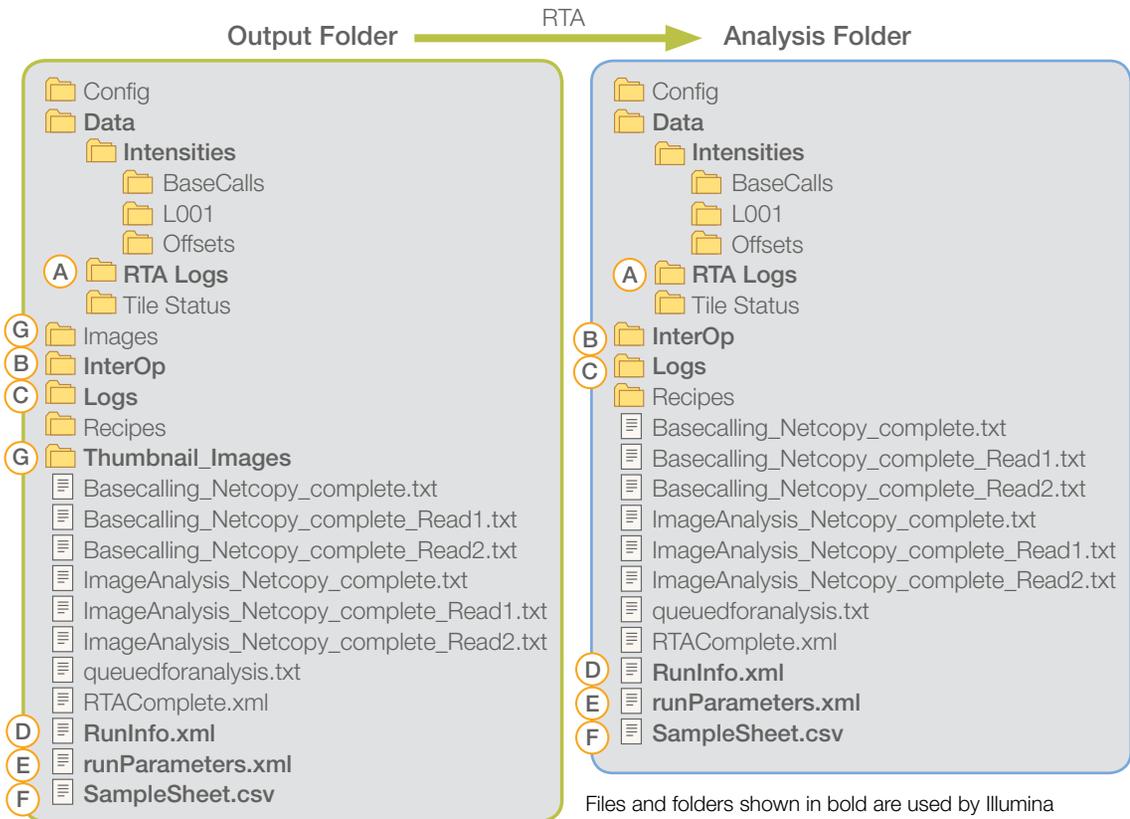


Folders Before Secondary Analysis

- A RTA Logs folder**—Contains log files that describe each step performed by RTA for each Read.
- B InterOp folder**—Contains binary files used by Sequencing Analysis Viewer (SAV) to summarize various primary analysis metrics, such as cluster density, intensities, quality scores, and overall run quality.
- C Logs folder**—Contains log files that describe every step performed by the instrument for each cycle.
- D RunInfo.xml**—Contains high-level run information, such as the number of Reads and cycles in the sequencing run.
- E runParameters.xml**—Contains a summary of run parameters and information about run components, such as the RFID of the flow cell and reagents associated with the run.
- F SampleSheet.csv**—Provides parameters for the run and subsequent analysis. At the start of the run, the sample sheet is copied to the root folder and renamed SampleSheet.csv. Copies are located in Data\Intensities and Data\Intensities\BaseCalls.
- G Images and Thumbnail_Images folders**—Contains focus images and thumbnails images. These folders are not required for secondary analysis and are not copied to the Analysis folder.



Files and folders shown in bold are used by Illumina Technical Support for troubleshooting a run.

Folders After Secondary Analysis Begins

- A RTA Logs folder**—Contains log files that describe each step performed by RTA for each Read.
- B InterOp folder**—Contains binary files used by Sequencing Analysis Viewer (SAV) to summarize various primary analysis metrics, such as cluster density, intensities, quality scores, and overall run quality.
- C Logs folder**—Contains log files that describe every step performed by the instrument for each cycle.
- D RunInfo.xml**—Contains high-level run information, such as the number of Reads and cycles in the sequencing run.
- E runParameters.xml**—Contains a summary of run parameters and information about run components, such as the RFID of the flow cell and reagents associated with the run.
- F SampleSheet.csv**—Provides parameters for the run and subsequent analysis. At the start of the run, the sample sheet is copied to the root folder and renamed SampleSheet.csv. Copies are located in Data\Intensities and Data\Intensities\BaseCalls.
- G Alignment folder**—Contains alignment (*.bam) and variant call (*.vcf) files. This folder is not created if you set up your run with the GenerateFASTQ workflow.
- H FASTQ files**—Provide intermediate analysis data for downstream third-party analysis. Files are located in Data\Intensities\BaseCalls.

Providing Files for Troubleshooting

Illumina Technical Support uses the files and folders shown in bold for troubleshooting. Maintenance logs, located in the root folder, can also be used for troubleshooting.

Use the bundle logs feature to group and zip the files to send to Illumina Technical Support. For more information, see the *MiSeq System User Guide (part # 15027617)*.

If Illumina Technical Support requests the the alignment folder (\Data\Intensities\BaseCalls), please zip and send the folder.

