LIMS User Guide

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Revision History

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Chapter 1

Overview

Illumina Laboratory Information Management System

The Illumina® Laboratory Information Management System (LIMS) is a high-speed, scalable system that enables positive sample tracking throughout the laboratory workflow. Illumina LIMS provides:

- 100% sample tracking
- Real-time quality metrics from image scanning
- Project repository of sample data
- File management of decoding, image, intensity, and analytical data files

During the laboratory processing, samples proceed through the workflow with positive sample tracking at each step, reducing the risk of misidentifying samples or skipping steps in the protocol. Additionally, Illumina LIMS allows you to generate genotyping reports and queue samples or plates for repeat processing.

System administrators can easily manage storage capacity and links to existing files. Configuration changes via the administrator's web client provide support for other network or direct-attached file systems. Similarly, backup and archive directories are fully configurable.

Audience and Purpose of this Guide

This guide is intended for lab technicians and lab managers who are using Illumina LIMS and IT personnel who are administering the system. It explains how to use the Illumina LIMS.

- Chapter 1 Overview—General information about Illumina LIMS, the workflow, the robot, and the software.
- Chapter 2 Administrative Tools—Instructions on setting up and managing Illumina LIMS and users.
- Chapter 3 Laboratory Management—Instructions on lab management tasks such as requeueing batches and decommissioning items from projects.
- Chapter 4 Reports—Information about how to generate and use all of the reports in Illumina LIMS.

Assay Protocol Tasks

Instructions on using Illumina LIMS during an Infinium®, GoldenGate®, or GoldenGate Indexing™ assay appear in the automated (robot) chapter of the respective assay protocol guides.

Project Management

For instructions on setting up institutes and projects in Illumina LIMS, see the Illumina LIMS Project Manager Guide.

Illumina Robot Control Software

Illumina LIMS works in conjunction with the Illumina automation control software to track the progress of items through the lab. Either you or the robot updates the Illumina LIMS database when a task is finished, so Illumina LIMS can queue the sample for the next task. For instructions about using the Illumina robot, consult the *Infinium Lab Setup and Procedures Guide* and appropriate Infinium and GoldenGate assay protocol guides.

If you have skipped a previous task, then the robot will not perform the current task. Instead, the dedicated robot PC will display an error stating that the plate, BeadChip or Universal Array Matrix is not queued for the task you are attempting to run. You can use the Illumina LIMS web client to learn what task the item is queued for (*Queue Status Report* on page 71).

Thermocycler Control Software

For instructions on using the Thermocycler Control Software (TCCS) and Illumina LIMS with GoldenGate projects, see the *Thermocycler Control Software User Guide*.

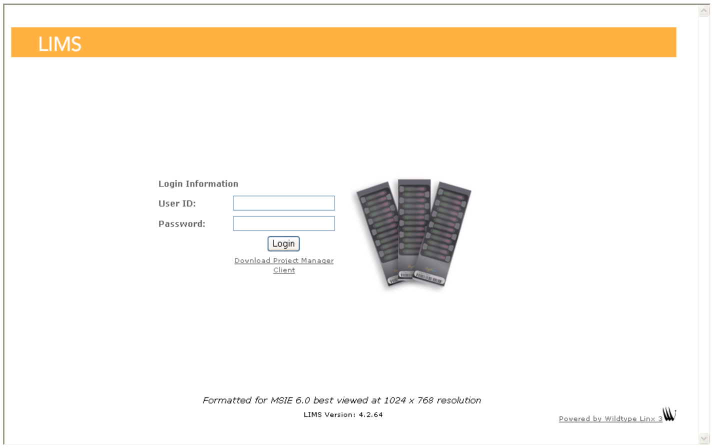
Launch the Illumina LIMS Web Client

The Illumina LIMS web client is accessible via a web browser. It is not installed on local machines.

To launch the Illumina LIMS Web Client

1. Open your web browser.
2. Type the address provided to you by the Illumina LIMS system administrator in the URL field.
3. Click **Enter**. The Illumina LIMS window opens.

Figure 1 Illumina LIMS Login



Formatted for MSIE 6.0 best viewed at 1024 x 768 resolution

LIMS Version: 4.2.64

4. Enter your user ID and password, and then click **Login**.

NOTE
Your user ID and password are set up by your LIMS administrator. See *Manage Users* on page 8.

Chapter 2

Administrative Tools

Manage Users

This section provides information about authentication methods, default administrative accounts, and checking user status.

Authentication Methods

Illumina LIMS can use either Windows authentication or database authentication. Windows authentication queries the local Windows domain for password authentication, while database authentication queries the Infinium or GoldenGate database. The authentication method is determined when Illumina LIMS is installed at your site.

Default Administrator Account

During installation a single administrator account will be created. The default user name and password are **infinium_admin**. You must have administrative access to create and manage user accounts, including other administrator accounts.

NOTE
Document and save the administrator password somewhere, so that Illumina support technicians can access Illumina LIMS if the system administrator becomes unavailable.

To create a user account

1. In the Illumina LIMS left sidebar, click **Admin Tools | Manage Users**. The Manage Users window opens.
2. Do one of the following:
   - If you are using Windows authentication, enter the user's Windows user name in the **New User** box.
   - If you are using database authentication, enter any unique user name in the **New User** box.
3. Enter a password in the **Password** box.
   If you are using Windows authentication, users will log in using their Windows password, so you do not need to tell them the account creation password.

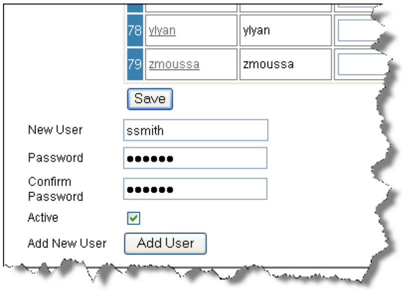
If you are using database authentication, you need to tell the password to the users, since they will log in with the password you set here. Only an administrator can change the password.

4 Enter the password again in the **Confirm Password** box.

NOTE
If the Windows domain ever becomes unavailable, Illumina support technicians can help you reset Illumina LIMS to use database authentication. If that happens, all users will need to log in using the password you entered when you created their accounts. Therefore we recommend that you adhere to a standard convention when creating passwords.

5 Select the **Active** check box to make the user account active in the system.

Figure 2 Add New User



78	ylyan	ylyan
79	zmoussa	zmoussa

New User: ssmith
Password: ●●●●●●
Confirm Password: ●●●●●●
Active: ☑

6 Click **Add User** to save the user account in the system.

User Status

User accounts may be active or inactive. An active account is one where the user can log in and perform tasks. If their account is inactive, users cannot log in.

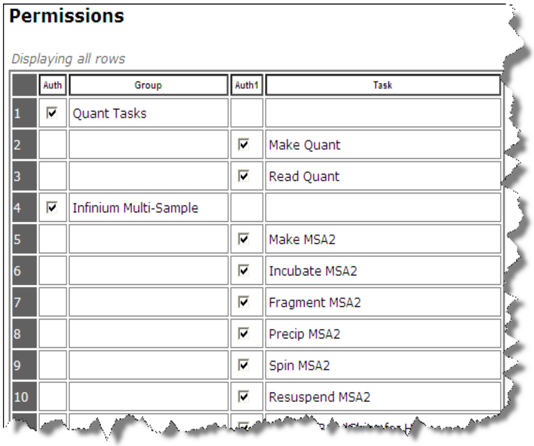
Add Permissions

The ability to view windows and perform tasks in Illumina LIMS is permission-dependent. When you create users, you must grant them appropriate permissions to the areas of the system that they need to access and to the task that they need to perform.

Group-Level and Task-Level Permissions

Every task in Illumina LIMS has an associated task-level permission. Related permissions, such as the set of Infinium HD Super tasks, are collected into a group.

Figure 3 Group-Level and Task-Level Permissions



Permissions

Displaying all rows

	Auth	Group	Auth1	Task
1	☑	Quant Tasks		
2			☑	Make Quant
3			☑	Read Quant
4	☑	Infinium Multi-Sample		
5			☑	Make MSA2
6			☑	Incubate MSA2
7			☑	Fragment MSA2
8			☑	Precip MSA2
9			☑	Spin MSA2
10			☑	Resuspend MSA2

Select the check box beside an individual task to give permission for just that task or select the check box beside the group to give permission for all tasks inside the group.

If a group-level task is selected, then clearing a check box beside a task inside the group has no effect.

Recommended Settings

- All users - Must have permission for the Authenticate task under the Management Client group. This enables them to use the Illumina LIMS Project Manager, Illumina automation control software, BeadArray Reader, GenomeStudio, iScan, HiScan, Thermocycler Control Software (for use with GoldenGate projects only), and Illumina Fluorometry Software, AutoCall.
- All lab personnel - Should have permission for the Tracking group so that they can assess the status of laboratory projects with tracking reports.
- Lab managers - Should have permission for the Lab Management group so they can perform managerial tasks, and permission for the Quality Control group so that they can run metrics reports.

- Lab technicians - Should have permission for the appropriate assay protocol, Quant, and Imaging groups so that they can perform tasks in the lab.

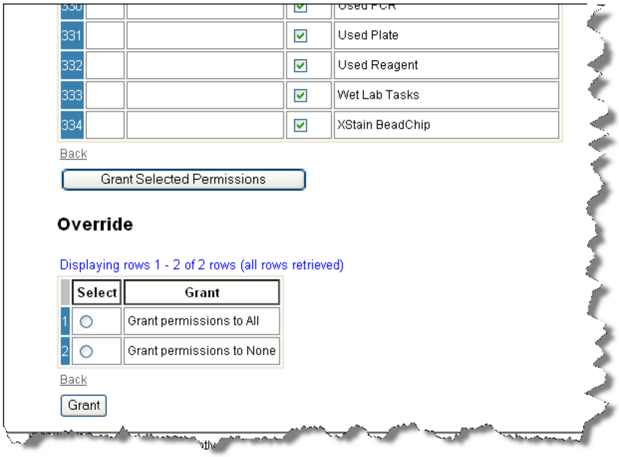
NOTE
You must purchase an Illumina LIMS Infinium license in order to run Infinium tasks and you must purchase an Illumina LIMS GoldenGate license in order to run GoldenGate tasks.

- Project managers - Should have permission for the Management Client group so that they can use Illumina LIMS Project Manager. In addition, they should have permission to the Lab Management, Quality Control, and Tracking groups so that they can run reports.

Assigning Permissions to a User

1 Click the user name in the **Edit/View** column. The Permissions window opens.

Figure 4 Grant Permissions



331			☑	Used Plate
332			☑	Used Reagent
333			☑	Wet Lab Tasks
334			☑	XStain BeadChip

Override

Displaying rows 1 - 2 of 2 rows (all rows retrieved)

	Select	Grant
1	○	Grant permissions to All
2	○	Grant permissions to None

2 Do one of the following:
- To grant universal permission for all tasks in the entire system, scroll to the Override section and select **Grant permissions to All**. Click **Grant**.
- To remove permission for all tasks in the entire system, select **Grant permissions to None**, and then click **Grant**.

- To grant limited permissions, select the check boxes beside groups or individual tasks. Remember that selecting a group automatically extends permission to perform all tasks in that group.

For suggestions and requirements regarding the permissions needed for various roles, see *Recommended Settings* on page 10.

3 When you finish granting permissions, click **Grant Selected Permissions**.

Manage Logs

Illumina LIMS maintains log files to help technical support scientists diagnose and solve problems. In general, you do not need to use the logs for any reason other than support purposes.

Types of Logs

Illumina LIMS maintains three type of log files:

- **LimsStatus #.#.log**: Logs all the internal server operations. This is the most complete log. The logs are numbered incrementally (1.0, 1.1, 1.2, 1.3, 2.0, 2.1, etc.)
- **Lims Request Response #.#.log**: Logs all the client/server requests and responses. The logs are numbered incrementally (1.0, 1.1, 1.2, 1.3, 2.0, 2.1, etc.)
- **yyyy.mm.dd.request.log**: Logs a combination of request/response information and short database-connection login information. This log is useful for tracking down database issues.

Naming Scheme

For each type of log, there may be multiple log files. The most recent log file is always numbered 00, and the oldest log file has the highest number.

Logging process

1. Illumina LIMS collects data until <log file>.00 log reaches 20 MB (configurable).
2. Illumina LIMS increments the number of the log file (e.g., LIMSStatus.00 changes to LIMSStatus.01) and stops logging information to that file.
3. Illumina LIMS opens a new file named <log file>.00 and begins logging information to that file.
4. When the second log file reaches the size limit, LIMS starts a third log file. All the numbers increment by 1 again: 01 becomes 02, and 00 becomes 01.
5. When there are the maximum number of log files, then the next time the numbers increment, the data in the last file are overwritten.

NOTE
To change the maximum number of log files or the maximum log file size contact your Illumina LIMS system administrator.

The speed with which the log files rotate is highly variable. Some tasks, such as scanning, generate a large amount of logged information and some labs are busier than others. Therefore, it is impossible to provide a rule of thumb for how long it takes to fill up a log file.

Viewing and Saving Log Files

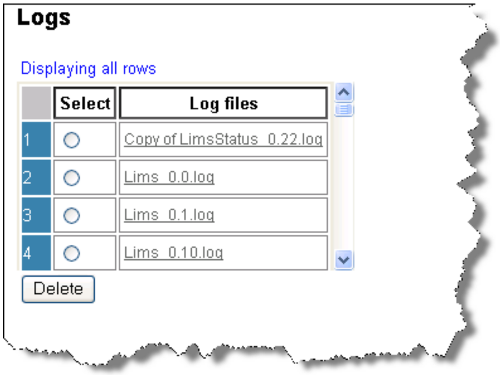
When you contact technical support, a technical support scientist may ask you to review a log file or send a copy of one.

NOTE
To help technical support scientists diagnose and solve problems, it is important to view or save the Illumina LIMS logs immediately.

To view log files

1 In the Illumina LIMS left sidebar, click **Admin Tools | Manage Logs**. The Manage Logs window opens.

Figure 5 Manage Logs



Logs

Displaying all rows

	Select	Log files
1	○	Copy of LimsStatus_0.22.log
2	○	Lims_0.0.log
3	○	Lims_0.1.log
4	○	Lims_0.10.log

2 Do one of the following:

- Right-click on any log file and select **Save Target As**. Save the file with a .txt extension, and then open it in an editor such as WordPad.

- Double-click on any log file to open it in Notepad.

NOTE
Some log files may be too large for the Notepad. If so, save the log file and open it with a different text viewer.

Enter Maintenance Mode

If you need to perform maintenance on the Illumina LIMS hardware or software, put the Illumina LIMS software in maintenance mode. This is a graceful way of easing users off the system without losing any data.

NOTE
You must have administrative permissions to access the Enter Maintenance Mode task.

To enter maintenance mode

1. In the Illumina LIMS left sidebar, click **Admin Tools | Enter Maintenance Mode**. The Enter Maintenance Mode window opens.
2. Enter the date and time when maintenance mode will end.
3. Click **Start** beside Refuse Future Connections. Current users may complete their tasks, but no one can start a new task until you bring the Illumina LIMS server software back online.

Install License

Install License allows you to install a new license file. Normally this is done by Illumina Customer Support staff, who will install your system license during initial system installation. If the system is upgraded, a new system license may be required. In this case, Illumina will provide instructions for installing the new license. Otherwise, do not use this task.

Chapter 3

Laboratory Management

Introduction

This section explains how to enter samples back into the laboratory workflow after they have been removed due to processing errors or deletion of partial batches. It also explains how to track the results of a Tecan robot run. You must have laboratory management access to Illumina LIMS to use Laboratory Management Tools.

Requeue Samples

This feature lets you re-enter a sample into the queue and make it available for creating new batches.

NOTE
This feature is not available for GoldenGate Indexing projects.

To requeue a sample

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Requeue for Make Sample Batch**. The Requeue Samples window opens.
2. Select the project that contains the samples you want to requeue, and click **Get Samples**. Samples that have been previously hybridized in the project appear.

NOTE
If the samples have not been hybridized, they do not appear in the list.

3. Select the check box beside each sample that you want to requeue, and then click **Save**.
4. Continue on to *Make Sample Batch* on page 22.

Make Sample Batch

This task allows you to combine samples that were requeued in the previous task, or by the project manager/scientist from Illumina LIMS Project Manager, into a batch for amplification.

NOTE
This capability applies to Infinium projects only. For GoldenGate projects, see the sections on Make Requeue Batch or Import Manual Batch in the Illumina LIMS Project Manager Guide.

To make a sample batch

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Make Sample Batch**. The Make Sample Batch window opens.
2. Select the product that you will use for the samples, and click **Select Product Type**. All the queued samples for that product appear in the Sample Listing window. A box beside the product list indicates the number of samples allowed for this batch type.
3. To add a sample to the batch, click the arrow beside the sample. As you add samples, a box beside the product list shows how many you have added so far.
4. When you finish assigning samples, click **Save** to have Illumina LIMS create the batch.
   A message like the following should appear: “Successfully completed task Make Sample Batch and created batch number 39,” where “39” is the batch number. Make a note of this number and relay it to the lab personnel who will run the batch.

Requeue for Hyb

This task re-hybridizes all samples within a sample plate and lets you requeue an amplified DNA plate for hybridization with another product. A plate may be hybridized up to three times (i.e., the first use followed by two re-hybridizations).

NOTE
For multi-use products, this process must be completed prior to re-hybridization of samples to the next beadchip product. See the appropriate assay protocol guide for instructions.

All hybridization plates can be used for GoldenGate and GoldenGate Indexing products. For Infinium products, only plates AMP and MSA can be used.

CAUTION
Before requeueing, make sure that there is enough sample volume in each well to hybridize to another BeadChip.

To requeue a plate for hybridization

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Requeue for Hyb**. The Requeue for Hyb window opens.
2. Scan the barcode of your amplification or hybridization plate and click **Get Plate Data**.
   The amplification plate barcode, current queue, and current product ID appear in the top part of the window. A list of all the available products appears in the Select Destination Product area.
3. For Infinium products, in the Select Destination Product area, click the part number of the new product for hybridization.
   For GoldenGate products, only the same product can be used.
   The new product and new queue information appear in the top part of the window.
4. Click **Save**.

Requeue for Image BeadChip

This task lets you requeue a BeadChip to image again.

1 In the Illumina LIMS left sidebar, click **Laboratory Management | Requeue for Image BeadChip**. The Requeue for Image BeadChip window opens.

2 Scan the barcode of your BeadChip and click **Get Sample Sections**.
The BeadChip is now ready to be imaged again.

NOTE
If the decode files have been deleted, LIMS will not allow the BeadChip to be requeued. Decode files are deleted based on how file retention has been configured.

Requeue for Make Quant

This task lets you requeue DNA plate to Make Quant again.

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Requeue for Make Quant**. The Requeue for Make Quant window opens.
2. Scan the barcode of the sample plate and click **Verify**.
3. Click **Save**.

NOTE
Only DNA plates originally queued to Make Quant can be requeued to Make Quant.

Decommission Item

This task lets you decommission items from your projects. A decommissioned item is removed from any queue that it is on and put onto the decommission queue. The decommissioned item can not be used in any workflow.

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Decommission Item**. The Decommission Item window opens.
2. Select the **Item Type**.
3. Scan the barcode of the item and click **Verify**.
4. Click **Save**.

Requeue APP

Pooled GoldenGate Indexing (MSI) samples can be requeued to the Make PCR MSI step to be able to reprocess MSI samples and rehybridize to new BeadChips.

To requeue an APP

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Requeue APP**. The Requeue APP window opens.
2. Enter the APP information and click **Verify**. A message above the **APP** field indicates if the APP has been verified.
3. Click **Save**.

Tecan Robot QC

The results of a Tecan robot run can be tracked. This task does not store robot QC data in Illumina LIMS.

To track Tecan robot run results

1. In the Illumina LIMS left sidebar, click **Laboratory Management | Tecan Robot QC**. The Tecan Robot QC window opens.
2. Enter the **Robot Name**.
3. Select the **QC Status** (Pass or Fail) depending on the results of the robot QC run.
4. Click **Save**. A message above the **Robot Name** field indicates that the Tecan Robot QC task has been successfully completed.

Chapter 4

Reports

Introduction

Illumina LIMS provides a number of reports that enable you to efficiently manage and retrieve genotyping data for samples. The reports can also be used to manage reagents and equipment.

Run Reports

The following instructions explain how to generate a report. The instructions apply equally to any report in the system. For specific information on a particular report, refer to the section named for that report.

To run a report

1. In the Illumina LIMS main window, click the **Reports** tab in the upper-right corner. The Reports window opens.
2. In the Illumina LIMS left sidebar, select one of the general types of reports. For information on each type, see:
   - *Lab Management Reports* on page 32
   - *Quality Control Reports* on page 53
   - *Tracking Reports* on page 62
3. Click a specific report to open it.
4. Enter or select the data for the report.
5. Select one of the following report formats when available:
   - **Export to CSV** to export the report to .csv (comma-separated value) files. You can open .csv files using Excel or Word, and then format or manipulate the data.
   - **Display on Page** to view the report in the lower portion of the window (HTML format).

   NOTE
   If you choose to display the report on the page, the heading row moves out of sight as you scroll through the data.
6. Run the report.

   NOTE
   Report results may vary dependent upon the type of project.

Lab Management Reports

Lab Management reports provide details about samples and batches within a project. There are 12 lab management reports:

- *Project Detail Report* on page 32
- *Project Summary Report* on page 35
- *Project AutoCall Report* on page 36
- *Reagent Usage Report* on page 38
- *AutoAccession Failure Report* on page 46
- *Product Inventory Report* on page 47
- *BeadChip Detail Report* on page 47
- *Processed DNA Well Usage Report* on page 49
- *PCR Detail Report* on page 49
- *MSI Project Plate Report* on page 50
- *MSI Task Report* on page 51
- *Robot Position Report* on page 51

Project Detail Report

This report provides details about your project, including the image date of scanning. Among other things, you can find out which samples have gone all the way through the assay protocol tasks and are ready to be scanned.

You must select the project and enter the hybridization **From Date.** Specifying a date range to constrain the results is optional for all projects except GoldenGate Indexing. To specify a date range, enter the **To Date**.

You can also enter a **Barcode** number to view information associated only with that barcode within the project.

NOTE
For GoldenGate Indexing projects, the query parameters must be seven days or less due to the potential of a large quantity of query results.

Table 1 Project Detail Report

Column	Description
AMP Batch	The batch ID.
AMP Plate	The amplification barcode.
AMP Well	The well coordinates for the sample in the amplification plate.
AMP Well Status	**Active**: Well can be used in downstream tasks. **Inactive**: Well cannot be used in downstream tasks.
ASE	The ASE plate barcode.
ASE Batch	The batch ID.
ASE Date	The date when ASE occurred.
ASE Pool Plate	The APP plate barcode.
Batch Status	**Active**: The batch is queued for amplification. **Completed**: The amplification plate has been created.
BeadChip	The unique BeadChip barcode.
Call Rate	The proportion of SNPs on an array that can be called as a specific genotype.
Hyb	The hybridization plate barcode.
Hyb Coord	The area of the BeadChip where the sample was hybridized.
Hyb Date	The date when hybridization occurred.
Image Date	The date and time when the BeadChip was scanned (i.e. imaged).
Master Oligo Set	The master part number that all of the indexed oligo pools are assigned to.
MUN/SUD	The MUN/SUD plate barcode.

Column	Description
MUN/SUD Well	The well coordinates for the sample in the MUN/SUD plate.
Oligo Pool	The oligo pool associated with the sample well.
P-SSID	Secondary System ID. Allows you to correlate your IDs with Illumina LIMS IDs, to track project data in your own databases.
Part Number	The part number associated with this product.
PartNum	The part number associated with this product (e.g., BeadChip type).
PCR	The PCR plate barcode.
PCR Date	The date when PCR occurred.
Product	The product description.
Project	The project name.
Quant Conc.	The concentration read from the quant plate.
Resusp Date	The date and time when resuspension occurred.
Sample	The sample name.
Sample Plate	The DNA plate barcode.
Sample Well	The well coordinates for the sample in the DNA plate.
Scan Count	Number of times that the BeadChip has been scanned.
Scanner Device	The name of the scanner used to scan the BeadChip.
Scanner Firmware Ver	The firmware version running on the scanner at the time it scanned the BeadChip.
Scanner Serial No.	The serial number of the scanner used to scan the BeadChip.
Scanner Software Ver	The software version running on the scanner at the time it scanned the BeadChip.

Column	Description
Section	The area of the BeadChip where the sample was hybridized.
SSC	Sample section column.
SSR	Sample section row.
SubSet Index	Identifies each of the individual oligo pools that make up a master oligo set.
Well Status	**Active**: Well can be processed through LIMS workflows. **Inactive**: Well cannot be processed.

Project Summary Report

This report shows the overall status of a project at a glance. The primary measure is the ratio of scans completed vs. scans expected.

Table 2 Project Summary Report

Column	Description
Created By	The user name of the project manager or scientist who created the project.
No. APPs Created /Remaining/Expected	The number of APPs created, remaining, and expected.
No. Batches Completed/Remaining/Created	The number of batches completed, remaining, and created.
No. Distinct Samples	The total number of samples.
No. Hybs Created /Remaining/Expected	The number of hybridizations created, remaining, and expected.

Column	Description
No. MUNs Created /Remaining/Expected	The number of MUNs created, remaining, and expected.
No. Products	The number of product part numbers associated with the project.
No. Oligo Pools	The number of oligo pools associated with the project.
No. Samples Resuspended/Remaining/Expected	The number of samples resuspended, remaining, and expected.
No. Samples Hyb'ed/Remaining/Expected	The number of samples hybridized, remaining, and expected.
No. Sample Plates	The number of sample plates associated with the project.
No. Scans Completed/Remaining/Expected	The number of scans completed, remaining, and expected.
No. SUDs Created /Remaining/Expected	The number of SUDs created, remaining, and expected.
P-SSID	Project Secondary System ID. Allows you to correlate your IDs with Illumina LIMS IDs, to track project data in your own databases.
Project	The project name.

Project AutoCall Report

This report indicates whether AutoCall has run for a given sample. AutoCall is the analysis software program that looks at each SNP (Single Nucleotide Polymorphism) in the sample and determines its genotype. For AutoCall to generate genotype calls, a cluster file must be linked to the product. For more information, see the Illumina LIMS Project Manager Guide.

Table 3 Project AutoCall Report

Column	Description
BeadChip	The BeadChip barcode.
Date	The date and time when AutoCall ran.
File Path	The path to the genotype call file (.gtc).
P-SSID	Project Secondary System ID. Allows you to correlate your IDs with Illumina LIMS IDs, to track project data in your own databases.
Project	The project name.
Queue	**Link Cluster File**: Indicates that you need to link a cluster file to the product before AutoCall can run. **AutoCall**: Indicates that the sample on that row is queued for AutoCall. **AutoCall Processing**: Appears very briefly to indicate that AutoCall is currently running for that sample. **AutoCall Complete**: Indicates that AutoCall has run successfully. **AutoCall Failed**: Indicates that AutoCall has failed.
Sample	The sample name.
Sample Plate	The sample plate barcode.
Section	The area on the BeadChip where the sample resides.
Status	**Success**: AutoCall ran and successfully generated genotype calls. **Fail**: AutoCall failed to run, or failed to complete successfully. If the network becomes unavailable, AutoCall will not be able to save the genotype call file to the network. In that case, the status might be **Complete**, but there would not be a file path, or the date might be incorrect. If this occurs, requeue the sample for AutoCall. For more information, see Requeue Products for AutoCall or Requeue for Autocall in the Infinium LIMS Project Manager Guide.
Well	The coordinates of the well in the sample plate.

Reagent Usage Report

This report lists any reagents used during the time period you designate.

You must select the **Assay Type** and enter the hybridization **From Date.** You can optionally enter the **To Date** to constrain the results or enter a **Barcode** number to view all other barcodes associated to it.

NOTE
Illumina recommends that only administrators run the Reagent Usage Report due to the volume of system processing required in order to retrieve a large amount of data.

Table 4 Reagent Usage Report

Column	Description
Actual Concentration	The actual concentration read from the quant plate, in nanograms per microliter (ng/µl).
Add MEL AM1	The AM1 barcode used in the Add MEL task.
Add Mel Date	The date the Add MEL task was run.
Add MEL MEL	The MEL barcode used in the Add MEL task.
Add MEL UB1	The UB1 barcode used in the Add MEL task.
Add Mel User	The logged in user for the Add MEL task.
Add MelMachine	The machine the Add MEL task was run on.
AMP Batch	The batch number
AMP Date	The date the Make AMP task was run.
AMP Machine	The machine that ran the AMP task.
AMP Plate	The amplification plate barcode.
AMP User	The logged in user for the AMP task.

Column	Description
AMP Well	The amplification plate well.
APP Plate	The APP plate barcode (for GoldenGate Indexing projects only).
App Well	The APP plate well (for GoldenGate Indexing projects only).
ASE Plate	The ASE plate barcode.
ASE Well	The ASE plate well.
Batch Status	**Active**: The batch is queued for amplification. **Completed**: The amplification plate has been created. **Deleted**: The amplification plate has been deleted from the queue.
BeadChip	The BeadChip barcode.
Bind MPB	The MPB barcode used in the Bind PCR task.
Call Rate	The proportion of SNPs on an array that can be called as a specific genotype.
Coat Date	The date the Coat task was run.
Coat Machine	The machine the Coat task was run on.
Coat xstain reagent 2	The xstain reagent 2 barcode used in the Coat BC2 task.
Coat User	The logged in user for the Coat task.
Coat xstain reagent 6	The xstain reagent 6 barcode used in the Coat BC2 task.
Frag AMP2 FRG	The FRG barcode used in the Frag AMP2 task.
Frag AMP3 FRG	The FRG barcode used in the Frag AMP3 task.
Frag Date	The date the Fragment AMP task was run.
Frag Machine	The machine that the Fragment task was run on.

Column	Description
Frag MSA1 fragment reagent 1	The fragment reagent 1 barcode used in the Frag MSA1 task.
Frag MSA2 fragment reagent 1	The fragment reagent 1 barcode used in the Frag MSA2 task.
Frag MSA3 fragment reagent 1	The fragment reagent 1 barcode used in the Frag MSA3 task.
Frag User	The logged in user for the Fragment task.
HYB Date	The date the hybridization task was run.
Hyb Duo BC2 xstain reagent 1	The xstain reagent 1 barcode used in the Hyb Duo BC2 task.
Hyb HC BC2 xstain reagent 1	The xstain reagent 1 barcode used in the Hyb HC BC2 task.
Hyb Machine	The machine the hybridization task was run on.
Hyb Machine	The machine the hybridization task was run on.
Hyb Multi BC2 / Use xstain reagent 1	The xstain reagent 1 barcode used in the Hyb Multi BC2 task.
HYB Plate	The hybridization plate barcode.
Hyb Single BC2 xstain reagent 1	The xstain reagent 1 barcode used in the Hyb Single BC2 task.
Hyb User	The logged in user for the hybridization task.
HYB Well	The hybridization plate well.
Image Date	The date the Image task was run.
Image Machine	The machine the Image task was run on.
Image User	The logged in user for the Image task.
Incubate Date	The date the Incubate task was run (not for GoldenGate

Column	Description
Incubate Machine	The machine that the Incubate task was run on (not for GoldenGate Indexing projects).
Incubate User	The logged in user for the Incubate task (not for GoldenGate Indexing projects).
Inoc IP1	The IP1 barcode used in the Inoc PCR task (not for GoldenGate Indexing projects).
Inoc UB1	The UB1 barcode used in the Inoc PCR task (not for GoldenGate Indexing projects).
Make AMP2 AMM	The AMM barcode used in the Make AMP2 task.
Make AMP2 MP1	The MP1 barcode used in the Make AMP2 task.
Make AMP3 AMM	The AMM barcode used in the Make AMP3 task.
Make AMP3 MP1	The MP1 barcode used in the Make AMP3 task.
Make ASE OB1	The OB1 barcode used in the ASE task.
Make Date	The date the Make task was run.
Make HYB Date	The date the Make Hyb task was run.
Make Hyb INT	The INT barcode used in the Make Hyb task.
Make Hyb Machine	The machine the Make Hyb task was run on.
Make Hyb MH1	The MH1 barcode used in the Make Hyb task.
Make Hyb UB2	The UB2 barcode used in the Make Hyb task.
Make Hyb User	The logged in user for the Make Hyb task.
Make Machine	The machine that the Make task was run on.
Make MSA1 make MSA reagent 1	The make MSA reagent 1 barcode used in the Make MSA1 task.

Column	Description
Make MSA1 MA2	The MA2 barcode used in the Make MSA1 task.
Make MSA1 make MSA reagent 3	The make MSA reagent 3 barcode used in the Make MSA1 task.
Make MSA2 make MSA reagent 1	The make MSA reagent 1 barcode used in the Make MSA2 task.
Make MSA2 MA2	The MA2 barcode used in the Make MSA2 task.
Make MSA2 make MSA reagent 3	The make MSA reagent 3 barcode used in the Make MSA2 task.
Make MSA3 make MSA reagent 1	The make MSA reagent 1 barcode used in the Make MSA3 task.
Make MSA3 MA2	The MA2 barcode used in the Make MSA3 task.
Make MSA3 make MSA reagent 3	The make MSA reagent 3 barcode used in the Make MSA3 task.
Make PCR MMP	The MMP barcode used in the Make PCR task.
Make User	The logged in user for the Make task.
Oligo Pool	The oligio pool associated with the sample.
PCR Date	The date the PCR task was run.
PCR Machine	The machine the PCR task was run on.
PCR Plate	The PCR plate barcode.
PCR User	The logged in user for the PCR task.
Pool ASE Date	The date the Add MEL task was run (for GoldenGate Indexing projects only).
Pool ASE IP1	The IP1 barcode used in the Pool ASE task (for GoldenGate Indexing projects only).
Pool ASE Machine	The machine the Add MEL task was run on (for GoldenGate

Column	Description
	Indexing projects only).
Pool ASE UB1	The UB1 barcode used in the Pool ASE task (for GoldenGate Indexing projects only).
Pool ASE User	The logged in user for the Add MEL task (for GoldenGate Indexing projects only).
Precip AMP2 PA1	The PA1 barcode used in the Precip AMP2 task.
Precip AMP3 PA1	The PA1 barcode used in the Precip AMP3 task.
Precip Date	The date the Precip AMP task was run.
Precip Machine	The machine the Precip task was run on.
Precip MSA1 precipitate reagent 1	The precipitate reagent 1 barcode used in the Precip MSA1 task.
Precip MSA2 precipitate reagent 1	The precipitate reagent 1 barcode used in the Precip MSA2 task.
Precip MSA3 precipitate reagent 1	The precipitate reagent 1 barcode used in the Precip MSA3 task.
Precip User	The logged in user for the Precip task.
Prepare BC2 xstain reagent 2	The xstain reagent 2 barcode used in the Prepare Single BC2 task.
Prepare BC2 hyb reagent 1	The hyb reagent 1 barcode used in the Prepare Single BC2 task.
Product	The product description.
Project	The project name.
Protocol	The protocol performed.

Column	Description
P-SSID	Project Secondary System ID. Allows you to correlate your IDs with Illumina LIMSIDs, to track project data in your own databases.
Resusp. Date	The date the Resuspend AMP task was run.
Resuspend AMP2 xstain reagent 1	The xstain reagent 1 barcode used in the Resuspend AMP2 task.
Resuspend AMP3 xstain reagent 1	The xstain reagent 1 barcode used in the Resuspend AMP3 task.
Resuspend Machine	The machine the Resuspend AMP task was run on.
Resuspend MSA1 xstain reagent 1	The xstain reagent 1 barcode used in the Resuspend MSA1 task.
Resuspend MSA2 xstain reagent 1	The xstain reagent 1 barcode used in the Resuspend MSA2 task.
Resuspend MSA3 xstain reagent 1	The xstain reagent 1 barcode used in the Resuspend MSA3 task.
Resuspend User	The logged in user for the Resuspend task.
Sample	The name of the sample or barcode.
Sample Plate	The DNA sample plate barcode.
Scanner Firmware Ver	The scanner firmware version.
Scanner Serial No.	The scanner serial number.
Section	The area on the BeadChip where the sample resides.
StartTime	The time when PCR started.
StopTime	The time when PCR stopped.
Thermocycler	The thermocycler the thermocycling was run on.

Column	Description
Type	Brand name of the array; various types of BeadChip (1x10 = 1 sample, 10 stripes).
Unit	The unit number of the thermocycler.
Wash BC2 xstain reagent 2	The xstain reagent 2 barcode used in the Wash BC2 task.
Wash BC2 WB1	The WB1 barcode used in the Wash BC2 task.
Wash BeadChip xstain reagent 2	The xstain reagent 2 barcode used in the Wash BeadChip task.
Wash Date	The date the Wash task was run.
Wash Machine	The machine the Wash task was run on.
Wash User	The logged in user for the Wash task.
Well	The DNA plate well.
XStain BC2 xstain reagent 9	The xstain reagent 9 barcode used in the XStain BC2 task.
XStain BC2 LTM	The LTM barcode used in the XStain BC2 task.
XStain BC2 xstain reagent 1	The xstain reagent 1 barcode used in the XStain BC2 task.
XStain BC2 xstain reagent 7	The xstain reagent 7 barcode used in the XStain BC2 task.
XStain BC2 xstain reagent 3	The xstain reagent 3 barcode used in the XStain BC2 task.
XStain BC2 xstain reagent 4	The xstain reagent 4 barcode used in the XStain BC2 task.
XStain BC2 xstain reagent 5	The xstain reagent 5 barcode used in the XStain BC2 task.

Column	Description
XStain Date	The date the XStain task was run.
XStain HD xstain reagent 9	The xstain reagent 9 barcode used in the XStain HD BeadChip task.
XStain HD xstain reagent 1	The xstain reagent 1 barcode used in the XStain HD BeadChip task.
XStain HD xstain reagent 8	The xstain reagent 8 barcode used in the XStain HD BeadChip task.
XStain HD xstain reagent 7	The xstain reagent 7 barcode used in the XStain HD BeadChip task.
XStain HD xstain reagent 3	The xstain reagent 3 barcode used in the XStain HD BeadChip task.
XStain HD xstain reagent 4	The xstain reagent 4 barcode used in the XStain HD BeadChip task.
XStain HD xstain reagent 5	The xstain reagent 5 barcode used in the XStain HD BeadChip task.
XStain Machine	The machine the XStain task was run on.
XStain User	The logged in user for the XStain task.
XUD Plate	The SUD/MUD plate barcode.

AutoAccession Failure Report

This report lists any BeadChips for which AutoAccession failed, along with the reason for failure. Since AutoAccession runs in the background, this report is a useful tool for viewing its status. If there are no failures, a message indicates that there are no AutoAccession failures to report at this time. For instructions about how to accession BeadChips, see the Illumina LIMS Project Manager Guide.

You can optionally add a date range or barcode to constrain the results.

Table 5 AutoAccession Failure Report

Column	Description
BeadChip	The barcode of the BeadChip that failed accession.
Comment	A system-generated explanation for the failure.
Date	The date of failed accession.

Product Inventory Report

This report lets you select one or more product types and generate a .csv file describing all of the individual BeadChips of that type that exist in the system. The report lists product name, part number, queue and all of the BeadChips in the entire Illumina LIMS system, not just within a project or institute.

Table 6 Product Inventory Report

Column	Description
BeadChip	The barcode of the individual BeadChip. There is one line in the table for every BeadChip of the selected product type(s).
Part Number	The part number associated with the product.
Product Name	The name that was assigned to the product when it was accessioned into the system.
Queued For	The task that the individual BeadChip is queued for.

BeadChip Detail Report

This report provides detailed information about the samples on an individual BeadChip. It also describes the BeadChip specifications and task history.

To generate this report, either:

- Scan the BeadChip barcode
- Search for the BeadChip in the Items on Queue report (*Queue Status Report* on page 71) and copy the barcode

Table 7 BeadChip Detail Report

Column	Description
Format	The product format: e.g., Slide 12 x 1 for a slide with twelve stripes.
Part Number	The part number associated with the product.
Product Line	The set of assay protocols that this BeadChip is designed for: e.g., Infinium HD.
Product Name	The name that was assigned to the product when it was accessioned into the system.
Sample Data	
Project	The project name.
DNA Plate	The barcode of the sample's original DNA plate.
DNA Well	The location of the well in the original DNA plate that held this sample.
Sample Name	The unique sample name.
Sample Section	The area on the BeadChip where the sample resides.
History	
Date	The date that the BeadChip entered the queue in the To Task column.
From Task	The task that the BeadChip completed immediately before entering the queue in the To Task column.
Time	The time that the BeadChip entered the queue in the To Task column.
To Task	The current task for which the BeadChip is queued.
User	The user processing the BeadChip for that task.

Processed DNA Well Usage Report

This report provides information about the processed DNA well usage for each project.

NOTE
This report is available for GoldenGate projects only.

Table 8 Processed DNA Well Usage Report

Column	Description
Batch	The batch ID.
MUN Plate	The MUN plate barcode.
Project	The project name.
Sample	The sample name or barcode.
Sample Plate	The sample plate barcode.
Uses Remaining	The number of uses remaining.
Well	The coordinates of the well in the sample plate.
Well	The coordinates of the well in the MUN plate.

PCR Detail Report

This report provides details about processed PCR plates.

Table 9 PCR Detail Report

Column	Description
Device	The thermocycler system.
Operator	The operator’s ID.
PCR	The PCR plate barcode.

Column	Description
PCR Date	The date when PCR occurred.
Protocol	The protocol performed.
Start Time	The time when PCR started.
Stop Time	The time when PCR stopped.
Total Time	The total number of minutes for PCR.
Unit	One block of the thermocycler.

MSI Project Plate Report

This report provides a view of all plate, OPA and BeadChip barcodes for an individual NSI project.

Table 10 MSI Project Plate Report

Column	Description
APP	The APP plate barcode.
ASE	The ASE plate barcode.
BeadChip	The barcode of the individual BeadChip.
HYB	The hybridization plate barcode.
Master Oligo Set	The master oligo set associated with the sample.
Oligo Pool	The oligo pool associated with the sample.
PCR	The PCR plate barcode.
Project	The project name.
Sample Plate	The DNA plate barcode.
Status	**Active**: The batch is queued for MSI.

Column	Description
	Completed: The MSI project plate has been created.
Subset Index	The subset index number.
SUD	The SUD plate barcode.
XT Batch ID	The XT batch number.

MSI Task Report

This report provides a view of which XT batches are queued to specific MSI tasks for processing in the lab.

Table 11 MSI Task Report

Column	Description
Plate	The plate barcode.
Sample Batch ID	The sample batch number.
XT Batch ID	The XT batch number.

Robot Position Report

This report provides a view of which XT batches are queued to specific MSI tasks for processing in the lab.

Table 12 Robot Position Report

Column	Description
Item	The item ID or barcode.
Machine	n/a

Column	Description
Position	n/a
Project	The project name.
Task	The name of the task.
Task Date	The date and time when the task was performed.

Quality Control Reports

These reports provide details about the DNA samples, and statistical information that allow you to measure the quality of your experimental data. There are five quality control reports:

- *Sample Quant Report* on page 53
- *Quant Standard Curve Report* on page 55
- *Sample Manifest Report* on page 55
- *Imaging Metrics Report* on page 57
- *Control Metrics Report* on page 59

Sample Quant Report

This report provides statistics about quantified samples. Run it after you have performed the Make Quant and Read Quant tasks. Use this report to review your sample quantification data.

You can query by institute to see all plates associated with an institute or by DNA to see information about a single plate. Select the query option, then select the input parameter. When you query by DNA, an additional **Barcode** field is provided to scan or enter the barcode.

The first six columns of the table contain the report data. The remaining columns contain information from the sample manifest.

Table 13 Sample Quant Report

Column	Description
Actual Conc (ng/µl)	The actual concentration read from the quant plate, in nanograms per microliter.
Comment	Any comment from the sample manifest.
Extract Method	The way in which the DNA was retrieved from the sample.
Institute	The institute name.

Column	Description
IsControl	Indicates whether this is a control sample.
I-SSID	Institute Secondary System ID. Allows you to correlate your IDs with Illumina LIMSIDs, to track project data in your own databases.
Parent 1	The sample name/barcode or plate well of the parent, if known.
Parent 2	The sample name/barcode or plate well of the other parent, if known.
QNT Plate	The quantified plate barcode.
Read QNT Date	The date when the Read Quant task was performed.
Replicate	The name or barcode of any duplicate sample in the same plate.
Sample	The sample name.
Sample Plate	The sample plate barcode.
Sex	The sex of the individual from which the sample was derived. **M**: Male **F**: Female **U**: Unknown
Species	The species from which the DNA sample was drawn.
Submitted Conc (ng/µl)	The concentration reported in the sample manifest, in nanograms per microliter.
Tissue Type	The type of tissue from which the DNA sample was drawn.
Vol. Received	The amount of sample submitted, in microliters.
Well	The coordinates of the well in the sample plate that contains the sample.
Well Status	Active: Well can be processed through LIMS workflows. Inactive: Well cannot be processed.

Column	Description
WGA Input (ng)	For cases where the sample was amplified before submission, this shows the original quantity of DNA.
WGA Method	(Whole Genome Amplification) Indicates whether the sample was amplified before submission.

Quant Standard Curve Report

This report returns the data from the standard plate used at Read Quant. It has several uses.

You can query by institute to see all the Standard Plates associated with an institute, or by QNT/QDNA to see the standard curve for a quant plate. Select the query type, then select the input parameter. When you query by QNT/QDNA, an additional **Barcode** field is provided to scan or enter the barcode.

The report displays the same columns regardless of whether you select an institute or a DNA sample.

Table 14 Quant Standard Curve Report

Column	Description
Concentration	The concentration of the well in the Standard Plate.
Institute	The institute name.
QNT Plate	The quantified (QNT or QDNA) plate barcode.
Read QNT Date	Date when quant (QNT or QDNA) was performed.
Read Value	The read value from the Fluorometer.
Standard Plate Well	The coordinates of the well in the standard plate.

Sample Manifest Report

This report returns the data from the sample manifest. It has several uses:

- To obtain data about a given plate.

- To ensure that a sample was accurately accessioned.
- To obtain statistics about a plate for which you did not run quant.
- To create a new sample manifest for accessioning a duplicate plate (e.g. a control DNA plate) into the system. To do this, export the report to a .csv file, change the barcode, and accession it.

You can query by institute to see all manifests associated with an institute, or by DNA to see the manifest for a single plate. Select the query type, then select the input parameter. When you query by DNA, an additional **Barcode** field is provided to scan or enter the barcode.

The report displays the same columns regardless of whether you select an institute or a DNA sample.

Table 15 Sample Manifest Report

Column	Description
Comment	Any comment from the sample manifest.
Extract Method	The way in which the DNA was retrieved from the sample.
Institute	The institute name.
IsControl	Indicates whether this is a control sample.
I-SSID	Institute Secondary System ID. Allows you to correlate your IDs with Illumina LIMSIDs, to track project data in your own databases.
Parent 1	The sample name/barcode or plate well of the parent, if known.
Parent 2	The sample name/barcode or plate well of the other parent, if known.
Replicate	The name or barcode of any duplicate sample in the same plate.
Sample	The sample name or barcode.
Sample Plate	The sample plate barcode.
Sex	The sex of the individual from which the sample was derived. **M**: Male

Column	Description
	F: Female **U**: Unknown
Species	The species from which the DNA sample was drawn.
Submitted Conc (ng/µl)	The concentration reported in the sample manifest, in nanograms per microliter.
Tissue Type	The type of tissue from which the DNA sample was drawn.
Vol. Received	The amount of sample submitted, in microliters.
Well	The coordinates of the well in the sample plate.
Well Status	**Active**: Well can be processed through LIMS workflows. **Inactive**: Well cannot be processed.
WGA Input (ng)	For cases where the sample was amplified before submission, this shows the original quantity of DNA in nanograms.
WGA Method	(Whole Genome Amplification) Indicates whether the sample was amplified before submission.

Imaging Metrics Report

This report provides statistical data about scans. You can export it to Excel and create graphs or plots to reveal patterns in recent scans or data about a given BeadChip.

To generate a report, you can query by BeadChip, date range, or project. After selecting the query type, click **Get List** to specify the input parameters.

Do one of the following to generate this report, either:

- **Query by BeadChip** - Scan or enter the BeadChip barcode
- **Query by Date Range** - Enter the imaging From Date. You can optionally enter the To Date to constrain the results. When the To Date is blank, the report retrieves all data up to today's date.
- **Query by Project** - Select the input project

The report shows the statistical results of the BeadChip image, telling the lab manager whether the BeadChip is likely to succeed in the analysis phase. This report, along with

Control Metrics, helps measure the quality of your experimental data by confirming whether the data are as you expect.

Table 16 Imaging Metrics Report

Column	Description
50th Green 50th Red 5th Green 5th Red 95th Green 95th Red mean Green mean Red	The percentile intensity values for the green and red channels.
50th Grn 5th 3 5th Grn 95th Grn	The percentile intensity values for the green channel.
BeadChip	The BeadChip barcode.
Focus Green Focus Red	The focus of the intensities for the green and red channels.
Image Date	The date and time when the BeadChip was scanned (*aka* imaged).
mean Grn	The mean intensity value for the green channel.
Product	The product description.
Product Rev	The revision of the product.
Project	The project name.
P-SSID	Project Secondary System ID. Allows you to correlate your IDs with Illumina LIMSIDs, to track project data in your own databases.

Column	Description
Reg Green Reg Red	The reg of the intensities for the green and red channels.
report_metrics_id	ID number assigned to the report metrics.
Scanner	The serial number of the scanner where the BeadChip was scanned.
Section	The area on the BeadChip where the sample resides.
section id	ID number for the selected section.
Sentrix Type	Brand name of the array; various types of BeadChip (1x10 = 1 sample, 10 stripes).
stdev Green stdev Red	The standard deviation of the intensities for the green and red channels.
stdev Grn	The standard deviation of the intensities for the green channel.

Control Metrics Report

This report details the behavior of the controls built into each BeadChip.

You must select the **Assay Type** and select **Get Products**. Then select the product name and enter the report **From Date.** You can optionally enter the **To Date** to constrain the results.

NOTE
This report and the Imaging Metrics report are drawn from tables populated by a background process that runs every few hours. Therefore, the data in these reports may lag behind the imaging by several hours.

Table 17 Control Metrics Report

Column	Description
BeadChip	The BeadChip barcode.
Green Extension1-HP 7040463	The value returned for this particular control. Each control is named in the format **Channel Type-of-control Code**. **Channel**: Green or Red **Type of Control**: See for an overview of Infinium Assay controls. **Code**: The bead number. It is possible to have the same control on multiple beads, enabling you to view the same information in different ways.
Image Date	The date and time when the BeadChip was scanned (*aka* imaged).
Product	The product description.
Product Rev	The revision of the product.
Project	The name of the project for which this assay was run.
P-SSID	Project Secondary System ID. Allows you to correlate your IDs with Illumina LIMSIDs, to track project data in your own databases.
quality_metrics_id	The ID number assigned to the quality metrics.
Scanner	The serial number of the scanner where the BeadChip was scanned.
Section	The area on the BeadChip where the sample resides.
section_id	The ID number assigned to the section.
Sentrix Type	Brand name of the array; various types of BeadChip (1 x10 = 1 sample, 10 stripes).

Infinium Assay System Controls

This table provides a brief overview of the Infinium system controls. For complete descriptions, see the System Controls chapter of the *Infinium Assay Lab Setup and Procedures* guide.

Table 18 Infinium Assay System Controls

Control	Description
Sample Independent	
Extension	Tests the extension efficiency of the A, T, G, and C nucleotides from a hairpin probe.
Hybridization	Tests the overall performance of the assay using synthetic targets instead of amplified DNA. The bead type IDs should result in signal with various intensities, corresponding to the concentration of the initial synthetic targets.
Staining	Shows the expected intensity of the biotin and DNP labeling controls. Tests the efficiency of the staining step.
Target Removal	Tests the efficiency of the stripping step after the extension reaction. The signals should be low compared to the hybridization controls, indicating that the targets were removed.
Sample Dependent	
Non-Polymorphic	Tests the overall performance of the assay, from amplification to detection, by querying a particular base in a non-polymorphic region of the genome. Enables you to compare assay performance across samples.
Non-Specific Binding	Monitors the specificity of the amplified DNA hybridization. The probe sequences should not bind to human sequences, and so the controls should have low intensity.
Stringency	Tests the stringency of the hybridization process.

Tracking Reports

Tracking reports tell you where things are in the system. There are six tracking reports:

- *Tran Report* on page 62
- *Task History Report* on page 66
- *History by User or Machine Report* on page 69
- *Item History Report* on page 70
- *List Items on Queue Report* on page 71
- *Queue Status Report* on page 71

Tran Report

This report provides data on a given transaction: who did it, what machine they used, etc. Either enter a particular transaction ID, or leave the box empty to view data on the most recent transaction. To obtain a specific transaction ID, use the *Task History Report* on page 66

Illumina LIMS creates a transaction record each time a task is saved into the system.

The Tran report contains several separate tables:

- *Task History*
- *Contents*
- *Attributes*
- *Conditions*
- *Comments*
- *Item History*

Task History

This section identifies each time a task is saved into the system.

Table 19 Tran Report (Task History)

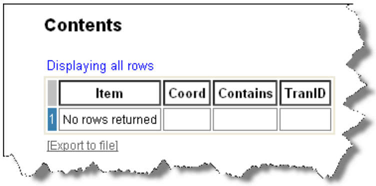
Column	Description
Item	Depending on the task, this may be a BeadChip, a sample, etc.

Column	Description
Login	The person who performed the task.
Machine	The machine on which the task was performed.
Queued From	The last task run for the item.
Queued To	The task for which the item is queued.
Task Date	The date and time when the task was saved.
Tran ID	The transaction ID

Contents

This section identifies the content, which is anything added to the item (i.e., a sample plate has samples as content).

Figure 6 Tran Report (Contents)



Contents

Displaying all rows

	Item	Coord	Contains	TranID
1	No rows returned			

[Export to file]

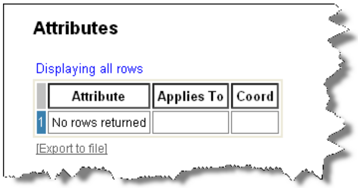
Table 20 Tran Report (Contents)

Column	Description
Contains	Anything that ever touched or was associated with the item: e.g., samples, reagents, institutes, etc.
Coord	If appropriate, coordinates for the relevant location: e.g., a section on a BeadChip or a well on a plate.
Item	Depending on the task, this may be a BeadChip, a sample, etc.
TranID	The transaction ID.

Attributes

This area of the report is not currently used.

Figure 7 Tran Report (Attributes)



Attributes

Displaying all rows

	Attribute	Applies To	Coord
1	No rows returned		

[Export to file]

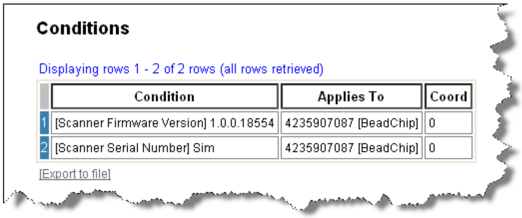
Table 21 Tran Report (Conditions)

Column	Description
Coord	If appropriate, the coordinates of the relevant location.
Applies To	The item and item type the attribute applies to.
Attribute	The information recorded.

Conditions

This section identifies the software and firmware used in the transaction.

Figure 8 Tran Report (Conditions)



Conditions

Displaying rows 1 - 2 of 2 rows (all rows retrieved)

	Condition	Applies To	Coord
1	[Scanner Firmware Version] 1.0.0.18554	4235907087 [BeadChip]	0
2	[Scanner Serial Number] Sim	4235907087 [BeadChip]	0

[Export to file]

Table 22 Tran Report (Conditions)

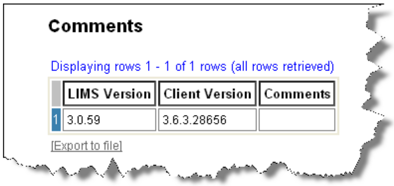
Column	Description
Applies To	The item and item type the condition applies to.
Condition	The information recorded.
Coord	If appropriate, the coordinates of the relevant location.

Comments

This section identifies the current versions of the Illumina LIMS web interface and Illumina LIMS Project Manager client interface.

Any comments associated with the task also appear in this table. Users cannot enter comments directly into Illumina LIMS, but sample manifests sometimes have comments and the system generates comments automatically for certain actions such as AutoAccession failures.

Figure 9 Tran Report (Comments)



Comments

Displaying rows 1 - 1 of 1 rows (all rows retrieved)

	LIMS Version	Client Version	Comments
1	3.0.59	3.6.3.28656	

[Export to file]

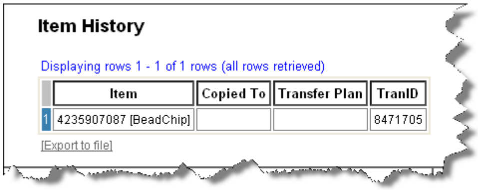
Table 23 Tran Report (Comments)

Column	Description
Client Version	The version of the client application (e.g., Illumina LIMS Project Manager, BeadScan, Infinium RobotControl, BeadStudio, etc.).
Comments	The comment text.
LIMS Version	The version of the Illumina LIMS web client.

Item History

This section identifies anything that was copied to the item. For example, in Make AMP2, DNA samples are copied to an AMP2 plate.

Figure 10 Tran Report (Item History)



Item History

Displaying rows 1 - 1 of 1 rows (all rows retrieved)

	Item	Copied To	Transfer Plan	TranID
1	4235907087 [BeadChip]			8471705

[Export to file]

Table 24 Tran Report (Item History)

Column	Description
Copied To	The object it was copied to: this could be another item, a task, etc.
Item	Depending on the task, this may be a BeadChip, a sample, etc.
TranID	The transaction ID.
Transfer Plan	The map that the robot uses to take contents from one container to the next.

Task History Report

This report provides information about every task that has occurred in the system. You can select any task to view, and optionally add a date range to constrain the results.

NOTE
You can enter a future end date when specifying the date range; the system collects data up through the present time and then stops.

Click **Latest Runs** to export a .csv file with data on the most recent execution of each task and on the queue associated with the task. See *Latest Run* below for more information.

Table 25 Task History Report

Column	Description
Comment	Any comments (usually system-generated) associated with the task.
Login	The person who performed the task.
Machine	The name of the machine on which the task was performed.
Queued From	The last task run for the item.
Queued To	The task for which the item is queued.
Task Date	The date and time when the task was performed.
Tran ID	The transaction ID of the task.

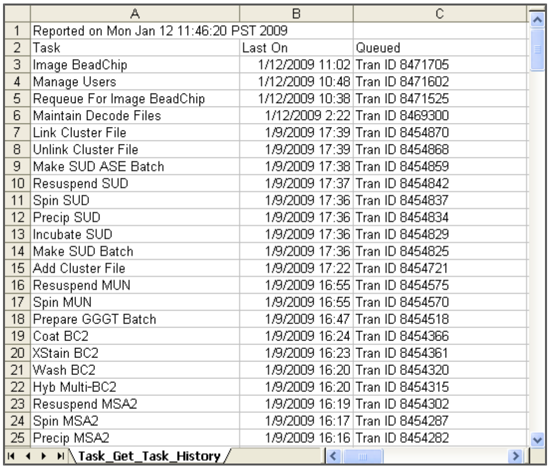
Latest Runs

Click **Latest Runs** to see a .csv report identifying the last time a task was run in the system. The .csv file has two sections.

Task Section

The Task section of the .csv report shows the date, time, and transaction ID for the last task that was run in this queue.

Figure 11 Task History Report, Latest Runs (Task)



	A	B	C
1	Reported on Mon Jan 12 11:46:20 PST 2009		
2	Task	Last On	Queued
3	Image BeadChip	1/12/2009 11:02	Tran ID 8471705
4	Manage Users	1/12/2009 10:48	Tran ID 8471602
5	Requeue For Image BeadChip	1/12/2009 10:38	Tran ID 8471525
6	Maintain Decode Files	1/12/2009 2:22	Tran ID 8469300
7	Link Cluster File	1/9/2009 17:39	Tran ID 8454870
8	Unlink Cluster File	1/9/2009 17:39	Tran ID 8454868
9	Make SUD ASE Batch	1/9/2009 17:38	Tran ID 8454859
10	Resuspend SUD	1/9/2009 17:37	Tran ID 8454842
11	Spin SUD	1/9/2009 17:36	Tran ID 8454837
12	Precip SUD	1/9/2009 17:36	Tran ID 8454834
13	Incubate SUD	1/9/2009 17:36	Tran ID 8454829
14	Make SUD Batch	1/9/2009 17:36	Tran ID 8454825
15	Add Cluster File	1/9/2009 17:22	Tran ID 8454721
16	Resuspend MUN	1/9/2009 16:55	Tran ID 8454575
17	Spin MUN	1/9/2009 16:55	Tran ID 8454570
18	Prepare GGGT Batch	1/9/2009 16:47	Tran ID 8454518
19	Coat BC2	1/9/2009 16:24	Tran ID 8454366
20	XStain BC2	1/9/2009 16:23	Tran ID 8454361
21	Wash BC2	1/9/2009 16:20	Tran ID 8454320
22	Hyb Multi-BC2	1/9/2009 16:20	Tran ID 8454315
23	Resuspend MSA2	1/9/2009 16:19	Tran ID 8454302
24	Spin MSA2	1/9/2009 16:17	Tran ID 8454287
25	Precip MSA2	1/9/2009 16:16	Tran ID 8454282

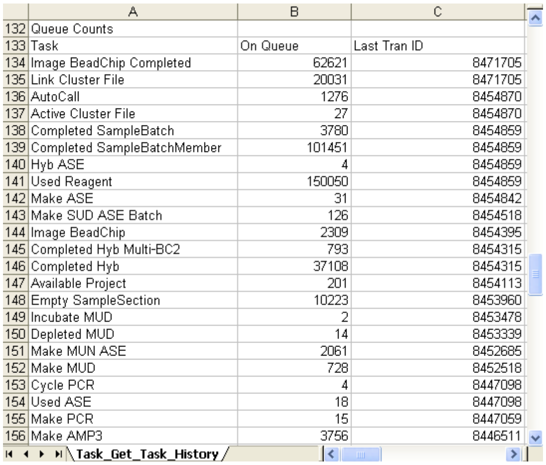
Table 26 Task History Report, Latest Runs (Task)

Column	Description
Last On	The date and time when the most recent task occurred.
Queued	The transaction ID associated with that execution of the task.
Task	Name of the task: e.g., Hyb Multi-BC2.

Queue Counts

The Queue Counts section of the .csv report shows the number of items in each queue, and the transaction ID of the most recent item added to the queue.

Figure 12 Task History Report, Latest Runs (Queue Counts)



	A	B	C
132	Queue Counts		
133	Task	On Queue	Last Tran ID
134	Image BeadChip Completed	62621	8471705
135	Link Cluster File	20031	8471705
136	AutoCall	1276	8454870
137	Active Cluster File	27	8454870
138	Completed SampleBatch	3780	8454859
139	Completed SampleBatchMember	101451	8454859
140	Hyb ASE	4	8454859
141	Used Reagent	150050	8454859
142	Make ASE	31	8454842
143	Make SUD ASE Batch	126	8454518
144	Image BeadChip	2309	8454395
145	Completed Hyb Multi-BC2	793	8454315
146	Completed Hyb	37108	8454315
147	Available Project	201	8454113
148	Empty SampleSection	10223	8453960
149	Incubate MUD	2	8453478
150	Depleted MUD	14	8453339
151	Make MUN ASE	2061	8452685
152	Make MUD	728	8452518
153	Cycle PCR	4	8447098
154	Used ASE	18	8447098
155	Make PCR	15	8447059
156	Make AMP3	3756	8446511

Table 27 Task History Report, Latest Runs (Queue Counts)

Column	Description
Last Tran ID	The transaction ID associated with the task.
On Queue	Number of times that items have been queued for the task.
Task	Name of the task: e.g., AutoCall.

History by User or Machine Report

This report lists the actions of a particular user or machine. If a robot appears to be malfunctioning, for example, use this report to get more data.

You can retrieve data by user name (login) or machine ID. You may optionally add a date range to constrain the results.

Table 28 History by User or Machine Report

Column	Description
Comment	Any comments (usually system-generated) associated with the

Column	Description
	task.
Login	The person who performed the task.
Machine	The name of the machine on which the task was performed.
Queued From	The last task run for the item.
Queued To	The task for which the item is queued.
Task Date	The date and time when the task was performed.
Tran ID	The transaction ID of the task.

Item History Report

This report provides information about items in the system, ranging from institutes to MSA2 plates to the xstain reagent 4 reagent.

To retrieve the history of any item, select the item type and enter its name or ID.

NOTE
If you do not know the ID, the List Items on Queue report (*List Items on Queue Report* on page 71) is often a quick way to find out.

Table 29 Item History Report

Column	Description
Content Added	The ID of any content that has been added to this item, such as a sample being added to a plate.
Item	The item ID or barcode.
Login	The person who performed the task.
Task	Identifies each task the item has completed, in chronological order.
Task Date	The date and time when the task was saved.
TranID	The transaction ID.

List Items on Queue Report

This report lists all the items in the selected queue. Select the queue.

Table 30 List Items on Queue Report

Column	Description
By	The login account of the person who performed the task.
Items	Depending on the task, this may be a BeadChip, a sample, etc.
Queued For	The task the item is queued for.
Queued On	The date and time when the item was queued for a task.
Routed From	The last task that was performed for the item.
TranID	The transaction ID.

Queue Status Report

Purpose

This report indicates the next task for up to 24 items. The items do not have to be of the same type. This information enables the laboratory technician to pick up the work at the correct point. Scan an item barcode into each field.

Table 31 Get Queue Status Report

Column	Description
Item	The ID of the scanned item.
Item Type	The item type.
Queued On	The date the item was queued for a task.
Queued To	The next task that the item is queued for.
Routed From	The previous task performed on the item.

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Technical Assistance

For technical assistance, contact Illumina Customer Support.

Table 32 Illumina General Contact Information

Illumina Website	http://www.illumina.com
Email	techsupport@illumina.com

Table 33 Illumina Customer Support Telephone Numbers

Region	Contact Number	Region	Contact Number
North America	1.800.809.4566	Italy	800.874909
Austria	0800.296575	Netherlands	0800.0223859
Belgium	0800.81102	Norway	800.16836
Denmark	80882346	Spain	900.812168
Finland	0800.918363	Sweden	020790181
France	0800.911850	Switzerland	0800.563118
Germany	0800.180.8994	United Kingdom	0800.917.0041
Ireland	1.800.812949	Other countries	+44.1799.534000

MSDSs

Material safety data sheets (MSDSs) are available on the Illumina website at http://www.illumina.com/msds.

Product Documentation

If you require additional product documentation, you can obtain PDFs from the Illumina website if PDFs are available. Go to http://www.illumina.com/support/documentation.ilmn. When you click on a link, you will be asked to log in to iCom. After you log in, you can view or save the PDF. To register for an iCom account, please visit https://icom.illumina.com/Account/Register.