

BIOLOGY RELATED INFORMATION STORAGE KIT

User Manual **SLIMS**

The Daley Lab

12/1/2010

SLIMS User Manual

v 1.1

Table of Contents

| | | |
|----------|--|-----------|
| 1 | Introduction | 4 |
| 1.1 | Overview | 4 |
| 1.2 | Layout | 5 |
| 2 | Getting Started | 6 |
| 2.1 | Logging In & Managing Accounts | 6 |
| 2.2 | Changing Your Password | 6 |
| 2.3 | Defining Constants | 7 |
| 2.4 | Loading Subjects, Containers and Samples..... | 7 |
| 3 | Viewing Data..... | 7 |
| 3.1 | Subjects | 7 |
| 3.2 | Containers..... | 7 |
| 3.3 | Samples..... | 8 |
| 4 | Searching Data | 8 |
| 4.1 | Simple Search | 8 |
| 4.2 | Power Search | 8 |
| 4.3 | SQL Query Search | 9 |
| 5 | Shopping Lists | 9 |
| 5.1 | What Are Lists | 9 |
| 5.2 | View Lists..... | 9 |
| 5.3 | List Creation..... | 10 |
| 5.3.1 | From Scratch | 10 |
| 5.3.2 | From Existing List | 11 |
| 5.3.3 | From a File..... | 11 |
| 5.4 | Editing Lists..... | 13 |
| 5.5 | Deleting Lists | 13 |
| 5.6 | List Tools..... | 13 |
| 5.6.1 | Make New 96-Well Containers..... | 13 |
| 5.6.2 | Make a 384-Well Plate from 96-Well Plates..... | 13 |
| 5.6.3 | Update Volumes | 13 |
| 5.6.4 | List Trimming | 14 |
| 5.6.5 | Sample Selector..... | 14 |
| 6 | Reports | 15 |
| 6.1 | Container: Custom Plating Sheet | 15 |
| 6.2 | Container: Sample Location Sheet..... | 15 |
| 7 | Supporting Tables..... | 15 |
| 8 | Tools | 15 |
| 8.1 | Editing Information | 15 |
| 8.2 | Creating Subjects | 16 |
| 8.2.1 | Individually | 16 |
| 8.2.2 | From a File..... | 16 |
| 8.3 | Creating Containers | 16 |
| 8.3.1 | From Scratch | 16 |
| 8.3.2 | From a File..... | 17 |

| | | |
|-----------|---|-----------|
| 8.3.3 | Cloning..... | 18 |
| 8.3.4 | 96 Well Plates from a List of Samples | 19 |
| 8.3.5 | 384 Well Plates from a List of Containers | 21 |
| 8.4 | Creating Samples | 22 |
| 8.4.1 | Individually | 22 |
| 8.4.2 | From Files..... | 22 |
| 8.4.2.1 | General Samples File | 23 |
| 8.4.2.2 | Specific Samples File | 23 |
| 8.5 | Customising View of Data..... | 24 |
| 8.6 | Plate Layout Viewer | 24 |
| 8.7 | Sample Selector | 24 |
| 8.7.1 | Defining Selection Criteria..... | 24 |
| 8.7.2 | Curating Results | 25 |
| 8.8 | History Viewers | 24 |
| 8.8.1 | Sample History Viewer..... | 24 |
| 8.8.2 | Container Content History Viewer | 25 |
| 8.9 | Handling Shipments..... | 24 |
| 8.9.1 | Shipping out/Returning Shipments..... | 24 |
| 8.9.2 | Viewing Shipments and Shipment History | 25 |
| 8.9.2.1 | Through a Container In the Shipment | 23 |
| 8.9.2.2 | Search Shipments | 23 |
| 8.10 | Sample File Attachments..... | 24 |
| 8.11 | Container Check-out/Check-in..... | 24 |
| 8.12 | Genotyped Information | 24 |
| 8.13 | Importing Data using BeadStudio-Generated CSV Files | 24 |
| 9 | Permissions..... | 27 |
| 10 | Term Guide | 28 |
| 10.1 | Samples..... | 28 |
| 10.2 | Containers..... | 28 |
| 10.3 | Controls..... | 29 |
| 10.4 | Users..... | 29 |
| 10.5 | Subjects | 29 |

1 Introduction

1.1 Overview

SLIMS manages information for subjects, the biological samples they have provided and the containers (plates or boxes of tubes) used to store and ship them. Each level of abstraction provides you with more power; you can choose to deal with wells individually, all the wells of a plate, all the samples from one subject, all the plates containing a sample from one subject, etc.

At each level, you can view, edit and create new entries. Data integrity is protected by validating input and controlling which users' accounts have privileges to edit and create different fields (see [Permissions](#)). Your account also keeps track of your role in the lab. Because statisticians and database administrators (so-called "dry lab" staff) may be interested in very different information than laboratory (or "wet lab") staff, SLIMS has tailored default view schemes that are fully customisable. This cuts down on the confusion caused by information overload. Your preferred view scheme is remembered every time you log in, so that you can make the system your own and maximize its efficiency (see [Customising View of Data](#)).

SLIMS features several new tools that expedite experiment operations while ensuring complete record keeping and facilitating intra-lab communications. The most broadly successful of these is a 'shopping cart' which allows users to create, store and share lists of subjects, samples and containers (see [Shopping Lists](#)). Lists can be created by anyone in the lab and populated by selecting elements singly, adding the results of a search or uploading a file. Being able to share these lists directly through SLIMS can be useful in labs spread over several rooms, buildings or disciplines because it imposes structured veins of communication with set vocabularies. It also reduces the use of personal spreadsheets which can become out of sync or indecipherable if the creator leaves.

Lists allow wet lab staff to perform batch operations like [volume updates](#) or [plate creations](#). When a new plate is designed in SLIMS, record keeping is automatically linked with the production of documents that aid in plate creation (a map of a plate's samples and a 'recipe' of sources detailing how much of which samples from where are to be used) (see [Reports](#)). Lists of plates can be used to design plates, serving cases such as the mechanical combination of [four 96-well plates into one 384-well](#) plate for TaqMan genotyping (Heid, et al., 1996). SLIMS integrates record-keeping and lab operations for this process by giving you a tool to design their new 384-well plate which in one stroke makes a record in the database and creates an import file necessary for machine operation. New plates can also be created without the use of lists, simply from pre-existing plates. A [plate cloning tool](#) allows you to make a new plate and sample records, adjust the volumes of the source well records and print off [documents for plate creation](#), all in one step.

To facilitate preparation for genotyping, SLIMS features a customisable, criteria-based [sample selector](#) and [plate layout design tool](#). Given a list of subjects in a study, the sample selector allows a user to define a hierarchical tree of criteria that SLIMS uses to retrieve the most appropriate sample for each subject. Once the initial selection process has been performed, the user can then manually curate the results: if they reject a particular sample, the 'next-best' will be presented and so on. When the final set of samples is ready, it is stored in a 'shopping cart' list. This list can then be used with the plating tool which designs plate layouts, makes plating documents for the wet lab and updates records of the new plate and the source samples.

All of the data updates that occur while using these tools—or any other SLIMS function—are logged in the supporting database. This automatic, detailed and reversible record keeping

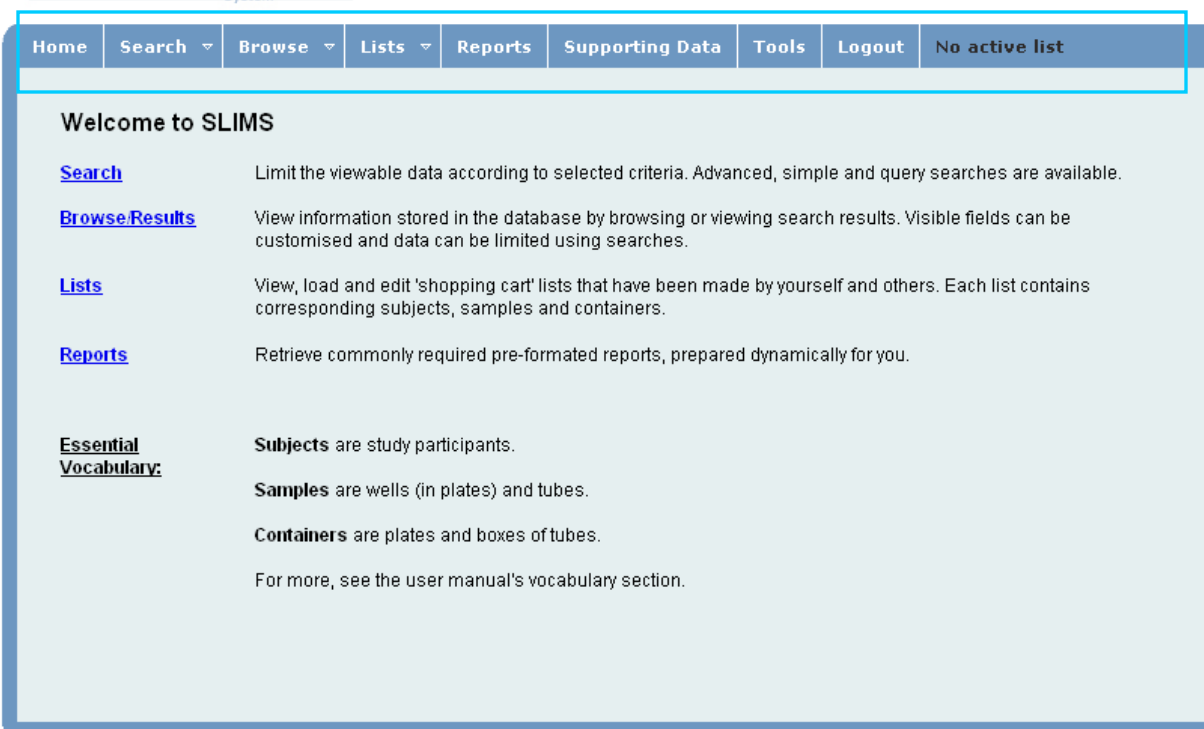
encourages lab members to use the system even if they are as yet unfamiliar with it by providing them with a safety net. Higher level data tracking is made possible by the availability of dynamically-filled, preformatted reports created using Jasper Reports technology (JasperSoft, 2009). Further, any search result or 'shopping cart' list can be exported to a delimited text file.

1.2 Layout

When you've logged into SLIMS (see [Logging In](#) if you're having trouble) you will see the screen below. Box A highlights the top navigation bar. This is the central navigation element for SLIMS. You will always see this bar at the top, except if you are in the middle of an operation that must either be cancelled or completed before anything else can be done. The options on the top bar are:

1. Home: This will bring you back to the front page (the one shown below).
2. Search
 - a. [Simple Search](#)
 - b. [Power Search](#)
 - c. [SQL Query Search](#)
3. Browse/Results: This will switch between the two depending on if a search is active.
 - a. [Subjects](#)
 - b. [Samples](#)
 - c. [Containers](#)
4. Lists
 - a. List Manager: create, load, open and close lists
 - b. [View List: Subjects](#) view the subjects in the active list
 - c. [View List: Samples](#) view the samples in the active list
 - d. [View List: Containers](#) view the containers in the active list
5. [Reports](#)
6. [Supporting Data](#)
7. Upload: tools to load subjects, samples and containers from files
8. Log out: important to do this every time you finish with SLIMS
9. "No active list": this will change to reflect the active list (the list you have most recently opened or created)


A



2 Getting Started


After installing SLIMS and setting up the database you need to do the following steps to populate the system with your data.

2.1 Logging In & Managing Accounts

The first time you log in to SLIMS, whatever you enter as login and password will work and will be stored as belonging to "First User". Once you are in, you can go to "Supporting Tables" then select "Users" from the drop down menu to edit your account (i.e. change the name and initials) using this button . From here, you can also create new accounts using the "New User" button. If you are not the first user to use the SLIMS, ask an admin to create an account for you. Changing the permissions of an account will also require the password to be changed. Be sure to mark down what the password was changed to before continuing.

2.2 Changing Your Password

If you want to change your password, you must be logged in as an admin user or ask someone who is an admin user to help you (go to "Supporting Tables" then select "Users" to see who are admin users).

As an admin, go to "Supporting Tables" then select "Users" from the drop down menu. Click  next to the user you want to change the password for, then use the password field.

2.3 Defining Constants

This step informs SLIMS of all the values for standardized fields in your lab. Clicking the “Supporting Tables” header button will bring you to a listing of all the tables you need to define values for. Any standardized-field values you will want a subject, sample or container to have must be defined before you can load your data. For more, see [Supporting Tables](#).

2.4 Loading Subjects, Containers and Samples



To load your inventory data into SLIMS, click on the “Upload” header button. You may load in your data starting with either subjects or containers. Samples can only be created once their subjects and containers are in the system, so they must be done last. Be sure that all standardized fields have all the appropriate entries to support your data. (If you want a container to have type ‘Box of Tubes’ but that type has not been created in the ‘Container Type’ supporting table, the container cannot be created.)

After each upload of subjects, containers, and samples, we suggest that you check over your new entries (see [Viewing Data](#)).

3 Viewing Data

3.1 Subjects



Subjects are people who participated in a study by donating a biological sample and responding to a survey. The naming structure of a subject ID is COHORT<Family ID>-<Individual ID> (ex: SAGE1001-1). There are two cohorts of subjects, SAGE (Study of Asthma Genes and the Environment) and CAPPS (Canadian *Asthma* Primary Prevention Study, abbreviated “Az” in IDs).





We have subject IDs along with information on their ethnicity, gender, mother’s ID and sometimes their father’s. This information is displayed by clicking on “Data -> Subjects”. From here, a subject’s information can be updated (if you have access privileges) using the edit button  (see [Editing Information](#)). You can also bring up a view of all the samples a subject has using this button . Using the top right drop-down menu, you can create a new subject (see [Creating Subjects](#)) or export all the information on subjects (limited by any searches currently active, see [Searching data](#)) to a tab-delimited text file suitable for opening in MS Excel.

3.2 Containers

A container is any object that is named and holds samples, for example it can be a plate or a box of tubes. Older plates didn’t have a uniform naming system however newer plates follow this format: <Cohort abbrev. Ex Az for CAPPS or SAGE for SAGE>_<Plate origin, ex: VAN for Vancouver or MON for Montreal>P<plate number><material type, ex: GEN for genomic or WGA for whole genome amplified> <concentration or dilution, ex: 1ng/ul or 1:100> <lot number>. A complete example name would be: Az_VANP8WGA 1:100 2.


When a container is made, information on the creator and date is stored, along with the container’s type, name, comments, the contents’ material type and whether they are stock. If a container is on site, its freezer, shelf and coordinates are kept. If a container is shipped out, the location it has been shipped to and the date of shipping is stored. A container should either have a freezer location, shipping details or must be marked as discarded. All this information can be viewed by clicking on “Browse -> Containers”, by searching for containers or by viewing the

containers in a list. From here, you can view a layout diagram using the layout button . If a container is a 384-well plate you can download an SDS file using this button: .

A container's information can be updated (if you have access privileges) using the edit button  (see [Editing Information](#)). You can bring up a view of all the contents of a container using this button:  and bulk-edit the volumes of all the contents using this button: . The clone-tool is accessed with this button:  and allows you to make a new plate based on the layout and samples in an existing plate (see [Creating Containers: Cloning](#)). Using the top right drop-down menu, you can create a new plate (see [Creating Containers: From Scratch](#)) or export all the information on containers (limited by any searches currently active, see [Searching data](#)) to a tab-delimited text file suitable for opening in MS Excel.

3.3 Samples

Samples are all the instances of any one subject's biological material. For example, samples with ID 'SAGE1001-1a' could be found simultaneously in a stock tube, a genomic dilution plate well and a WGA plate well, each of which would be an instance of the sample. More than one sample can have the same sample ID; samples are uniquely identified by their container's name and their location in that container (row and column).

This identifying information plus volume, concentration, dilution, contamination state, comments, barcode and parent sample (ex: if the material in a well came from another well, which was it) can be viewed by clicking on "Browse/Results -> Samples" from the top menu. From here, a sample's information can also be updated (if you have access privileges) using the edit button  (see [Editing Information](#)). Using the top right drop-down menu, you can create a new sample (see [Creating Samples](#)), export all the information on samples (limited by any searches currently active, see [Searching data](#)) to a tab-delimited text file suitable for opening in MS Excel or customize your view of sample data (see [Customising View of Data](#)).

4 Searching Data

4.1 Simple Search

This is a simple keyword search that allows you to quickly search for containers or samples by name. Whether the search retrieves only *exact* matches to your query or not depends on the "Exact" checkbox beside the search field. The search is not case sensitive. The result of this search will affect all data viewable (ex: if you search exactly for a plate named 'Container A', the only samples that will be displayed in the sample view screen will be those that are in 'Container A').

4.2 Power Search

This is a complex, powerful search tool that allows you to limit the visibility of all data based on any fields. For example, if you search for samples by cohort (ex 'SAGE') and sample type (ex 'blood'), the only samples that will be displayed in the sample view screen will be those that match these criteria *and* the only containers that will be displayed in the container view screen will be those that have one of these samples within them. See section [Term Guide](#) for a definition of every field available for searching.

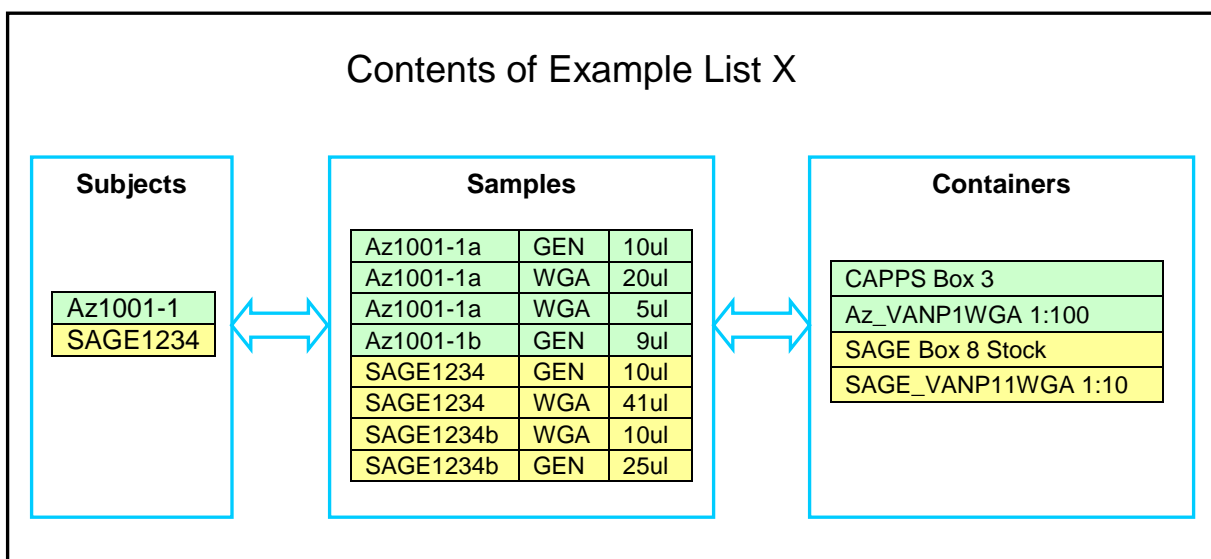
4.3 SQL Query Search

This tool allows you to input a SQL query directly to the database and retrieve the results in tab-delimited text file format. This should only be used with a query written by someone with SQL experience.

5 Shopping Lists

5.1 What Are Lists

SLIMS's shopping lists serve the same function as shopping carts in commercial sites like Amazon.ca, except instead of choosing CDs and books you can cherry pick a collection of samples, subjects or containers. Lists can be created and accessed by anyone which allows lists to be shared between users. They are also saveable, 'save as'-able and editable which allows users to collaboratively work on and develop multiple versions of lists. Lists can be used to batch edit samples, select samples for subjects or to make new plates.



5.2 View Lists

In order to view an existing list, go to "Lists -> List Manager". You will be presented with an option to select a list from a drop-down menu or to search for your desired.

If you select a list from the drop down menu, then simply press "Load List" and your list will be shown to you.

If you want to search for a list, you can do so by list name, creator, modifier, date created or date last modified. Searching will bring up a set of lists that matched your criteria and you may select one by clicking the "Load" button next to it.

When a list is loaded, it will be displayed and will also cause samples in your list to be highlighted when seen in data view screens (ex. when viewing a list of samples resulting from a search, like below).

Home Search Results Lists Reports Supporting Data Tools Logout Active list: dummy samples

Samples -- 17 items Cancel Search What would you like to do? Go

| Update List | Sample | Sample Type | Material Type | Stock | Volume (ul) | Concentration (ng/ul) | Collection Date | Extraction Date | Contaminated | Comments |
|-------------------------------------|------------|-------------|---------------|-------|-------------|-----------------------|-----------------|-----------------|--------------|---------------------------------------|
| <input type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 6.0 | 44.0 | 2003-12-22 | | no | |
| <input type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 5.0 | 44.0 | 2003-12-22 | | no | |
| <input checked="" type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 127.0 | 44.0 | 2003-12-22 | | no | |
| <input type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 10.0 | 1111.0 | 2003-12-22 | | no | test |
| <input type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 35.0 | 20.0 | 2003-12-22 | | no | TEST |
| <input type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 35.0 | 20.0 | 2003-12-22 | | no | TEST |
| <input type="checkbox"/> | SAGE1087-1 | Epithelial | WGA | no | 35.0 | 20.0 | 2003-12-22 | | no | |
| <input type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 6.0 | 44.0 | 2003-12-22 | | no | |
| <input type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 5.0 | 44.0 | 2003-12-22 | | no | |
| <input type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 53.0 | 75.0 | 2003-12-22 | | no | Tube prepared for CNG but never sent. |
| <input checked="" type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 127.0 | 44.0 | 2003-12-22 | | no | |
| <input type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 10.0 | 1111.0 | 2003-12-22 | | no | test |
| <input type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 35.0 | 20.0 | 2003-12-22 | | no | TEST |
| <input type="checkbox"/> | SAGE1087b | ST Cells | WGA | no | 35.0 | 20.0 | 2003-12-22 | | no | TEST |

In List

5.3 List Creation

5.3.1 From Scratch

To create and populate a list from scratch, you must first create a new list. To do this, go to "Lists -> List Manager" and press the "Create Empty List" button. This will prompt you for a name for your list. After naming your list, it has been created and is ready to be updated with added samples.

To populate your list you may either browse samples or use search results. Once viewing the samples you would like to add to your list, all you need to do is tick the check box next to each sample you want to add (the 'select all' button in the first header column may come in handy here (See boxes A and B in the figure below)) and then press "Update List" (See box C in the figure below). If you have not first created a list to add samples to, this button will appear as "Create List" and will prompt you for a new list name.

| Sample | Sample Type | Material Type | Stock | Volume (ul) |
|------------|-------------|---------------|-------|-------------|
| SAGE1087-1 | Epithelial | WGA | no | 6.0 |
| SAGE1087-1 | Epithelial | WGA | no | 5.0 |
| SAGE1087-1 | Epithelial | WGA | no | 127.0 |
| SAGE1087-1 | Epithelial | WGA | no | 10.0 |

5.3.2 From Existing List

If you would like to create a list pre-populated with samples from another list or—put differently—you would like to make a copy of a list, you must first load and view the list off of which you want to base yours. Then by selecting 'Save list as' from the action menu in the top right you will be asked to name your new list. If your name is accepted, the new list will be created, populated and loaded. You may then use it or edit it as you like without affecting the original list.

5.3.3 From a File

If you would like to create a list and populate it with elements from a file, you can use the "Create List From File" button in the List Manager. You have four choices for list population, (see drop down menu):

1. **Subject Based**
This will populate a list based on your file of subjects, each described by cohort and subject ID. It will add the subjects you've indicated in the file, all their samples, and all containers those samples are in.
Your input must be a tab delimited txt with one line for every subject with the following format: [cohort tag][tab][subject ID]
A cohort tag can be either Az, CAPPS, SAGE, FA or NFA.
Subject IDs are composed of digits and dashes *only* without any cohort indicator.
For example: "Az 1001-1"
2. **Sample ID Based**
This will populate a list based on your file of samples, each described by their sample ID. It will add the samples you've indicated in the file, the subjects these samples came from, and all containers these samples are found in.
Your file must be a txt with one sample ID (ex: Az1001-1b) on each line
3. **Specific Sample Based**
This will populate a list based on your file of specific samples (and containers) as described by their sample IDs, the containers they're in and where they are in their containers. The subjects in your list will include all the subjects these samples came from.

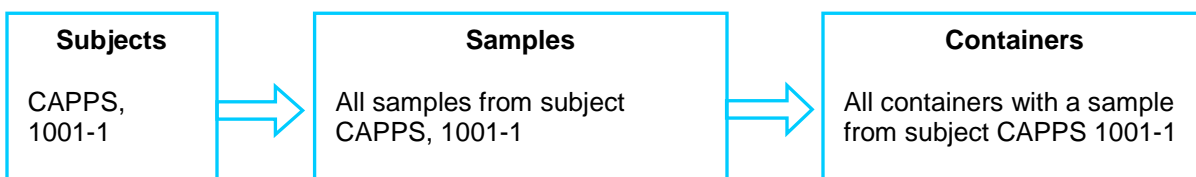
Your file must be a tab delimited txt with one line for every sample, in the following format: [sample ID][tab][container name][tab][row letter][tab][column number]
For example: "Az1001-1 Az_VANP4WGA 1:100 A 3"

4. Container Based

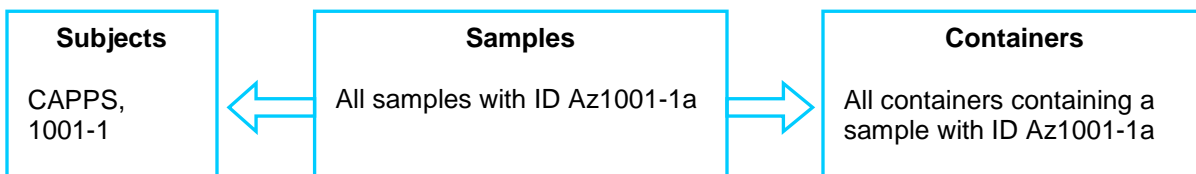
This will populate a list based on your file of containers, each described by their name. It will add the containers you've indicated in the file, all their samples and the subjects those samples came from.

Your file must be a txt with one container name (ex: Az_VANP4WGA 1:100) on each line

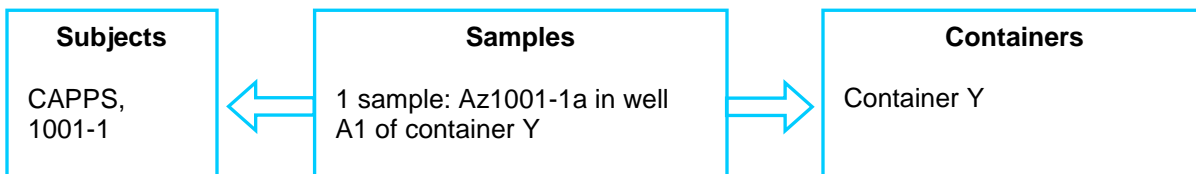
Contents of Example List X:
Created from Subject CAPPS, 1001-1

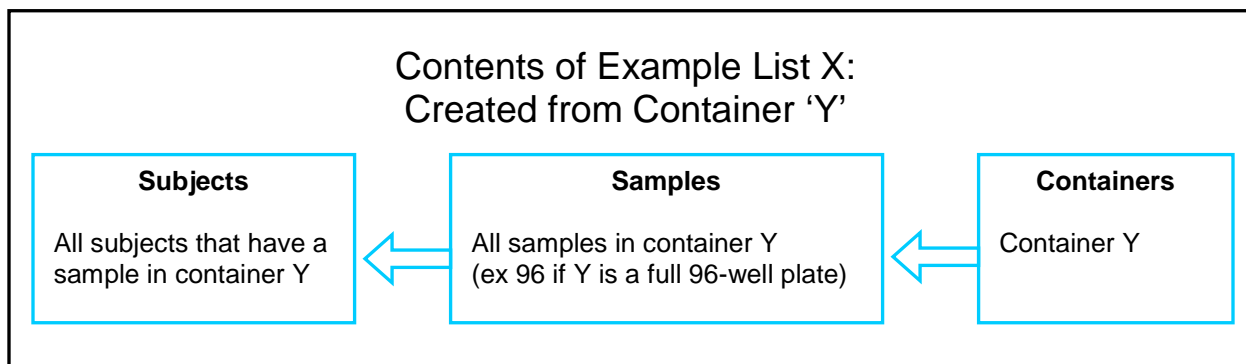


Contents of Example List X:
Created from Sample ID Az1001-1a



Contents of Example List X:
Created from Container 'Y', well A1 (sample ID: Az1001-1a)





5.4 Editing Lists

You can edit the contents of a list from any data view screen by checking or un-checking the tick boxes next to a sample and then pressing "Update List" in the first column of the list header. The select all and deselect all buttons (under "Update List") may be useful. The blue rows in a view screen indicate that a sample is part of your currently loaded list.

5.5 Deleting Lists

You can delete lists that were created by yourself or another user with lower privileges than what you hold. Lists can be searched by the creator to simplify list deletion. To delete a list, first load the list that needs to be deleted, then click on the delete button.

5.6 List Tools

5.6.1 Make New 96-Well Containers

See [Creating Containers: 96 Well Plates from a List of Samples](#).

5.6.2 Make a 384-Well Plate from 96-Well Plates

See [Creating Containers: 384 Well Plates from a List of Containers](#).

5.6.3 Update Volumes

To update the volumes of all samples in a list:

1. Make or load a list of samples you want to update
2. Go to the "View List: Samples" page under the top header bar option "Lists"
3. From the top-right dropdown box, select "Update all volumes in list" and press "Go"
4. Use the drop down box (box A) to decide how to update the volumes. Your options are:
 - a. decrease (decrease all volumes by the value entered)
 - b. increase (increase all volumes by the value entered)
 - c. set to (change all volumes to the value entered)
5. Enter the value in the box next to box A, this must be a numeric value and can have a decimal point
6. If your list has any volumes that are unknown, you will be warned and those samples will not be affected
7. If you are trying to decrease volumes by an amount that not every sample can support, then you will be warned and will not be able to execute the update. Try removing the samples with insufficient volume from your list and updating those separately, either

through a new list (see [List Trimming](#)) or each individually from the “Active List: View Samples” page (see [Editing Information](#))

Update the volumes of 12 samples:

Decrease by

uL

The lowest volume in your list of samples is: 2.0 uL.

OK

Cancel

5.6.4 List Trimming

The trim list tool can be accessed from the top-right dropdown box on any view page by selecting “Trim List” and pressing “Go”. This tool allows you to modify existing lists based on specified criteria. You have two sets of functional options:

1. Results Destination
- a. Edit

your active list be trimmed according to your criteria.
- b. Save As

a *new* list will be created from your active list and your criteria. Your active list will not be changed at all.
2. Trimming Action
- a. Keep

Keep only those elements in the list that satisfy your criteria. (ex: if you select Material Type: WGA, then your result list will have only WGA samples)
- b. Remove

Remove all elements from the list that satisfy the criteria below. (ex: if you select Material Type: WGA, then your result list will have not have any WGA samples)

These options are presented in the top box of the Trim Tool screen (boxes A1 and A2 respectively) and each must be selected before you can continue. If you select to make a new list (‘Save As’) you need to enter a name for your new list.

After selecting how the Trim Tool will work, you can specify your criteria in the lower fields (Box B and lower). When you have finished your selections, scroll to the bottom of the page, select what view of your resulting list you’d like to see, and click “Trim” to trim your list.

Home

Search

Browse

Lists

Reports

Supporting Data

Tools

Logout

Active list: samples to WGA for Montreal Plating III SB v2

Trim List Tool

Trim your active list by choosing to keep or remove all the entries that satisfy the criteria you define below.

To deselect rows or select multiple values use <Ctrl> + mouse click.

If no values for a field are selected, the viewable data will not be restricted by that field.

To start, select how this trim will affect your list:

1)

Make changes to the active list.

Make a new list from the results of this trim. (Your original active list will be unchanged and your active list will be switched to the new list)

Enter a name for your new list:

2)

Keep *only* those elements in the list that satisfy the criteria below. (ex: if select Material Type: WGA below, then your list will have only WGA samples)

Remove *all* elements from the list that satisfy the criteria below. (ex: if select Material Type: WGA below, then your list will not have any WGA samples)

Container Fields

Container Name

Exact

Is not

Container Alias

Container Type

384 Well Plate

96 Well Plate

Box of Tubes

CNG Barcoded Tube

(To Be) Shipped Out?

No

Yes

Discarded?

No

Shipped To

CNG

GABRIEL

Genome Quebec

Date Shipped

Comments

Exact

Is not

5.6.5 Sample Selector

See [Tools: Sample Selector](#).

14

6 Reports

6.1 Container: Custom Plating Sheet

This is a file particularly useful when making a new plate. Every line corresponds to one well or tube in the plate being created. In the 'Sources' section, it lists the source samples' containers, their locations within them, a barcode (either of a plate or of a tube) if applicable and how much volume of each source is to be used. In the 'Destination' section, it lists where material from each source sample is to be put and how much buffer needs to be added to each destination sample (either well or tube).

To get this file, go to the 'Reports' page and select 'Container: Custom Plating Sheet' from the drop down. Enter the name of the new container you are making in the text box, select the format you want and press 'Get Report'.


6.2 Container: Sample Location Sheet

This is a file particularly useful when making a new plate as it lists the locations for all the source samples of a plate. Every line corresponds to one well or tube in the plate being created. The columns describe which samples are being used, where they are (which freezer, what shelf and what specific location), what box or plate they are in (source container and source container alias), what the barcode of the source plate or tube is (if applicable), what well or location in the box the source sample is in ("source well") and finally where in the new plate this source sample is going to be put ("Dest Well").

To get this file, go to the 'Reports' page and select 'Container: Sample Location Sheet' from the drop down. Enter the name of the new container you are making in the text box, select the format you want and press 'Get Report'.


7 Supporting Tables

These tables list all the supporting data for SLIMS. Here you will find system constants like container types, sample types, freezers, users etc. All users can view this data but only admin users can edit the entries or create new ones. Values must exist in these tables before they can be used in the rest of the system. For example, SLIMS will not let you assign a plate or box of tubes to a freezer that has not yet been created in the freezers table. This allows data in your inventory to stay consistent so that the same freezer doesn't end up with a dozen names with different capitalizations and spellings.

To view a table, select it from the drop down menu. To create a new entry, use the button on the top right. To edit the entries, use the edit button  on the far right of each row. For a description of the tables (which appear as fields of other objects) check the [Term Guide](#).

8 Tools

8.1 Editing Information

When viewing any entry, a  button appears at the far right of the row. Pressing this button will open a screen allowing you to edit any permissible field by either entering a new value or selecting an option from a drop-down menu. For a description of all data fields, see the [Term Guide](#). When you are finished, you can press the "Update" button to submit your changes. If what you have entered is invalid, red text at the top of the editing box will tell you to what the problem

is. If all the information entered is valid, the “Update” button will bring you back to the entries listing you were at previously.

8.2 Creating Subjects

8.2.1 Individually

From the subject view page, you can select “Create a new subject” from the dropdown menu in the top right-hand corner. This will lead you to a page where you can enter information for your new subject. For a description of each of these fields, see the [Term Guide](#). When you are finished, you can press the “Add” button to submit your changes. If what you have entered is invalid, red text at the top of the editing box will tell you to what the problem is. If all the information entered is valid, the “Add” button will bring you back to the subject view page you were at previously.

8.2.2 From a File

This tool (found under header “Upload”) will create new subjects in SLIMS from a file you prepare and select. Your file must be a tab delimited txt with one line for every subject. Every line must have a value for each of the following fields, see below for what to enter if the field is unknown or blank.

| Field | Description |
|------------|--|
| Cohort | For existing cohorts, see the power search listing. If you want to use a new cohort, this will need to be created by an admin user. |
| Subject ID | Subject's ID within its cohort, ie "1001-1" (not Az1001-1) |
| Family ID | The subject's family ID within its cohort (ex "1001") |
| Gender | "M" or "F", or "0" if unknown |
| Consent | Whether we have consent from this subject or not ("y" or "n"). "0" if unknown |
| Mother ID | Father's ID within its cohort, ie "1001-4" or "0" if unknown |
| Father ID | Mother's ID within its cohort, ie "1001-5" or "0" if unknown |
| Ethnicity | For existing ethnicities, see the power search listing. If you want to use a new ethnicity, this will need to be created by an admin user. |
| Comments | 0" if none. (must not contain any apostrophes.) |

8.3 Creating Containers

8.3.1 From Scratch

From the container view page, you can select “Create a new container” from the dropdown menu in the top right-hand corner. This will lead you to a page where you can enter information for your new container. For a description of each of these fields, see the [Term Guide](#). When you are finished, you can press the “Add” button to submit your changes. If what you have entered is invalid, red text at the top of the editing box will tell you to what the problem is. If all the

information entered is valid, the “Add” button will bring you back to the container view page you were at previously.

Sample Information Management System

Add Container

Container Name

Material Type

Stock?

Container Type

freezer

Shelf

Discarded?

Shipped Out?

Shipped Date - - (YYYY MM DD)

Shipped To

comments

8.3.2 From a File

This tool (found under header “Upload”) will create new containers in SLIMS from a file you prepare and select. Your file must be a tab delimited txt with one line for every container. Every line must have a value for each of the following fields, see below for what to enter if the field is unknown or blank (if nothing is indicated, the field must have a real value).

| Field | Description |
|-------------------------|--|
| Container Name | The systematic name of this container. |
| Container Alias | Non systematic name for a container. What is actually written on the container if it differs from the systematic name, or what the container was once known as. "0" if none. |
| Initials of Plate Maker | The initials of the plate maker(s), or "0" if unknown. |
| Date on Plate | The date written on the container (format: yyyy-mm-dd), or "0" if none. |
| Container Type | For existing container types, see the power search listing. If you want to use a new container type, this will need to be created by an admin user. |
| Stock | Whether the wet lab considers this container only to have stock contents (like a box of extracted DNA tubes or a stock (1:1 dilution) WGA plate) |
| Material Type | For existing material types, see the power search listing. If you want to use a new material type, this will need to be created by an admin user. |
| Valid | Whether this container is valid or not ("y" or "n"). |
| Freezer Name | For existing freezers, see the power search listing. If you want to use a new freezer, this will need to be created by an admin user. "-1" if unknown. |
| Shelf | The shelf the container is on in the freezer, "-1" if unknown. |

| | |
|------------------|---|
| Location Details | The specifics of where the container is on the shelf in the freezer, "-1" if unknown. |
| Discarded | Whether this container has been discarded or not ("y" or "n"). |
| Shipping Status | Whether this container has been shipped-out, or returned. "y" for shipped out, "r" for returned, "n" for N/A. |
| Shipment Name | The name of the shipment. "0" if unknown or N/A. |
| Ship Date | When this container was shipped out (format: yyyy-mm-dd). "0" if unknown or N/A. |
| Shipped To | Where this container was shipped to, or "0" if N/A. For existing shipped to locations, see the power search listing. If you want to use a new shipping location, this will need to be created by an admin user. |
| Comments | "0" if none. (must not contain any apostrophes.) |

8.3.3 Cloning

New 96 and 384 well plates can be created using the layout of a currently existing plate, in SLIMS this is known as "cloning". When viewing a listing of containers, the plates will have this button



at the far right which will let you make a clone of that row's plate. Clicking this button will take you to a screen that will let you set the new plate's properties (1st section) and adjust all samples involved. When cloning a plate, a volume of sample must be taken out of each well of the original plate to put in each well of the new plate, this value can be set in the first box of the second section (box A in the image below). The most common action for this step will be to set the amount each well of the original plate will be decreased by, however an option is also available to set the volume of each well of the original plate to the same amount, using the "Set to" option in the dropdown box. The following boxes in this section (box B in the image below) allow you to set the properties of the samples in the new plate. With the first box, you can set the final volume to be in each well and with the second or third box you can set the concentration or dilution, one of which must be filled out. Finally, pressing "Clone" will execute the cloning and bring you to a view page listing all the samples in your plate (this may take a few seconds).

If you want a Sample Location Sheet or a Custom Plating Sheet for the plate you just created, go to the reports page (see [Reports](#)).

For a description of each of the fields on this page, see the [Term Guide](#).

Set New Container Properties for Clone of *Asthma Plate 18 GEN 1:100*

New Plate's Properties

Plate Name

Material Type

freezer

Shelf

Comments

Sample Properties

Update volumes of original (source) plate's samples: **A**

Set volumes of new cloned plate's samples: **B**

Set concentrations of new cloned plate's samples:

Set dilutions of new cloned plate's samples: (ex: 1:100)

8.3.4 96 Well Plates from a List of Samples

Lists can be used to make new plates or boxes of tubes from existing samples. If you want to make a 96-well plate from the samples in your list, first load and view the list then choose "Create and Populate a 96 Well Plate" from the top-right drop-down menu.

The first screen this brings you to shows you how many plates you will need (*at least*, as you add +/- controls, the number may increase) and allows you to decide if you want to consider phenotype status in plate layout. If you do, choosing "Yes" will allow you to select which phenotype(s) you want to base case/control status on. If a subject is affected by any of the phenotypes selected, they will be considered a "case". Cases and controls will be spread evenly among the plates you create. You will only have the chance to decide if you want phenotype status considered in plate layout *once* per list you are plating. Cases and controls will be randomly assigned to plates, though their ratio will be the same on each plate. Click "Create Plate 1" to start making plates.

The second screen you're brought to will let you create the container you will be populating. At this point you will need to fill out the standard container creation form (see [Creating Containers: From Scratch](#)).

Now you can add controls to your plate, either select a pre-existing layout from the drop down menu or define your own using the "Custom Controls" button.

Finally, you want to add samples to your plate. If you the samples you are adding do not fill the plate, you are given the option to choose a plating direction, either by row or by column.

For each sample you must specify (a) how much DNA (green column 1) or volume (green column 2) of an original sample is to be used in the creation of it's corresponding new sample, (b) what the volume of the new sample in the new container will be (green column 3), (c) the new samples'

concentrations or dilutions (these values can be copied from the original samples using the 'originals' button) (green column 4) and (d) any comments that should be stored with the new samples (green column 5). To apply the same value to all subjects, use the box in the head to enter your value (box A) and press the "All" button (button B). If you have filled in any 2 columns, you can have SLIMS generate the other values using the "Calculate" buttons. The "Maximum" button allows you to take the most amount possible from each sample. If rows are too wide, use the "Customize sample data view" option of the drop down box to the right to hide some columns. When you are finished, click 'Validate'.

If you are having difficulty reading and inputting information because the view is too cluttered, try customizing your view using the "Customize Sample Data View" option in the top right drop-down menu (see [Customising View of Data](#)).

| Plate | Amplification Date | Comments | DNA from Source to be Used (ng) | Volume of Original to be Used (ul) | Volume of New Sample (ul) | New Concn (x ng/ul) or Dilution (x:xxx) | New Comments |
|-------|--------------------|----------|---------------------------------|------------------------------------|---------------------------|---|----------------------|
| | | | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> |
| | | | All | All | All | All | All |
| | | | Maximum | Calculate | Calculate | Originals | |
| | | | Calculate | | | Calculate | |
| | | | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> |
| | | | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> |
| | | | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> |
| | | | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> | <input type="text"/> |

If you have more plates to make you will be brought back to the first screen and must press "Create Plate 2" to make your next plate. If you have made all your plates, you will be brought to a summary screen that will show you all you've done and let you download a 'Plating Recipe' which will summarize for each sample: where it is, how much of it you will need, which well this volume is to go in and if it needs to be diluted.

If your plate is not going to be full (that is, the sum of controls and samples is less than the total number of wells) then SLIMS presents you with a choice of how to layout your samples: either plating them by row or by column. See below for an example.

Specify Sample Properties

For each sample, specify (a) how much DNA (green column 1) or volume (green column 2) of an original sample is to be used in the creation of it's corresponding new sample, (b) what the volume of the new sample in the new container will be (green column 3), (c) the new samples' concentrations or dilutions (these values can be copied from the original samples using the 'originals' button) (green column 4) and (d) any comments that should be stored with the new samples (green column 5). If rows are too wide, use the "Customize sample data view" option of the drop down box to the right to hide some columns. When you are finished, click 'Validate'.

What would you like to do? ▼

Note: This plate will have less than 96 wells full, which sample layout scheme would you prefer? Select one below.
Green are +/- controls, **blue** are samples and white are empty wells.

☒ By row ☐ By column

| | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|-----|-----|-----|
| A1 | A2 | A3 | A4 | A5 | A6 | A7 | A8 | A9 | A10 | A11 | A12 |
| B1 | B2 | B3 | B4 | B5 | B6 | B7 | B8 | B9 | B10 | B11 | B12 |
| C1 | C2 | C3 | C4 | C5 | C6 | C7 | C8 | C9 | C10 | C11 | C12 |
| D1 | D2 | D3 | D4 | D5 | D6 | D7 | D8 | D9 | D10 | D11 | D12 |
| E1 | E2 | E3 | E4 | E5 | E6 | E7 | E8 | E9 | E10 | E11 | E12 |
| F1 | F2 | F3 | F4 | F5 | F6 | F7 | F8 | F9 | F10 | F11 | F12 |
| G1 | G2 | G3 | G4 | G5 | G6 | G7 | G8 | G9 | G10 | G11 | G12 |
| H1 | H2 | H3 | H4 | H5 | H6 | H7 | H8 | H9 | H10 | H11 | H12 |

| | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|-----|-----|-----|
| A1 | A2 | A3 | A4 | A5 | A6 | A7 | A8 | A9 | A10 | A11 | A12 |
| B1 | B2 | B3 | B4 | B5 | B6 | B7 | B8 | B9 | B10 | B11 | B12 |
| C1 | C2 | C3 | C4 | C5 | C6 | C7 | C8 | C9 | C10 | C11 | C12 |
| D1 | D2 | D3 | D4 | D5 | D6 | D7 | D8 | D9 | D10 | D11 | D12 |
| E1 | E2 | E3 | E4 | E5 | E6 | E7 | E8 | E9 | E10 | E11 | E12 |
| F1 | F2 | F3 | F4 | F5 | F6 | F7 | F8 | F9 | F10 | F11 | F12 |
| G1 | G2 | G3 | G4 | G5 | G6 | G7 | G8 | G9 | G10 | G11 | G12 |
| H1 | H2 | H3 | H4 | H5 | H6 | H7 | H8 | H9 | H10 | H11 | H12 |

Validate

| Update List | Sample | Material Type | Volume (ul) | Concentration (ng/ul) | Dilution | Barcode | Container | Row | Column | Parent | Contaminated | Comments | DNA from Source to be Used (ng) | Volume of Original to be Used (ul) | Volume of New Sample (ul) | New Concentration (x ng/ul) or Dilution (fold) | New Container |
|-------------|--------|---------------|-------------|-----------------------|----------|---------|-----------|-----|--------|--------|--------------|----------|---------------------------------|------------------------------------|---------------------------|--|---------------|
|-------------|--------|---------------|-------------|-----------------------|----------|---------|-----------|-----|--------|--------|--------------|----------|---------------------------------|------------------------------------|---------------------------|--|---------------|

8.3.5 384 Well Plates from a List of Containers

SLIMS provides a tool to create 384 well plates from four (or fewer) 96 well plates and produce the SDS import file necessary for machine operation. The steps for this process are as follows:

1. Select or create a list of containers that includes the plates you would like to use in making a new 384 well plate. This list can be of any length. If you are unfamiliar with making a list, see the [List Creation](#) section for instructions.
2. View your container list (see [View Lists](#)) and select the "Create 384 well plates from 96 well plates" option from the top right drop-down menu. Press "Go".
3. In the first section (box A in the figure below), enter the information for your new 384 well plates. The final names for the 384 well plates will be composed as follows: <Plate name root>_<Batch>_<Barcode>. The deck location for each plate will be stored in the comments.
4. Choose which plates you would like to include in your 384 well plate by ticking their respective boxes (box B in the figure below).
5. For each plate to be included, decide where you would like them to go in the new plate. Use the diagram on the right (section C in the figure below) and the roman numerals I, II, III and IV to indicate which plate should correspond to which layout. For example, if in the figure below we entered "2" as the placement for a plate, well A1 of that plate would be put into A2 of the new plate, A2 would be put into A4, B1 into C2, etc.
6. Press "finish". This will create your new 384 well plate and bring up your SDS import file, if you had it created. Finally, you will be brought to a view page listing all the samples in your new plate (this may take a few seconds).
7. If you would like an SDS import file to be created for any 384 well plate, search for the plate by name and use the [SDS](#) button in your search results.
8. Don't forget to update a plate's discard status if it's thrown away!

Specify New Plate Name and Layout

New 384-Well Plate Details:

Plate name root:
(ex: SAGE_VANP9/10/11/12GEN)

Batch:

Individual Plates:

| Barcode | Deck Location | Plate Maker's Initials |
|----------------------|---------------|------------------------|
| <input type="text"/> | P1 | <input type="text"/> |

☒ To be stored Freezer:
Shelf:
Location:

☐ To be discarded

New 384-Well Plate Layout:

Select at most 4 96-well plates to create a new 384-well plate and set their order/layout on the new plate using the diagram on the right.

| Use Plate? | Order (Q1,Q2,Q3,Q4) | Source Plate |
|--------------------------|----------------------|---------------------------|
| <input type="checkbox"/> | <input type="text"/> | SAGE_VANP10WGA 1:10 DUMMY |
| <input type="checkbox"/> | <input type="text"/> | SAGE_VANP11WGA 1:10 DUMMY |
| <input type="checkbox"/> | <input type="text"/> | SAGE_VANP12WGA 1:10 DUMMY |
| <input type="checkbox"/> | <input type="text"/> | SAGE_VANP13WGA 1:10 DUMMY |
| <input type="checkbox"/> | <input type="text"/> | SAGE_VANP14WGA 1:10 DUMMY |

(This may take a few seconds)

A

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 |
|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| A | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| B | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| C | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| D | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| E | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| F | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| G | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| H | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| I | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| J | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| K | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| L | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| M | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| N | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |
| O | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 | Q1 | Q2 |
| P | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 | Q3 | Q4 |

8.4 Creating Samples

8.4.1 Individually

From the sample view page, you can select "Create a new sample" from the dropdown menu in the top right-hand corner. This will lead you to a page where you can enter information for your new sample. For a description of each of these fields, see the [Term Guide](#). When you are finished, you can press the "Add" button to submit your changes. If what you have entered is invalid, red text at the top of the editing box will tell you to what the problem is. If all the information entered is valid, the "Add" button will bring you back to the sample view page you were at previously.

8.4.2 From Files

This tool (found under header "Upload") will create new samples in SLIMS from two files you prepare and select. The first of the two files is called the General Samples file, this will have one line every sample ID. The second file is the Specific Samples file and will have one line for every sample. You will upload the files one at a time. Your files must be tab delimited 'txt's and every

line must have a value for each of the following fields. (See below for what to enter if the field is unknown or blank.)

8.4.2.1 General Samples File

| Field | Description |
|-----------------|--|
| Sample ID | (ex: Az1001-1a or SAGE1234) |
| Cohort | (ex: CAPPS or SAGE). For existing cohorts, see the power search listing. If you want to use a new cohort, this will need to be created by an admin user. |
| Subject ID | Subject's ID within its cohort, ie "1001-1" (not Az1001-1) |
| Valid | Whether the sample is valid ("y" or "n"). "0" if unknown. |
| Sample Type | The type of biological material this sample is or was extracted from (ie blood, epithelial etc). For existing sample types, see the power search listing. If you want to use a new sample type, this will need to be created by an admin user. |
| Collection Date | The date this sample (the unextracted version) was collected (format: yyyy-mm-dd). "0" if unknown. |
| Extraction Date | The date DNA was extracted from the unextracted version of this sample (format: yyyy-mm-dd). "0" if unknown. |
| Comments | "0" if none. (Must not contain any apostrophes.) |

8.4.2.2 Specific Samples File


| Field | Description |
|----------------|---|
| Container name | The container this sample is in. New containers can be made individually through SLIMS's interface in the browse containers screen. |
| Row | The row in the container the sample is in |
| Column | The column in the container the sample is in |
| Sample ID | (ex: Az1001-1a or SAGE1234) |
| Barcode | The barcode on a tube or plate if the sample has one, "0" if none. |
| Material Type | What type of material this content is (WGA, genomic, unextracted, etc). For existing material types, see the power search listing. If you want to use a new material type, this will need to be created by an admin user. |
| Volume | The volume of the content in ul, -1 for unknown, 0 for empty. |
| Concentration | The concentration of the content in ng/ul, -1 for unknown. |
| Dilution | The dilution of the content (ex 1:1 or 1:100), "0" for unknown or N/A. |

| | |
|-----------------------|---|
| Parent Sample ID | The sample ID of the sample this sample came from (ex: if this sample was made from material taken from another tube 'x', then tube tube 'x' would be the parent sample) "-2" if N/A or "-3" if unknown. |
| Parent Container name | The container name of the sample this sample came from (ex: if this sample was made from material taken from another tube 'x', then tube tube 'x' would be the parent sample) "-2" if N/A or "-3" if unknown. |
| Parent Row | The row of the sample this sample came from (ex: if this sample was made from material taken from another tube 'x', then tube tube 'x' would be the parent sample) "-2" if N/A or "-3" if unknown. |
| Parent Column | The column of the sample this sample came from (ex: if this sample was made from material taken from another tube 'x', then tube tube 'x' would be the parent sample) "-2" if N/A or "-3" if unknown. |
| Contaminated | If the tube/well is contaminated ("y" or "n"). "0" if unknown. |
| Quantification Date | The date this content was inventoried (format: yyyy-mm-dd). "0" if unknown or N/A. |
| Amplification Date | The date this sample was amplified (format: yyyy-mm-dd). "0" if unknown or N/A. |
| Comments | "0" if none. (Must not contain any apostrophes.) |

8.5 Customising View of Data

From any samples view page, you can determine what information is shown for samples and in what order. Selecting the "" option of the drop down menu in the top right brings you to a page that lists all the information available to view (for a description of each of these fields, see the [Term Guide](#)). You can select which data you'd like

8.6 Plate Layout Viewer

When viewing a list of containers, this button:  will take you to a diagram of its container. The diagram will show you what is in which wells and the volumes of each sample.

8.7 Sample Selector

This tool allows you to select one sample for each member of a list of subjects according to criteria you define.

8.7.1 Defining Selection Criteria

Your first step is to make/load your list of subjects and define the selection (decision) tree that will determine your sample preferences.

1. Make sure the list you want to use is the active one.
2. From the top-right dropdown on the subject list view page, choose "Select samples for subjects in list"
3. To define your selection tree, select your first criterion from the box on the left (box A) and press 'Add' (button B). (Scroll down to see descriptions of each option.) If further specifications for your choice are required, you will be brought to a sub-criterion definition screen. For example, if the most important criteria for your decision is whether a sample's

material type is 'genomic' or 'wga' then the first option you would choose from box A would be "Material Type". Then in the sub-criterion definition screen you would pick genomic and wga, in that order.

- After selecting a criterion (and perhaps defining it further), you will see your updated selection tree to the right (box D).
- For each branch of your tree, keep selecting criteria from box A until you are satisfied. When you have fully defined your first branch, press the 'Done Branch' button (button C) to finalize your current branch and move on to the next. When you have finished all your branches, you will have completed the selection tree definition stage of sample selection.

Branch 2: Select Your Level 3 Criterion:

Select a Criterion

- Types —
- Stock Samples Only
- Physical Properties —
- Concentration
- Volume
- Amount of DNA
- Dilution
- Maximize Concentration
- Maximize Volume
- Maximize Amount of DNA
- Genotyping —
- Previously Genotyped
- Genotyping Call Rate
- Never Genotyped
- Dates —
- Collection Date Range
- Extraction Date Range
- Amplification Date Range
- Most Recent Collection Date
- Most Recent Extraction Date
- Most Recent Amplification Date

Add **B**

Done Branch **C**

Current Selection Tree:

| Most Preferred | Level 1 | Level 2 | Level 3 |
|----------------------------|------------------------|---------------------------------------|---------------|
| Selection Branch 1: | Material Type: Genomic | Sample Type: Blood | |
| Selection Branch 2: | Material Type: Genomic | Sample Type: Multiple: Blood & Buccal | You are here. |
| Selection Branch 3: | Material Type: Genomic | Sample Type: Buccal Swab | |
| Selection Branch 4: | Material Type: Genomic | Sample Type: Epithelial | |
| Selection Branch 5: | Material Type: WGA | | |
| Least Preferred | | | |

8.7.2 Curating Results

Once you have fetched your samples, you must curate your results to make sure they are appropriate. Pay special attention to the comments field.

Under the header "Subjects Without Qualifying Samples" you will find subjects without any samples that match your selection criteria.

Under the header "Best-Match Sample Candidates" you will find the best match samples found according to your selection tree and any rejections you might have made. If you have accepted a subject's sample, no more samples belonging to that subject will be shown here.

You should review all the samples in this list and decide if you would like to keep or reject each one. To make this process easier, try sorting by comments, container names etc. Use the radio buttons on the left (box A) or right-most columns to indicate if you want to accept or reject a sample.

When you have finished, press the submit button. The samples you have rejected will be refetched and the next-best matches will be presented. If there are no more potential matches for your criteria, you will be brought to a summary screen where you can review all your final results. If you are satisfied, scroll to the bottom of the screen where you can enter the name for the list that will store your results.

Pressing cancel at any time will clear your selection tree and results and bring you back to the main page

Sample Selector Results: 13 Candidate Samples For Review

Subjects Without Qualifying Samples

The following subjects do not have any samples that match any of your selection profiles.

- SAGE 1207
- SAGE 1338
- SAGE 2745
- SAGE 2646-1
- SAGE 1045-2
- SAGE 1050-1
- SAGE 1050-2
- SAGE 1311-1
- SAGE 2702-1
- SAGE 2702-2
- SAGE 2706-1

Best-Match Sample Candidates

The following samples are the best matches found according to your profiles and any rejections you might have made. Subjects for whom you have accepted a sample will not have any samples shown below.

Review all the samples below and decide if you would like to keep or reject each one. To make this process easier, try sorting by comments, container names etc. Use the radio buttons on the left to accept or reject a sample.


(This may take some time)

| Accept | Reject | Container Contents | Sample | Material Type | Sample Type | Volume (ul) | Concentration (ng/ul) | Stock | Dilution | Barcode | Container | Row | Column | Parent | Contaminated | Collection Date | Extraction Date |
|----------------------------------|-----------------------|----------------------------------|--------|---------------|---------------|-------------|-----------------------|-------|----------|---------|-----------------------|-----|--------|---------|--------------|-----------------|-----------------|
| <input checked="" type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> | 2688-4 | Az1146-1a | Genomic Blood | 0.0 | 10.0 | no | | | Az_VANP3GEN E 10ng-ul | 1 | | Unknown | no | | 2004-07-11 |
| <input checked="" type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> | 4356-6 | Az1175-1_yr1 | Genomic Blood | 330.0 | 0.82 | yes | | | CAPPS Yr 1 Box 5 | B | 3 | N/A | no | 1995-11-30 | 1996-07-11 |


8

This consists of the Sample History Viewer and the Container Content History Viewer. Both these tools allow you to quickly find the sample you want in the container you want.

8.8.1 Sample History Viewer

The Sample History Viewer allows users to see where a sample, specified by the user, originates from and where it went. To use, simply click on the  icon on the Sample page to view the Sample History Viewer.

8.8.2 Container Content History Viewer

The Container Content History Viewer allows users to see all the containers that have ever contained a specified sample. To use, simply click on the  icon on the Sample page to view the Container Content History Viewer.

8.9 Handling Shipments

Users are able to look at a history of where a sample has been shipped (for genotyping).

8.9.1 Shipping out/Returning Shipments



From the "What would you like to do?" dropdown menu, you can choose Shipping Options. Through the dialogue box that appears, you can specify the shipment status, shipment name, shipment date, shipment location (genotyping centers), and additional comments regarding the

shipment. There are two methods you can use to specify which containers you want to ship/return. The first way is through your list; it will ship/return all the containers in your list. The second way is through the items you have checked on the Containers page; it will ship/return all the checked items on the page.

8.9.2 Viewing Shipments and Shipment History

There are two ways to view shipments: one is through one of the containers in the shipment and the other is through a search.


8.9.2.1 Through a container in the shipment

By clicking on the  icon on the Container page, you can view all the shipments that container has been in. If you click on the  icon on the shipment history page, you can view all the containers in that shipment.

8.9.2.2 Search shipments

You can search shipments through the Simple Search feature if you select “Shipment” from the dropdown menu. All the shipment names will be listed in a multiselect box. You can specify the shipment(s) you want to view. After, you will be shown a list of all the containers in those shipment(s) will appear.


8.10 Sample File Attachments

Files related to a sample can be attached to the sample. To attach a file, simply click on the  icon and a list of all files associated with that sample will be shown. To add a new file, go through the “What would you like to do?” menu and select “Attach a new file”.

8.11 Container Check-out/Check-in

This feature allows user to check-in or check-out a container so other users in the lab are able to determine which user has the sample. This feature can be accessed through the “What would you like to do?” dropdown menu. You can either checkout all the containers in your list or all the containers you checked on the Containers page. Additional comments can be left regarding the checkout, it will be in its own field separate from the comments that belong to the container.

8.12 Genotyped Information

This tool can be accessed through its icon  on the Sample page. A new page showing genotyping information regarding the specified sample will come up. The page has information on the Allele 1, Allele 2 and the SNP (RS number) of that genotype run.

8.13 Importing Data using BeadStudio-Generated CSV Files

This import tools allows users to batch import Container Content, Sample, Container, Subject, Genes, SNP, and Genotype data from sets of BeadStudio-generated CSV files. Most files will work after being generated by BeadStudio, however some may need slight modifications. An extra file will also need to be created to show the relationship between the datasets.

9 Permissions

To protect data from accidental changes, users have varied permissions in SLIMS. This means that depending on a user’s rights in SLIMS, they may be able to perform some actions but not others. An overview of these rights levels and their permitted actions can be found in the file Permissions.xls

10 Term Guide

In this section you will find explanations of fields used in SLIMS, organised by the main element they are associated with.

10.1 Samples

| Field | Description |
|--------------------|---|
| BARCODE | The barcode on a tube or plate, if the sample has one |
| VALID | Whether this sample is valid |
| CONTAMINATED | If the tube/well is contaminated |
| PARENT | The sample this sample came from (ex the tube that material was taken from to fill a well) |
| SAMPLE TYPE | The type of biological material this sample is or was extracted from (ie blood, epithelial etc) |
| MATERIAL TYPE | What type of material this sample is (WGA, genomic, unextracted, etc) |
| ROW | The row in the container the sample is in |
| COLUMN | The column in the container the sample is in |
| VOLUME | The volume of the sample in ul, -1 for unknown |
| CONCENTRATION | The concentration of the sample in ng/ul, -1 for unknown |
| DILUTION | The dilution of the sample (ex 1:100), 1:1 for stock and blank for unknown or N/A |
| COLLECTION DATE | The date this sample (the unextracted version) was collected |
| EXTRACTION DATE | The date DNA was extracted from the biological material of this sample |
| AMPLIFICATION DATE | What date this sample was amplified, will be null if non WGA |
| QUANTIFIED | The date this sample was inventoried |

10.2 Containers

| Field | Description |
|-----------------|--|
| CONTAINER NAME | The systematic name of this container |
| CONTAINER ALIAS | Non systematic name for a container. What is actually written on the container if it differs from the systematic name, or what the container was once known as |
| DATE | The date written on the container |
| INITIALS | The initials of the plate maker(s) |
| CONTAINER TYPE | What type of container this is (96 well plate, box of tubes, etc) |
| VALID | Whether the container is valid (explanation of this should be in comments field) |
| STOCK | Whether the wet lab considers this container only to have stock contents (like a box of extracted DNA tubes or a stock WGA plate) |
| MATERIAL TYPE | What kind of material is in this container (all WGA, all genomic, a mix of these etc) |

| | |
|--------------|---|
| FREEZER | Which freezer this container is in |
| SHELF | The shelf the container is on in the freezer |
| LOCATION | The specifics of where the container is on the shelf in the freezer |
| DISCARDED | Whether this container has been discarded or not |
| SHIP STATUS | Whether this container is shipped out, returned, or neither. |
| SHIPPED DATE | When this container was/will be shipped out |
| SHIPPED TO | Where this container was/will be shipped out to |

10.3 Controls

| Field | Description |
|--------------|---|
| CONTROL NAME | The name of this kind of control |
| TYPE | Whether it's a negative or positive control |

10.4 Users

| Field | Description |
|------------|---|
| FULL NAME | User's full name |
| LOGIN | User's login |
| PASSWORD | User's password |
| RIGHTS | What level of permissions does this user have, see Permissions.xls for description of different levels. |
| COMMENTARY | Comments field |
| USER TYPE | What type of user this is (system admin, dry lab, wet lab etc) |
| INITIALS | The user's initials (especially useful for wet lab because this is what is written on plates) |

10.5 Subjects

| Field | Description |
|------------|--|
| COHORT | The cohort this subject belongs to |
| SUBJECT ID | The subject's ID within its cohort (ex 1001-1) |
| FAMILY ID | The subject's family ID within its cohort (ex 1001) |
| MOTHER ID | The subject's mother's "ID" field (a string representing the subject ID like 1001-4, <i>not</i> the database ID of the subject's mother (ie not a tblsubject.subjectID value)) |
| FATHER ID | The subject's father's "ID" field (a string representing the subject ID like 1001-5 <i>not</i> the database ID of the subject's mother (ie not a tblsubject.subjectID value)) |
| GENDER | The subject's gender |
| HASCONSENT | Whether we have consent from the subject |
| ETHNICITY | The subject's ethnicity |
| "COMMENT" | Comments |

