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Overview

Intended for whole-genome sequencing of small genomes, the Local Run Manager Resequencing analysis module aligns reads against the specified reference, and then performs variant analysis.

Compatible Library Types

The Resequencing analysis module is compatible with specific library types represented by library kit categories on the Create Run screen. For a current list of compatible library kits, see the [Local Run Manager support page](#) on the Illumina website.

Input Requirements

In addition to sequencing data files generated during the sequencing run, such as base call files, the Resequencing analysis module requires a reference genome.

A reference genome provides the chromosome and start coordinate in the alignment output file. When setting up run and analysis parameters, specify the path to the reference genome associated with each sample to be sequenced.

About This Guide

This guide provides instructions for setting up run parameters for sequencing and analysis parameters for the Resequencing analysis module. For information about the Local Run Manager dashboard and system settings, see the *Local Run Manager Software Guide (document # 1000000002702)*.

Set Parameters

- 1 If needed, log in to Local Analysis Software.
- 2 Select **Create Run**, and select **Resequencing**.
- 3 Enter a run name that identifies the run from sequencing through analysis.
The run name can contain alphanumeric characters, spaces, and the following special characters:
`~. !@#\$%-_{ }.
- 4 **[Optional]** Enter a run description to identify the run.
The run description can contain alphanumeric characters, spaces, and the following special characters:
`~. !@#\$%-_{ }.

Specify Run Settings

- 1 Select the library prep kit from the Library Prep Kit drop-down list.
- 2 Specify the number of index reads.
 - ▶ 0 for a run with no indexing
 - ▶ 1 for a single-indexed run
 - ▶ 2 for a dual-indexed run
- 3 Select the read type for the run, if a change is possible.
- 4 Enter the number of cycles for the run.
- 5 **[Optional]** For Custom Primers, specify any custom primer information to be used for the run by selecting

the appropriate checkboxes.

Custom primer options vary based on your instrument or Local Run Manager implementation.

Specify Module-Specific Settings

- 1 Select an alignment method from the Aligner drop-down list.
 - ▶ **BWA-MEM**—(Default) Optimized for Illumina sequencing data and reads ≥ 70 bp.
 - ▶ **BWA-Backtrack Legacy**—Use with legacy data or reads < 70 bp.
- 2 Select a variant calling method from the Variant Caller drop-down list.
 - ▶ **Starling**—Calls SNPs and small indels, and summarizes depth and probabilities for every site in the genome.
 - ▶ **GATK**—(Default) Calls raw variants for each sample, analyzes variants against known variants, and then calculates a false discovery rate for each variant.
- 3 Select the **On/Off** toggle to enable or disable the following settings.
 - ▶ **Export to gVCF**—Off by default. When enabled, analysis includes gVCF files that contain information about all sites within the region of interest. If Starling is the selected variant calling method, this setting is turned on automatically.
 - ▶ **Flag PCR Duplicates**—On by default. When enabled, PCR duplicates are flagged in the BAM files and not used for variant calling. PCR duplicates are defined as 2 clusters from a paired-end run where both clusters have the exact same alignment position for each read.
 - ▶ **Indel Realignment**—Off by default. When enabled, regions containing indels are locally realigned to minimize the number of mismatches.
 - ▶ **Reverse Complement**—(Only available with Nextera Mate Pair library prep kits) Off by default. When enabled, all reads are reverse-complemented as they are written to FASTQ files.

Specify Samples for the Run



Specify samples for the run using the following options:

- ▶ **Enter samples manually**—Use the blank table at the bottom of the Create Run screen.
- ▶ **Import sample sheet**—Navigate to an external file in a comma-separated values (*.csv) format.

After you have populated the samples table, you can export the sample information to an external file. You can use this file as a reference when preparing libraries or import the file when configuring another run.

Enter Samples Manually

To manually enter sample information, you must first select a Library Prep Kit in the Run Settings section.

- 1 Adjust the samples table to an appropriate number of rows.
 - ▶ In the Rows field, use the up/down arrows or enter a number to specify the number of rows to add to the table. Select  to add the rows to the table.
 - ▶ Select  to delete a row.
 - ▶ Right-click on a row in the table and use the commands in the contextual menu.
- 2 Enter a unique sample ID in the Sample ID field.
Use alphanumeric characters, dashes, or underscores. Spaces are not allowed in the Sample ID field.
- 3 **[Optional]** Enter a sample description in the Sample Description field.
Use alphanumeric characters, dashes, or underscores. Spaces are not allowed in the Sample Description field.
- 4 If you have a plated kit, select an index plate well from the Index well drop-down list and skip to step 7.

- 5 If applicable, specify an Index 1 sequence.
- 6 If applicable, specify an Index 2 sequence.

**NOTE**

During analysis, the iSeq™ 100, MiniSeq™, and NextSeq™ Systems automatically reverse complement the i5 indexes in custom library prep kits. Make sure that the i5 indexes are in the forward orientation.

- 7 Select a reference genome from the Genome Folder drop-down list.
- 8 **[Optional]** Enter a project name in the Sample Project field.
Use alphanumeric characters, dashes, or underscores. Spaces are not allowed in the Sample Project field.
- 9 **[Optional]** Select **Export Sample Sheet** to export the sample information in *.csv format.
The exported sample sheet can be used as a template or imported when creating new runs.
- 10 Select **Save Run**.

Import Sample Sheet

- 1 If you do not have a sample sheet to import, see *Enter Samples Manually on page 4* for instructions on how to create and export a sample sheet. Edit the file as follows.
 - a Open the sample sheet in a text editor.
 - b Enter the sample information in the [Data] section of the file.
 - c Save the file. Make sure that the sample IDs are unique.
- 2 Select **Import Sample Sheet** at the top of the Create Run screen and browse to the location of the sample sheet.
Make sure that the information in the sample sheet is correct. Incorrect information can impact the sequencing run.
- 3 When finished, select **Save Run**.

Analysis Methods

The Resequencing analysis module performs the following analysis steps and then writes analysis output files to the Alignment folder.

- ▶ Demultiplexes index reads
- ▶ Generates FASTQ files
- ▶ Aligns to a reference
- ▶ Identifies variants

Demultiplexing

Demultiplexing compares each Index Read sequence to the index sequences specified for the run. No quality values are considered in this step.

Index reads are identified using the following steps:

- ▶ Samples are numbered starting from 1 based on the order they are listed for the run.
- ▶ Sample number 0 is reserved for clusters that were not assigned to a sample.

- ▶ Clusters are assigned to a sample when the index sequence matches exactly or when there is up to a single mismatch per Index Read.

FASTQ File Generation

After demultiplexing, the software generates intermediate analysis files in the FASTQ format, which is a text format used to represent sequences. FASTQ files contain reads for each sample and the associated quality scores. Any controls used for the run and clusters that did not pass filter are excluded.

Each FASTQ file contains reads for only one sample, and the name of that sample is included in the FASTQ file name. FASTQ files are the primary input for alignment.

Adapter Trimming

The Resequencing analysis module performs adapter trimming by default.

During longer runs, clusters can sequence beyond the sample DNA and read bases from a sequencing adapter. To prevent sequencing into the adapter, the adapter sequence is trimmed before the sequence is written to the FASTQ file. Trimming the adapter sequence avoids reporting false mismatches with the reference sequence and improves alignment accuracy and performance.

Adapter Sequences

When using the Resequencing analysis module, the following adapter sequences are trimmed depending on the selected library prep method:

- ▶ IDT-ILMN TruSeq DNA-RNA UD Indexes 24 Indexes
 - ▶ Read 1: AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
 - ▶ Read 2: AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT
- ▶ IDT-ILMN TruSeq DNA-RNA UD Indexes 96 Indexes
 - ▶ Read 1: AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
 - ▶ Read 2: AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT
- ▶ Nextera DNA, Nextera XT, Nextera XT v2
 - ▶ Read 1: CTGTCTCTTATACACATCT
- ▶ Nextera DNA CD Indexes - 24 Indexes Tubed
 - ▶ Read 1: CTGTCTCTTATACACATCT
- ▶ Nextera DNA CD Indexes - 96 Indexes Plated
 - ▶ Read 1: CTGTCTCTTATACACATCT
- ▶ Nextera DNA
 - ▶ Read 1: CTGTCTCTTATACACATCT+AGATGTGTATAAGAGACAG
- ▶ TruSeq DNA-RNA CD Indexes 96 Indexes
 - ▶ Read 1: AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
 - ▶ Read 2: AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT
- ▶ TruSeq DNA-RNA Single Indexes Set A&B
 - ▶ Read 1: AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
 - ▶ Read 2: AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

Alignment

During the alignment step, reads are aligned against the entire reference genome using the Burrows-Wheeler Aligner (BWA), which aligns relatively short nucleotide sequences against a long reference sequence. BWA automatically adjusts parameters based on read lengths and error rates, and then estimates insert size distribution.

The Resequencing analysis module provides the option of using BWA-MEM or BWA-Backtrack Legacy for the alignment step.

BWA-MEM

BWA-MEM is the most recent version of the Burrows-Wheeler Alignment algorithm. Optimized for longer read lengths of ≥ 70 bp, BWA-MEM has a significant positive impact on detection of variants, especially insertions and deletions.

BWA-Backtrack

BWA-Backtrack is an earlier version of the Burrows-Wheeler Aligner algorithm that aligns sequencing read lengths in < 70 bp segments. Use this version for very short reads, or when consistency is required with previous study data.

Variant Calling

Variant calling records single nucleotide polymorphisms (SNPs), insertions/deletions (indels), and other structural variants in a standardized variant call format (VCF).

For each SNP or indel called, the probability of an error is provided as a variant quality score. When Indel Realignment is enabled, reads are realigned around candidate indels to improve the quality of the calls and site coverage summaries.

The Resequencing analysis module provides the option of using Starling or GATK for variant calling.

Starling


Starling calls both SNPs and small indels, and summarizes depth and probabilities for every site in the genome. Starling produces a VCF file for each sample that contains variants.

Starling treats each insertion or deletion as a single mismatch. Base calls with more than two mismatches to the reference sequence within 20 bases of the call are ignored. If the call occurs within the first or last 20 bases of a read, the mismatch limit is increased to 41 bases.

GATK



The Genome Analysis Toolkit (GATK) calls raw variants for each sample, analyzes variants against known variants, and then calculates a false discovery rate for each variant. Variants are flagged as homozygous (0/0 or 1/1) or heterozygous (0/1 or 1/0) in the VCF file sample column. For more information, see www.broadinstitute.org/gatk.

View Analysis Results

- 1 From the Local Analysis Software dashboard, select the run name.
- 2 From the Run Overview tab, review the sequencing run metrics.
- 3 To change the analysis data file location for future requeues of the selected run, select the **Edit**  icon,

and edit the output run folder file path.

The file path leading up to the output run folder is editable. The output run folder name cannot be changed.

- 4 **[Optional]** Select the **Copy to Clipboard**  icon to copy the output run folder file path.
- 5 Select the Sequencing Information tab to review run parameters and consumables information.
- 6 Select the Samples & Results tab to view the analysis report.
 - ▶ If analysis was requeued, select the appropriate analysis from the Select Analysis drop-down list.
 - ▶ From the left navigation bar, select a sample ID to view the report for another sample.
- 7 **[Optional]** Select the **Copy to Clipboard**  icon to copy the Analysis Folder file path.

Analysis Report

Analysis results are summarized on the Samples & Results tab. The report is also available in a PDF file format for each sample and as an aggregate report in the Analysis folder.

Sample Information

Column Heading	Description
Sample ID	The sample ID provided when the run was created.
Sample Name	The sample name provided when the run was created.
Run Folder	The name of the run folder.
Total PF Reads	The total number of reads passing filter.
Percent Q30 Bases	The percentage of bases called with a quality score \geq Q30.

Read Level Statistics

Column Heading	Description
Total Aligned Reads	The total number of reads that aligned to the reference for each read (Read 1 and Read 2).
Percent Aligned Reads	The percentage of reads that aligned to the reference for each read (Read 1 and Read 2).

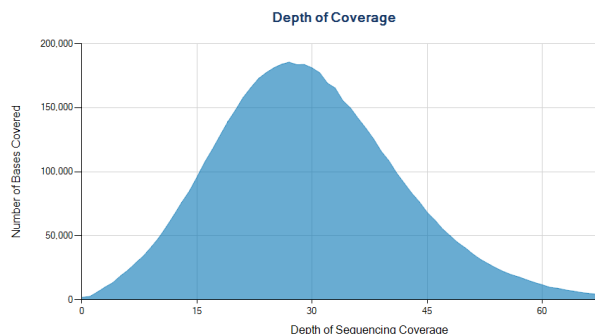
Base Level Statistics

Column Heading	Description
Total Aligned Bases	The total number of bases that aligned to the reference for each read (Read 1 and Read 2).
Percent Aligned Bases	The percentage of aligned bases averaged over cycles per read (Read 1 and Read 2).
Mismatch Rate	The percentage of bases that did not align to the reference averaged over cycles per read (Read 1 and Read 2).

Coverage Histogram

The coverage histogram shows the depth of sequencing coverage across the number of bases covered. The depth of coverage is calculated by the number of bases aligned to a given reference position averaged over all positions.

Figure 1 Coverage Histogram (Example)



Small Variants Summary

Row Heading	Description
Total Passing	The total number of variants passing filter for single nucleotide variations (SNVs), insertions, and deletions.
Percent Found in dbSNP	The percentage of variants called by the variant caller that are also present in dbSNP.
Het/Hom Ratio	The ratio of the number of heterozygous SNPs and number of homozygous SNPs detected for the sample.
Ts/Tv Ratio	The ratio of transitions and transversions in SNPs. <ul style="list-style-type: none"> • Transitions are variants of the same nucleotide type (pyrimidine to pyrimidine, C and T; or purine to purine, A and G). • Transversions are variants of a different nucleotide type (pyrimidine to purine, or purine to pyrimidine).

Fragment Length Summary

The fragment length summary section lists the average length of the sequenced fragment for the selected sample, the minimum fragment length, the maximum fragment length, and the range of variability listed as standard deviation. To account for potential outliers, the minimum and maximum are calculated from values within ~ 3 standard deviations, excluding the lower and upper 0.15% of the data.

Duplicate Information

The duplicate information section lists the percentage of clusters for a paired-end sequencing run that are considered to be PCR duplicates. PCR duplicates are defined as 2 clusters from a paired-end run where both clusters have the exact same alignment positions for each read.

Analysis Output Files

The following analysis output files are generated for the Resequencing analysis module and provide analysis results for alignment and variant calling. Analysis output files are located in the Alignment folder.

File Name	Description
Demultiplexing (*.demux)	Intermediate files containing demultiplexing results.
FASTQ (*.fastq.gz)	Intermediate files containing quality scored base calls. FASTQ files are the primary input for the alignment step.
Alignment files in the BAM format (*.bam)	Contains aligned reads for a given sample.
Variant call files in the VCF format (*.vcf)	Contains information about variants found at specific positions in a reference genome.
Variant call files in the genome VCF format (*.genome.vcf)	Available when the Export to gVCF setting is enabled, these files contain the genotype for each position, whether called as a variant or called as a reference.

Demultiplexing File Format

The process of demultiplexing reads the index sequence attached to each cluster to determine from which sample the cluster originated. The mapping between clusters and sample number is written to a demultiplexing (*.demux) file for each tile of the flow cell.

The demultiplexing file naming format is **s_1_X.demux**, where X is the tile number.

Demultiplexing files start with a header:

- ▶ Version (4-byte integer), currently 1
- ▶ Cluster count (4-byte integer)

The remainder of the file consists of sample numbers for each cluster from the tile.

When the demultiplexing step is complete, the software generates a demultiplexing file named **DemultiplexSummaryF1L1.txt**.

- ▶ In the file name, **F1** represents the flow cell number.
- ▶ In the file name, **L1** represents the lane number.
- ▶ Demultiplexing results in a table with one row per tile and one column per sample, including sample 0.
- ▶ The most commonly occurring sequences in index reads.

FASTQ File Format

FASTQ is a text-based file format that contains base calls and quality values per read. Each record contains 4 lines:

- ▶ The identifier
- ▶ The sequence
- ▶ A plus sign (+)
- ▶ The Phred quality scores in an ASCII + 33 encoded format

The identifier is formatted as:

@Instrument:RunID:FlowCellID:Lane:Tile:X:Y ReadNum:FilterFlag:0:SampleNumber

Example:

```
@SIM:1:FCX:1:15:6329:1045 1:N:0:2
TCGCACTCAACGCCCTGCATATGACAAGACAGAATC
+
<>;##=><9=AAAAAAAAAA9#:<#<;<<<????#=#
```

BAM File Format

A BAM file (*.bam) is the compressed binary version of a SAM file that is used to represent aligned sequences. SAM and BAM formats are described in detail at samtools.github.io/hts-specs/SAMv1.pdf.

BAM files use the file naming format of **SampleName_S#.bam**, in which # is the sample number determined by the order that samples are listed for the run.

BAM files contain a header section and an alignment section:

- ▶ **Header**—Contains information about the entire file, such as sample name, sample length, and alignment method. Alignments in the alignments section are associated with specific information in the header section.
- ▶ **Alignments**—Contains read name, read sequence, read quality, alignment information, and custom tags. The read name includes the chromosome, start coordinate, alignment quality, and match descriptor string.

The alignments section includes the following information for each read or read pair:

- ▶ **RG**—Read group, which indicates the number of reads for a specific sample.
- ▶ **MD**—Mismatching positions/bases.
- ▶ **AS**—Paired-end alignment quality.
- ▶ **NM**—Edit distance tag, which records the Levenshtein distance between the read and the reference.
- ▶ **XS**—Suboptimal alignment score.

BAM files are suitable for viewing with an external viewer, such as IGV or the UCSC Genome Browser.

BAM index files (*.bam.bai) provide an index of the corresponding BAM file.

VCF File Format

Variant Call Format (VCF) is a common file format developed by the genomics scientific community. It contains information about variants found at specific positions in a reference genome. VCF files end with the .vcf or .vcf.gz suffixes.

The VCF file header includes the VCF file format version and the variant caller version and lists the annotations used in the remainder of the file. The last line in the header contains the column headings for the data lines. Each of the VCF file data lines contains information about one variant.

VCF File Headings

Heading	Description
CHROM	The chromosome of the reference genome. Chromosomes appear in the same order as the reference FASTA file.
POS	The single-base position of the variant in the reference chromosome. For SNVs, this position is the reference base with the variant. For indels, this position is the reference base immediately preceding the variant.
ID	The rs number for the SNP obtained from dbSNP.txt, if applicable. If multiple rs numbers exist at this location, the list is delimited by semicolons. If a dbSNP entry does not exist at this position, a missing value marker ('.') is used.
REF	The reference genotype. For example, a deletion of a single T is represented as reference TT and alternate T. An A to T single nucleotide variant is represented as reference A and alternate T.

Heading	Description
ALT	The alleles that differ from the reference read. For example, an insertion of a single T is represented as reference A and alternate AT. An A to T single nucleotide variant is represented as reference A and alternate T.
QUAL	A Phred-scaled quality score assigned by the variant caller. Higher scores indicate higher confidence in the variant and lower probability of errors. For a quality score of Q, the estimated probability of an error is $10^{-(Q/10)}$. For example, the set of Q30 calls has a 0.1% error rate. Many variant callers assign quality scores based on their statistical models, which are high in relation to the error rate observed.

VCF File Annotations

Heading	Description
FILTER	If all filters are passed, PASS is written in the filter column. <ul style="list-style-type: none"> • LowDP—Applied to sites with depth of coverage below a cutoff. • LowGQ—The genotyping quality (GQ) is below a cutoff. • LowQual—The variant quality (QUAL) is below a cutoff. • LowVariantFreq—The variant frequency is less than the given threshold. • R8—For an indel, the number of adjacent repeats (1-base or 2-base) in the reference is greater than 8. • SB—The strand bias is more than the given threshold. Used with the Somatic Variant Caller and GATK.
INFO	Possible entries in the INFO column include: <ul style="list-style-type: none"> • AC—Allele count in genotypes for each ALT allele, in the same order as listed. • AF—Allele Frequency for each ALT allele, in the same order as listed. • AN—The total number of alleles in called genotypes. • CD—A flag indicating that the SNP occurs within the coding region of at least 1 RefGene entry. • DP—The depth (number of base calls aligned to a position and used in variant calling). • EXON—A comma-separated list of exon regions read from RefGene. • FC—Functional Consequence. • GI—A comma-separated list of gene IDs read from RefGene. • QD—Variant Confidence/Quality by Depth. • TI—A comma-separated list of transcript IDs read from RefGene.
FORMAT	The format column lists fields separated by colons. For example, GT:GQ. The list of fields provided depends on the variant caller used. Available fields include: <ul style="list-style-type: none"> • AD—Entry of the form X,Y, where X is the number of reference calls, and Y is the number of alternate calls. • DP—Approximate read depth; reads with MQ=255 or with bad mates are filtered. • GQ—Genotype quality. • GQX—Genotype quality. GQX is the minimum of the GQ value and the QUAL column. In general, these values are similar; taking the minimum makes GQX the more conservative measure of genotype quality. • GT—Genotype. 0 corresponds to the reference base, 1 corresponds to the first entry in the ALT column, and so on. The forward slash (/) indicates that no phasing information is available. • NL—Noise level; an estimate of base calling noise at this position. • PL—Normalized, Phred-scaled likelihoods for genotypes. • SB—Strand bias at this position. Larger negative values indicate less bias; values near 0 indicate more bias. Used with the Somatic Variant Caller and GATK. • VF—Variant frequency; the percentage of reads supporting the alternate allele.
SAMPLE	The sample column gives the values specified in the FORMAT column.

Genome VCF Files

Genome VCF (gVCF) files are VCF v4.1 files that follow a set of conventions for representing all sites within the genome in a reasonably compact format. The gVCF files include all sites within the region of interest in a single file for each sample.

The gVCF file shows no-calls at positions with low coverage, or where a low-frequency variant occurs. For low-frequency variants, it must occur often enough that the position cannot be called to the reference. A genotype (GT) tag of `./.` indicates a no-call.

If the genotypes of interest feature is turned on, the gVCF file may show variant calls of interest that are requested by the user. These calls may have a filter value of “ForcedReport”, indicating that the calls were force written to the gVCF file.

For more information, see sites.google.com/site/gvcftools/home/about-gvcf.

Supplementary Output Files

The following output files provide supplementary information, or summarize run results and analysis errors. Although these files are not required for assessing analysis results, they can be used for troubleshooting purposes. All files are located in the Alignment folder unless otherwise specified.

File Name	Description
AdapterTrimming.txt	Lists the number of trimmed bases and percentage of bases for each tile. This file is present only if adapter trimming was specified for the run.
AnalysisLog.txt	Processing log that describes every step that occurred during analysis of the current run folder. This file does not contain error messages. Located in the root level of the run folder.
AnalysisError.txt	Processing log that lists any errors that occurred during analysis. This file will be empty if no errors occurred. Located in the root level of the run folder.
CompletedJobInfo.xml	Written after analysis is complete. Contains information about the run, such as date, flow cell ID, software version, and other parameters. Located in the root level of the run folder.
DemultiplexSummaryF1L1.txt	Reports demultiplexing results in a table with one row per tile and one column per sample.
ErrorsAndNoCallsByLaneTileReadCycle.csv	A comma-separated values file that contains the percentage of errors and no-calls for each tile, read, and cycle.
Mismatch.htm	Contains histograms of mismatches per cycle and no-calls per cycle for each tile.
ResequencingRunStatistics.xml	Contains summary statistics specific to the run. Located in the root level of the run folder.
Summary.xml	Contains a summary of mismatch rates and other base calling results.
Summary.htm	Contains a summary web page generated from Summary.xml.

Analysis Folder

The analysis folder holds the files generated by the Local Run Manager software.

The relationship between the output folder and analysis folder is summarized as follows:

- ▶ During sequencing, Real-Time Analysis (RTA) populates the output folder with files generated during image analysis, base calling, and quality scoring.
- ▶ RTA copies files to the analysis folder in real time. After RTA assigns a quality score to each base for each cycle, the software writes the file RTAComplete.txt to both folders.


- ▶ When the file RTAComplete.txt is present, analysis begins.
- ▶ As analysis continues, Local Run Manager writes output files to the analysis folder, and then copies the files back to the output folder.

Folder Structure

 **Alignment**—Contains *.bam and *.vcf files, and files specific to the analysis module.

 **<Time Stamp>**

 **Fastq**—Contains binary files used by Sequencing Analysis Viewer (SAV).

 Sample1_S1_L001_R1_001.fastq.gz

 Undetermined_S0_L001_R1_001.fastq.gz

 AnalysisError.txt

 AnalysisLog.txt

 **Data**

 **Intensities**

 **BaseCalls**

 **L001**—Contains one subfolder per cycle, each containing *.bcl files.

 **L001**—Contains *.locs files, 1 for each tile.

 **RTA Logs**—Contains log files from RTA software analysis.

 **InterOp**—Contains binary files used by Sequencing Analysis Viewer (SAV).

 **Logs**—Contains log files describing steps performed during sequencing.

 **Queued**—A working folder for software; also called the copy folder.

 CompletedJobInfo.xml

 QueuedForAnalysis.txt

 [WorkflowName]RunStatistics

 RTAComplete.xml

 RTAComplete.txt

 RunInfo.xml

 runParameters.xml

Alignment Folders

When analysis begins, the Local Run Manager creates an Alignment folder named **Alignment_#**, where # is a sequential number.

If you created the run by importing the information for a run that has already been analyzed, the Alignment folder is named **Alignment_Imported_#**.

Custom Analysis Settings

Custom analysis settings are intended for technically advanced users. If settings are applied incorrectly, serious problems can occur.

Add a Custom Analysis Setting

- 1 From the Module-Specific Settings section of the Create Run screen, select **Show Advanced Settings**.
- 2 Select **+ Add custom setting**.
- 3 In the custom setting field, enter the setting name as listed in the Available Analysis Settings section.
- 4 In the setting value field, enter the setting value.
- 5 To remove a setting, select **X**.

Available Analysis Settings

- ▶ **Adapter Trimming**—By default, adapter trimming is enabled in the Resequencing analysis module. To specify a different adapter, use the Adapter setting. The same adapter sequence is trimmed for Read 1 and Read 2.
 - ▶ To specify 2 adapter sequences, separate the sequences with a plus (+) sign.
 - ▶ To specify a different adapter sequence for Read 2, use the AdapterRead2 setting.

Setting Name	Setting Value
Adapter	Enter the sequence of the adapter to be trimmed.
AdapterRead2	Enter the sequence of the adapter to be trimmed.

- ▶ **Quality Score Trim**—The BWA alignment algorithm automatically trims the 3' ends of non-indexed reads with low quality scores. By default, the value is set to 15.

Setting Name	Setting Value
QualityScoreTrim	Enter a value greater than 0.

- ▶ **Variant Frequency**—Filters variants with a frequency less than the specified threshold.

Setting Name	Setting Value
VariantFrequencyFilterCutoff	Enter a threshold value. With GATK or Starling, the default value is 0.20.

- ▶ **Indel Repeat Cutoff**—Filters insertions and deletions when the reference has a 1-base or 2-base motif over 8 times (by default) next to the variant.

Setting Name	Setting Value
IndelRepeatFilterCutoff	Enter a threshold value. The default value is 8.

- ▶ **Variant Genotyping Quality**—Filters variants with a genotype quality (GQ) less than the specified threshold.

Setting Name	Setting Value
VariantMinimumGQCutoff	Enter a value less than 99. With GATK, the default value is 30. With Starling, the default value is 20.

- ▶ **Variant Quality Cutoff**—Filters variants with a quality (QUAL) less than the specified threshold. QUAL

indicates the confidence of the variant call.

Setting Name	Setting Value
VariantMinimumQualCutoff	Enter a threshold value. With GATK, the default value is 30. With Starling, the default value is 20.

Revision History

Document	Date	Description of Change
Document # 1000000002705 v02	January 2021	Updated software descriptions for Resequencing v3.0, which includes updates to: <ul style="list-style-type: none"> • Software requirements. • Updated run name and description requirements. • Updated parameter settings for library prep kit and index decoupling.
Document # 1000000002705 v01	June 2018	Added i5 index sequence instruction when creating custom prep kit sample sheets for use on the iSeq, MiniSeq, and NextSeq systems.
Document # 1000000002705 v00	January 2016	Initial release.

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

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



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