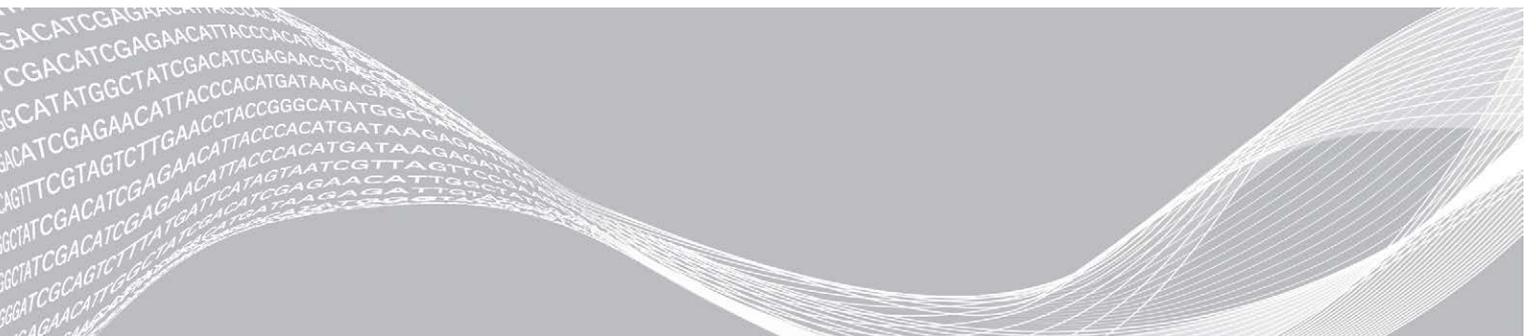


Illumina DRAGEN COVID Pipeline

Software Guide



Use of this product is covered by patents owned by and licensed to Illumina, Inc. Payment for this product conveys the limited, non-transferable right to use this product for its intended use in accordance with its documentation and any other associated terms and conditions. A representative, non-exhaustive list of such patents is located at www.illumina.com/patents. No right under any other patent or for any other use is conveyed expressly, by implication, or by estoppel.

This document and its contents are proprietary to Illumina, Inc. and its affiliates ("Illumina"), and are intended solely for the contractual use of its customer in connection with the use of the product(s) described herein and for no other purpose. This document and its contents shall not be used or distributed for any other purpose and/or otherwise communicated, disclosed, or reproduced in any way whatsoever without the prior written consent of Illumina. Illumina does not convey any license under its patent, trademark, copyright, or common-law rights nor similar rights of any third parties by this document.

The instructions in this document must be strictly and explicitly followed by qualified and properly trained personnel in order to ensure the proper and safe use of the product(s) described herein. All of the contents of this document must be fully read and understood prior to using such product(s).

FAILURE TO COMPLETELY READ AND EXPLICITLY FOLLOW ALL OF THE INSTRUCTIONS CONTAINED HEREIN MAY RESULT IN DAMAGE TO THE PRODUCT(S), INJURY TO PERSONS, INCLUDING TO USERS OR OTHERS, AND DAMAGE TO OTHER PROPERTY, AND WILL VOID ANY WARRANTY APPLICABLE TO THE PRODUCT(S).

ILLUMINA DOES NOT ASSUME ANY LIABILITY ARISING OUT OF THE IMPROPER USE OF THE PRODUCT(S) DESCRIBED HEREIN (INCLUDING PARTS THEREOF OR SOFTWARE).

© 2022 Illumina, Inc. All rights reserved.

All trademarks are the property of Illumina, Inc. or their respective owners. For specific trademark information, see www.illumina.com/company/legal.html.

Revision History

Document	Date	Description of Change
Document # 1000000158680 v02	March 2022	<ul style="list-style-type: none"> Updated installation instructions to clarify requirement to uninstall previous software versions. Updated DRAGEN Server v1 and v2 content throughout to v2 and v3 respectfully. Updated content throughout for v1.1.0 release.
Document # 1000000158680 v01	October 2021	<ul style="list-style-type: none"> Added new commands to the Running the Illumina DRAGEN COVID Pipeline section. Added command for uninstalling prior Illumina DRAGEN COVID Pipeline version in the Install the Illumina DRAGEN COVID Pipeline section. Updated content throughout for v1.0.1 release and compatibility with new ARTIC v4 primers. Updated output folders and files in Analysis Methods and Output Structure sections. Updated the detected sequence variants depth criteria to "greater than or equal to 10" in Variant Calling and Consensus Sequence Generation for Research Use Only section.
Document # 1000000158680 v00	April 2021	Initial release.

Table of Contents

Revision History	iii
Overview	1
Installation Requirements	1
Storage Requirements	1
Install the Illumina DRAGEN COVID Pipeline	2
Running the System Check	2
Running the Illumina DRAGEN COVID Pipeline	3
Process Lane Subsets or Multiple Flow Cells	4
Analysis Methods	4
Detection Algorithm	5
Output Structure	6
Variant Calling and Consensus Sequence Generation for Research Use Only ..	7
Uninstall Illumina DRAGEN COVID Pipeline	7
DRAGEN COVID Lineage Tools	7
Outputs	9
Technical Assistance	10

Overview

The Illumina DRAGEN COVID Pipeline analyzes sequencing reads of RNA libraries prepared using ARTIC v3, v4 or v4.1 gene panel assays. The Illumina DRAGEN COVID Pipeline uses the Illumina DRAGEN Bio-IT Platform to perform analysis to determine the presence of SARS-CoV-2 and generates results in BAM, VCF, and FASTA formats.

The Illumina DRAGEN COVID Pipeline requires a sample sheet. For information on creating a sample sheet, see *BCL Convert Software Guide (document # 100000094725)*.

In addition to SARS-CoV-2 analysis, the Illumina DRAGEN COVID Pipeline performs small variant calling for samples that meet the minimum threshold of SARS-CoV-2 virus targets detected. The minimum threshold is configurable with a default of 90 targets. See the options in *Running the Illumina DRAGEN COVID Pipeline on page 3*. The Illumina DRAGEN COVID Pipeline generates a consensus sequence in FASTA format. Variant calls and consensus sequences are generated for informational purposes only and not for patient reporting.

Installation Requirements

Illumina DRAGEN COVID Pipeline contains the following minimum operating requirements.

The Illumina DRAGEN COVID Pipeline is compatible with a DRAGEN Server v3 and v4.

By default, the software includes the following items:

- ▶ Linux CentOS 7.3 operating system, or later.

The following additional software is required before installing Illumina DRAGEN COVID Pipeline.

- ▶ Docker version 18.09, or later.

Storage Requirements

The DRAGEN Server provides NVMe SSD located in `/staging` directory to use as the software output directory.

Network-attached storage is required for long-term storage.

Analysis output is automatically written to the `/staging/dragen-covid-pipeline_analysis_<timestamp>` to make sure the DRAGEN Server processes read and write data on the NVMe SSD. You can modify this location using the command-line.

Before beginning analysis, develop a strategy to copy data from the DRAGEN Server to a network-attached storage. Delete output data on the DRAGEN Server as soon as possible.

The following are the run and analysis output sizes for each sequencing system per 36 bp. Output folder size can vary based on the number of positive samples. The following table are recommended storage requirements.

Sequencing System	Run Folder Output (GB)	Analysis Output (GB)
NovaSeq 6000 SP flow cell	20	60
NovaSeq 6000 S4 flow cell	225–240	860
NextSeq 500/550 and 550Dx HO flow cell	12	30

Install the Illumina DRAGEN COVID Pipeline

Use the instructions in this section to install the Illumina DRAGEN COVID Pipeline.

Illumina recommends running Docker as a non-root user by adding the user to the docker group. It is possible to run the Illumina DRAGEN COVID Pipeline as root but not recommended. For more information, see the Docker website.

If you currently have DRAGEN COVID Pipeline or Illumina DRAGEN COVIDSeq Test Pipeline installed, you must uninstall it. The installation script will uninstall any other DRAGEN software as well.

- 1 Download the Illumina DRAGEN COVID Pipeline installer package from the the Illumina support website.
- 2 Install Docker 18.09 or later using the install instructions for CentOS provided in the Docker documentation.
- 3 Install the DRAGEN Server license using the instructions provided in the [Illumina DRAGEN Server Site Prep & Installation Guide](#).
- 4 Download the Illumina DRAGEN COVID Pipeline installation script provided in the email from Illumina. The link expires after 1 week.

5 Store the install script in the `/staging` directory.

6 To run the software in a screen virtual terminal, enter the following command: `screen`.

```
screen -S <name>
```

In addition to other uses, the command avoids terminating the execution due to terminal inactivity.

7 To update the run script permissions, enter the following command:

```
chmod +x /staging/install_dragen-covid-pipeline-RUO-v1.1.0.run
```

8 Remove older versions of the product, enter one of the following commands:

- ▶ DRAGEN COVIDSeq Test Pipeline: `/staging/uninstall_covidseq-x.x.x.sh`
- ▶ Illumina DRAGEN COVID Pipeline: `/staging/uninstall_dragen-covid-pipeline-RUO-x.x.x.sh`

Where `x.x.x` is the older version to be removed.

9 To run the installation script, enter the following command:

```
/staging/install_dragen-covid-pipeline-RUO-1.1.0.run
```

The script also removes the previously installed DRAGEN software. Depending on your previous version of DRAGEN, you might need to power cycle your server after install.

Running the System Check

Make sure that the system is functioning properly by running the `check_dragen-covid-pipeline-1.1.0.sh` script. The self-test script checks the following functions:

- ▶ If all required services are running.
- ▶ If the proper Docker image is installed.
- ▶ If the Illumina DRAGEN COVID Pipeline successfully runs on a test data set.

The self-test runs for approximately five minutes. If the self-test prints a failure message, contact Illumina Technical Support and provide the `/staging/check_dragen-covid-pipeline_<timestamp>.tgz` output file.

To detach from the screen process at anytime, enter `ctrl-a d`.

Running the Illumina DRAGEN COVID Pipeline

The Illumina DRAGEN COVID Pipeline is started by selecting the shell script using the command line, and then running the software with Docker. Analysis outputs are located in the `/staging/dragen-covid-pipeline_analysis_<timestamp>` directory.

This location ensures that the server is on an optimized NVMe SSD.

Do not move files or press CTRL+C when the app is running. Moving files during the analysis can cause the analysis to fail or provide incorrect results. Pressing CTRL+C stops the analysis and might cause an error. If an error does occur, restart the server.

- 1 If detached from the screen process, enter the following command to reattach to screen:

```
screen -r name
```

- 2 To run the Illumina DRAGEN COVID Pipeline, enter the following command-line argument:

```
dragen-covid-pipeline.sh --runFolder <FULL_PATH_TO_RUN_FOLDER>
```

- 3 **[Optional]** Enter any of the other following available commands:

Option	Description
<code>--alignerMinScore</code>	Optional. Default 22. The minimum score to use for alignment.
<code>--ampliconThreshold</code>	Specifies the minimum number of SARS-CoV-2 targets detected for the sample to have a result of SARS-CoV2-Detected. The default value is 90.
<code>--analysisFolder</code>	Full path to the alternative analysis folder. For high performance, the folder must be on an NVMe SSD partition. Make sure to use a different folder than the test data folder <code>/staging/illumina/covid</code> . If the Illumina DRAGEN COVID Pipeline is uninstalled, the test data folder is deleted.
<code>--callabilityThreshold</code>	Optional. Default 10. The callability threshold for variant calling.
<code>--disableFilterReads</code>	Optional. Default false. If this flag is set, the pipeline will NOT filter reads to remove all unaligned reads and reads that align to the human control sequences.
<code>--disableScrubReads</code>	Optional. Default false. If this flag is set, the pipeline will NOT run NCBI's SRA Human Read Scrubber.
<code>--fastMode</code>	Turns off alignment, variant calling, and consensus sequence FASTA generation to improve speed.
<code>--fastqFolder</code>	Full path to the FastQ folder. Use of this command requires the specification of a sample sheet using the <code>--sampleSheet</code> command. Do not use this command if you are using the <code>--runFolder</code> command.
<code>--help</code>	Displays a help screen, and then exits.
<code>--lane</code>	To exclude BCL Convert on a single lane, set the option to the value 1, 2, 3, or 4.
<code>--primers</code>	Optional. Default v3. Set this argument to v4 to use the V4 ARTIC primers, or v4.1 to use the experimental V4.1 ARTIC primers.
<code>--runFolder</code>	Full path to the BCL folder. Do not use this command if you are using the <code>--fastqFolder</code> command.
<code>--sampleSheet</code>	Full path to the sample sheet. If your sample sheet is not located in the root directory of your run folder or is not named <code>SampleSheet.csv</code> , the <code>--sampleSheet</code> command is required.
<code>--version</code>	Displays the version of the software, and then exits.

Process Lane Subsets or Multiple Flow Cells

To analyze a subset of lanes, create a copy of the sample sheet, and then remove all samples that are not in the lanes to process. Specify this new sample sheet on the command line.

To process a single lane, use the `--lane` option with the value set to 1, 2, 3, or 4. The option restricts demultiplexing BCL to FASTQ to the specified lane and increases overall performance. Only include samples from the specified lane in your sample sheet.

To analyze multiple flow cells, perform multiple, serial executions of the software. Only initiate a new analysis after the previous is completed. Running multiple executions of the software concurrently on the same server can cause the analysis to fail or produce incorrect results.

Each flow cell includes a separate run folder.

Analysis Methods

The Illumina DRAGEN COVID Pipeline performs analysis using the following steps. Each of the first seven steps creates a subfolder in `Logs_intermediates` subfolder under the analysis folder.

- Validates the sample sheet fields.
This step generates the `SampleSheetValidation` subfolder.
- Converts BCL data in the run folder to FASTQ sample data. All samples from the run are available as FASTQ files compressed in a gzip. If the `--lane` option is used, only samples in the specified lane are available as FASTQ files.
This step generates the `FastqGeneration` subfolder.
- For each sample, Illumina DRAGEN COVID Pipeline determines the presence of SARS-CoV-2 and an internal (human) control. The read coverage per target is compared to a fixed target threshold to determine covered targets. The number of covered targets is then used to detect SARS-CoV-2 (\geq `virusThreshold`) and the internal control (\geq `humanThreshold`).
The step generates the `VirusDetection` subfolder.
- For each sample, Illumina DRAGEN COVID Pipeline scrubs the original set of FASTQ files to remove human reads using the NCBI Human Read Scrubber algorithm. This step is optional, by default it is enabled but to disable provide the `--disableScrubReads` flag at run time. This step generates the `ScrubbedReads` subfolder.
- For each sample with a result of SARS-CoV-2 Detected and at least 90 SARS-CoV-2 targets detected, Illumina DRAGEN COVID Pipeline aligns FASTQ files to the SARS-CoV-2 reference genome. To change the number of targets detected from the default of 90, use the `--ampliconThreshold` option at run time. To change the aligner minimum score from the default of 22, use the `--alignerMinScore` option at run time.
This step generates the `MapAlign` subfolder.
- For each sample with a result of SARS-CoV-2 Detected and at least 90 SARS-CoV-2 targets detected, Illumina DRAGEN COVID Pipeline performs variant calling to determine any variants present in the sample with respect to the SARS-CoV-2 reference genome. To change the number of targets detected from the default of 90, use the `--ampliconThreshold` option at run time. To change the variant callability threshold from the default of 10, use the `--callabilityThreshold` option at run time. This step produces VCF files containing detected variants for each processed sample. See [Variant Calling and Consensus Sequence Generation for Research Use Only on page 7](#) for more information.
This step generates the `VariantCalling` subfolder.

- 7 For each sample with a result of SARS-CoV-2 Detected and at least 90 SARS-CoV-2 targets detected, Illumina DRAGEN COVID Pipeline generates a consensus genome in FASTA format using variant calls and coverage metrics as input. To change the number of targets detected from the default of 90, use the `--ampliconThreshold` option at run time. See [Variant Calling and Consensus Sequence Generation for Research Use Only on page 7](#) for more information. This step generates the `ConsensusFasta` subfolder.
- 8 For each sample, Illumina DRAGEN COVID Pipeline generates a filtered BAM file with unaligned reads removed. This step is optional, by default it is enabled but to disable provide the `--disableFilterReads` flag at run time. This step generates the `FilteredReads` subfolder.
- 9 The Illumina DRAGEN COVID Pipeline generates a combined coverage report (`coverage.csv` file) that determines if the sample had greater than or equal to 30x coverage.

For information about downstream analysis using third-party software, see [DRAGEN COVID Lineage Tools on page 7](#).

Detection Algorithm

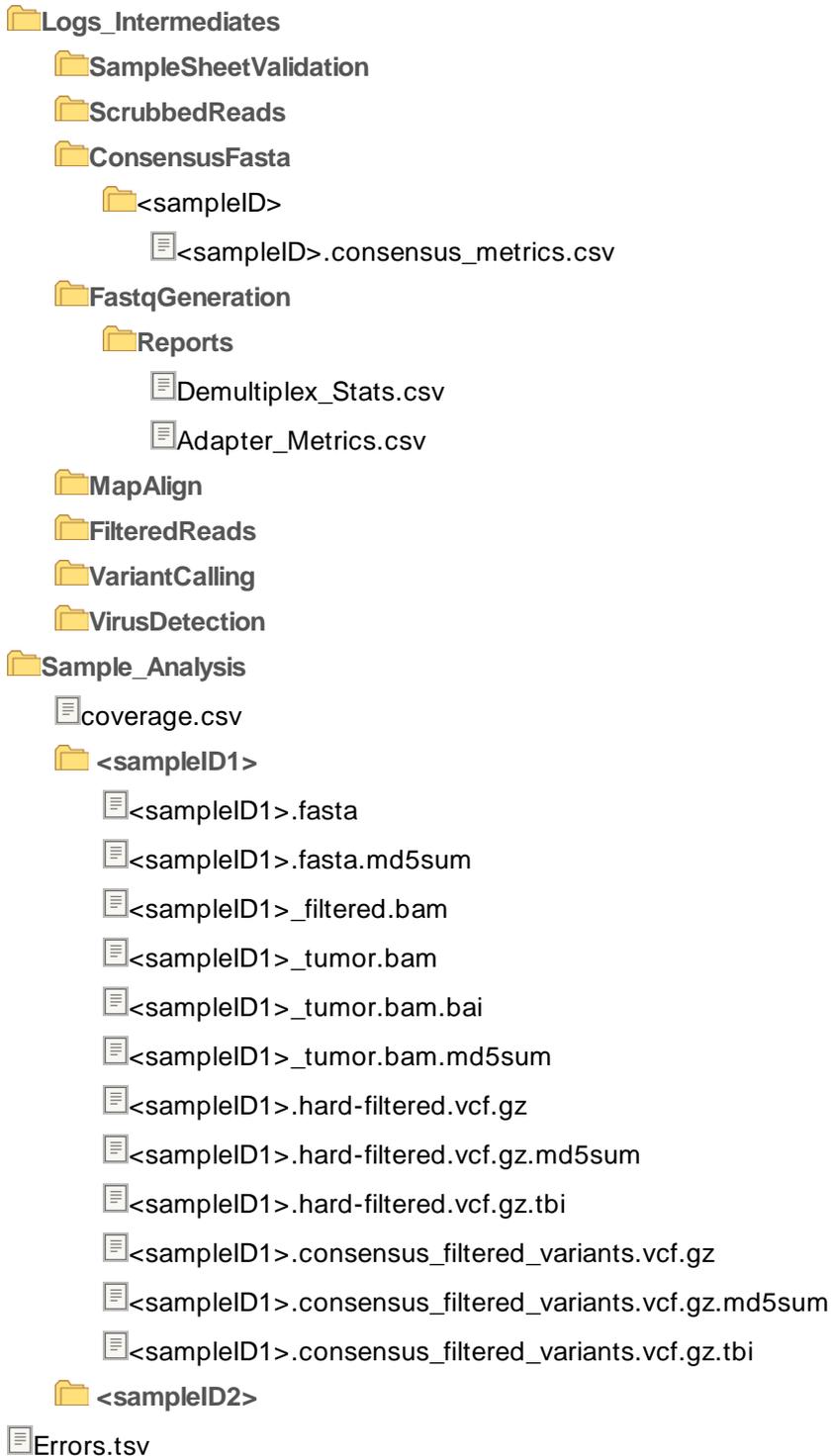
The Illumina DRAGEN COVID Pipeline uses a kmer based algorithm to detect SARS-CoV-2 and any external controls. The algorithm uses a kmer reference database to match kmers from the sequencing read to kmers from the SARS-CoV-2 reference genome (NC_0455). To create the kmer reference list, the SARS-CoV-2 reference genome is split in 32 bp kmers, and then any kmers that contain cross-reactivity are removed. To measure cross-reactivity, the kmer reference list uses the NCBI database of 100k human and animal pathogens. Bat and pangolin viruses are not included because of the similarity to the SARS-CoV-2 genome.

The kmer algorithm is performed using the following process:

- 1 The sequencing read is split into 32 bp kmers.
- 2 The kmers are matched to the kmer reference list.
- 3 Each of the reference kmers is labeled with a corresponding amplicon from either SARS-CoV-2 or external control.
- 4 If an amplicon contains at least 150 matched read and reference kmers, the amplicon is detected.
- 5 If the following number of amplicons are present, the algorithm detects SARS-CoV-2 or the external control.
 - ▶ SARS-CoV-2 is detected if there are at least 5 SARS-CoV-2 amplicons.
 - ▶ External control is detected if there are at least 3 external control amplicons.

Output Structure

The Illumina DRAGEN COVID Pipeline outputs results in the following folder structure. Key output files are shown below.



 AnalysisLog.txt

 run.log

 task_duration.csv

Variant Calling and Consensus Sequence Generation for Research Use Only

Illumina DRAGEN COVID Pipeline performs variant and consensus sequence generation for each sample with a result of SARS-CoV-2 Detected and at least 90 SARS-CoV-2 virus targets detected. To change the number of targets detected from the default of 90, use the `--ampliconThreshold` option at run time. Variant calls and consensus sequences are for information purposes only and should not be used for patient reporting.

Variant calling and consensus sequence generation is not performed for invalid samples.

The variant calling output file is generated in VCF 4.2 file format and located in `Sample_Analysis/<Sample ID>/<Sample ID>.hard-filtered.vcf.gz`.

The consensus filtered variant calling output file is located in `Sample_Analysis/<Sample ID>/<Sample ID>.consensus_filtered_variants.vcf.gz`.

To generate a consensus sequence in FASTA format, detected sequence variants that meet the following criteria are applied to the SARS-CoV-2 reference sequence (NCBI Accession NC_045512.2).

- ▶ All DRAGEN quality filters pass.
- ▶ Allele frequency is greater than or equal to 0.5.
- ▶ Depth is greater than or equal to 10.

Regions of sequence with coverage below 10 are masked as low-confidence. Hard-masking is applied, and all bases in low-confidence regions are converted to "N". A soft-masked sequence is also provided and indicates all low-confidence regions with lower case characters.

The hard-masked consensus FASTA is available in `Sample_Analysis/<Sample ID>/<Sample ID>.fasta`.

Uninstall Illumina DRAGEN COVID Pipeline

The Illumina DRAGEN COVID Pipeline includes an uninstall script located in the `/usr/local/bin` called `uninstall_dragen-covid-pipeline-1.1.0.sh`.

The uninstall script removes the following assets:

- ▶ All scripts (`dragen-covid-pipeline.sh`, `check_dragen-covid-pipeline-1.0.1.sh`, `uninstall_dragen-covid-pipeline-1.0.1.sh`).
- ▶ The Illumina DRAGEN COVID Pipeline Docker image.
- ▶ Data stored in `/staging/illumina/dragen-covid-pipeline`.

The script does not uninstall Docker.

To uninstall the Illumina DRAGEN COVID Pipeline, enter the following command as root.

```
/usr/local/bin/uninstall_dragen-covid-pipeline-1.1.0.sh
```

DRAGEN COVID Lineage Tools

The DRAGEN COVID Lineage Tools has been updated to patch a bug related to the NextClade software. This will be the last update made to this product. Illumina support for the DRAGEN COVID Lineage Tools is being discontinued. Customers can continue to use this version of the software, or to get the latest versions of Pangolin and NextClade they can download those tools directly.

- ▶ Pangolin: <https://github.com/cov-lineages/pangolin>
- ▶ NextClade: <https://docs.nextstrain.org/projects/nextclade/en/latest/user/nextclade-cli.html>

You can use the DRAGEN COVID Lineage Tools software package for complimentary downstream analysis for Illumina DRAGEN COVID Pipeline.

DRAGEN COVID Lineage Tools packages the third-party software applications Pangolin and NextClade, which provide lineage and clade determination of viral RNA sequences found in FASTA files. The DRAGEN COVID Lineage Tools software package is not supported by Illumina Technical Support.

The software is packaged as a Docker image and deployed as a TAR file.

Load and run DRAGEN COVID Lineage Tools, as follows.

- 1 Download the TAR file from the Illumina DRAGEN COVID Pipeline support page.

- 2 To extract the image, load the TAR file into Docker by entering the following command:

```
docker load < dragen-covid-lineage-tools-1.1.0.tar
```

- 3 To see all the images on your server, enter the following command:

```
docker images
```

The response displays all docker images on the system, which should include the image **dragen-covid-lineage-tools:1.0.1**.

- 4 To run the image as a container, enter the following command:

```
docker run -t -v {PATH_TO_FASTA_FOLDER}:/opt/illumina/fasta-folder:ro -v
  {PATH_TO_ANALYSIS_FOLDER}:/opt/illumina/analysis-folder:rw dragen-
  covid-lineage-tools:1.0.1 --max-indel 400 --max-ambig 0.6
```

For descriptions of the options used, refer to the following table:

Option	Description
{PATH_TO_ANALYSIS_FOLDER}	Set to an absolute folder path on your server. The analysis output is saved to the folder location.
{PATH_TO_FASTA_FOLDER}	Set to an absolute folder path on your server that contains your FASTA files. FASTA files can be nested inside the root folder. For example, the output from the Illumina DRAGEN COVID Pipeline produces a Sample_Analysis folder, which contains {Sample_ID} subfolders. Inside of the subfolders are the sample FASTA files. Point to the root Sample_Analysis folder and the software recursively finds all the nested FASTA files.
--max-ambig	Specifies the maximum proportion of Ns allowed for Pangolin to attempt assignment. The default value is 0.5.
--update-nextclade	This feature is disabled in this version of the dragen-covid-lineage-tools and is locked to the current latest version of 1.10.2
--update-pangolin	This feature is disabled in this version of the dragen-covid-lineage-tools and is locked to the current latest version of 3.1.19. Make sure the server is connected to the internet for the update to occur.

Option	Description
<code>--max-indel</code>	For Nextclade: Maximum amount of insertions, deletions, duplications, or ambiguous seed matches allowed to proceed with alignment. Alignments with long indels are slow to compute and require substantial memory in the current implementation. Alignment of sequences with indels longer than this value, will not be attempted and a warning will be emitted. Default:400.

Outputs

The DRAGEN COVID Lineage Tools software generates the following outputs:

Output	Path	Description
Combined Clade Report	<code>./analysis-folder/combined_clade_report.csv</code>	A combined CSV file containing all sample clade reports.
Combined FASTA	<code>./analysis-folder/combined_fasta.fasta</code>	A concatenated file of all processed FASTA files.
Combined Lineage Report	<code>./analysis-folder/combined_lineage_report.csv</code>	A combined CSV file containing all sample lineage reports.
Log File	<code>./analysis-folder/covid-lineage-tools- <timestamp>.log</code>	Details the functions performed by the software and any errors encountered.
Per Sample Clade Reports	<code>./analysis-folder/{sample-id}/{sample-id}.clade_report.csv</code> <code>./analysis-folder/{sample-id}/{sample-id}.clade_report.tsv</code> <code>./analysis-folder/{sample-id}/{sample-id}.clade_report.json</code>	Clade reports produced by NextClade for each sample. The report is named after the sample ID found in the FASTA file name. NextClade generates the same report in following file formats: <ul style="list-style-type: none"> • csv • tsv • json For example, the file <code>sample1.fasta</code> would have the following reports: <ul style="list-style-type: none"> • <code>sample1.clade_report.csv</code> • <code>sample1.clade_report.tsv</code> • <code>sample1.clade_report.json</code>
Per Sample Lineage Report	<code>./analysis-folder/{sample-id}/{sample-id}.lineage_report.csv</code>	A lineage report produced by Pangolin for each sample. The report is named after the sample ID found in the FASTA file name. For example, the file <code>sample1.fasta</code> would have a report with the name <code>sample1.lineage_report.csv</code> .

Technical Assistance

For technical assistance, contact Illumina Technical Support.

Website: www.illumina.com
Email: techsupport@illumina.com

Illumina Technical Support Telephone Numbers

Region	Toll Free	International
Australia	+61 1800 775 688	
Austria	+43 800 006249	+43 1 9286540
Belgium	+32 800 77 160	+32 3 400 29 73
Canada	+1 800 809 4566	
China		+86 400 066 5835
Denmark	+45 80 82 01 83	+45 89 87 11 56
Finland	+358 800 918 363	+358 9 7479 0110
France	+33 8 05 10 21 93	+33 1 70 77 04 46
Germany	+49 800 101 4940	+49 89 3803 5677
Hong Kong, China	+852 800 960 230	
India	+91 8006500375	
Indonesia		0078036510048
Ireland	+353 1800 936608	+353 1 695 0506
Italy	+39 800 985513	+39 236003759
Japan	+81 0800 111 5011	
Malaysia	+60 1800 80 6789	
Netherlands	+31 800 022 2493	+31 20 713 2960
New Zealand	+64 800 451 650	
Norway	+47 800 16 836	+47 21 93 96 93
Philippines	+63 180016510798	
Singapore	1 800 5792 745	
South Korea	+82 80 234 5300	
Spain	+34 800 300 143	+34 911 899 417
Sweden	+46 2 00883979	+46 8 50619671
Switzerland	+41 800 200 442	+41 56 580 00 00
Taiwan, China	+886 8 06651752	
Thailand	+66 1800 011 304	
United Kingdom	+44 800 012 6019	+44 20 7305 7197
United States	+1 800 809 4566	+1 858 202 4566
Vietnam	+84 1206 5263	

Safety data sheets (SDSs)—Available on the Illumina website at support.illumina.com/sds.html.

Product documentation—Available for download from support.illumina.com.



Illumina

5200 Illumina Way

San Diego, California 92122 U.S.A.

+1.800.809.ILMN (4566)

+1.858.202.4566 (outside North America)

techsupport@illumina.com

www.illumina.com

For Research Use Only. Not for use in diagnostic procedures.

© 2022 Illumina, Inc. All rights reserved.

illumina[®]