as many variables as possible. In order to reconstruct the aggregate dataset requested by WHO the following variables are mandatory to report: Age, PlaceOfInfection, Precondition, HealthcareWorker, Hospitalisation, DateOfHospitalisation, DateOfDischarge, IntensiveCare, DateOfICUHDU, RespSupport, Outcome and DateOfDeath (UNK is allowed for most variables).
- To allow for severity and vaccine breakthrough infection analysis, please report the following variables:
    - *One of:* Hospitalisation, DateOfHospitalisation, DateOfDischarge
    - *One of:* IntensiveCare, DateOfICUHDU, RespiratorySupport
    - *One of:* Outcome, DateOfDeath
    - VaccStatus and/or (VaccDose1, 2, 3, 4 DateOfOnset), BrandDose1, 2, 3, 4
- **Report in a timely manner** even if outcome information is not known; outcome can be updated when information becomes available.
- **If reporting of case-based data is incomplete or not timely, please also report "NCOVAGGR" and "NCOVVARIANT" (see below).** If reporting of case-based data is complete, then "NCOVAGGR" and "NCOVVARIANT" do not need to be reported.

Countries collecting aggregated surveillance data should:

- **Report recordtype "NCOVAGGR"**. All variables should be reported. Data should be aggregated by week of sampling for cases and week of death for deaths. If this is not possible (e.g. data are by week of notification) please inform ECDC.
- **Report recordtype "NCOVVARIANT"**. All variables should be reported if possible. Data should be aggregated by the week samples were taken. If this is not possible (e.g. data are by week of notification) please inform ECDC.

If detailed case-based data are available for the subset of cases which are genetically characterised (e.g. by sequencing or PCR-based assays), please report these separately using the recordtype "NCOV" even if you report a less detailed dataset using "NCOV" or otherwise report "NCOVAGGR". Please use a specific datasource with a suffix "-WGS" or contact ECDC in this case. TESSy helpdesk can help you create such a datasource.

Reporting of NCOVTEST

NCOVTEST has been implemented for the reporting of aggregated number of tests by method, age-group and subnational region. These data are used for the calculation of testing rates and positivity rates at subnational level (NUTS2/GAUL1 for most countries; however because data on number of cases at subnational level are currently collected from public sources, testing data are required by *health regions for Portugal* and *counties for Norway*) and used for the *maps* in support of the Council Recommendation on a coordinated approach to the restriction of free movement in response to the COVID-19 pandemic in the EU/EEA.

If data on number of tests disaggregated by method, age-group and region are not available, then testing data can be reported at subnational level without any further disaggregation (by reporting the number of tests in the AgeUNK variable and with LabMethod = UNK). A data source has been created for each country for the reporting of NCOVTEST (e.g.: FR-NCOVTEST). If further clarification on reporting is needed, please email *influenza@ecdc.europa.eu* and copy *tessy@ecdc.europa.eu*.

Reporting SARS-CoV-2 variants

The variable **VirusVariant** in NCOV and the recordtype **NCOVVARIANT** are there for assessing the frequency of SARS-CoV-2 variants in a sample (representative and/or targeted) for each country, as well as collecting case-based information linked to clinical, epidemiological and other reported data. As of 28 May 2021, the coded value list for the variable VirusVariant in both NCOV and NCOVVARIANT will be aligned with the list of variants of interest and of concern published by ECDC: *https://www.ecdc.europa.eu/en/covid-19/variants-concern.* Each variant case should be reported only once and in the most specific category available both in NCOV and NCOVVARIANT. For example, a variant of sublineage AY.4.2 should be reported only as AY.4.2 and not as the parental lineage B.1.617.2.

When reporting to NCOV:

Report samples that have been selected for either sequencing directly or by using a variant screening method.
Report **VirusVariant** when the identified virus is carrying one or more of the representative amino acid substitutions described in the relevant coded value. If several apply, choose the most specific variant (highest number of matching amino acid substitutions) (Table).
Report **Wild_Type** for **all** cases that have been screened or sequenced, irrespective of whether the sample has been screened for all of the mutations in order to exclude all of the variants in the list. For example, if you have screened for N501Y and it was negative, but you didn't screen for E484K, you should still report the virus as Wild_Type. **Reporting all cases will enable ECDC/WHO Euro to generate a meaningful denominator of all sequenced/genotyped viruses.**
VirusVariantOther is intended to be used for reporting variants that are of concern or under investigation in your country but are not defined in the coded value list. Please include enough information for ECDC/WHO Euro to be able to clearly identify the variant. Novel variants of potential public health relevance should also be reported via EWRS.
Report where possible the variable **SequencingCategory** to allow identification of cases sequenced as part of representative or targeted surveillance.

When reporting to NCOVVARIANT:

For each variant (specified in the variable **VirusVariant**) please report the numbers of variants identified via sequencing or screening in the variables **NumberRepresentative**, **NumberTargeted** depending on whether the samples are sequenced as part of representative surveillance or targeted surveillance. For further details please refer to: *https://www.ecdc.europa.eu/en/publications-data/guidance-representative-and-targeted-genomic-sars-cov-2-monitoring*. If the reason for sequencing is not known, please report the numbers in the variable **NumberUNK.**
If you are able to distinguish variants detected through targeted surveillance as imported or locally acquired, please report these numbers in the variables NumberTargetedImported and NumberTargetedLocal, respectively. This is particularly important for B.1.1.529 (Omicron) sublineages. Also note that each virus should only be reported once, using the most specific variant available (e.g. a BA.2 virus should be reported once in the BA.2 category and not be reported as B.1.1.529).
Report **Wild_Type** for **all** cases that have been screened or sequenced, irrespective of whether the sample has been screened for all of the mutations in order to exclude all of the variants in the list. For example, if you have screened for N501Y and it was negative, but you didn't screen for E484K, you should still report the virus as Wild_Type. **Reporting all cases will enable ECDC/WHO Euro to generate a meaningful denominator of all sequenced/genotyped viruses.**
VirusVariantOther is intended to be used for reporting variants that are of concern or under investigation in your country but are not defined in the coded value list. Please include enough information for ECDC/WHO Euro to be able to clearly identify the variant. Novel variants of potential public health relevance should also be reported via EWRS.
The number of any of the variants should be based on the date of sampling.
Screening and partial sequencing results:
Report variants where you have confidence in the results; a variant screening (e.g. using a SNP or other PCR-based assay) or partial sequencing (using NGS amplicon or Sanger sequencing) result that only covers some signature mutations is still enough to report a variant if the result can clearly distinguish the virus from the other variants in the coded-value list. Signature mutations for the variant in the sequenced region should be present. Ideally S-gene amino acids 1-800 (2 400 bp) or the entire S-gene should be sequenced to also monitor the S1/S2 cleavage site and other regions of interest. The B.1.351/501Y.V2 variant has variable reported mutation profiles, so it is recommended to use the minimum set: D80A, D215G, E484K, N501Y, A701V.

Table. Example of variants of concern and how to report to TESSy based on the laboratory methods used for their identification

Variant	NSP6	S1: NTD	S1:RBD	S1/S2	S2	Methods	Reporting
B.1.617.2	**-**	T19R, G142D, E156G, Δ157-158	**L452R, T478K**	**D614G, P681R**	D950N	1) Specific RT-PCRs to detect characteristic mutations 2) Sequencing of at least amino acids 1-700	1) Report based on your interpretation* the closest that describes your finding 2) B.1.617.2
B.1.351	**Δ106-108**	D80A, D215G	K417N, **E484K, N501Y**	D614G	**A701V**	1) Specific RT-PCRs to detect characteristic mutations 2) Sequencing at least 69-70 (no deletion), D80A, D215G, E484K, N501Y, A701V	1)If only 1 PCR-based assay for E484K or N501Y or Orf1a del (Δ3675-3677) used/is positive: report the respective variable/coded value or Wild_Type (if negative) If several SNP assays used/are positive: report based on your interpretation* the closest that describes your finding (either one of the single mutations if you cannot distinguish the lineage or B.1.351) 2) B.1.351
P.1	**Δ106-108**	L18F, T20N, P26S, D138Y, R190S	K417T, **E484K, N501Y**	D614G, H655Y	T1027I, V1176F	1) Specific RT-PCRs to detect characteristic mutations 2) Sequencing at least 69-70 (no deletion), D80A, D215G, E484K, N501Y, A701V	1)If only 1 PCR-based assay for E484K or N501Y or Orf1a del (Δ3675-3677) used/is positive/are positive: report the respective variable/coded value or Wild_Type (if negative) If several SNP assays used/are positive: report based on your interpretation* the closest that describes your finding (either one of the single mutations if you cannot distinguish the lineage or P.1) 2) P.1

* Interpretation should be based on the genetic information and if needed and possible taking into account the prevalence of the VOC in the setting (based on confirmatory sequencing of at least a subset of viruses). If several VOCs are circulating and your PCR-based methods cannot distinguish between them, then only the common characteristic mutation should be reported or sequencing should be used to further define the exact variant.

Preparing data

For all recordtypes, data may be entered directly in TESSy for individual records ('Manually create a record'). For any batch reporting by file upload (CSV or XML format) please note that once the data has been exported from your national database it needs to be in a format that TESSy can accept (see 'checking metadata').

Checking metadata

The TESSy metadata define the fields and valid data formats for input to TESSy for a given subject.

To ensure data can be saved correctly in TESSy, please check the data are correctly formatted according to the most recent metadata set.

Changes to the metadata for the subject of this Reporting Protocol are described in:

- *Changes to current metadata* – changes since the last Reporting Protocol.
- *Annex Metadata change history* – all preceding changes.

It is especially important to focus on:

- **Field formats**

  Many fields require that data are formatted in a specific way. For example, dates must be in the **YYYY-MM-DD** format; dates in the DD/MM/YYYY format will be rejected.

- **Coded values**

  Some fields only permit the use of specific values (coded values). For example, **M**, **F**, **UNK**, or **Other** are the coded values for *Gender* and any other value in a *Gender* field will be rejected.

The metadata file contains all the definitions and rules you need to comply with to format your data correctly for every subject (usually a disease). The file can be downloaded as an Excel file from the TESSy documents website.

By filtering the fields in the file by subject, you can see the fields required for your subject and the rules applying to these fields.

The *Tessy User Guide* provides an overview of how you work with the metadata file, and the TESSy user documentation provides in-depth details on metadata.

Submitting your data

Data are submitted through the TESSy web interface (go to **Upload**). Previously reported data can be found through the review tab (see below).

The *Tessy User Guide* provides an overview of how you submit files to TESSy and in-depth descriptions of all the upload methods.

Finalising your submission

The compliance of your data with the validation rules in the metadata is checked automatically during the data upload process.

The result of your upload – i.e. rejected or validated – is displayed immediately after the check in the **Validation details** webpage has completed. Please review the result carefully:

- If your file has been rejected, there will be a message explaining each instance of non-compliance with the metadata that you need to correct.

- If your file has been validated, there might be warnings and remarks relating to possible data quality issues or to potential overwriting of existing records that you should consider.

When you file has been validated and you are satisfied that all corrections have been made, please ensure prompt approval – unapproved uploads can block the approval of other uploads.

- The TESSy user documentation provides information on reviewing validation results and adjusting reporting periods to avoid overwriting existing records.
- General training and guidance on reporting is available on the *TESSy website*. A training video on reporting COVID-19 data is available in the *ECDC virtual academy*.

TESSy HelpDesk

Email:	*TESSy@ecdc.europa.eu*
Telephone number:	**+46-(0)8-5860 1601**
Availability:	9:00 – 16:00 Stockholm time, Monday to Friday (except ECDC Holidays)

Changes to COVID-19 disease metadata

RecordType: NCOV: RecordType Version 5: Update 2021-09-24

- Added variable SequencingCategory to collect information on reason for sequencing
- Updated coded value list for variable VirusVariant to capture all variants of interest and of concern listed on the ECDC website: *https://www.ecdc.europa.eu/en/covid-19/variants-concern*
- Added variable VaccDose3 and 4 and Brandose3 and 4 and updated coded value list for VaccStatus to capture cases receiving a third and fourth vaccination dose
- Updated coded value list for BrandDose1, BrandDose2 and BrandDose3.

See *NCOV metadata recordtype version for variable descriptions.*

RecordType: NCOVAGGR: RecordType Version 4: Update 2021-05-28

- Removed sequencing related variables

See *NCOVAGGR metadata* for variable descriptions.

New RecordType: NCOVVARIANT: RecordType Version 1

- New RecordType to collect number of detections by variant of interest or of concern as part of representative or targeted surveillance

See *NCOVAGGR metadata* for variable descriptions.

RecordType: NCOVCLASSIFICATION: Inactivated 2021-07-26

- The RecordType was inactivated as WHO Geneva will stop collecting transmission classifications from countries and displaying these data on the global COVID dashboard *https://covid19.who.int* as of week starting 26 July.

Information on changes to the metadata for other subjects is available on the TESSy documentation website.

Annex - Coronavirus disease 2019 (COVID-19) metadata

Revisions of COVID-19 disease metadata set

The COVID-19 metadata have been developed based on WHO case reporting form[2]. The most recent metadata set is available from the TESSy website under technical guidelines and tools tab (as shown below).

Current record type versions

Table 1 shows the record type versions to be used when reporting COVID-19 (Record type: NCOV) data to TESSy.

Table 1: COVID-19 record type versions

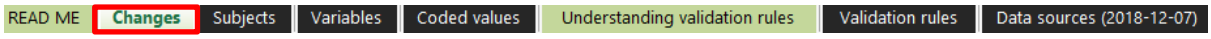
Record	Type of data	Record type version
NCOV	Case-based	5
NCOV	Case-based	4
NCOV	Case-based	3
NCOV	Case-based	2 (inactivated from 2020-12-02)
NCOVTEST	Case-based[3]	2
NCOVTEST	Case-based[3]	1 (inactivated from 2020-10-31)
NCOVAGGR	Aggregated	4
NCOVAGGR	Aggregated	3 (inactivated from 2021-06-11)
NCOVAGGR	Aggregated	2 (inactivated from 2020-10-31)
NCOVCLASSIFICATION	Case-based	1 (inactivated from 2021-07-26)
NCOVVARIANT	Case-based[3]	1

[2] World Health Organization, 2020: Interim case reporting form for 2019 Novel Coronavirus (2019-nCoV) of confirmed and probable cases, available at: https://www.who.int/docs/default-source/coronaviruse/20200121-2019-ncov-reporting-form.pdf?sfvrsn=96eff954_4

[3] Note NCOVTEST and NCOVVARIANT are “case-based” recordtype as they allow multiple rows for the same week. However the number of tests/variants are reported in an aggregated way.

NCOV metadata change history

When you open a metadata set, the Excel file has a tab 'Changes', recording historical changes.



NCOV metadata recordtype version 5

Common TESSy variables

Record Identifier (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be:

- unique within the national COVID-19 disease surveillance system
- anonymous.

Record type (mandatory)

Field: RecordType

Coding: NCOV

The record type defines the structure and the format of the data reported. The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: 5

The version of the record type defines the current structure of the data reported. The current version of the NCOV record type is 5.

This variable is not mandatory as TESSy concludes the record type version from the metadataset indicated by default. However, the variable RecordTypeVersion can override this default.

Subject (mandatory)

Field: Subject

Coding: NCOV

The subject describes the disease to be reported.

Data source (mandatory)

Field: DataSource

Coding: Pre-assigned as CountryCode-NCOV to each country; can be modified by National Coordinator

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. The descriptions of the surveillance systems submitted to TESSy should be kept up to date and will be used to assist with data interpretation.

Reporting country (mandatory)

Field: ReportingCountry

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-mm-dd (preferred)
yyyy-Www
yyyy-mm
yyyy-Qq
yyyy

This is the date used by the national surveillance institute/organisation in case reports and official statistics. The date used for statistics can vary from country to country but is preferably date of notification for NCOV as defined in WHO case reporting form.

The date the case was notified to the national health authorities (notification date) is the preferred date used for statistics.

Status (mandatory)

Field: Status

Coding: NEW/UPDATE
DELETE

The field 'Status' is used for updating data; the default is 'New/Update'. By choosing 'Delete' the selected record (or batch of data) will remain in TESSy but be marked as inactive; this data can be used to reconstruct data for a given date in the past.

Epidemiological variables

In alphabetic order by field.

Age (mandatory)

Field: Age

Coding: Numerical (0-120)
UNK = Unknown

Age of patient in years as reported in the national system at the time of disease onset.

Age in months

Field: AgeMonth

Coding: Numerical (0-23)
NA = Not applicable
UNK = Unknown

Age of patient in months as reported in the national system for cases <2 years of age at the time of disease onset.

Brand of COVID-19 vaccination dose 1

Field: BrandDose1

Coding: VaccineCOVID:
AZ = Vaxzevria – AstraZeneca
BECNBG = Inactivated – Beijing CNBG
BHACOV = Covaxin – Bharat
CHU = Chumakov - Covi-Vac
COM = Comirnaty – Pfizer/BioNTech
CVAC = Curevac-CVnCOV

HAYATVAC = Hayat VAC
JANSS = Ad26.COV 2.5 – Janssen
MOD = mRNA-1273 – Moderna
NVX = Novavax – Covovax
NVXD = Novavax – Nuvaxovid
QAZVAQ = QazCovid-In
SGSK = Sanofi GSK - Subunit
SIICOV = Covishield – SII
SIN = CoronaVac – Sinovac
SPU = Sputnik V – Gamaleya
SPUL = Gamaleya - Sputnik-Light
SRCVB = EpiVacCorona – SRCVB
WUCNBG = Inactivated – Wuhan CNBG
ZFUZ = Sino-Uzbek - ZF-UZ-VAC
UNK = UNKNOWN

Brand of COVID-19 vaccination dose 1.

Brand of COVID-19 vaccination dose 2

Field: BrandDose2

Coding: VaccineCOVID:
AZ = Vaxzevria – AstraZeneca
BECNBG = Inactivated – Beijing CNBG
BHACOV = Covaxin – Bharat
CHU = Chumakov - Covi-Vac
COM = Comirnaty – Pfizer/BioNTech
CVAC = Curevac-CVnCOV
JANSS = Ad26.COV 2.5 – Janssen
HAYATVAC = Hayat VAC
MOD = mRNA-1273 – Moderna QAZVAQ = QazCovid-In
NVX = Novavax – Covovax
NVXD = Novavax – Nuvaxovid
SGSK = Sanofi GSK - Subunit
SIICOV = Covishield – SII
SIN = CoronaVac – Sinovac
SPU = Sputnik V - Gamaleya
SPUL = Gamaleya - Sputnik-Light
SRCVB = EpiVacCorona – SRCVB
WUCNBG = Inactivated – Wuhan CNBG
ZFUZ = Sino-Uzbek - ZF-UZ-VAC
UNK = UNKNOWN

Brand of COVID-19 vaccination dose 2.

Brand of COVID-19 vaccination dose 3

Field: BrandDose3

Coding: VaccineCOVID:
AZ = Vaxzevria – AstraZeneca
BECNBG = Inactivated – Beijing CNBG
BHACOV = Covaxin – Bharat

CHU = Chumakov - Covi-Vac
COM = Comirnaty – Pfizer/BioNTech
CVAC = Curevac-CVnCOV
JANSS = Ad26.COV 2.5 – Janssen
HAYATVAC = Hayat VAC
MOD = mRNA-1273 – Moderna QAZVAQ = QazCovid-In
NVX = Novavax – Covovax
NVXD = Novavax – Nuvaxovid
SGSK = Sanofi GSK - Subunit
SIICOV = Covishield – SII
SIN = CoronaVac – Sinovac
SPU = Sputnik V – Gamaleya
SPUL = Gamaleya - Sputnik-Light
SRCVB = EpiVacCorona – SRCVB
WUCNBG = Inactivated – Wuhan CNBG
ZFUZ = Sino-Uzbek - ZF-UZ-VAC
UNK = UNKNOWN

Brand of COVID-19 vaccination dose 3.

Brand of COVID-19 vaccination dose 4

Field: BrandDose1

Coding: VaccineCOVID:
AZ = Vaxzevria – AstraZeneca
BECNBG = Inactivated – Beijing CNBG
BHACOV = Covaxin – Bharat
CHU = Chumakov - Covi-Vac
COM = Comirnaty – Pfizer/BioNTech
CVAC = Curevac-CVnCOV
HAYATVAC = Hayat VAC
JANSS = Ad26.COV 2.5 – Janssen
MOD = mRNA-1273 – Moderna
NVX = Novavax – Covovax
NVXD = Novavax – Nuvaxovid
QAZVAQ = QazCovid-In
SGSK = Sanofi GSK - Subunit
SIICOV = Covishield – SII
SIN = CoronaVac – Sinovac
SPU = Sputnik V – Gamaleya
SPUL = Gamaleya - Sputnik-Light
SRCVB = EpiVacCorona – SRCVB
WUCNBG = Inactivated – Wuhan CNBG
ZFUZ = Sino-Uzbek - ZF-UZ-VAC
UNK = UNKNOWN

Brand of COVID-19 vaccination dose 4.

Classification (mandatory)

Field: Classification

Coding: CONF = Confirmed
PROB = Probable

Case classification according to the ECDC/WHO case definition.

Clinical Symptoms

Field: ClinicalSymptoms
Coding: ASY = Asymptomatic
CONJ = Conjunctival injection
COUGH = Dry or productive cough
DIARR = Diarrhoea
FEVER = History of fever/chills
HEAD = Headache
IRR = Irritability/confusion
O = Other, please specify
PAIN = Pain
PAINABDO = Pain - abdominal
PAINCHEST = Pain - chest
PAINJOINT = Pain - joint
PAINMUSC = Pain - muscular
PAINOTH = Pain - other
RUNOS = Runny nose
SBREATH = Shortness of breath
SORETHR = Sore throat
UNK = Unknown
VOMIT = Nausea/vomiting
WEAK = General weakness

Onset of clinical symptoms.

Clinical symptoms – other

Field: ClinicalSymptomsOther
Coding: Text
UNK = Unknown

Other reported clinical symptoms not found in the list of possible values.

Complications

Field: Complications
Coding: AKI = Acute renal injury
ARDS = Acute respiratory distress syndrome
BRONCH = Bronchiolitis
ENCEPH = Encephalitis
HEARTFAIL = Heartfailure
MULTIFAIL = Multi-organ failure
MYOCARD = Myocarditis
NONE = None
O = Other (please specify separately)
OTHBAC = Other secondary bacterial infection
PIMS=Paediatric Inflammatory Multisystem Syndrome - Temporally Associated with SARSCoV2
PNEU = Bacterial pneumonia (secondary)
SEPSIS = Sepsis
STILLBIRTH = Still birth as pregnancy outcome in a case
UNK = Unknown

Complications at any time.

Date of death (mandatory for cases where outcome is DIEDNCOV, DIEDOTHER, DIEDUNK)
Field: DateOfDeath
Coding: *yyyy-mm-dd*
UNK= Unknown
Exact date for date of death. If not applicable, please use 'UNK'.

Date of hospital discharge (mandatory for hospitalised cases)
Field: DateOfDischarge
Coding: *yyyy-mm-dd*
UNK= Unknown
Date of discharge from hospital (exact date only). If not applicable, please use 'UNK'.

Date of Hospitalisation (mandatory if Hospitalisation = Y)
Field: DateOfHospitalisation
Coding: *yyyy-mm-dd*
UNK= Unknown
If not applicable, please use 'UNK'.

Date of admission to ICU or HDU (mandatory if IntensiveCare = Y)
Field: DateOfICUHDU
Coding: *yyyy-mm-dd*
Date of admission to intensive care unit or high dependency unit

Date of Onset of Disease
Field: DateOfOnset
Coding: *yyyy-mm-dd*
UNK= UnknownDate of onset of disease. Not applicable in asymptomatic cases. If not applicable, please use 'Unk'.

Gender
Field: Gender
Coding: F = Female
M = Male
O = Other (for example, transsexual)
UNK = Unknown
Gender of the reported case.

Laboratory genotyping method
Field: GenotypingMethod
Coding: LabGenoNCOV
WGS= Whole Genome Sequencing
SangerSequencing= Sanger Sequencing
SNPassay= SNP PCR-based assay
S_gene_target_failure= failure to detect via a PCR-based assay
O = Other, please specify
Genotyping method used for identifying the virus variant.

Laboratory genotyping method – other

Field: GenotypingmethodOther

Coding: Text

UNK=Unknown

Other reported genotyping method used for idenitifying the virus variant not found in the list of possible values in GenotypingMethod.

Healthcare worker setting

Field: HCWSetting

Coding:
PRIMCLIN = Primary care clinic, GP practice
COMCARE = Community care, home care
TESTSITE = Dedicated COVID-19 diagnostic respiratory sample collection site, in- or outside hospital
HOSP-NoS = Hospital, not specified
HCOV-ICU = Hospital, COVID-19 ICU ward
HCOV-O = Hospital, COVID-19 other (non-ICU) ward
HOTH-ICU = Hospital, non-COVID-19 ICU ward
HOTH-O = Hospital, non-COVID-19 other (non-ICU) ward
LTCF-NoS = LTCF, not specified
LTCF-GNH = LTCF, general nursing home
LTCF-RH = LTCF, residential home
LTCF-MIX = LTCF, mixed facility
LTCF-SPEC = LTCF, specialised facility
O = Other healthcare setting
NA = Not applicable
UNK = Unknown

Main working environment of the HCW in the 14 days before onset of symptoms. If the HCW was working in more than one setting, select the setting with the majority of working time, e.g. a GP working 55% of the time in a clinic and 45% of the time performing house visits, select PRIMCLIN. LTCF is defined according to HAI-Net HALT definitions. Specialised facilities include LTCFs for mentally and physically disabled, psychiatric LTCFs, rehabilitation centres, palliative care facility and sanatoria.

Healthcare worker type

Field: HCWType

Coding: *See metadataset*

Type of healthcare worker. Occupations codes are categorised in four broad categories (medical doctors, nursing professionals and midwives, students and other) with optional detailed subcategories. Codes are aligned with Eurostat (ISCO) for denominator data to calculate occupation-specific risks. For definitions, see Eurostat. *Definitions and data collection specifications on health care statistics (non-expenditure data). Version 10 July 2016.*

Healthcare worker (mandatory)

Field: HealthCareWorker

Coding:
N = No
Y = Yes
UNK = Unknown

Information on whether the case is a healthcare worker or not.

Healthcare worker details

Field: HealthcareWorkerDetails

Coding: Free text

Details about HCW type or setting (free text).

Hospitalisation (mandatory)
Field: Hospitalisation

Coding: N = No
UNK = Unknown
Y = Yes

Admission to hospital.

Imported
Field: Imported
Coding: N = No
Y = Yes
UNK = Unknown

Patient travelled outside the reporting country in the 14 days prior to symptom onset.

Infection source

Field: InfectionSource
Coding: CA = Community-associated
HA-D = Definite healthcare-associated
HA-P = Probable healthcare-associated
IA = Indeterminate association
UA = Unknown association, insufficient data
UNK = Unknown

Source or origin of COVID-19 infection. See *definition* for cut-offs of number of days of stay in a healthcare facility associated with a category. For healthcare workers and re-admissions, case-by-case evaluation of exposure in healthcare facility and/or community.

InfluenzaCoinfectionDetail
Field: (Sub)typing details for influenza coinfection
Coding: AH1pdm09 = A(H1)pdm09
AH1N1pdm09 = A(H1N1)pdm09
AH3 = A(H3)
AH3N2 = A(H3N2)
Aunk = A not-subtyped
B = B no lineage
BVic = B/Victoria
BYam = B/Yamagata

(Sub)typing details for influenza coinfection.

InfluenzaVaccination
Field: Influenza vaccination
Coding: N = No
Y = Yes
UNK = Unknown

Current seasonal influenza vaccination.

Intensive care (mandatory)
Field: IntensiveCare
Coding: N = No
UNK = Unknown
Y = Yes

Case required care in an intensive care unit or high dependency unit (unit with capabilities for more intensive observation, treatment and nursing care than can be provided on a regular ward).

Laboratory method

Field: LabMethod

Coding: LabMethodNCOV:

ANTIGEN = Antigen detection

GENOSEQ = Genotyping/Sequencing

ISOV = Isolation of virus

NEU = Neutralisation

NUC = NAAT by RT-PCR, other or not specified

NUC1 = NAAT by a single gene RT-PCR assay used for 1st detection of 2019-nCoV

NUC2 = NAAT by a single gene RT-PCR assay used for 2nd confirmatory detection of 2019-nCoV

NUCPAN = NAAT by a pan-coronavirus RT-PCR assay

O = Other

SCONV = Seroconversion or fourfold titre rise

SIGG = NCOV specific IgG-antibodies

SIGM = NCOV specific IgM-antibodies

SIGMG = NCOV specific IgM- and IgG antibodies

UNK = Unknown

Laboratory method used to make diagnosis.

Number of days in ICU or HDU

Field: NumberDaysICUHDU

Coding: Numerical
NA = Not applicable
UNK = Unknown

Total number of days patient spent in ICU or HDU.

Outcome (mandatory)

Field: Outcome

Coding: ALIVE = Alive, recovered, cured
DIEDNCOV = COVID-19 was the main or contributing cause of death
DIEDOTHER = Death not related to COVID-19 infection
DIEDUNK = Cause of death unknown
STILLTREATMENT = Still on medical treatment (not recovered)
UNK = Unknown outcome

Outcome refers to the patient's vital status resulting from COVID-19. If death occurred due to other disease, 'DIEDOTHER' should be reported. If the patient is still ill at the time of reporting, code the outcome as 'STILLTREATMENT'. The outcome should be updated when the final outcome is known. ECDC will send reminders to countries to update outcome of cases reported as "STILLTREATMENT" two weeks after they are reported.

Date PCR Episode 1

Field: PCREpisode1

Coding: *yyyy-mm-dd*
UNK= Unknown

If **ReinfectionCase=Y**, date of positive PCR test for episode1 of infection

Place of infection (mandatory)

Field: PlaceOfInfection
Coding: NUTS_GAUL
UNK = Unknown

The probable place of infection should be provided at the NUTS 3 level. If the probable case of infection is not an EU/EEA country, then use GAUL nomenclature.

Place of residence

Field: PlaceOfResidence
Coding: NUTS_GAUL
UNK = Unknown

Place of residence of patient at the time of disease onset. Select the most detailed NUTS(EU/EEA) or GAUL(nonEU/EEA) level possible.

Pneumococcal vaccination

Field: PneumococcalVaccination

Coding: N = No
Y = Yes
UNK = Unknown

Recent pneumococcal vaccination.

Precondition (repeatable field, mandatory)

Field: Precondition
Coding: ASPL = Asplenia
ASTH = Asthma
CANC = Cancer, malignancy
CARDIACDIS = Cardiac disorder, excluding hypertension
DIAB = Diabetes
HIV = HIV/other immune deficiency
HYPERT = Hypertension
KIDNEY = Kidney-related condition, renal disease
LIVER = Liver-related condition, liver disease
LUNG = Chronic lung disease, excluding asthma
NEUROMUS = Neuromuscular disorder, chronic neurological
O = Other precondition, please specify
OBES = Obesity
PREG = Pregnancy, trimester is unknown
PREG1 = Pregnancy, 1st trim, the 1st trim is from week 1 to the end of week 12
PREG2 = Pregnancy, 2nd trim, the 2nd trim is from week 13 to the end of week 26
PREG3 = Pregnancy, 3rd trim, the 3rd trim is from week 27 to the end of the pregnancy
PREGPOST = Post-partum (<6 weeks)
SMOKE = Current smoking
TB = Tuberculosis

Precondition – other

Field: PreconditionOther
Coding: Text

UNK = Unknown

Details of underlying conditions, if Precondition is coded as 'other', but is known. If multiple other preconditions, separate by a semicolon (;) within the same field.

Prior medication

Field: PriorMedic

Coding: ACE = Angiotensin converting enzyme inhibitors (ACE inhibitors)
ARB = Angiotensin II receptor blockers (ARBs)
NSAID = Non-steroidal anti-inflammatory (NSAID)
UNK = Unknown

Whether patient took any of Angiotensin converting enzyme inhibitors, Angiotensin II receptor blockers or Non-steroidal anti-inflammatory drugs prior to disease onset.

Date RAT episode 1

Field: RATEpisode1

Coding: *yyyy-mm-dd*
UNK= Unknown

If **ReinfectionCase=Y**, date of positive RAT test for episode1 of infection.

Reinfection case

Field: ReinfectionCase

Coding: Y = Yes
N = No
UNK = Unknown

Reinfection according to the *suspected case definition* for reinfection.

Respiratory support (mandatory)

Field: RespSupport
Coding: ECMO = Extracorporeal membrane oxygenation
N = No
O = Other, please specify
OXYGEN = Oxygen therapy
UNK = Unknown
VENT = Ventilator including non-invasive positive pressure ventilation

Level of respiratory support given to patient.

Respiratory support - Other

Field: RespSupportOther
Coding: Text
UNK = UnknownOther respiratory support not found in the list of possible values.

Sequence Episode 1

Field: SequenceEpisode1

Coding: TEXT
UNK = Unknown

If **ReinfectionCase = Y**, sequencing information for episode 1 of infection. Sequence identifier for whole genome or gene sequence, based on which the sequence read data can be retrieved from external database such as GISAID, GenBank or other db (except ENA). GISAID isolate sequence

accession number should be reported in format EPI_ISL_402123, GenBank MK334047.1. Please report ENAId in WgsEnaId variable.

Positive serology episode 1

Field: SerologyEpisode1

Coding: Y = Yes
N = No
UNK = Unknown

If **ReinfectionCase = Y**, result of serology for first episode of infection.

Setting

Field: Close contact setting

Coding: FAM = Family setting
HCS = Health care setting
LTCF = Long term care facility
O = Other location, please specify
PRI = Prison
UNK = Unknown
WORK = Work place
DET = Migrant detention centre

Close contact setting with a probable or confirmed case in the 14 days prior to symptom onset.

Close contact setting - other

Field: SettingOther

Coding: Text

Other close contact setting.

Severity of episode 1

Field: SeverityEpisode1

Coding: SymptomsSeverity:
ASY = Asymptomatic
HOSP = Hospitalised
ICU = Intensive care
SYMP = Symptomatic
UNK = Unknown

If **ReinfectionCase = Y**, provide information on severity of the first episode (Symptomatic; Hospitalisation; Intensive care) highest severity takes priority.

Symptomatic

Field: Symptomatic

Coding: ASY = Asymptomatic
SYMP = Symptomatic
UNK = Unknown

Date COVID-19 vaccination dose 1

Field: VaccDose1

Coding: *yyyy-mm-dd*
UNK= Unknown

Date of first COVID-19 vaccination dose.

Date COVID-19 vaccination dose 2

Field: VaccDose2

Coding: *yyyy-mm-dd*

UNK= Unknown

Date of second COVID-19 vaccination dose.

Date COVID-19 vaccination dose 3

Field: VaccDose3

Coding: *yyyy-mm-dd*

UNK= Unknown

Date of third COVID-19 vaccination dose.

Date COVID-19 vaccination dose 4

Field: VaccDose4

Coding: *yyyy-mm-dd*

UNK= Unknown

Date of fourth COVID-19 vaccination dose.

Vaccination status COVID-19

Field: VaccStatus

Coding: VaccStatusCOVID:

1DOSE = 1 dose

2DOSE = 2 doses

3DOSE = 3 doses

4DOSE= 4 doses

DOSEUNK = Vaccinated with unknown number of doses

NOTVACC = 0 dose unvaccinated

UNK = Unknown vaccination status

Indicates if the case is vaccinated and number of vaccine doses received.

Variant episode 1 (Updated coded value list)

Field: VariantEpisode1

Coding: VirusVariantNCOV:

B.1.1.7+E484K = mutations: del 69-70, del 144, E484K, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H

B.1.616 = B.1.616 (mutations: D215G, D614G, 142del, G669S, H66D, H655Y, N1187D, Q949R, V483A, Y144V)

B.1.617 = B.1.617 lineage or any sublineage of B.1.617(common mutations: D614G, L452R, P681R)

CLUSTER_5 = Denmark cluster 5 associated with mink (defined by mutations: del 69-70, Y453F, I692V, M1229I)

E484K = detected via an SNP assay specific for E484K

N501Y = detected via an SNP assay specific for N501Y

ORF1a(del3675-3677) = Variants carrying ORF1a deletion (del 3675-3677)

P.1 = P.1 variants (L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F)

S_GENE_DELETION = Variant virus with deletion in S-gene (defined by mutation: del 69-70 or by negative S-gene RT-PCR)

UNK = Sequence information unknown or not available

VARIANT_OTHER = Novel variant of potential concern. Provide details in VirusVariantOther

WILD_TYPE = None of the variants described for this variable

Y453F = Y453F associated with farmed minks; defined by mutation: Y453F

B.1.525 = B.1.525 (mutations: E484K, D614G, Q677H)

B.1.427/B.1.429 = B.1.427/B.1.429 (mutations: L452R, D614G)

P.1 = P.1 variants (L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F)

P.3 = P.3 (mutations: E484K, N501Y, D614G, P681H)

B.1.617.1 = B.1.617.1 (mutations: L452R, E484Q, D614G, P681R)

B.1.617.2 = B.1.617.2 (mutations: L452R, T478K, D614G, P681R)

B.1.617.3 = B.1.617.3 (mutations: L452R, E484Q, D614G, P681R)

B.1.620 = B.1.620 (mutations: S477N, E484K, D614G, P681H)

B.1.621 = B.1.621 (mutations: R346K, E484K, N501Y, D614G, P681H)

B.1.351 = B.1.351 (defined by mutations: D80A, D215G, E484K, N501Y, A701V)

B.1.1.7 = B.1.1.7 (mutations: del69-70, del144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H)

C.37= C.37 (mutations L452Q, F490S, D614G)

AY.4.2 = AY.4.2 (mutations: L452R, T478K, D614G, P681R, A222V, Y145H)

BA.1 = BA.1 or B.1.1.529 with mutations del69-70, ins214EPE, S371L, G496S, T547K

BA.2 = BA.2 or B.1.1.529 with mutations V213G, T376A, R408S

BA.2.75 = BA.2 sub-lineage with mutations D339H, G446S, N460K, and R493Q in the RBD, and mutations K147E, W152R, F157L, I210V, and G257S in the N-terminal domain of the Spike protein

BA.2+L452X = BA.2 and any of its sub-lineages with mutations at position 452 of the Spike protein

BA.3 = BA.3 or B.1.1.529 with mutations del69-70, ORF1a:A3657V, ORF3a:T22V

BA.4 = BA.4 or B.1.1.529 with mutations L452R, F486V, del69-70, NSP7b: L11F, N:

P151S, ORF1a: Δ141-143

BA.5 = BA.5 or B.1.1.529 with mutations L452R, F486V, del69-70

If **ReinfectionCase = Y**, information on variant virus of SARS-CoV-2 for episode 1 of infection according to mutation pattern of specific concern identified by sequence analysis of the case, or in some cases by a specific RT-PCR pattern. If several apply, choose the most specific variant (highest number of matching mutations).

Viral coinfection

Field: ViralCoinfection

Coding: INFL = Influenza

RSV = RSV (Respiratory syncytial virus)

OTHCOR = Other coronavirus

O = Other respiratory viral pathogen, please specify

UNK = Unknown

Viral co-infection/co-detection.

Viral coinfection – other

Field: ViralCoinfectionOther

Coding: Text

UNK = Unknown

Details of other viral co-infection is ViralCoinfection is coded as 'other', but is known.

Virus variant of SARS-CoV-2 (updated coded value list)

Field: VirusVariant

Coding: VirusVariantNCOV:

B.1.1.7+E484K = mutations: del 69-70, del 144, E484K, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H

B.1.616 = B.1.616 (mutations: D215G, D614G, 142del, G669S, H66D, H655Y, N1187D, Q949R, V483A, Y144V)

B.1.617 = B.1.617 lineage or any sublineage of B.1.617(common mutations: D614G, L452R, P681R)

CLUSTER_5 = Denmark cluster 5 associated with mink (defined by mutations: del 69-70, Y453F, I692V, M1229I)

E484K = detected via an SNP assay specific for E484K

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ORF1a(del3675-3677) = Variants carrying ORF1a deletion (del 3675-3677)

P.1 = P.1 variants (L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F)

P.3 = P.3 (mutations: E484K, N501Y, D614G, P681H)

S_GENE_DELETION = Variant virus with deletion in S-gene (defined by mutation: del 69-70 or by negative S-gene RT-PCR)

UNK = Sequence information unknown or not available

VARIANT_OTHER = Novel variant of potential concern. Provide details in VirusVariantOther

WILD_TYPE = None of the variants described for this variable

Y453F = Y453F associated with farmed minks; defined by mutation: Y453F

B.1.525 = B.1.525 (mutations: E484K, D614G, Q677H)

B.1.427/B.1.429 = B.1.427/B.1.429 (mutations: L452R, D614G)

P.3 = P.3 (mutations: E484K, N501Y, D614G, P681H)

B.1.617.1 = B.1.617.1 (mutations: L452R, E484Q, D614G, P681R)

B.1.617.2 = B.1.617.2 (mutations: L452R, T478K, D614G, P681R)

B.1.617.3 = B.1.617.3 (mutations: L452R, E484Q, D614G, P681R)

B.1.620 = B.1.620 (mutations: S477N, E484K, D614G, P681H)

B.1.621 = B.1.621 (mutations: R346K, E484K, N501Y, D614G, P681H)

B.1.351 = B.1.351 (defined by mutations: D80A, D215G, E484K, N501Y, A701V)

B.1.1.7 = B.1.1.7 (mutations: del69-70, del144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H)

C.37= C.37 (mutations L452Q, F490S, D614G)

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BA.2+L452X = BA.2 and any of its sub-lineages with mutations at position 452 of the Spike protein

BA.3 = BA.3 or B.1.1.529 with mutations del69-70, ORF1a:A3657V, ORF3a:T22V

BA.4 = BA.4 or B.1.1.529 with mutations L452R, F486V, del69-70, NSP7b: L11F, N:

P151S, ORF1a: Δ141-143

BA.5 = BA.5 or B.1.1.529 with mutations L452R, F486V, del69-70

COVID-19 case with a variant virus of SARS-CoV-2 according to mutation pattern of specific concern identified by sequence analysis of the case, or in some cases by a specific RT-PCR pattern. If several apply, choose the most specific variant (highest number of matching mutations).

Virus variant type other specified

Field: VirusVariantOther

Coding: TEXT

Specified variant type not captured in the coded values for VirusVariant variable as indicated in VARIANT_OTHER response for VirusVariant variable.

Sequencing category (new)

Field: SequencingCategory

Coding: SequencingCategoryNCOV

REP = Representative

BREAK = Targeted - vaccine breakthrough

OUTBREAKS = Targeted – outbreaks

TRAVEL = Targeted – travel

UNUSUAL = Targeted – unusual events

UNK = Unknown

The representative category should cover specimens collected as part of sampling for sequencing that are considered, as far as possible, representative of COVID-19 cases at the time of sampling. Representativeness should be true most importantly in regard to age/age groups, time points (week in most cases), geographic areas within the country and spectrum of disease.

With increasing vaccine coverage infections in vaccinated individuals will most likely constitute the majority of the representative sample; in this case vaccine breakthrough infections should be reported in the sequencing category "representative". **In case of vaccinated cases please ensure to report the variables on vaccination status (VaccStatus, BrandDose1-3, VaccDose1-3).**

For further details please refer to *https://www.ecdc.europa.eu/sites/default/files/documents/Guidance-for-representative-and-targeted-genomic-SARS-CoV-2-monitoring.pdf*

Wgs ENA identifier

Field: WgsEnaId

Coding: Text

European Nucleotide Archive (ENA) run identifier, based on which the sequence read data can be retrieved. Starts with ERR or SRR, i.e. not the sample or experiment which ERS/ERX or SRS/SRX.

Wgs Sequence read archive (RA) identifier

Field: WgsSequenceId

Coding: Text

Sequence identifier for whole genome or whole or partial gene sequence, based on which the sequence read data can be retrieved from external database such as GISAID, GenBank or other db (except ENA). GISAID isolate sequence accession number should be reported in format EPI_ISL_402123, GenBank MK334047.1. Please report ENAId in WgsEnaId variable.

NCOVAGGR metadata

The NCOVAGGR metadata, **recordtype version 4** is used for reporting of aggregated data on cases and deaths. Aggregated data should be reported by week. Note that sequencing related variables have been removed. Data on variants of interest and of concern should be reported using NCOVVARIANT.

Common TESSy variables

Record type (mandatory)

Field: RecordType

Coding: NCOVAGGR

The record type defines the structure and the format of the data reported. The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: 4

The version of the record type defines the current structure of the data reported. If the dataset is changed, the version changes to the next higher integer. The current version of the NCOVAGGR record type is 3.

This variable is not mandatory as TESSy concludes the record type version from the metadataset indicated. The variable RecordTypeVersion allows to override this default.

Subject (mandatory)

Field: Subject

Coding: NCOV

The subject describes the disease to be reported.

Data source (mandatory)

Field: DataSource

Coding: Pre-assigned as CountryCode-NCOVAGGR to each country; can be modified by National Coordinator

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. The descriptions of the surveillance systems submitted to TESSy should be kept up to date and will be used to assist with data interpretation.

Reporting country (mandatory)

Field: ReportingCountry

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week for which the reported data refer.

Epidemiological variables

Age 00-04 Males

Field: Age00-04M

Coding: Numeric

Number of confirmed cases among males in age group 0-4 years, newly reported for week of reporting.

Age 05-09 Males

Field: Age05-09M

Coding: Numeric

Number of confirmed cases among males in age group 5-9 years, newly reported for week of reporting.

Age 10-14 Males

Field: Age10-14M

Coding: Numeric

Number of confirmed cases among males in age group 10-14 years, newly reported for week of reporting.

Age 15-19 Males

Field: Age15-19M

Coding: Numeric

Number of confirmed cases among males in age group 15-19 years, newly reported for week of reporting.

Age 20-24 Males

Field: Age20-24M

Coding: Numeric

Number of confirmed cases among males in age group 20-24 years, newly reported for week of reporting.

Age 25-29 Males

Field: Age25-29M

Coding: Numeric

Number of confirmed cases among males in age group 25-29 years, newly reported for week of reporting.

Age 30-39 Males

Field: Age30-39M

Coding: Numeric

Number of confirmed cases among males in age group 30-39 years, newly reported for week of reporting.

Age 40-49 Males

Field: Age40-49M

Coding: Numeric

Number of confirmed cases among males in age group 40-49 years, newly reported for week of reporting.

Age 50-59 Males

Field: Age50-59M

Coding: Numeric

Number of confirmed cases among males in age group 50-59 years, newly reported for week of reporting.

Age 60-64 Males

Field: Age60-64M

Coding: Numeric

Number of confirmed cases among males in age group 60-64 years, newly reported for week of reporting.

Age 65-69 Males

Field: Age65-69M

Coding: Numeric

Number of confirmed cases among males in age group 65-69 years, newly reported for week of reporting.

Age 70-74 Males

Field: Age70-74M

Coding: Numeric

Number of confirmed cases among males in age group 70-74 years, newly reported for week of reporting.

Age 75-79 Males

Field: Age75-79M

Coding: Numeric

Number of confirmed cases among males in age group 75-79 years, newly reported for week of reporting.

Age 80+ Males

Field: Age80+M

Coding: Numeric

Number of confirmed cases among males in age group 80+ years, newly reported for week of reporting.

AgeUNKM

Field: AgeUNKM

Coding: Numeric

Number of confirmed cases among males with unknown age, newly reported for week of reporting.

Age 00-04 Females

Field: Age00-04F

Coding: Numeric

Number of confirmed cases among females in age group 0-4 years, newly reported for week of reporting.

Age 05-09 Females

Field: Age05-09F

Coding: Numeric

Number of confirmed cases among females in age group 5-9 years, newly reported for week of reporting.

Age 10-14 Females

Field: Age10-14F

Coding: Numeric

Number of confirmed cases among females in age group 10-14 years, newly reported for week of reporting.

Age 15-19 Females

Field: Age15-19F

Coding: Numeric

Number of confirmed cases among females in age group 15-19 years, newly reported for week of reporting.

Age 20-24 Females

Field: Age20-24F

Coding: Numeric

Number of confirmed cases among females in age group 20-24 years, newly reported for week of reporting.

Age 25-29 Females

Field: Age25-29F

Coding: Numeric

Number of confirmed cases among females in age group 25-29 years, newly reported for week of reporting.

Age 30-39 Females

Field: Age30-39F

Coding: Numeric

Number of confirmed cases among females in age group 30-39 years, newly reported for week of reporting.

Age 40-49 Females

Field: Age40-49F

Coding: Numeric

Number of confirmed cases among females in age group 40-49 years, newly reported for week of reporting.

Age 50-59 Females

Field: Age50-59F

Coding: Numeric

Number of confirmed cases among females in age group 50-59 years, newly reported for week of reporting.

Age 60-64 Females

Field: Age60-64F

Coding: Numeric

Number of confirmed cases among females in age group 60-64 years, newly reported for week of reporting.

Age 65-69 Females

Field: Age65-69F

Coding: Numeric

Number of confirmed cases among females in age group 65-69 years, newly reported for week of reporting.

Age 70-74 Females

Field: Age70-74F

Coding: Numeric

Number of confirmed cases among females in age group 70-74 years, newly reported for week of reporting.

Age 75-79 Females

Field: Age75-79F

Coding: Numeric

Number of confirmed cases among females in age group 75-79 years, newly reported for week of reporting.

Age 80+ Females

Field: Age80+F

Coding: Numeric

Number of confirmed cases among females in age group 80+ years, newly reported for week of reporting.

AgeUNKF

Field: AgeUNKF

Coding: Numeric

Number of confirmed cases among females with unknown age, newly reported for week of reporting.

Age Gender Unknown

Field: AgeGenderUnk

Coding: Numeric

Number of confirmed cases with unknown age and gender, newly reported for week of reporting.

Deaths 00-04 Males

Field: Deaths00-04M

Coding: Numeric

Number of deaths among confirmed cases in males aged 0-4 years, newly reported for week of reporting.

Deaths 05-09 Males

Field: Deaths05-09M

Coding: Numeric

Number of deaths among confirmed cases in males aged 5-9 years, newly reported for week of reporting.

Deaths 10-14 Males

Field: Deaths10-14M

Coding: Numeric

Number of deaths among confirmed cases in males aged 10-14 years, newly reported for week of reporting.

Deaths 15-19 Males

Field: Deaths15-19M

Coding: Numeric

Number of deaths among confirmed cases in males aged 15-19 years, newly reported for week of reporting.

Deaths 20-24 Males

Field: Deaths20-24M

Coding: Numeric

Number of deaths among confirmed cases in males aged 20-24 years, newly reported for week of reporting.

Deaths 25-29 Males

Field: Deaths25-29M

Coding: Numeric

Number of deaths among confirmed cases in males aged 25-29 years, newly reported for week of reporting.

Deaths 30-39 Males

Field: Deaths30-39M

Coding: Numeric

Number of deaths among confirmed cases in males aged 30-39 years, newly reported for week of reporting.

Deaths 40-49 Males

Field: Deaths40-49M

Coding: Numeric

Number of deaths among confirmed cases in males aged 40-49 years, newly reported for week of reporting.

Deaths 50-59 Males

Field: Deaths50-59M

Coding: Numeric

Number of deaths among confirmed cases in males aged 50-59 years, newly reported for week of reporting.

Deaths 60-64 Males

Field: Deaths60-64M

Coding: Numeric

Number of deaths among confirmed cases in males aged 60-64 years, newly reported for week of reporting.

Deaths 65-69 Males

Field: Deaths65-69M

Coding: Numeric

Number of deaths among confirmed cases in males aged 65-69 years, newly reported for week of reporting.

Deaths 70-74 Males

Field: Deaths70-74M

Coding: Numeric

Number of deaths among confirmed cases in males aged 70-74 years, newly reported for week of reporting.

Deaths 75-79 Males

Field: Deaths75-79M

Coding: Numeric

Number of deaths among confirmed cases in males aged 75-79 years, newly reported for week of reporting.

Deaths 80+ Males

Field: Deaths80+M

Coding: Numeric

Number of deaths among confirmed cases in males aged 80+ years, newly reported for week of reporting.

DeathsUNKM

Field: DeathsUNKM

Coding: Numeric

Number of deaths among confirmed cases in males with unknown age, newly reported for week of reporting.

Deaths 00-04 Females

Field: Deaths00-04F

Coding: Numeric

Number of deaths among confirmed cases in females aged 0-4 years, newly reported for week of reporting.

Deaths 05-09 Females

Field: Deaths05-09F

Coding: Numeric

Number of deaths among confirmed cases in females aged 5-9 years, newly reported for week of reporting.

Deaths 10-14 Females

Field: Deaths10-14F

Coding: Numeric

Number of deaths among confirmed cases in females aged 10-14 years, newly reported for week of reporting.

Deaths 15-19 Females

Field: Deaths15-19F

Coding: Numeric

Number of deaths among confirmed cases in females aged 15-19 years, newly reported for week of reporting.

Deaths 20-24 Females

Field: Deaths20-24F

Coding: Numeric

Number of deaths among confirmed cases in females aged 20-24 years, newly reported for week of reporting.

Deaths 25-29 Females

Field: Deaths25-29F

Coding: Numeric

Number of deaths among confirmed cases in females aged 25-29 years, newly reported for week of reporting.

Deaths 30-39 Females

Field: Deaths30-39F

Coding: Numeric

Number of deaths among confirmed cases in females aged 30-39 years, newly reported for week of reporting.

Deaths 40-49 Females

Field: Deaths40-49F

Coding: Numeric

Number of deaths among confirmed cases in females aged 40-49 years, newly reported for week of reporting.

Deaths 50-59 Females

Field: Deaths50-59F

Coding: Numeric

Number of deaths among confirmed cases in females aged 50-59 years, newly reported for week of reporting.

Deaths 60-64 Females

Field: Deaths60-64F

Coding: Numeric

Number of deaths among confirmed cases in females aged 60-64 years, newly reported for week of reporting.

Deaths 65-69 Females

Field: Deaths65-69F

Coding: Numeric

Number of deaths among confirmed cases in females aged 65-69 years, newly reported for week of reporting.

Deaths 70-74 Females

Field: Deaths70-74F

Coding: Numeric

Number of deaths among confirmed cases in females aged 70-74 years, newly reported for week of reporting.

Deaths 75-79 Females

Field: Deaths75-79F

Coding: Numeric

Number of deaths among confirmed cases in females aged 75-79 years, newly reported for week of reporting.

Deaths 80+ Females

Field: Deaths80+F

Coding: Numeric

Number of deaths among confirmed cases in females aged 80+ years, newly reported for week of reporting.

DeathsUNKF

Field: DeathsUNKF

Coding: Numeric

Number of deaths among confirmed cases in females with unknown age, newly reported for week of reporting.

Deaths Age Gender Unknown

Field: DeathsAgeGenderUnk

Coding: Numeric

Number of deaths among confirmed cases with unknown age and gender, newly reported for week of reporting.

Cases Healthcare Workers

Field: CasesHCW

Coding: Numeric

Number of confirmed cases among healthcare workers, newly reported for week of reporting.

Deaths Healthcare Workers

Field: DeathsHCW

Coding: Numeric

Number of deaths among confirmed cases in healthcare workers, newly reported for week of reporting.

Discharged

Field: Discharged

Coding: Numeric

Number of confirmed cases newly discharged from hospital for the week of reporting.

Hospitalised

Field: Hospitalised

Coding: Numeric

Number of newly hospitalised confirmed cases during the week of reporting.

Number of free ICU beds

Field: ICUBedsFree

Coding: Numeric

Number of free adult ICU beds as of Wednesday for the week of reporting. Number of ICU beds as of Wednesday previous week not occupied by either COVID-19 patients or other patients requiring intensive care.

Total number of ICU beds

Field: ICUBedsTotal

Coding: Numeric

Total number of adult ICU and HDU beds (occupied and free beds for any patient requiring intensive care) as of Wednesday for the week of reporting. Use the same definition of ICU/HDU as used for the routine national reporting of COVID-19 patients in the ICU.

Number of COVID-19 patients in the ICU

Field: ICUPatientsCOVID

Coding: Numeric

Number of probable and confirmed COVID-19 patients in adult ICU/HDU as of Wednesday for the week of reporting.

Number of cases

Field: NumberOfCases

Coding: Numeric

Number of all confirmed cases for the week of reporting.

Number of deaths

Field: NumberOfDeaths

Coding: Numeric

Number of deaths among confirmed cases for the week of reporting.

Reinfection cases

Field: ReinfectionCases

Coding: Numeric

Total number of suspected reinfection cases according to the *suspected reinfection case definition* for the reporting week.

Ventilated

Field: Ventilated

Coding: Numeric

Number of cases treated with mechanical ventilation or ECFO or admitted in intensive care unit (ICU) for the week of reporting (ie total number being ventilated, under ECFO or in ICU during the reporting week).

NCOVTEST metadata

The NCOVTEST metadata, **recordtype version 2** is used for reporting of aggregated data on the number of tests by method, age-group and region per week.

Common TESSy variables

Record Identifier (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be

- unique within the national COVID-19 disease surveillance system
- anonymous.

Record type (mandatory)

Field: RecordType

Coding: NCOVTEST

The record type defines the structure and the format of the data reported. The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: 2

The version of the record type defines the current structure of the data reported. If the dataset is changed, the version changes to the next higher integer. The current version of the NCOVTEST record type is 2.

This variable is not mandatory as TESSy concludes the record type version from the metadataset indicated. The variable RecordTypeVersion allows to override this default.

Subject (mandatory)

Field: Subject

Coding: NCOV

The subject describes the disease to be reported.

Data source (mandatory)

Field: DataSource

Coding: Pre-assigned as CountryCode-NCOVTEST to each country; can be modified by National Coordinator

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. The descriptions of the surveillance systems submitted to TESSy should be kept up to date and will be used to assist with data interpretation.

Reporting country (mandatory)

Field: ReportingCountry

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics
Coding: yyyy-Www
The week for which the reported data refer.

Epidemiological variables

Type of test

Field: LabMethod
Coding: ANTIGEN = Antigen detection
NUC = NAAT by RT-PCR
UNK = Unknown
Type of test.

Region of test (mandatory)

Field: RegionTest
Coding: Country/NUTS1 or 2/GAUL1/Country specific
Region where the tests were performed.

Age 00-04

Field: Age00-04
Coding: Numeric
Number of tests performed among persons aged 0-4 years.

Age 05-09

Field: Age05-09
Coding: Numeric
Number of tests performed among persons aged 5-9 years.

Age 10-14

Field: Age10-14
Coding: Numeric
Number of tests performed among persons aged 10-14 years

Age 15-19

Field: Age15-19
Coding: Numeric
Number of tests performed among persons aged 15-19 years

Age 20-24

Field: Age20-24
Coding: Numeric
Number of tests performed among persons aged 20-24 years

Age 25-29

Field: Age25-29
Coding: Numeric
Number of tests performed among persons aged 25-29 years

Age 30-39
Field: Age30-39
Coding: Numeric
Number of tests performed among persons aged 30-39 years

Age 40-49
Field: Age40-49
Coding: Numeric
Number of tests performed among persons aged 40-49 years

Age 50-59
Field: Age50-59
Coding: Numeric
Number of tests performed among persons aged 50-59 years

Age 60-64
Field: Age60-64
Coding: Numeric
Number of tests performed among persons aged 60-64 years

Age 65-69
Field: Age65-69
Coding: Numeric
Number of tests performed among persons aged 65-69 years

Age 70-74
Field: Age70-74
Coding: Numeric
Number of tests performed among persons aged 70-74 years

Age 75-79
Field: Age75-79
Coding: Numeric
Number of tests performed among persons aged 75-79 years

Age 80+
Field: Age80+
Coding: Numeric
Number of tests performed among persons aged 80+ years

Age UNK
Field: AgeUNK
Coding: Numeric
Number of tests performed among persons where the age was not known

NCOVVARIANT metadata

The NCOVVARIANT metadata, **recordtype version 1** is used for reporting of aggregated data on variants of interest and of concern per week.

Common TESSy variables

Record Identifier (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be

- unique within the national COVID-19 disease surveillance system
- anonymous.

Record type (mandatory)

Field: RecordType

Coding: NCOVVARIANT

The record type defines the structure and the format of the data reported. The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: 1

The version of the record type defines the current structure of the data reported. If the dataset is changed, the version changes to the next higher integer. The current version of the NCOVVARIANT record type is 1.

This variable is not mandatory as TESSy concludes the record type version from the metadataset indicated. The variable RecordTypeVersion allows to override this default.

Subject (mandatory)

Field: Subject

Coding: NCOVVARIANT

The subject describes the disease to be reported.

Data source (mandatory)

Field: DataSource

Coding: Pre-assigned as CountryCode-NCOVVARIANT to each country; can be modified by National Coordinator

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. The descriptions of the surveillance systems submitted to TESSy should be kept up to date and will be used to assist with data interpretation.

Reporting country (mandatory)

Field: ReportingCountry

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week of sampling.

Epidemiological variables

Virus variant of SARS-CoV-2

Field: VirusVariant

Coding: VirusVariantNCOV:

B.1.1.7+E484K = mutations: del 69-70, del 144, E484K, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H

B.1.616 = B.1.616 (mutations: D215G, D614G, 142del, G669S, H66D, H655Y, N1187D, Q949R, V483A, Y144V)

B.1.617 = B.1.617 lineage or any sublineage of B.1.617(common mutations: D614G, L452R, P681R)

CLUSTER_5 = Denmark cluster 5 associated with mink (defined by mutations: del 69-70, Y453F, I692V, M1229I)

E484K = detected via an SNP assay specific for E484K

N501Y = detected via an SNP assay specific for N501Y

ORF1a(del3675-3677) = Variants carrying ORF1a deletion (del 3675-3677)

S_GENE_DELETION = Variant virus with deletion in S-gene (defined by mutation: del 69-70 or by negative S-gene RT-PCR)

UNK = Sequence information unknown or not available

VARIANT_OTHER = Novel variant of potential concern. Provide details in VirusVariantOther

WILD_TYPE = None of the variants described for this variable

Y453F = Y453F associated with farmed minks; defined by mutation: Y453F

B.1.525 = B.1.525 (mutations: E484K, D614G, Q677H)

B.1.427/B.1.429 = B.1.427/B.1.429 (mutations: L452R, D614G)

P.1 = P.1 variants (L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F)

P.3 = P.3 (mutations: E484K, N501Y, D614G, P681H)

B.1.617.1 = B.1.617.1 (mutations: L452R, E484Q, D614G, P681R)

B.1.617.2 = B.1.617.2 (mutations: L452R, T478K, D614G, P681R)

B.1.617.3 = B.1.617.3 (mutations: L452R, E484Q, D614G, P681R)

B.1.620 = B.1.620 (mutations: S477N, E484K, D614G, P681H)

B.1.621 = B.1.621 (mutations: R346K, E484K, N501Y, D614G, P681H)

B.1.351 = B.1.351 (defined by mutations: D80A, D215G, E484K, N501Y, A701V)

B.1.1.7 = B.1.1.7 (mutations: del69-70, del144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H)

C.37= C.37 (mutations L452Q, F490S, D614G)

AY.4.2 = AY.4.2 (mutations: L452R, T478K, D614G, P681R, A222V, Y145H)

BA.1 = BA.1 or B.1.1.529 with mutations del69-70, ins214EPE, S371L, G496S, T547K

BA.2 = BA.2 or B.1.1.529 with mutations V213G, T376A, R408S

BA.2.75 = BA.2 sub-lineage with mutations D339H, G446S, N460K, and R493Q in the RBD, and mutations K147E, W152R, F157L, I210V, and G257S in the N-terminal domain of the Spike protein

BA.2+L452X = BA.2 and any of its sub-lineages with mutations at position 452 of the Spike protein

BA.3 = BA.3 or B.1.1.529 with mutations del69-70, ORF1a:A3657V, ORF3a:T22V

BA.4 = BA.4 or B.1.1.529 with mutations L452R, F486V, del69-70, NSP7b: L11F, N: P151S, ORF1a: Δ141-143

BA.5 = BA.5 or B.1.1.529 with mutations L452R, F486V, del69-70

COVID-19 case with a variant virus of SARS-CoV-2 according to mutation pattern of specific concern identified by sequence analysis of the case, or in some cases by a specific RT-PCR pattern. If several apply, choose the most specific variant (highest number of matching mutations).

Virus variant type other specified

Field: VirusVariantOther

Coding: TEXT

Specified variant type not captured in the coded values for VirusVariant variable as indicated in VARIANT_OTHER response for VirusVariant variable.

Number of sequences from representative surveillance

Field: NumberRepresentative

Coding: Numeric

Number of the specific variant detected from representative surveillance.

The representative surveillance should cover specimens collected as part of sampling for sequencing that are considered, as far as possible, representative of COVID-19 cases at the time of sampling. Representativeness should be true most importantly in regard to age/age groups, time points (week in most cases), geographic areas within the country and spectrum of disease.

With increasing vaccine coverage infections in vaccinated individuals will most likely constitute the majority of the representative sample; in this case vaccine breakthrough infections should be reported as part of representative surveillance.

Refer to *https://www.ecdc.europa.eu/sites/default/files/documents/Guidance-for-representative-and-targeted-genomic-SARS-CoV-2-monitoring.pdf* for more details.

Number of sequences from targeted surveillance

Field: NumberTargeted

Coding: Numeric

Number of the specific variant detected from targeted surveillance.

With increasing vaccine coverage infections in vaccinated individuals will most likely constitute the majority of the representative sample; in this case vaccine breakthrough infections should be reported as part of representative surveillance.

Refer to *https://www.ecdc.europa.eu/sites/default/files/documents/Guidance-for-representative-and-targeted-genomic-SARS-CoV-2-monitoring.pdf* for more details.

Number of sequences from targeted surveillance - imported

Field: NumberTargetedImported

Coding: Numeric

Number of the specific variant detected from targeted surveillance which were considered to be imported (travelled outside the reporting country in the 14 days prior to symptom onset).

Number of sequences from targeted surveillance – locally acquired

Field: NumberTargetedLocal

Coding: Numeric

Number of the specific variant detected from targeted surveillance which were considered to be acquired within the reporting country.

Number of sequences with unknown reason for sequencing

Field: NumberUNK

Coding: Numeric

Number of the specific variant where the reason for sequencing was not known.