Field Name	Data Type
wwtp_name	string
sample_id	unique sample id (a string 20 characters
pooled	category
samples_in_pool	string (comma-separated list)
sample_collect_date	date ([yyyy]-[mm]-[dd]) or comma-separa
received_by_lab_date	date ([yyyy]-[mm]-[dd]) or comma-separa
selected_for_sequencing	category
reason_not_sequenced	category
date_sent_seq	date ([yyyy]-[mm]-[dd])
seq_run_type	category
major_seq_method	integer
major_seq_method_desc	string
genome_coverage	float
total_raw_reads	integer
coverage_above_thresh	category
selected_for_deposition	category
date_deposited	date ([yyyy]-[mm]-[dd])
date_deposition_accepted	date ([yyyy]-[mm]-[dd])
sra_accession	string
biosample_accession	string
seq_vendor	string
pcr_target_avg_conc	float
sequencing_run_id	integer
addl_seq_method_notes	string
major_lab_method	integer

Description

The name of the Wastewater Treatment Plant (WWTP), or the name of the septic or other treatment system to waswetwater wh...

An uniqe ID assigned to a wastewater sample selected for sequencing. It must be unique for this NWSS reporting jurisdiction. V...

Was this sample pooling before sequening?

If sample is pooled, comma separated list of the sample_id's that were pooled, if not pooled write N/A. **Pooled samples must within 7 days of each other.**

The date of sample collection; for composite samples, specify the date on which sample collection began. For pooled samples,

The date sample arrived in Biobot's laboratory. For pooled samples, a comma separated list of arrival dates for all consistent samples_in_pool)

Was this sample selected for sequencing (Yes or No)?

If sample was not sequenced, succinctly indicate why?

Date sample was sent to Biobot's sequencing vendor

Choose one of the following: standard sequencing, re-run due to low coverage, method validation

A number used to distinguish major sequencing methods

Description of sequencing method

% of SARS-CoV-2 genome covered at 10x or more

Number of total sequencing reads

Did the sequencing meet the minimum QC criteria (Yes or No)? (currently 20% of SARS-CoV-2 genome covered at >= 10x, mi...

Was the sequencing run selected for deposition in NCBI? (this will generally be "yes" if "coverage_above_thresh" is "yes", if co... be deposited)

Date the sample was submitted for deposition to the NCBI repository (or other CDC-specified repository)

Date the deposition was accepted to the NCBI repository and went live

Accession number for SRA experiment

Biosample ID from NCBI

Vendor that performed the sequencing

Concentration of the PCR target back-calculated to unconcentrated sample basis (from NWSS). This will be the N...

Numeric ID to distinguish multiple sequencing runs of the same biological sample

Additional details on sequencing methodology, as needed (e.g., minor changes too small to be included in 'major_lab_method'...

A number used to distinguish major lab methods at the reporting jurisdiction level.

Value Set	Units
[string, length less than or equal to 40 characters]	[none]
[sample id]	[none]
vs_yn	[none]
[string];	[none]
[date not after tomorrow's date] (or list thereof)	[none]
[date not after tomorrow's date] (or list thereof)	[none]
vs_ynp	[none]
vs_reason_not_sequenced	[none]
[date not after tomorrow's date]; [empty]	[none]
vs_seq_run_type	[none]
[greater than or equal to 0]; [empty]	[none]
[string]; [empty]	[none]
[0 to 100]; [empty]	[none]
[0 or greater]; [empty]	[none]
vs_yne	[none]
vs_yne	[none]
[date not after tomorrow's date]; [empty]	[none]
[date not after tomorrow's date]; [empty]	[none]
[string, length less than or equal to 40 characters]; [empty]	[none]
[string, length less than or equal to 40 characters]; [empty]	[none]
[string]; [empty]	[none]
[any positive float other than 0]; 0 (if no amplification observed)	[units specified
[0 or greater]	[none]
[string of any length--free text description]	[none]
[greater than or equal to 0]	[none]

Dependent Fields

None

None

None
If 'pooled' is "yes", then this must have a non-empty value

None

None

None
If 'selected for sequencing' is "no", then this must have a non-empty value

None
If 'date_sent_seq' has a non-empty value, then this must have a non-empty value
If 'date_sent_seq' has a non-empty value, then this must have a non-empty value
If 'date_sent_seq' has a non-empty value, then this must have a non-empty value
If 'selected_for_deposition' has a non-empty value, then this must also have a non-empty value
If 'selected_for_deposition' has a non-empty value, then this must also have a non-empty value
If 'selected_for_deposition' has a non-empty value, then this must also have a non-empty value

None

Empty if selected_for_deposition is "no"

Empty if selected_for_deposition is "no"
If 'date_deposition_accepted is non-empty, then this must also have a non-empty value
If 'date_deposition_accepted' is non-empty, then this must also have a non-empty value
If 'date_sent_seq' has a non-empty value, then this must have a non-empty value
None
If 'date_sent_seq' has a non-empty value, then this must have a non-empty value

None
None

Note that we may add to these value sets as we test additional sequencing protocols, etc

This includes only new value sets (for fields from NWSS, we use the NWSS values sets)

vs_reason_not_sequenced	Description	vs_seq_run_type	
ANOTHER_SAMPLE_SELECTED	Another sample from this same	STANDARD	standard seque
NOT_DETECTED	SARS-CoV-2 was not detected	RERUN	re-run of a samp
CT_ABOVE_THRESHOLD	SARS-CoV-2 was detected in t	METHOD_VAL	method validati
TRIBAL_TERRITORY_OPTOUT	This location is from a tribal na	[empty]	No sequencing
SAMPLE_SELECTION_ERROR	Due to lab error, we were unable to send this sample for seque		

vs_ynp	Description
YES	selected for sequencing
NO	not selected for sequencing
POOLED	pooled with another sample before sequencing
run	
ncing	