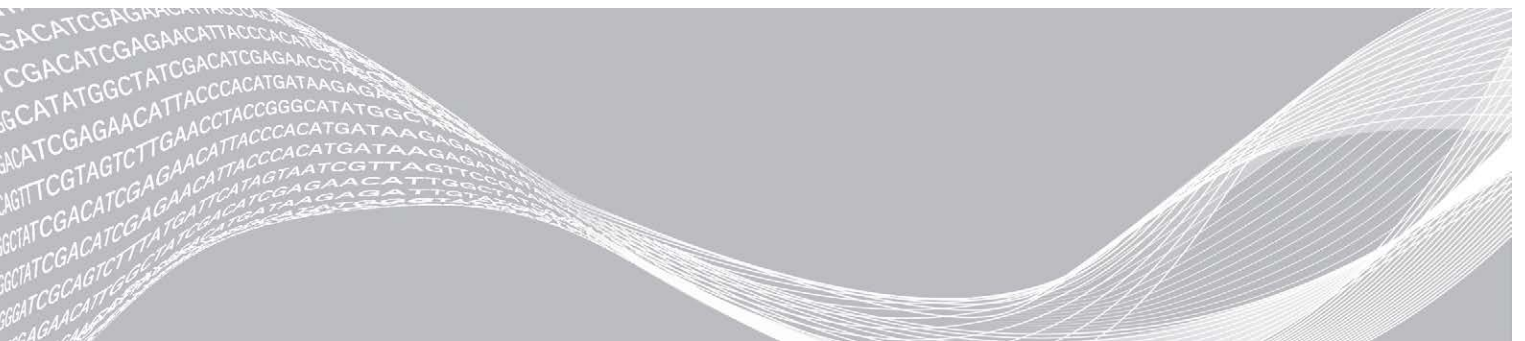


# Illumina LIMS

## Software Guide



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

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

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

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

© 2019 Illumina, Inc. All rights reserved.

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

## Revision History

Document	Date	Description of Change
Document # 1000000032951 v02	August 2019	Removed reference to WG# barcode numbering in the <i>Searching for an Institute and DNA and BCD Samples</i> text.
Document # 1000000032951 v01	December 2018	Added procedure on adding a sample batch.
Document # 1000000032951 v00	June 2017	Initial release.

# Table of Contents

<b>Introduction</b> .....	<b>1</b>
Access Features .....	1
<b>Chapter 1 Illumina LIMS Project Manager Software</b> .....	<b>2</b>
Overview .....	2
Project Manager .....	7
Laboratory Manager .....	26
Resources .....	28
<b>Chapter 2 Illumina LIMS Web Client</b> .....	<b>30</b>
Overview .....	30
Administrative Tools .....	30
Laboratory Management .....	34
Reports .....	35
<b>Technical Assistance</b> .....	<b>53</b>

## Introduction

The Illumina® Laboratory Information Management System (LIMS) software is comprised of two components:

- ▶ Illumina LIMS Project Manager, a server application that lets scientists or project managers:
  - ▶ Set up institutes, projects, and investigators
  - ▶ Accession samples
  - ▶ Add global control sample plates
  - ▶ Accession products
  - ▶ Add cluster files

For more information on using the Project Manager, see *Illumina LIMS Project Manager Software* on page 2

- ▶ Illumina LIMS web client that enables positive sample tracking throughout the laboratory workflow by providing:
  - ▶ 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

For more information on using the web client, see *Illumina LIMS Web Client* on page 30

## Access Features

Access to the Illumina LIMS Project Manager or Illumina LIMS web client is done one of two ways:

- ▶ Windows authentication
- ▶ Database authentication

Confirm your log on method with your system administrator.

Your lab manager or system administrator sets up user accounts and determines the features that are available to you. To request changes to your account, contact your system administrator.

# Illumina LIMS Project Manager Software

Overview .....	2
Project Manager .....	7
Laboratory Manager .....	26
Resources .....	28

## Overview

The Illumina LIMS Project Manager lets you easily accession experimental and control samples into the system using familiar sample sheet definitions. When you assign samples to an Infinium project, Project Manager automatically queues them for processing in batches that match the Illumina reagent and BeadChip packages. You can also create customized Infinium batches manually.

To use the Project Manager, you must have Management Client access. For more information on permissions, see *Manage Users on page 30*.

## Illumina LIMS Project Manager Workflow

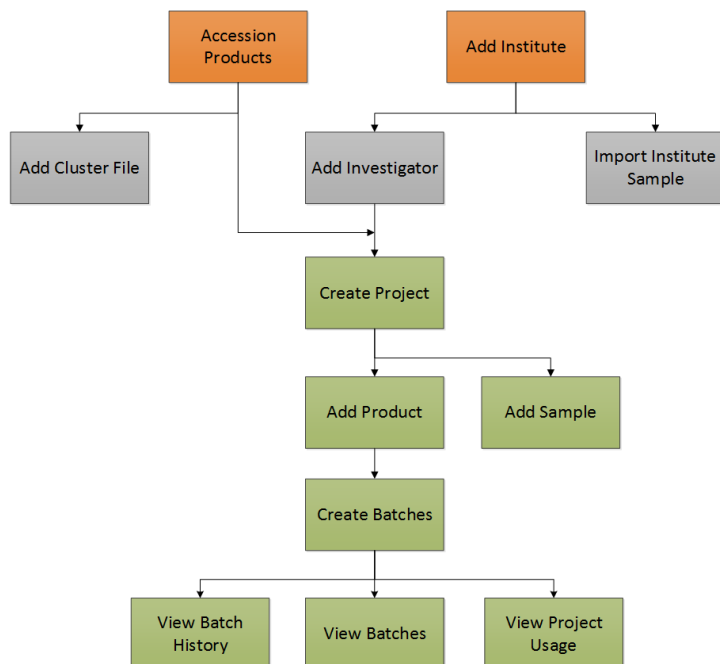
The following diagram illustrates the Project Manager workflow. For more detail on any of the steps, see the corresponding section.



### NOTE

While products can be accessioned into the system prior to adding institutes, there must be a product in the system in order to create a project.

Figure 1 Illumina LIMS Project Manager Workflow



## Installing the Illumina LIMS Project Manager Client

- 1 In the URL field of your web browser, type the address provided by the system administrator. The Illumina LIMS window opens.
- 2 Select **Download Project Manager Client**.  
The Illumina LIMS Project Manager client is installed. When complete, the **Log into LIMS Project Manager** window opens, and the Illumina lims-manager icon is added to your desktop.
- 3 Set the Java Security configuration by doing the following:
  - ▶ In the Control Panel, select **Java 32-bit**.
  - ▶ Select the **Security** tab.
  - ▶ In the exception list, add the LIMS website address.
  - ▶ Select **OK** and exit the Control Panel.

## Getting Started

- 1 Select the Illumina lims-manager icon.  
The **Log into LIMS Project Manager** window opens.  
The first time you use the Project Manager you must configure the client server.
  - a Select **Configure**.
  - b Enter or edit the Display Name, Host, Port, and Context, then select **OK**.
  - c To add additional servers, select **New Server** then enter the Display Name, Host, Port, and Context.
  - d To delete a server, select the server from the list, and then select **Delete**.

If you do not know your configuration parameters, consult your Illumina LIMS system administrator.

- 2 Do one of the following:
  - ▶ If you are using Windows authentication, enter your Windows user name and password in the **Log into LIMS Project Manager** window.
  - ▶ If you are using database authentication, enter the user name and password that were established for your Illumina LIMS user account.

If you do not know what form of authentication is being used, contact your system administrator.

- 3 Select **Login**.  
The Illumina LIMS Project Manager window opens.



### NOTE

The first time you log in to the Project Manager, the Illumina LIMS Project Manager End-User Software License Agreement opens. Read the agreement, then select **Agree** to continue.

The instructions in this guide assume that you are logged in to Project Manager.

## Configuration Tools

The configuration of email ,connection timeouts, date and time formats, and log settings can be modified. To access these configuration options in the Project Manager window select **Tools | Options**. The table that follows describes the options on each tab.

Option	Description
Email	Sets the SMTP Server used for email.
Connection	Sets connection parameters. <b>Server Communication</b> —Select the number of seconds of lost connection time before server communications timeout. A 0 setting indicates no time outs. <b>Automatic Logoff</b> —Select the number of seconds of inactivity before the user is automatically logged off. A 0 setting indicates that the users are never logged off automatically. Select whether to display a warning message prior to logoff and whether to reactivate the prior task after re-login.
Date/Time Format	Sets the date and time format to be used.
Log Settings	Enables or disables logs.

## View Events and Communications

### View Event Logs

Project Manager logs all events that occur during a session. These logs are often used when troubleshooting system issues.

The first time you log in, the Event Log is automatically displayed. The Event Log lists the events that have occurred in the current session.

- ▶ To remove the Event Log pane, from the Illumina LIMS Project Manager menu bar select **View | Event Log**.
- ▶ To redisplay the Event Log, from the Illumina LIMS Project Manager menu bar select **View | Event Log**.
- ▶ Select to increase or decrease the **Max Lines** (maximum number of lines) in the Event Log pane as needed.
- ▶ Select **Clear** in the Event Log pane to delete the contents of the list.

### View Request/Response Exchanges

You can view all the requests and responses between the server and the local client. If you call technical support, a technical support scientist may request that you turn this on.

The first time you log in, the Request/Response pane is automatically displayed. The Request/Response pane shows the code that is being executed.

- ▶ To remove the Request/Response pane, from the Illumina LIMS Project Manager menu bar select **View | Request/Response**.
- ▶ To redisplay the Request/Response pane, from the Illumina LIMS Project Manager menu bar select **View | Request/Response**.
- ▶ Select **Clear** in the Request/Response pane to delete the contents of the list.

### Email the Request/Response Log

- 1 In the Request/Response pane, select **Save to File** .
- 2 Name the file with a .txt (text file) extension.
- 3 In the Request/Response pane, Select **Mail** .  
An email dialog box opens populated with the email address for technical support.
- 4 Enter your email address in the **From** box.
- 5 **[Optional]** Enter a subject line or comments.



Comments will appear in the body of the message.

- 6 Select **Add**, and then navigate to the location of the text file you created and select it.
- 7 Select **Send**.

## Manage Display

Project Manager lets you modify the viewing options.

### Reset All Windows

You can reset the Illumina LIMS Project Manager window to display the viewing panes in the default configuration.

- ▶ From the menu bar select **View | Reset All Windows** so that all the viewing panes will be displayed and in their default location.  
The changes takes effect the next time you open and log in to Project Manager.

## Manage Table Contents

The contents of most tables can be copied for pasting into a spreadsheet or text file. Additionally, the order in which the rows of data are displayed can be sorted by a specified column.

- ▶ Copy table contents by placing the cursor within any table display, right-click, and select **Copy**. Open the destination application (for example, an Excel spreadsheet) where you want to paste the table contents, right-click, and select **Paste**
- ▶ Click the column header to toggle the sort order between ascending, descending, or original order based on the contents of the column selected.

## Manage Forms

A form can be saved, loaded, or saved as an image in the Project Manager. Using the form options lets you save the input data and later load that data without having to manually reenter it.

- ▶ To save a form, select **Save Form**. Name and save the selected workflow form to an XML format.
- ▶ To load a form, select **Load Form**. Locate and select the form that you want to view.
- ▶ To capture an image of a workflow pane, select **Form Screen Shot**. Enter a name for the image of the workflow pane, and select **Save** to save the image in PNG format.

## Report Bugs

- 1 In the Project Manager window, select **Report Bug**.  
The Email window opens. The following information is automatically included in the email:
  - ▶ Your email address
  - ▶ Subject
  - ▶ Comments about the last event you performed
  - ▶ A screen shot of the last event you performed
- 2 In the **To** field, enter the email address of your Illumina LIMS system administrator.
- 3 Enter additional comments if necessary.
- 4 Add or remove attachments if necessary.
  - ▶ To add a file to the attachment list, select the add icon, choose the file to add, and then select **Open**.
  - ▶ To remove a file from the attachments list, select the file from the list, then select the delete icon.

- 5 Select **Send** to send the bug report.

## Administrator Tools

The system administrator controls user access and application values from the Administration page.

- ▶ From the menu bar select **Tools | Administrator**.

## User Manager

Illumina LIMS users can be added and their permissions can be controlled through the User Manager.

- ▶ In the Administration page, select **User Manager**.  
A list of existing users is displayed.

## Add User

- 1 In the Administration window, select the Add User icon.
- 2 Enter the user name and password information, and then select **Save**.  
See [Add User on page 6](#) to set up user permissions.

## Edit Password

Use this feature to edit passwords for users logging in using database authentication.

- 1 Select a user from the list.
- 2 Select the Edit User icon.
- 3 Enter the new password information, and then select **Save**.

## Edit Permissions

- 1 Select a user from the list.  
The user's permissions are displayed for each Illumina LIMS task. A check in the Allowed column indicates that the user has permission to perform that task.
- 2 To modify the user's permissions do one of the following:
  - ▶ Select **Allow All** to allow the user to perform all Illumina LIMS tasks.
  - ▶ Select **Select Individual Tasks** to allow the user to perform only selected Illumina LIMS tasks and do one of the following:
    - ▶ Check the box in the Allowed column next to each individual task that you want the user to have permission to perform.
    - ▶ Select **Check All** to allow the user to perform all Illumina LIMS tasks.
    - ▶ Select **Uncheck All** to disallow the user to perform any Illumina LIMS tasks.
  - ▶ Select **Copy Permissions of** to copy the permissions of another user. Select a user whose permissions are to be copied from the drop-down menu.
- 3 Select **Save**.

## App Values

This feature lets you create and edit application values, and create new categories.

- ▶ In the Administration window, select **App Values**.  
The list of application values is displayed in alphabetical order.

## Edit Application Values

- 1 Double-click on the parent type folder that contains the application (app) value type you want to edit.
- 2 Select the + sign beside any folder to view more information, drilling down until you see the app value that you want to edit.
- 3 Select the value that you want to edit.
- 4 Select **Edit App Value**.
- 5 Enter the new App Value and select **Save**.

## Add Category


- 1 Select **New Category**.
- 2 Enter the new Parent Type category and select **Save**.

## Add Application Value

- 1 Double-click on the folder that contains the parent type you want to update.
- 2 Select the + sign beside any folder to view more information, drilling down until you see the folder where you want to add the app value.
- 3 Select the folder that will contain the new app value.
- 4 Select **New App Value**.
- 5 Enter the new label or name in the App Value Type field.
- 6 Enter specific information about the App Value Type in the App Value field, such as the directory path, value, or setting.  
Active and inactive settings are defined as follows:
  - ▶ **Active:** Anyone can do work associated with the application.
  - ▶ **Inactive:** No one can do any work associated with the project.
- 7 Select **Save**.  
The new app value and its type are added to the parent category folder.

## Exit Project Manager

To exit Project Manager do one of the following from the Illumina LIMS Project Manager window:

- ▶ Select **Logoff**.
- ▶ Select **File | Exit**.
- ▶ Select  in the upper right corner.

## Project Manager

The Project Manager area provides tools for creating and managing individual projects for each institute. Every project, investigator, sample, and batch is associated with a single institute. Products are available to all institutes.

## Adding and Managing Institutes

An institute is a group, institution, department, or other entity that has projects in Illumina LIMS. Every project must be associated with an institute.

### Adding an Institute

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Select **New Institute**.  
The Add New Institute pane opens.
- 3 Enter the institute name and any ancillary contact information that you wish to include.  
The only required information is the institute name.
- 4 If the institute has a system ID that allows the LIMS data to connect to its own backend database, enter the ID here.  
This ID appears on all institute-based reports as I-SSID (institute secondary system ID).
- 5 Select **Save**.

### Modifying an Institute

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Find the appropriate institute.  
For more information, see [Searching for an Institute on page 8](#).
- 3 Highlight the institute and select **Institute Detail**, or double-click the institute.  
The Institute Detail pane opens.
- 4 Select the institute name.  
The institute details are displayed.
- 5 Make any changes to the institute's contact information, and then select **Save**.



#### NOTE

You cannot change the name of the institute.

### Searching for an Institute

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 In the **Search By** drop-down list, select the type of information you want to search by:
  - ▶ Institute Name
  - ▶ Project Name
  - ▶ Investigator Name
  - ▶ Sample Container Barcode (ie, DNA plate barcode)
- 3 In the **Search Criteria** field, type the text to search on (eg, RMS Lab, or the DNA barcode number for a sample plate).  
The field is not case-sensitive.

- 4 **[Optional]** If you do not know the full name, enter a wild card (\*) to represent the missing text. For example (assuming that you are searching by institute):
- ▶ e\* searches for all institutes whose names begin with “e”
  - ▶ \*e\* searches for all institutes whose names contain “e”
  - ▶ \*e searches for all institutes whose names end in “e”
- To list all institutes, leave the field empty.
- 5 Select **Search**.  
The results of the search appear at the bottom of the pane.

## Sample Manifest

The sample manifest defines the DNA or BCD samples that are run through the lab. It can contain data for any number of plates, each of which can contain from 1 to 96 samples. To accession the sample manifest data, see [Accessioning Institute Samples on page 10](#).

The data in a sample manifest are specific to a single institute. If you import the sample manifest into an institute other than the one named in the file, you are prompted to confirm.

## DNA and BCD Sample Manifests

The sample manifest must contain the following information in the specific cells as indicated:

- ▶ A1: Institute Name
- ▶ A2: Date Received
- ▶ A3: Comments
- ▶ B1: The institute name accessioned for the samples listed in this manifest

The sample manifest must contain the columns listed in the following table. The columns can be in any order. DNA Input (ng) and Institute Sample Group should be used only in the BCD manifest.

**Table 1 DNA and BCD Sample Manifest Columns**

Column	Description
Comments*	Any supplementary data about the sample.
Conc (ng/μl)	The concentration of DNA in the sample, in nanograms per microliter.
DNA Input (ng)	(BCD manifests only) DNA input in Bisulfite conversion.
Extraction Method	The method by which the DNA was extracted from the tissue.
Institute Plate Label	The DNA barcode for the sample plate.
Institute Sample Group	(BCD manifest only) Required for methylation projects (for example, Disease vs. Normal).
Institute Sample Label	The name assigned by the institute to identify this sample.
Is Control	<b>0:</b> Experimental sample <b>1:</b> Control sample
Mass of DNA used in WGA	The mass of DNA used for this sample in WGA, if WGA was the extraction method.
Parent 1*	The sample name or plate well of the parent, if known.
Parent 2*	The sample name or plate well of the other parent, if known.
Replicate(s)*	The name or barcode of any duplicate sample in the same plate.

Column	Description
Row	(Optional) The row number of the sample in the sample manifest. Integers only. These numbers enable you to make sure that you have entered all the data for each plate (eg, 96 samples for the first plate and 72 samples for the second).
Sex	The sex of the individual from whom the sample was drawn. <b>M</b> : Male <b>F</b> : Female <b>U</b> : Unknown
Species	The species from which the DNA sample was drawn.
Tissue Source	The type of tissue from which the DNA was drawn.
Volume (µl)	The amount of sample, in microliters.
Well	The coordinates of the well in the sample plate (eg, A01 or H10).
WGA Method (if Applicable*)	The type of whole-genome amplification that was used to extract the DNA, if WGA was the extraction method.

\*This column must be present in the file but does not need to contain any information.

## Accessioning Institute Samples

To make samples available to projects within an institute, accession the sample manifest data into the institute. To begin, save the sample manifest as a comma-separated value (\*.csv) file. A manifest can contain any number of sample plates. For more information on the construction of the sample manifest, see [Sample Manifest on page 9](#).



### CAUTION

If you are generating the \*.csv file from an Excel spreadsheet, before saving it as a \*.csv file, review the Excel file to make sure that the final column has data in every row. If the last column is empty, Excel discards all commas after the last complete column in the row. This offsets the values for the rest of the file and causes errors upon import.

Projects only have access to samples that have been accessioned into the institute. Samples cannot be accessioned into more than one institute. This helps protect proprietary data.

## Accessioning Samples to an Institute

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Find the appropriate institute.  
For more information, see [Searching for an Institute on page 8](#).
- 3 Highlight the institute, and then select **Institute Detail**.  
The Institute Detail pane opens.
- 4 Select **Institute Samples**.
- 5 Select **Import Institute Samples**.
- 6 Select a sample manifest file (\*.csv), and then select **Open**.



### NOTE

If you import a sample manifest into an institute that is different from the institute name in the sample manifest, you are prompted to confirm.

The Import Manifest Detail pane opens and shows a row for each sample plate. For a detailed list of the columns in the sample manifest, see [Import Manifest Detail Fields on page 11](#).



#### NOTE

By default, the **Quant Samples** checkbox is selected for every sample plate. When you save, the sample plates are queued for the Make Quant task. You cannot assign sample plates to projects until they have completed the Read Quant task and are placed in the Available Sample Plates queue.

- 7 If you do not want to quantify a sample plate, deselect that plate. When you save, any sample plate that is not selected for Quant is immediately made available to assign to a project.
- 8 Select any sample plate in the Import Manifest Detail pane to view information about each well in the plate.

**Table 2 Import Manifest Detail Fields**

Column	Description
IsControl	<b>0:</b> The well in this row contains an experimental sample. <b>1:</b> The well in this row contains a control sample.
Parent 1	The sample name or plate well of the parent, if known.
Parent 2	The sample name or plate well of the other parent, if known.
Quant Samples	Indicates whether to quantify the samples in the sample plate. If the checkbox is selected, Project Manager automatically queues the samples for Make Quant. You cannot add these samples to a project until Read Quant is complete.
Replicates	The name or barcode of any duplicate sample in the same plate.
Sample	The sample name.
Sample Plate	The sample DNA plate barcode.
Sex	The sex of the individual from which the sample was derived. <b>M:</b> Male <b>F:</b> Female <b>U:</b> Unknown
Species	The species from which the DNA sample was drawn.
Well	The coordinates of the well in the sample plate (eg, A01 or H10).

- 9 Make sure that the species count specified on the Import Manifest Detail matches the number of species represented in the sample set.
- 10 Select **Save** to finish importing the samples into the institute. The imported samples appear at the bottom of the Institute Samples list. For more information, see the Sample Plate Fields table.

**Table 3 Sample Plate Fields**

Column	Description
IsControl	<b>0:</b> This plate is not a control plate. <b>1:</b> This plate is a control plate. Control plates are visible to all institutes in Project Manager.
Number of Samples	The number of samples on the plate.
Project Count	The number of projects to which this plate has been assigned.
Sample Container Id	System-generated database key.
Sample Plate	The sample plate name or barcode.

## Validating Samples

Project Manager automatically validates all the fields in the manifest when it is saved. If all sample plate data are valid, the row appears in green. If there is an error in the sample plate data (eg, the IsControl column has a value other than 0 or 1), the sample plate appears in red.

Possible causes for errors include:

- ▶ A plate has the same ID as a sample plate that is already in the system
- ▶ There is a missing value in one of the fields (eg, a blank volume)
- ▶ There is a character value in a numeric field

If an error occurs, correct the data in the sample manifest \*.csv file and reimport the samples.

## Viewing Institute Samples

The Institute Samples pane lists sample plates that are available for all projects in the institute.

- ▶ Select a sample plate to show detailed information from the sample manifest in the Plate Detail pane.

**Table 4 Sample Plate Detail Fields**

Column	Description
Comment	Any comments from the sample manifest.
Conc (ng/μl)	The concentration of DNA in the sample, in nanograms per microliter.
IsControl	<b>No:</b> The well in this row contains an experimental sample. <b>Yes:</b> The well in this row contains a control sample.
Parent 1	The sample name or plate well of the parent, if known.
Parent 2	The sample name 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.
Sex	The sex of the individual from which the sample was derived. <b>M:</b> Male <b>F:</b> Female <b>U:</b> Unknown
Species	The species from which the DNA sample was drawn.
Tissue Type	The type of tissue from which the DNA sample was drawn.
Volume (μl)	The amount of sample, in microliters.
Well	The coordinates of the well in the sample plate (eg, A01 or H10).

## Adding and Managing Investigators

Investigators are the scientists associated with an institute. An investigator can only be associated with one institute. Every project must have a principal investigator.

### Adding an Investigator

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Find the desired institute.  
For more information, see [Searching for an Institute on page 8](#).
- 3 Highlight the institute, and then select **Institute Detail**.



- 4 Select **Investigators**.
- 5 In the Investigators pane, select **New Investigator** and enter the required information.
  - ▶ First name
  - ▶ Last name
  - ▶ Email address
  - ▶ Phone #1
- 6 Select **Save**.  
The investigator appears in the Investigators list at the top of the pane.

## Updating an Investigator

You can only modify investigator contact information, the name cannot be changed.

- 1 In the Institute Detail pane, select **Investigators**.
- 2 In the Investigators pane, select the investigator.  
The investigator's personal information appears at the bottom of the pane.
- 3 Modify the contact information as needed, and then select **Save**.

## Product Accessioning

Accessioning is the process of adding new products to the database. After a product is accessioned, it is available to projects in any institute. To accession a product, the following files are required:

- ▶ Product Definition file (\*.xml): contains fields describing the specific product format.
- ▶ Bead Pool Manifest file (\*.bpm): provides information about every locus on the product.
- ▶ For multispecies products, all bead pool manifests associated with the product must be imported.
- ▶ **[Optional]** Cluster file (\*.egt): Provide the cluster positions required for generating genotype calls with Autocall. For more information, see [Cluster File Manager on page 14](#).



### NOTE

Multiuse products (eg, HumanOmni1-quad Multi-Use) must be accessioned even if the single-use version of the same product is already in the database (eg, HumanOmni1-quad).

## Accessioning Products

- 1 In the left pane, select **Product Manager**.
- 2 In the Product Manager frame, select **Product Accession**.  
The Product Accession window opens.
- 3 Select **Browse**, navigate to the definition file (\*.xml), and select **Open**.  
The product information automatically populates.
- 4 For multispecies products, the number of species associated with the product is displayed, select **Next**.  
The BPM Import pane opens.
- 5 For each species associated with the imported product, select by species to add or modify the **Bead Pool Manifest**.
- 6 Navigate to the bead pool manifest file (\*.bpm), and select **Open**.  
The selected manifest path and file name are displayed.
- 7 Select **Next**.

- 8 Review Product accession Detail, and then select **Save**.  
It can take a few moments for the product accession to complete.  
When accession is complete, the product appears in the **Available Products** list.

**NOTE**

Following product accession, cluster files can be added. For more information, see *Cluster File Manager* on page 14.

## Accessioning Individual BeadChips

In addition to accessioning product definitions into the system, you must accession each individually barcoded item. The information that needs to be accessioned can be downloaded via MyIllumina. For more information, see *Technical Assistance* on page 53.

**NOTE**

Before accessioning an individual BeadChip, you must have already accessioned its associated part number.

- 1 Access the BeadChip map data using the **Decode File Client**.
- 2 Navigate to the data destination folder and save files.
- 3 Open a window to display the contents of the data destination folder.
- 4 Navigate to the AutoLoad folder defined for your system.  
For more information about configuring system folders, see the *Illumina LIMS Web Client* on page 30.
- 5 Drag the BeadChip barcode folder into the AutoLoad folder.  
The next time that the Illumina Project Manager polls the AutoLoad folder, it accessions the items it finds there. If the accession is successful, the BeadChip is queued for the appropriate task.

**NOTE**

The product must be accessioned before the individual item can be accessioned.

If the accession fails, the DMAP files are moved automatically to the autoloading\_failure folder on the LIMS server, and an error appears in the AutoAccession Failure report. For more information about reports, see the *Illumina LIMS Web Client* on page 30.

## Cluster File Manager

Cluster files (\*.egt, \*.egtp) provide cluster definitions. For the AutoCall program to generate genotype calls, you must link a cluster file to each product. For single-species, each product can have one or more associated cluster files, but only one cluster file can be active at any time. For multi-species, each product can have one or more associated cluster files, and only one cluster file per species can be active at any time.

For standard products, import the cluster file using the Cluster File Manager. Custom BeadChips do not come with a cluster file. To create the cluster file, run the BeadChip against your samples, analyze the data in GenomeStudio, and export a cluster file. Import the file into the Project Manager using the Cluster File Manager.

Adding another cluster file is also useful if you wish to change the cluster definitions as you gather more data. To do this, customize the cluster file in GenomeStudio and export it. Importing multiple cluster files lets you continue to refine the file as you gather more data.

After each modification, it is recommended that you requeue the samples using the latest cluster file.

**NOTE**

AutoCall does not work with Methylation products.

## Viewing Cluster Files

- 1 In the left pane, select **Cluster File Manager**.
- 2 Select the **Product Name**, and then select **Next**.  
The active and inactive cluster files are displayed. The active cluster file appears in green.

## Adding a Cluster File

- 1 In the Cluster File Manager window, select the Product Name, and then select **Next**.
- 2 Select **Add Cluster File** to add a file to the list.
- 3 Navigate to the cluster file (\*.egt, \*.egtp), and then select **Open**.  
When the cluster file finishes importing, it is added to the list in the Manage Cluster Files window. The default status is Inactive.

**NOTE**

More than one cluster file can be added, however, only one can be active for a product or species at a given time .

## Activating a Cluster File

- 1 In the Cluster File Manager window, select the Product Name, and select **Next**.
- 2 Select the cluster file that you want to use for this product.
- 3 Select **Activate Cluster File**.  
The file you select applies to all revisions of the product. The active cluster file appears in green.

**NOTE**

If you activate a different cluster file for this product, the previously active cluster file automatically becomes inactive.

## Inactivating Cluster Files

- 1 In the Cluster File Manager window, select the Product Name, and then select **Next**.
- 2 Select **Inactivate Cluster Files**.  
The status of all listed files is set to inactive.

## Adding and Managing Projects

Most of the work done in Illumina LIMS is associated with a project, which in turn is associated with an institute. The project defines the available products, sample plates, and batches.

Before adding a project, you must have already done the following:

- ▶ Added investigators (see [Adding and Managing Investigators on page 12](#))
- ▶ Accessioned products (see [Product Accessioning on page 13](#))

## Adding a Project

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Find the desired institute.  
For more information, see [Searching for an Institute on page 8](#).
- 3 Highlight the institute, and then select **Institute Detail**.
- 4 Select **Projects**.
- 5 Select **New Project**.
- 6 Enter the project name.
- 7 If the project has a system ID that allows the LIMS data to connect to its own backend database, enter the ID.  
This ID appears on all the project-based LIMS reports as P-SSID (project secondary system ID).
- 8 Select the principal investigator.  
If the investigator does not appear in the list, go to the Investigators pane and add a record for the investigator. For more information, see [Adding and Managing Investigators on page 12](#).



### NOTE

If a newly added investigator does not appear in the list, select **Refresh Project** to refresh the screen.

- 9 Enter or select a starting date (mm/dd/yyyy) and a due date (mm/dd/yyyy).



### NOTE

The starting date and due date are for tracking purposes only, and have no effect on how the project is run.

- 10 Select the products that will be used in the project.  
You can select multiple products at one time, except for MSI products.



### NOTE

If a product does not appear in the list, go to the Product Manager and accession the product into the system. For more information, see [Product Accessioning on page 13](#).

When you assign sample plates to the project, a separate batch is created for each product. For more information on sample plates, see [Viewing Sample Plates on page 20](#).

- 11 Select **Save**.  
The project appears in the Projects list at the top of the page.

## Adding Products to an Existing Project

You can add new products to a Infinium project at any time. The product must be accessioned into the system before it can be added to a project. For more information, see [Accessioning Products on page 13](#).

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Find the desired institute.  
For more information, see [Searching for an Institute on page 8](#).
- 3 Highlight the institute, and then select **Institute Detail**.

- 4 Select **Projects**.
- 5 Highlight a project in the Projects pane.  
The project data appears at the bottom of the pane.
- 6 Select **Add Product**.  
The Assign Products to Project dialog box opens.
- 7 Assign products to the project:
  - ▶ Select one or more products from the **Available** list and select > to move them to **Assign to Project**.
  - ▶ Select < to move items from the **Assign to Project** list back to the **Available** list.
- 8 Select **Add Product/Build Batches**.  
The products are added to the Project Detail window.
- 9 When prompted, indicate whether you want to create batches for all samples.  
If you select **No**, you can still batch old samples for the new product by using the Import Manual Batch function. For more information, see [Importing Manual Batches on page 17](#).  
When Project Manager finishes adding the products, they appear on the list of products for the project.
- 10 Select **Save** in the Project Detail window.
- 11 If you chose to batch existing samples for the new product, select the **Batches** tab. The new batches appear on the list along with the product and batch creation date.

## Importing Manual Batches

This feature lets you create a customized batch of samples from a single project. By exporting sample data as a \*.csv file and then sorting and filtering the data, you can quickly assemble the batch regardless of how many samples the project contains.

- 1 Run the Project Detail report from the Illumina LIMS web client, and export it to a \*.csv file.
- 2 Edit the \*.csv file to create a batch import file.
- 3 Import the file into the project.

See the following sections for more detailed instructions.



### NOTE

Illumina LIMS can automatically batch your samples as well. For more information, see [Assigning Sample Plates on page 21](#).

## Defining the Batch

This section explains how to create the batch import file from an Illumina LIMS report. To create manual batches, you must have previously accessioned the samples, quantified them if necessary, and assigned them to a project. For more information, see [Accessioning Institute Samples on page 10](#). The samples should be in one or more DNA plates.

- 1 Log in to the Illumina LIMS web client.
- 2 Select the **Reports** tab, and then in the left pane, select **Lab Management | Project Detail Report**.
- 3 Select a project from the list.
- 4 Select **Export to CSV**, and then select **Run Report**. Select to **Save** or **Open** the \*.csv file.  
The \*.csv file contains information about every sample in the project.

- 5 Edit the information in the \*.csv file to refine the list to only the samples you want to batch.
  - ▶ To import samples from one DNA source plate, prepare a batch import file as shown in [Figure 2](#).
  - ▶ To import samples from multiple DNA source plates, prepare a batch import file as shown in [Figure 3](#).
- 6 Save the edited Project Detail Report \*.csv file to a new batch import \*.csv file with the following structure:



**NOTE**

The column field names must exactly match the names listed below.

**Table 5 Project Detail Report fields**

Cell	Description
A1	Column header <b>Product Part Number</b>
B1	The actual product number. The product part number can be found using the Product Inventory Report.
A3	<b>Sample Plate</b> column that lists the sample plate barcode(s). You can batch samples from more than one plate.
B3	<b>Sample Wells</b> column that lists the well for each sample you want to batch. The maximum number of samples you can batch is 96.

**Figure 2 Sample Batch Import File from One DNA Source Plate**

	A	B	C	D	E	F
1	Product Part Number	11208819				
2						
3	Sample Plate	Sample Well				
4	WG0003121-DNA	A01				
5	WG0003121-DNA	A02				
6	WG0003121-DNA	B01				
7	WG0003121-DNA	B02				
8	WG0003121-DNA	C01				
9	WG0003121-DNA	C02				
10	WG0003121-DNA	D01				
11	WG0003121-DNA	D02				
12	WG0003121-DNA	E01				
13	WG0003121-DNA	E02				
14	WG0003121-DNA	F01				
15	WG0003121-DNA	F02				
16	WG0003121-DNA	G01				
17	WG0003121-DNA	G02				
18	WG0003121-DNA	H01				
19	WG0003121-DNA	H02				
20	WG0003121-DNA	A01				
21	WG0003121-DNA	A02				
22	WG0003121-DNA	B01				
23						

**Figure 3** Sample Batch Import File from Multiple DNA Source Plates

	A	B	C	D
1	Product Part Number	20005176		
2				
3	Sample Plate	Sample Well		
4	WG8000001-DNA	A01		
5	WG8000001-DNA	C01		
6	WG8000001-DNA	E01		
7	WG8000001-DNA	G01		
20	WG8000002-DNA	A05		
21	WG8000002-DNA	C05		
22	WG8000002-DNA	E05		
23	WG8000002-DNA	G05		
36	WG8000003-DNA	A09		
37	WG8000003-DNA	C09		
38	WG8000003-DNA	E09		
39	WG8000003-DNA	G09		
52	WG8000007-DNA	B01		
53	WG8000007-DNA	C01		
54	WG8000007-DNA	F01		
55	WG8000007-DNA	G01		
68	WG8000008-DNA	B05		
69	WG8000008-DNA	C05		
70	WG8000008-DNA	F05		
71	WG8000008-DNA	G05		
84	WG8000009-DNA	B09		
85	WG8000009-DNA	C09		

STcherrypicking\_WG8000001-80000

### Importing the Batch

- 1 In the Institute Detail pane, select **Projects**.
- 2 Highlight a project in the Projects pane.  
The project data appears at the bottom of the pane.
- 3 Select the **Batches** tab.  
Batches that are currently associated with the project are displayed.
- 4 Select **Import Manual Batch**.
- 5 Browse to the sample batch import file (\*.csv), and then select **Open**.  
Project Manager imports the batch data and queues the batch for amplification. The new batches appear in the list with the date and time of import.

### Modifying Project Status

Projects can have one of four status codes.

- ▶ **Active**—Default state when a project is added. The project can be modified, and anyone can do work associated with the project.
- ▶ **Inactive**—Set to Inactive to put a project on hold. No one can do any work associated with the project. You can only change the status to Active, or to Awaiting Archive.
- ▶ **Awaiting Archive**—Set inactive projects to archive. No work can be done on the project, nor can the status of the project be changed. A poller runs at set intervals and archives the data to an archive folder on the file server.

- ▶ **Archived**—When the archive completes, the project status is automatically updated to Archived. Once the status is set to Archived, the IT department can back up the files.

## Viewing Sample Plates

The Sample Plates tab lists the sample plates that are assigned to your project, by name or barcode. It indicates whether the plate is a control plate, and identifies the number of wells.

### Viewing Sample Plates Associated With the Project

- 1 In the Institute Detail pane, select **Projects**.
- 2 Highlight a project in the Projects pane.  
The project data appears at the bottom of the pane.
- 3 Select the **Sample Plates** tab.  
Plates that are currently associated with the project are listed.

**Table 6 Project Sample Plate Fields**

Column	Description
Barcode	The barcode of the sample plate.
Number of wells	The number of sample wells in the plate.

### Viewing Sample Plate Details for a Project

- 1 In the Projects pane, highlight a project.  
The project data appears at the bottom of the pane.
- 2 Select the **Sample Plates** tab.  
Plates that are currently associated with the project are listed.
- 3 In the Institute Detail pane, select **Projects**.
- 4 Double-click a plate name in the Sample Plates tab.  
The Displaying Plate Detail pane opens. It displays information about every sample well on the plate.

**Table 7 Plate Detail Fields**

Column	Description
Comment	Any comments regarding the samples.
IsControl	<b>No:</b> The well in this row contains an experimental sample. <b>Yes:</b> The well in this row contains a control sample.
Conc (ng/μl)	The concentration of DNA in the sample, in nanograms per microliter.
Parent 1	The sample name or plate well of the parent, if known.
Parent 2	The sample name 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.
Sex	The sex of the individual from which the sample was derived. <b>M:</b> Male <b>F:</b> Female <b>U:</b> Unknown
Species	The species from which the DNA sample was drawn.



Column	Description
Tissue Type	The type of tissue from which the DNA sample was drawn.
Volume (µl)	The amount of sample, in microliters.
Well	The coordinates of the well in the sample plate (eg, A01 or H10).

## Assigning Sample Plates

After you have accessioned sample plates into the institute, you can assign them to projects. When you assign a sample plate to a project, the Project Manager automatically batches the samples and starts the laboratory workflow.



### NOTE

You can also add batches manually. For more information, see [Importing Manual Batches on page 17](#).

Automatically generated batches consist of samples on a single plate. For multiuse products, Illumina LIMS assigns as many 24-sample batches as possible from each plate, with the remaining samples filling out the last batch. For multisample products, the batches can contain 48 or 96 samples. For optimal processing, make sure that the sample plates contain multiples of the number of samples per batch, which results in full batches for every run.

## Assigning Sample Plates to a Project

- In the Projects pane, highlight a project.  
The project data appears at the bottom of the pane.
- Select the **Sample Plates** tab.  
Plates that are currently associated with the project are listed.
- Select **Assign Sample Plates**.  
The Assign Samples to Project dialog box opens. It lists all the available sample plates in the institute. To add another plate to this list, see [Accessioning Institute Samples on page 10](#).
- Select one or more samples from the Available list and select > to assign them to the project.
- Select **Add Samples/Build Batches**.  
The sample plates appear in the Sample Plates tab.  
If the project contains one or more multispecies products, the Analysis Assignment Needed dialog box opens. Batches that require species assignments to associate the species name in the sample manifest with the species name in the bead pool manifest (\*.bpm) are highlighted in red.
- To set assignments, select **Assign Species** for each batch highlighted in red.  
The Set Analysis Assignment dialog box opens; unassigned samples are highlighted in red in the Sample pane.
- Select one or more samples in the **Sample** pane, choose the appropriate species in the **Product** pane, and then select **Assign**.  
Alternatively, if all highlighted samples are assigned to a selected species in the Product pane, select **Assign to all unassigned**.
- When all samples are assigned to the appropriate analysis species, select **Set Batch Assignments**.  
The Analysis Assignment Needed dialog opens and batches are highlighted in green if species assignment was successful.
- Select **Build Batches**.

## Viewing Project Samples

- ▶ Select a plate name in the Sample Plates tab to view sample plate details for a project. The Displaying Plate Detail pane displays information about every sample well on the plate. For information about the columns in this table, see the following.

**Table 8 Plate Detail Fields**

Column	Description
Comment	Any comments regarding the samples.
IsControl	<b>No:</b> The well in this row contains an experimental sample. <b>Yes:</b> The well in this row contains a control sample.
Conc (ng/μl)	The concentration of DNA in the sample, in nanograms per microliter.
Parent 1	The sample name or plate well of the parent, if known.
Parent 2	The sample name 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.
Sex	The sex of the individual from which the sample was derived. <b>M:</b> Male <b>F:</b> Female <b>U:</b> Unknown
Species	The species from which the DNA sample was drawn.
Tissue Type	The type of tissue from which the DNA sample was drawn.
Volume (μl)	The amount of sample, in microliters.
Well	The coordinates of the well in the sample plate (eg, A01 or H10).

## Batch Detail

The Batch Detail tab provides detailed information about the project batches.

- 1 In the Institute Detail pane, select **Projects**.
- 2 In the Projects pane, highlight a project.  
The project data appears at the bottom of the pane.
- 3 Select the **Batch Detail** tab.  
The batch detail appears. For information about the columns in this tab, see the table that follows.

**Table 9 Batch Detail Fields**

Column	Description
Amplification Plate	The amplification plate ID.
Batch	The batch number.
Product Name	The name of the product (eg, HumanHap300-Duo). For multiuse products, this is the first BeadChip that is hybridized in the series. Make sure that the Product Name column is associated with the proper batch number for the product. <b>Note:</b> Multiuse products list multiple batch numbers for the same plate. It is important to note the batch number of the first BeadChip that is processed in the series.
Source Plate	The source plate ID.
Task	The current queue of the batch.

## Monitoring Project Usage

The Project Usage tab provides information about the samples that have been hybridized to a BeadChip.

If you adjust the cluster files during a project, you may wish to reanalyze all the project samples. The Project Usage tab has a **Requeue Products for AutoCall** function that lets you requeue the samples per product to AutoCall, to regenerate genotyping call files.

- 1 In the Institute Detail pane, select **Projects**.
- 2 In the Projects pane, highlight a project.  
The project data appears at the bottom of the pane.
- 3 Select the Project Usage tab.  
Sample information for the project appear. For information about the columns in this table, see [Project Usage Fields on page 23](#).
- 4 To requeue all the samples for a product in this project to AutoCall, select **Requeue Products for AutoCall**.  
A list of all products in this project appears.
- 5 Select the products that you want to reanalyze, and then select **Requeue**.



### NOTE

If you are reanalyzing due to adjustments in a cluster file, remember that each cluster file is specific to a product. Therefore, you may not need to reanalyze the samples for every product.

**Table 10 Project Usage Fields**

Column	Description
Barcode	The barcode of the individual BeadChip.
Date Completed	The date and time when the batch amplification was completed.
Date Created	The date and time when the batch was added to the project.
Product Name	The name of the product (eg, HumanHap300-Duo).
Sample Name	The sample name.
Sample Section	The section of the BeadChip where the sample was hybridized.
Status	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> The samples in the batch have been amplified. <b>Deleted:</b> The batch was deleted.

## Viewing Project Batches

- 1 In the Institute Detail pane, select **Projects**.
- 2 In the Projects pane, highlight a project.  
The project data appears at the bottom of the pane.
- 3 Select the **Batches** tab.  
Batch information appears. For information about the columns on this tab, see the tables that follow.

**Table 11 Batches Fields**

Column	Description
Completed Date	The date and time when the samples were amplified.
Created Date	The date and time when the batch was created.
Format	The format of the product (eg, 1x10, 1x12, 96x1).
LIMS Task	The task that is being performed for this batch: <ul style="list-style-type: none"> <li>• Multiuse BeadChip options: Make AMP2</li> <li>• Single-use BeadChip options: Make MSA# (where # is the MSA version), Make AMP# (where # is the AMP version)</li> </ul>
Number of Transfers	The number of wells from the sample plate that have been assigned to this batch.
Product Name	The name of the product (eg, HumanHap300-Duo).
Sample Batch ID	Project Manager automatically assigns a number to each batch. Select the batch number to open the Batch Detail window.
Status	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> The samples in the batch have been amplified. <b>Deleted:</b> The batch was deleted.

- To view detailed information about a batch, select the batch number. The Displaying Batch Detail window opens and shows information about every sample well in the batch.

**Table 12 Batch Detail Fields**

Column	Description
Analysis Species	The species of the associated analysis file.
BeadChip	The barcode number of the BeadChip.
BeadChip Queue	The BeadChip status.
Id	The sample plate identification number.
Institute	The name of the institute.
Project	The name of the selected project.
Sample	The name of the sample.
Sample Plate	The name or barcode of the original sample plate.
Sample Species	The species of the sample.
Sample Well	The coordinates of the well in the sample plate (eg, A01 or H10).
Status	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> The samples in the batch have been amplified. <b>Deleted:</b> The batch was deleted.

## Deleting Project Batches

- In the Institute Detail pane, select **Projects**.
- Highlight a project in the Projects pane.  
The project data appears at the bottom of the pane.
- Select the **Batches** tab
- Highlight one or more batches in the list and select **Delete**.  
Completed batches cannot be delete, only active batches can be deleted.

## Viewing Batch History

The Batch History pane shows historical batch data for all projects in the institute. To view batch data for a single project, see [Viewing Project Batches on page 23](#).

- 1 In the left pane, select **Project Manager**.  
The Institute Search pane opens.
- 2 Find the appropriate institute.  
For more information, see [Searching for an Institute on page 8](#).
- 3 Highlight the institute and select **Institute Detail**.
- 4 Select **Batch History**.  
The batch history information appears.

**Table 13 Batch History Fields**

Column	Description
Assay Type	The assay type: WGGT or GGGT.
Batch ID	Project Manager automatically assigns a number to each batch. Select the batch number to open the Batch Detail window.
Number of Transfers	The number of wells from the sample plate that were assigned to this batch.
Plate	Barcode number for amplification plate.
Queue	The current task the amplification plate is queued for.
Status	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> The samples in the batch have been amplified. <b>Deleted:</b> The batch was deleted.

- 5 Select any batch to open a Batch Detail window.  
The window shows information about every sample in the batch.

**Table 14 Batch History Detail Fields**

Column	Description
Item	The name or barcode of the original sample plate.
Alpha Coordinate	The coordinates of the well in the sample plate (eg, A01 or H10).
appvaluetype	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> The samples in the batch have been amplified. <b>Deleted:</b> The batch was deleted.
Item	The name or barcode of the sample inside the well.
Item	The Barcode number of the BeadChip.
Sample Container Id	Project Manager automatically assigns a number to each batch.
Task	The BeadChip status.

## Requeue for Autocall

Requeue for Autocall allows samples for an institute to be requeued via project, batch, or BeadChip. Select the attribute to requeue by and the detail pane populates with items available for requeue.

- 1 In the Institute Detail pane, select **Requeue for Autocall**.
- 2 Select an attribute (Project, Batch, or BeadChip) from the **Requeue for Autocall by** drop-down menu.  
The details display in the lower portion of the pane and vary depending upon the selected attribute.

- 3 Select the checkbox for each project, batch, or BeadChip to requeue, and then select **Save**.
- 4 Select **Refresh** to display the list with the requeued items removed.

## Laboratory Manager

The Laboratory Manager is a high level view of which projects are queued, and their status. It also includes an option to unarchive projects. Only administrators or project managers should have access to the administrative tasks.

### Laboratory Manager Status Reports

The Laboratory Manager Status Report provides a view of project batch status reports.

- 1 In the left pane, select **Laboratory Manager | Status Reports | Project Batches**.  
The Laboratory Manager Project Batches pane opens.

**Table 15 Project Batches Fields**

Field	Description
Active Batches	The number of current batches waiting to run.
Completed Batches	The number of completed batches.
Project ID	ID number associated with the project.
Project Name	The name of the project (eg, HumanHap300-Duo).

- 2 Select a project to view the details.

**Table 16 Selected Project Fields**

Field	Description
Number of Items on Queue	The quantity of a specific task that is in the queue for the selected project.
Queue	A list of the current tasks that are queued for the selected project.

- 3 Select a queue item to display the queue detail.

### Unarchive Project

Use Unarchive Project to restore an archived file back to its originally stored location.

- 1 In the left pane, select **Laboratory Manager | Tasks | Unarchive Project**.  
The Unarchived Project pane lists the archived projects.

**Table 17 Unarchive Project Fields**

Field	Description
Project Name	Name of selected project.
Status	Shows if the project is archived or unarchived.
Number of Files	The number of files archived for the project.
Archive Date	Date the project was originally archived.

- 2 Select a project in the list.  
All archived files related to the selected project appear.

**Table 18 Selected Unarchive Project Fields**

Field	Description
File Type	The file type of the archived project.
Archive File Share	Location where the archived file is stored.
Original File Share	Original location of the archived file.

- 3 Select one or more files from the list, and then select **Unarchive**.  
A dialog box opens, asking if you have moved all the files back to the archived location. All associated files must be located on the archived file share so that Illumina LIMS can move the files back to their original location. If necessary, consult your system administrator for assistance.

## Prepare Sample Batch

You can create a multi-project batch using the Prepare Sample Batch task in Project Manager. Before creating a batch, you must have already accessioned the samples, quantified them (if required), and assigned them to a project. (For more information on this process, see *Accessioning Institute Samples on page 10*.) You also need the multi-project batch template file, found on the Illumina LIMS downloads page of the Array Software support section on [support.illumina.com](http://support.illumina.com).

- 1 Log in to Illumina LIMS Project Manager.
- 2 In the left pane, navigate to **Laboratory Manager | Tasks | Prepare Sample Batch**.  
The Prepare Sample Batch pane opens.
- 3 Select **Browse**.  
The Select a Batch File dialog opens.
- 4 Navigate to the folder that contains the batch template file (\*.csv), select it, and then select **Open**.  
The batch appears in Batch Information pane. If there is a problem with the formatting of the batch file and Illumina LIMS is unable to read it, an error message is displayed.
- 5 Configure the batch template file as follows, and then click **Save**.

**Table 19 Batch File Configuration**

Field	Description
Product Part Number	The product part number.
Row 2	Leave blank.
Project	The project name.
Source	The source barcode.
SourceWell	The well for each source you want to batch.



### NOTE

You can enter up to 96 unique samples from any project in Project Manager in the multi-project batch file.

- 6 Select **Browse**, select your file, and then select **Save**.  
All samples appear on the Prepare Sample Batch task. Any errors are displayed in red in the Status column on a per-sample basis.
- 7 If all samples appear as **OK**, select **Save** to create the batch.

## Resources

Project Manager has three tools to help you quickly find information.

Tool	Description
<i>Available Products</i>	Provides instant information about every product in the system
<i>Item Tracker</i>	Lets you drill down for information on any item or queue in the system
<i>Laboratory Manager</i>	Provides a high-level view of projects that are queued and their status.

In addition to the tools available in Project Manager, the Illumina LIMS web client provides a wide variety of reports. For more information, see the *Illumina LIMS Web Client on page 30*.

## Available Products

The Available Products tool provides quick access to information about every product that has been accessioned into the system.

The Available Products pane opens on the BeadChip tab with the list of BeadChip products displayed.

**Table 20 Available BeadChip Products Fields**

Field	Description
Accessioned By	The user that added the product to the system.
Accessioned On	The date and time that the product was added.
BPM Path	The network path for the BPM (Bead Pool Manifest).
Is Latest Revision	Gives a true or false statement to indicate whether this is the most recent revision of the product.
Num. of Samples	The number of samples that can be hybridized onto the BeadChip.
Part Number	The part number that identifies this product. Each individual BeadChip has its own barcode, but multiple BeadChips can have the same part number.
Product Line	The platform associated with this product.
Product Name	The name of the product (eg, HumanHap300-Duo).
Rev	The revision of the product.
Species	The species represented in the product.

## Item Tracker

The Item Tracker is a system-wide tracking tool that displays information about any item (reagent, institute, cluster file, etc.) or queue in the system.

The first time you log in, the Item Tracker pane is automatically displayed.

- In the Item Tracker pane, do one of the following:
  - ▶ Select **Item Type** to see a list of physical or logical objects such as reagents, institutes, or cluster files.
  - ▶ Select **Item Queue** to see every queue in the system, from Active Cluster File to XStain BC2.
- Select the + sign beside any item to view more information.
- Continue to drill down until you see the information that you need.



**NOTE**

Some items may take longer to appear than other items. For example, Samples often take some time, because there can be hundreds of samples in the system.

- 4 To remove the Item Tracker pane, from the Illumina LIMS Project Manager menu bar select **View | Item Tracker**.
- 5 To redisplay the Item Tracker, from the Illumina LIMS Project Manager menu bar select **View | Item Tracker**.

## Types of Information

The lowest drill down level contains four types of information:

### Attributes

**Table 21 Attribute Fields**

Field	Description
Name	The item name.
Value	The item value.

### Contents

**Table 22 Contents Fields**

Field	Description
Coord	The exact location of the item. For example, A01 denotes the location of a sample in a plate.
Item	The individual item barcode.
Type	The item type (eg, sample).

### Queues

**Table 23 Queues Fields**

Field	Description
Task	The current queue that the item is on.

### Queue History

**Table 24 Queue History Fields**

Field	Description
By	Logged in user when task was run.
Date	The date and time when the item changed from one queue to another.
From	The original queue.
To	The new queue.
Tran Id	The transfer identification number.

Some types of information are irrelevant to a particular item and will be blank.

# Illumina LIMS Web Client

Overview .....	30
Administrative Tools .....	30
Laboratory Management .....	34
Reports .....	35

## Overview

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 lets you 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 using the administrator's web client provide support for other network or direct-attached file systems. Similarly, backup and archive directories are fully configurable.

## Illumina Automation 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 information on using the robot, see the *Infinium Lab Setup and Procedures Guide* and the *Infinium assay protocol guide*.

If you have skipped a previous task, then the robot will not perform the current task. Instead, the dedicated robot PC displays an error stating that the plate or BeadChip 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 52).

## Launch the Illumina LIMS Web Client

The Illumina LIMS web client is accessible from a web browser.

- 1 In the URL field, type the address provided by the Illumina LIMS system administrator, and select **Enter**.
- 2 Enter your user ID and password, and then select **Login**.



### NOTE

Your user ID and password are configured by your Illumina LIMS administrator. See *Manage Users* on page 30.

## Administrative Tools

The Admin Tools include the following administrative functions.

- ▶ *Manage Users*—Authenticate, set status, and grant user permissions.
- ▶ *Manage Logs*—View and save logs for use in troubleshooting.
- ▶ *Enter Maintenance Mode*—Restrict user access to the system for system maintenance.
- ▶ *Install License*—Update license when directed by Illumina Technical Support.

## 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 database. The authentication method is determined during installation.

## Default Administrator Account

During installation a single administrator account is 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 to provide Illumina support technicians access to Illumina LIMS if the system administrator becomes unavailable.

## Create a User Account

- 1 In the left pane, click **Admin Tools | Manage Users**.
- 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.  
If you are using database authentication, you need to provide users with the password you create here.  
Only an administrator can change the password.
- 4 Re-enter the password in the **Confirm Password** box.



### NOTE

If the Windows domain becomes unavailable, Illumina technical support can help you reset Illumina LIMS to use database authentication. In this case, users must log in using the password that was created when you created their accounts. It is recommended that you adhere to a standard convention when creating passwords.

- 5 Select the **Active** check box to activate the user account.
- 6 Select **Add User** to save the user account.

## User Status

User accounts may be active or inactive. When an account is active the user can log in and perform tasks. When an account is inactive, the user cannot access the system.

## Add Permissions

The ability to view windows and perform tasks in Illumina LIMS is permission based. When users are created they must be granted permissions to the areas of the system that they need to access in order to perform their work functions.

## 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.

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 within the group has no effect.

## Recommended Settings by Role

- ▶ **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, and Illumina fluorometry software, AutoCall.
- ▶ **All lab personnel**—Should have permission for the Tracking group to let them 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.

- ▶ **Project managers**—Should have permission for the Management Client group to let them use Illumina LIMS Project Manager. In addition, they should have permission to the Lab Management, Quality Control, and Tracking groups to run reports.

## Assigning Permissions to a User

- 1 In the **Edit/View** column, select the user name.
- 2 In the Permissions window, do one of the following:
  - ▶ To grant universal permission for all tasks in the system, scroll to the Override section and select **Grant permissions to All**, and then click **Grant**.
  - ▶ To remove permission for all tasks in the system, select **Grant permissions to None**, and then click **Grant**.
  - ▶ To grant limited permissions, select the check boxes beside groups or individual tasks. Keep in mind 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 by Role on page 32](#).
- 3 When you finish granting permissions, select **Grant Selected Permissions**.

## Manage Logs

Illumina LIMS maintains log files to help technical support scientists diagnose and solve problems. These logs are typically only used for troubleshooting 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 researching database issues.

## Log Naming Scheme

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

## Logging Process

- 1 Data is collected until <log file>.00 reaches 20 MB (configurable).
- 2 When the configured log file size is reached, the number of the log file is incremented by 1. (eg, LIMSStatus.00 changes to LIMSStatus.01) and stops logging information to that file.
- 3 A new file named <log file>.00 is created and begins logging the most recent information to that file.
- 4 When the second log file reaches the size limit, a third log file is created. All the numbers increment by 1 again: 01 becomes 02, and 00 becomes 01.
- 5 When the maximum number of log files are created, the next time the numbers increment, the data in the last file is 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 increment is variable and is dependent on the tasks being performed and how busy your lab is.

## Viewing and Saving Log Files

Use log files to troubleshoot system issues.



### NOTE

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

- 1 In the left pane, select **Admin Tools | Manage Logs**.  
The Manage Logs window opens.
- 2 Do one of the following:
  - ▶ Right-click on any log file and select **Save Link 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

When maintenance on the Illumina LIMS hardware or software is needed, put the Illumina LIMS software in maintenance mode. This lets current users complete their tasks while preventing other users from starting a new task until the maintenance mode is finished.



### NOTE

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

- 1 In the left pane, select **Admin Tools | Enter Maintenance Mode**.
- 2 On the Enter Maintenance Mode window, enter the date and time when maintenance mode will end.
- 3 Select **Start**.

## Install License

Install License lets you install a new license file. This is typically done by Illumina Customer Support staff, who installs the system license during initial system installation. If the system is upgraded, a new system license may be required. In this case, Illumina technical support will provide instructions for installing the new license. Unless instructed to do so, do not use this task.

## Laboratory Management

This section provides information on entering samples back into the laboratory workflow after they have been removed due to processing errors or deletion of partial batches. It also provides information on tracking the results of a Tecan robot run. You must have Laboratory Management permissions to use Laboratory Management Tools.

## Requeue for Image BeadChip

This task lets you requeue a BeadChip to be reimaged.

- 1 In the left pane, select **Laboratory Management | Requeue for Image BeadChip**.
- 2 In the Requeue for Image BeadChip window, scan the barcode of your BeadChip and click **Get Sample Sections**.

The BeadChip is now ready to be reimaged.



### NOTE

If the decode files have been deleted, Illumina 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

Use this to requeue DNA plate to Make Quant.

- 1 In the left pane, select **Laboratory Management | Requeue for Make Quant**.
- 2 In the Requeue for Make Quant window, scan the barcode of the sample plate and select **Verify**.
- 3 Select **Save**.



### NOTE

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

## Decommission Item

Use this to decommission items from your projects. A decommissioned item is removed from any queue that it is on and puts it into the decommission queue. The decommissioned item cannot be used in any workflow.

- 1 In the left pane, select **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 Select **Save**.

## Tecan Robot QC

Use this to track the results of a Tecan robot run. This task does not store robot QC data in Illumina LIMS.

- 1 In the left pane, select **Laboratory Management | Tecan Robot QC**.
- 2 In the Tecan Robot QC window, enter the **Robot Name**.
- 3 Select the **QC Status** (Pass or Fail) depending on the results of the robot QC run.
- 4 Select **Save**.  
A message above the **Robot Name** field indicates that the Tecan Robot QC task has been successfully completed.

## Reports

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

### Run Reports

This section provides information on running a report. The instructions apply all reports in the system. For information on a particular report, refer to the section named for that report.

- 1 In the upper-right corner of the Illumina LIMS main window, select **Reports**.
- 2 In the left pane, select one of the report categories.  
For information on each type, see:
  - ▶ [Lab Management Reports on page 36](#)
  - ▶ [Quality Control Reports on page 44](#)
  - ▶ [Tracking Reports on page 49](#)
- 3 Select a specific report to open it.
- 4 Enter or select the data for the report.
- 5 Select one of the following report formats:
  - ▶ **Export to CSV** to export the report to \*.csv (comma-separated value) files. 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

When reports are displayed 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 eight lab management reports.

### Project Detail Report

This report provides details about your project, including the image date of scanning. Included in the report is information on 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. To specify a date range, enter the **To Date**.

Optionally, a **Barcode** number can be entered to view information associated only with that barcode within the project.

**Table 25 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	<b>Active:</b> Well can be used in downstream tasks. <b>Inactive:</b> Well cannot be used in downstream tasks.
Analysis Species	The species of the associated analysis file.
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	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> 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 (ie, imaged).
MUN/SUD	The MUN/SUD plate barcode.
MUN/SUD Well	The well coordinates for the sample in the MUN/SUD plate.
Oligo Pool	The oligo pool associated with the sample well.



Column	Description
P-SSID	Secondary System ID. Lets you 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 (eg, 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 Species	The species of the sample.
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.
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	<b>Active:</b> Well can be processed through Illumina LIMS workflows. <b>Inactive:</b> 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 versus scans expected.

**Table 26 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.
No. MUNs Created /Remaining/Expected	The number of MUNs created, remaining, and expected.

Column	Description
No. Products	The number of product part numbers 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 Software on page 2*.

**Table 27 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	<b>Link Cluster File:</b> Indicates that you need to link a cluster file to the product before AutoCall can run. <b>AutoCall:</b> Indicates that the sample on that row is queued for AutoCall. <b>AutoCall Processing:</b> Appears very briefly to indicate that AutoCall is currently running for that sample. <b>AutoCall Complete:</b> Indicates that AutoCall has run successfully. <b>AutoCall Failed:</b> 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	<b>Success:</b> AutoCall ran and successfully generated genotype calls. <b>Fail:</b> 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 <b>Complete</b> , 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 <i>Illumina LIMS Project Manager Software on page 2</i> .
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 28 Reagent Usage Report**

Column	Description
Actual Concentration	The actual concentration read from the quant plate, in nanograms per microliter (ng/ $\mu$ l).
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.
AMP Well	The amplification plate well.
ASE Plate	The ASE plate barcode.
ASE Well	The ASE plate well.
Batch Status	<b>Active:</b> The batch is queued for amplification. <b>Completed:</b> The amplification plate has been created. <b>Deleted:</b> 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	The fragment reagent barcode used in the Frag MSA1 task.
Frag MSA2 fragment reagent	The fragment reagent barcode used in the Frag MSA2 task.
Frag MSA3 fragment reagent	The fragment reagent 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.
Incubate Machine	The machine that the Incubate task was run on.
Incubate User	The logged in user for the Incubate task.
Inoc IP1	The IP1 barcode used in the Inoc PCR task.
Inoc UB1	The UB1 barcode used in the Inoc PCR task.
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.
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.

Column	Description
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.
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.
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	The precipitate reagent barcode used in the Precip MSA1 task.
Precip MSA2 precipitate reagent	The precipitate reagent barcode used in the Precip MSA2 task.
Precip MSA3 precipitate reagent	The precipitate reagent 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	The hyb reagent barcode used in the Prepare Single BC2 task.
Product	The product description.
Project	The project name.
Protocol	The protocol performed.
P-SSID	Project Secondary System ID. Allows you to correlate your IDs with Illumina LIMS IDs, 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.

Column	Description
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.
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.
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 information on accessioning BeadChips, see the *Illumina LIMS Project Manager Software on page 2*.

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

**Table 29 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 30 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, do one of the following:
  - ▶ Scan the BeadChip barcode
  - ▶ Search for the BeadChip in the Items on Queue report (*Queue Status Report on page 52*) and copy the barcode

**Table 31 BeadChip Detail Report**

Column	Description
Format	The product format (eg, 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 (eg, Infinium HD).
Product Name	The name that was assigned to the product when it was accessioned into the system.
<b>Sample Data</b>	
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.
<b>History</b>	
Date	The date that the BeadChip entered the queue in the To Task column.

Column	Description
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.

## Robot Position Report

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

**Table 32 Robot Position Report**

Column	Description
Date	The date and time when the task was performed.
Item	The item ID or barcode.
Machine	n/a
Project	The project name.

## 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

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 33 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.
IsControl	Indicates whether this is a control sample.
I-SSID	Institute Secondary System ID. Allows you to correlate your IDs with Illumina LIMS IDs, 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.



Column	Description
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 Illumina 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.
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 can be used to 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 34 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 can be used to:

- ▶ Obtain data about a given plate.
- ▶ Make sure that a sample was accurately accessioned.
- ▶ Obtain statistics about a plate for which you did not run quant.

- ▶ Create a new sample manifest for accessioning a duplicate plate (eg, 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 35 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 LIMS IDs, 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. <b>M:</b> Male <b>F:</b> Female <b>U:</b> 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	<b>Active:</b> Well can be processed through Illumina LIMS workflows. <b>Inactive:</b> 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. It can be exported to Excel to create graphs or plots to reveal patterns in recent scans or data about a given BeadChip.

You can query by BeadChip, date range, or project.

- 1 Select **Get List** to specify the input parameters.
- 2 Do one of the following:
  - ▶ **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, and indicates if 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 is as you expect.

**Table 36 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.
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 LIMS IDs, to track project data in your own databases.
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 refine 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 37 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 <b>Channel Type-of-control Code</b> . <b>Channel:</b> Green or Red <b>Type of Control:</b> See <i>Infinium Assay System Controls</i> on page 48 for an overview of Infinium Assay controls. <b>Code:</b> 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.
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 LIMS IDs, 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 Lab Setup and Procedures Guide*.

**Table 38 Infinium Assay System Controls**

Control	Description
<b>Sample Independent</b>	
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.
<b>Sample Dependent</b>	
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

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 50](#)

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

The Tran report contains several separate tables:

- ▶ **Task History**—Identifies each time a task is saved into the system.
- ▶ **Contents**—Identifies the content, which is anything added to the item (ie, a sample plate has samples as content).
- ▶ **Attributes**—Not currently used.
- ▶ **Conditions**—Identifies the software and firmware used in the transaction.
- ▶ **Comments**—Identifies the current versions of the Illumina LIMS web client 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.
- ▶ **Item History**—Identifies anything that was copied to the item. For example, in Make AMP2, DNA samples are copied to an AMP2 plate.

**Table 39 Task History Table**

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

**Table 40 Contents Table**

Column	Description
Contains	Anything that ever touched or was associated with the item (eg, samples, reagents, institutes, etc.)
Coord	If appropriate, coordinates for the relevant location (eg, 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.

**Table 41 Attributes Table**

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.

**Table 42 Conditions Table**

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.

**Table 43 Comments Table**

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

**Table 44 Item History Table**

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 refine 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* for more information.

**Table 45 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.

Column	Description
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 view a \*.csv report identifying the last time a task was run in the system. The \*.csv file has two sections.

- ▶ **Task**—Shows the date, time, and transaction ID for the last task that was run in this queue.
- ▶ **Queue Counts**—Shows the number of items in each queue, and the transaction ID of the most recent item added to the queue.

**Table 46 Task Section**

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 (eg, Hyb Multi-BC2).

**Table 47 Queue Counts Section**

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 (eg, AutoCall).

## History by User or Machine Report

This report lists the actions of a particular user or machine. For example, if a robot appears to be malfunctioning, use this report to gather more data.

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

**Table 48 History by User or Machine 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.

## 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 52*) is often a quick way to find out.

**Table 49 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 50 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

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 51 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.



# Technical Assistance

For technical assistance, contact Illumina Technical Support.

Website: [www.illumina.com](http://www.illumina.com)  
Email: [techsupport@illumina.com](mailto:techsupport@illumina.com)

## Illumina Customer Support Telephone Numbers

Region	Toll Free	Regional
North America	+1.800.809.4566	
Australia	+1.800.775.688	
Austria	+43 800006249	+43 19286540
Belgium	+32 80077160	+32 34002973
China	400.066.5835	
Denmark	+45 80820183	+45 89871156
Finland	+358 800918363	+358 974790110
France	+33 805102193	+33 170770446
Germany	+49 8001014940	+49 8938035677
Hong Kong	800960230	
Ireland	+353 1800936608	+353 016950506
Italy	+39 800985513	+39 236003759
Japan	0800.111.5011	
Netherlands	+31 8000222493	+31 207132960
New Zealand	0800.451.650	
Norway	+47 800 16836	+47 21939693
Singapore	+1.800.579.2745	
South Korea	+82 80 234 5300	
Spain	+34 911899417	+34 800300143
Sweden	+46 850619671	+46 200883979
Switzerland	+41 565800000	+41 800200442
Taiwan	00806651752	
United Kingdom	+44 8000126019	+44 2073057197
Other countries	+44.1799.534000	

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

Product documentation—Available for download from [support.illumina.com](http://support.illumina.com).



Illumina  
5200 Illumina Way  
San Diego, California 92122 U.S.A.  
+1.800.809.ILMN (4566)  
+1.858.202.4566 (outside North America)  
techsupport@illumina.com  
www.illumina.com

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

© 2019 Illumina, Inc. All rights reserved.

**illumina**<sup>®</sup>