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MarkVCID2 Virtual Biorepository Sample Tracking Instructions Manual

v.3.1.22
MarkVCID Consortium

By the MGH Neurological Clinical Research Institute and MarkVCID Coordinating Center.

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MarkVCID2 Virtual Biorepository

This is an instructional guide on how to use the MarkVCID Virtual Biorepository sample tracking platform to store and ship your samples.

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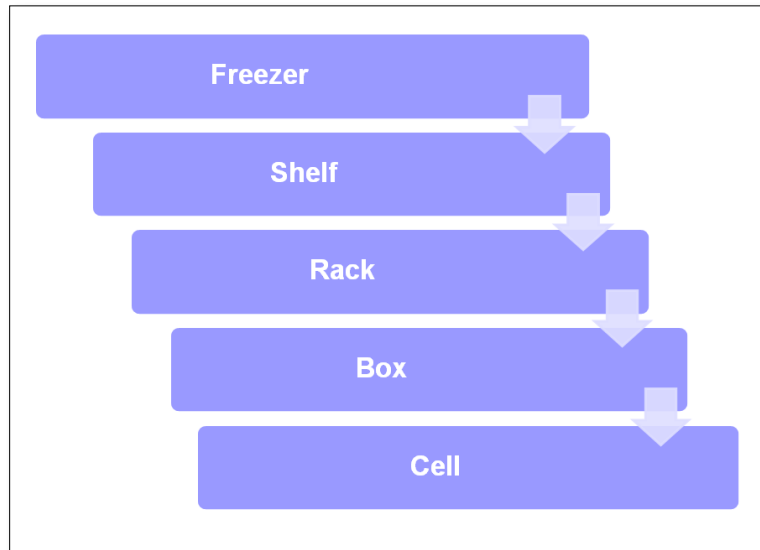
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General Concepts

MarkVCID Virtual Biorepository Storage Structure

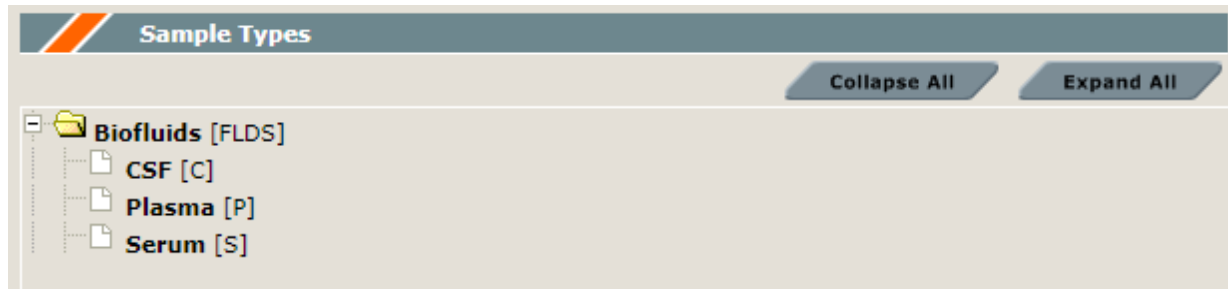
Specimen locations are tracked in the MarkVCID Virtual Biorepository sample tracking system using a hierarchical scheme, starting with all freezers located at a given site:

- Shelves within a freezer
- Racks located on a shelf
- Boxes being held in a rack
- Cells within a box, each holding an individual specimen



Sample Nomenclature

Samples in the MarkVCID Virtual Biorepository are organized by type, starting with general sample categories (biofluids) narrowing down to specific sample types. When top-level categories are expanded, the corresponding sub-types appear as follows:



Labels

Each biospecimen, regardless of its storage conditions, must have a barcoded label affixed to its container so it can be tracked in the MarkVCID Virtual Biorepository (Please refer to MarkVCID Label Printing Guide to learn how to print labels). This section describes the information contained on a label.

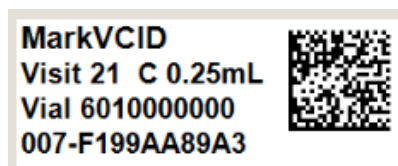
Printed labels contain both a barcode and human-readable text. Although both sets of information overlap, they are not entirely identical. When scanned, the barcode contains all information necessary for a sample to be recognized by the MarkVCID Virtual Biorepository software.

Biospecimen Labels

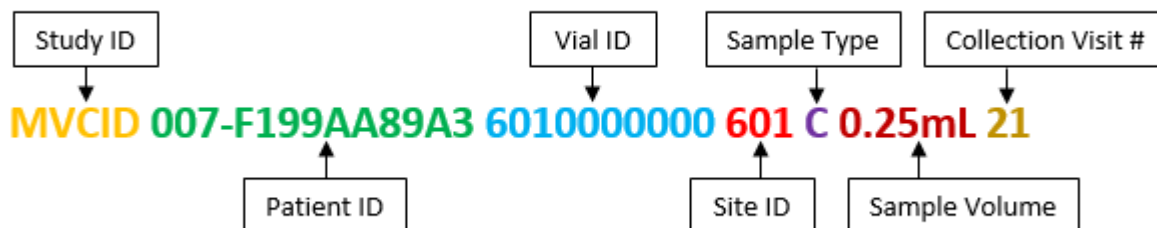
All biospecimens tracked in the MarkVCID Virtual Biorepository will have a text label containing the following information:

- Study Name
- Patient ID
- Vial ID – Identifies the individual specimens. The biorepository requires a unique Vial ID for every specimen associated with the consortium.
- Site ID – Identifies the specimen collection site.
- Sample Type – Identifies the type of specimen contained in the associated vial. *Abbreviation of the type must be used in the label barcode.*
- Sample Volume – Required for biofluids (measured in milliliters).
- Timepoint or Collection Visit # - Enumeration is done per sample type.
- Barcode for automated sample processing into the system.

Biospecimen Label Example:



Example biospecimen 'barcode' string: MVCID 007-F199AA89A3 601000000 601 C 0.25mL 21



Box ID

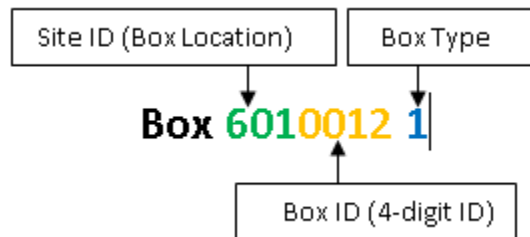
All boxes containing Biorepository samples will have an associated box ID. The box ID will be affixed to the exterior of a storage box. Box information must be entered in the system before importing the scanned strings of the biospecimens.

The following items are typically included within the box information:

- Site ID – A three-digit identifier specific to the study site where the box originated.
- Box ID – A four-digit identifier that is unique for each box at a given site.
- Box Type – Indicates the number of cells within a box (individual storage spaces). For example, type 1 indicates a typical 9x9 box.

Example box 'barcode' string: "Box 6010012 1"

Note: You must enter the word 'Box' before box ID and box type.



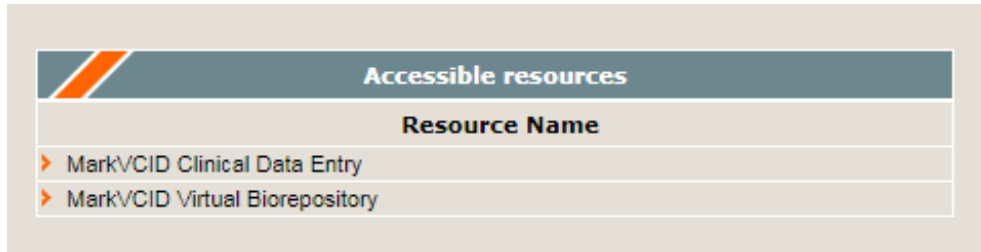
Accessing the MarkVCID Biorepository Platform

The MarkVCID Virtual Biorepository is accessible in most major Internet browsers and can be found at the following address (URL): <https://ncr10.partners.org/MarkVCID/BR>

You must receive a registered Username and Temporary Password from the MarkVCID Coordinating Center to access the virtual biorepository.

The screenshot shows a login form with a dark blue background. It contains two white input fields: "Username:" and "Password:". Below the fields is a light-colored button labeled "Enter".

Selecting the MarkVCID tab will display a list of all permitted system resources. The user can access the Virtual Biorepository by clicking the “MarkVCID Virtual Biorepository” link.



Management Tab

Upon entering the MarkVCID Virtual Biorepository, the following homepage will be displayed (the “Barcodes” tab):



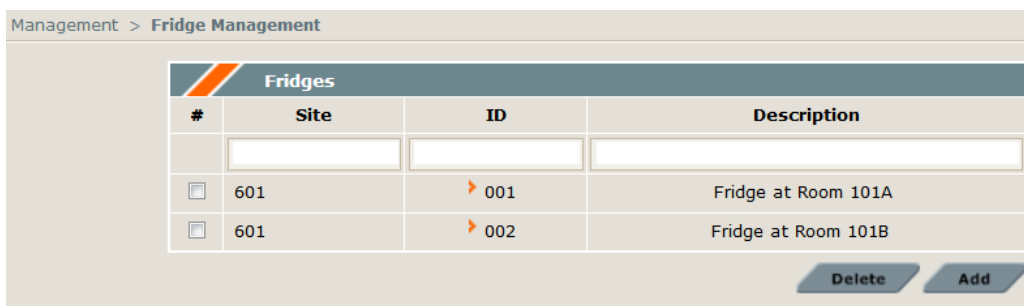
To view and manage aspects of the biorepository, click the *Management* tab. Here you can view, create and edit four main items in the virtual biorepository:

- Fridge
- Box
- Sample
- Sample Type

Fridge Management

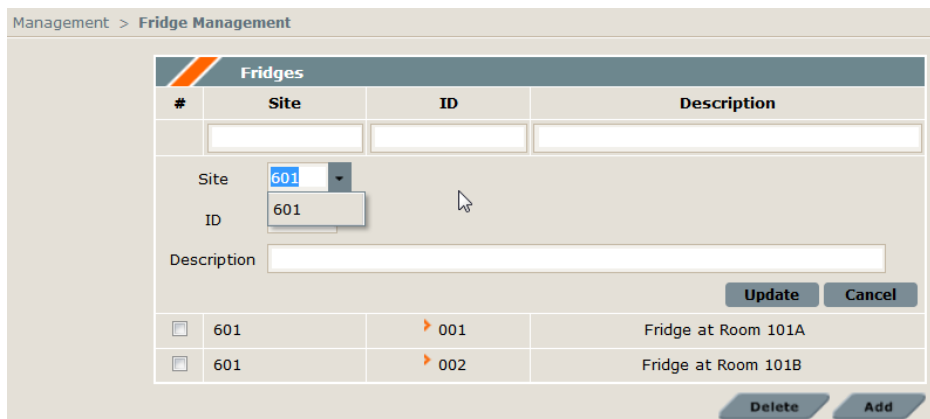


On the “Fridge Management” page, you can create, edit and view fridges at your respective site. For example, for Site 601, only fridges located at Site 601 are shown in the ID column of the *Fridge* table.



Adding a New Fridge:

1. Click the “Add” button and a new row will be created.
2. Create a unique three-character alphanumeric ID value. A description of the fridge can also be entered, but this is not required (example: ‘Fridge at Room 101A,’ as seen in the screenshot below).
3. Click “Update” to save the new fridge information.



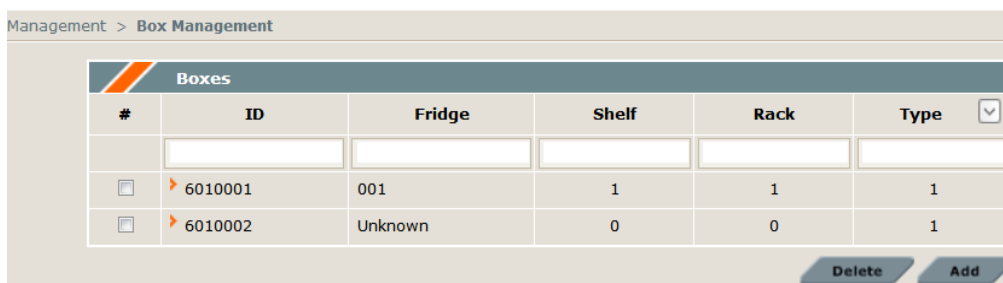
4. You can edit the fridge information by clicking any fridge’s ID number. You can leave the fridge creation process by clicking the “Cancel” button.

Box Management



In the “Box Management” page, you can create, edit, and view boxes. Like fridge access, you can only view boxes located at your assigned site. You should use the site number that was assigned to you by the MarkVCID Coordinating Center as part of your participation in the Consortium. This site number can be found on the MarkVCID website (<https://markvcid.partners.org/research-site-ids>) for reference.

All box IDs begin with the user’s site ID followed by four digits.



Adding a New Box

1. Click the “Add” button on the “Box Management” page.
2. Type a seven-digit box ID. The ID’s first three digits must be your site ID. The next four digits can be any between 0001 and 9999. **Note:** you cannot view boxes located at other sites. If you create a box with another site’s ID, you will not be able to view it in the Boxes table.
3. Select the “Fridge” in which the Box will be located.
4. Type a “Shelf” number (optional).
5. Type a “Rack” number (optional).
6. Select a “Box” type. (1 indicates a typical 9x9 = 81 cells box, if you use a box type other than 9x9, the NCRI Help Desk or the system administrator will be able to configure it on request)
7. Click the “Update” button to create the box.

8. You can make changes to any of your site's boxes by locating it in the Boxes table and clicking its ID.

#	ID	Fridge	Shelf	Rack	Type
<input type="checkbox"/>	6010001	001	1	1	1
<input type="checkbox"/>	6010002	Unknown	0	0	1
<input type="checkbox"/>	6010003	Unknown	1	1	1

Note: You can delete selected boxes that do not contain samples in the Boxes table. The system will not allow you to delete boxes that contain one or more samples.

Sample Management

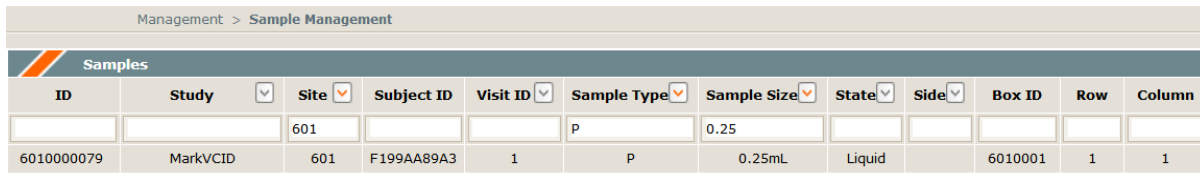


The "Sample Management" page displays vials located at your site. The table displays all relevant parameters for each sample located at the user's site.

ID	Study	Site	Subject ID	Visit ID	Sample Type	Sample Size	State	Side	Box ID	Row	Column
6010000001	MarkVCID	601	F199AA89A3	1	S	0.25mL	Liquid		6010002	1	1
6010000079	MarkVCID	601	F199AA89A3	1	P	0.25mL	Liquid		6010001	1	1
6010000078	MarkVCID	601	F199AA89A3	1	S	0.25mL	Liquid		6010001	1	2
6010000077	MarkVCID	601	F199AA89A3	1	S	0.25mL	Liquid		6010001	1	3
6010000080	MarkVCID	601	F199AA89A3	1	S	0.25mL	Liquid		6010001	1	4
6010000085	MarkVCID	601	F199AA89A3	1	S	0.25mL	Liquid		6010001	1	5
6010000086	MarkVCID	601	F199AA89A3	1	S	0.25mL	Liquid		6010001	1	6

Searching for a Sample at Your Site

It is inefficient to manually browse through the repository for a specific sample/set of samples located at your site. Please search by typing in the search textbox and selecting the appropriate filter dropdowns located directly under the table's column titles. Press the "Enter" button on your keyboard (or "Return" for Apple computers). You can use as many or as few of the filters as you'd like during a search. For example, below is a search for all samples with sample type P, of sample size 0.25mL, collected at site 601. The system will search through all samples located at site 601 and will only display those that meet all selected criteria.

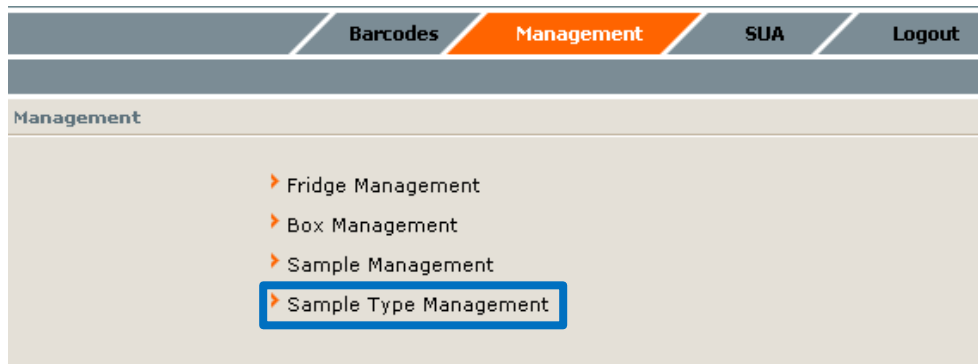


Management > Sample Management

Samples




ID	Study	Site	Subject ID	Visit ID	Sample Type	Sample Size	State	Side	Box ID	Row	Column
6010000079	MarkVCID	601	F199AA89A3	1	P	0.25mL	Liquid		6010001	1	1

Sample Type Management



Unlike the previous management pages, the "Sample Type Management" page shows all sample types stored in the Biorepository. Site users cannot enter or edit sample types in the "Samples Type Management" page. Accessing this page only gives site users knowledge of all existing sample type categories and individual sample types stored and tracked in the virtual biorepository.



Sample type categories are designated with the  icon and can be expanded by clicking the adjacent  icon. Individual sample types are designated with the  icon.

Each sample type displays the sample type name followed by its code. This code also appears on the vial's label.

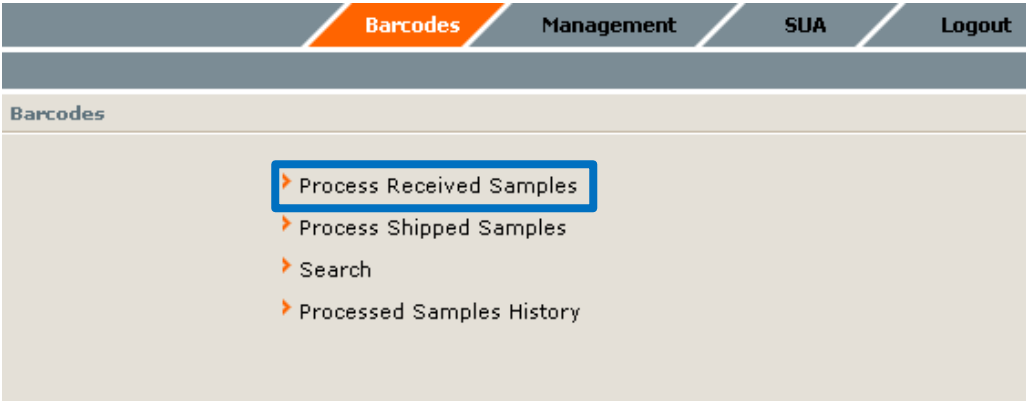
Barcodes Tab

Processing Received Samples (samples collected at your site)

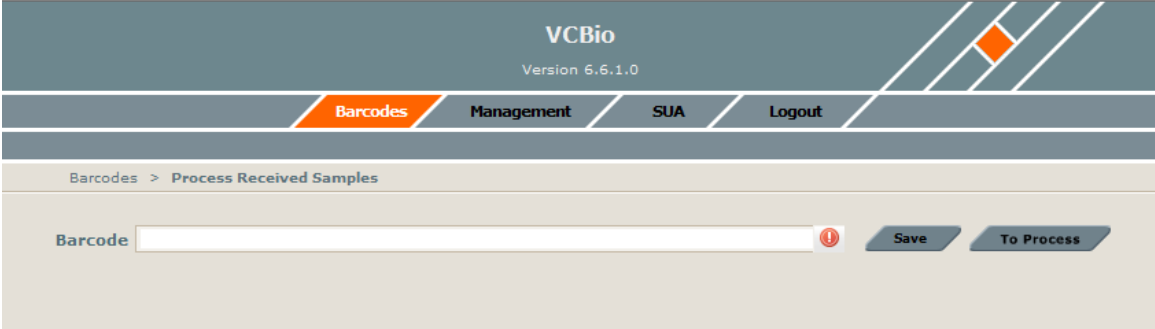
The samples collected and stored at your site need to be processed into the sample tracking system to track the location and status of the sample. The “Process Received Samples” section allows you to process the samples into the system by scanning in the barcoded samples.

Processing Received Samples

Click “Process Received Samples”.



You will then be brought to the next screen “Process Received Samples”.



Placing Samples in a Box

Once sample(s) are placed in a box for storage, a box label (with the box id to identify the box) should be affixed to the outer surface of the box. Cells in the box should be filled starting at the top left corner, filling left to right in a single row (**Mark the starting cell of your box if the box does not have any markers to identify the cell numbers. This will help locate the samples correctly when a sample request is made in the future**). Once a row is filled, the row below is filled from left to right, and so on. For example, in the box below a group of CSF and plasma samples would be placed in the box as shown:

		Column								
		1	2	3	4	5	6	7	8	9
Row	1	c	c	c	c	p	p	p	p	p
	2	p	p	#	#	#				
				---	---	---				
	3									
	4									
	5									
	6									
	7									
	8									
9										

A scanned box will usually contain more than one sample. The image below displays an example of a string output with multiple scanned biospecimens.

```
Box 6010001 1 MVCID F199AA89A3 6010000079 601 S 0.25mL 1 MVCID F199AA89A3 6010000078 601 S
0.25mL 1 MVCID F199AA89A3 6010000077 601 S 0.25mL 1 MVCID F199AA89A3 6010000080 601 S
0.25mL 1 MVCID F199AA89A3 6010000085 601 S 0.25mL 1 MVCID F199AA89A3 6010000086 601 S
0.25mL 1
```

IMPORTANT: You must scan and place your samples in the order explained above because the samples are processed in the same order in the system.

Example of how the following strings are processed in the system:


```
Box 6010001 1 MVCID F199AA89A3 6010000079 601 S 0.25mL 1 MVCID F199AA89A3 6010000078 601 S
0.25mL 1 MVCID F199AA89A3 6010000077 601 S 0.25mL 1 MVCID F199AA89A3 6010000080 601 S
0.25mL 1 MVCID F199AA89A3 6010000085 601 S 0.25mL 1 MVCID F199AA89A3 6010000086 601 S
0.25mL 1
```

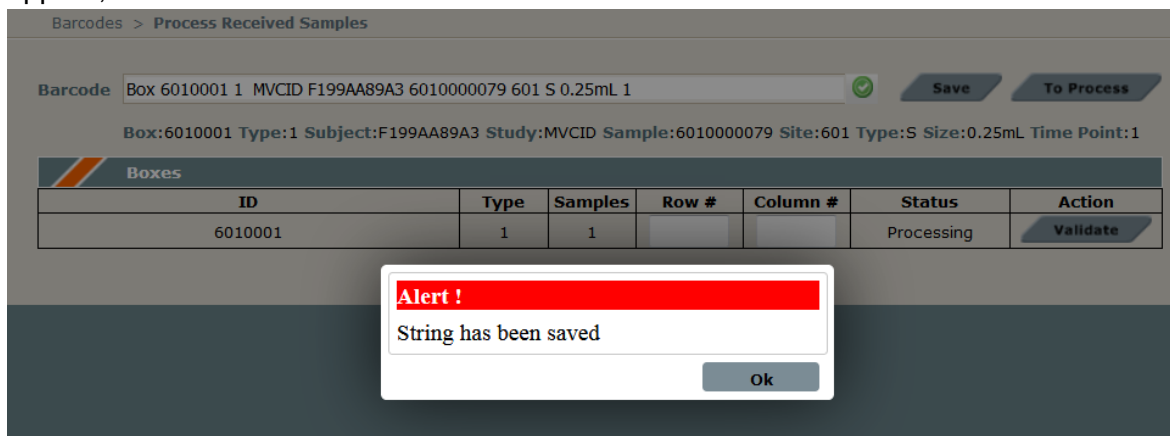
The cell locations of the vial ids will be tracked as follows for box 6010001:

Vial ID	Row #	Column #
6010000079	1	1
6010000078	1	2
6010000077	1	3
6010000080	1	4
6010000085	1	5
6010000086	1	6

Scanning Barcodes

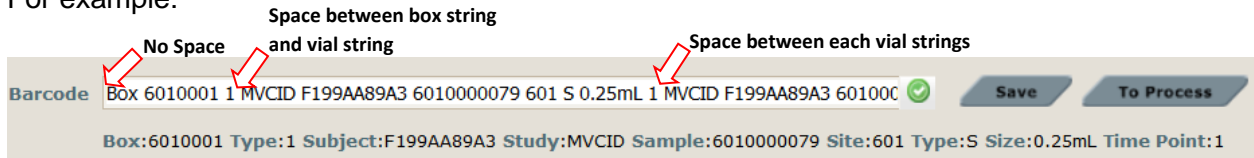
Once a label has been affixed to a sample’s vial, it must then be scanned into the system using the following procedure:

1. Open a word document on your computer. Once a scan gun (supplied to each participating consortium site) is connected to a computer, any barcodes scanned while the scanner is connected will be entered as text wherever the computer’s cursor is placed. In this way, the scanner acts like a keyboard—if you have a word document open on the connected computer, barcode text will be “typed” into the document as labels are scanned. To prevent errors or the need to rescan any of your samples, it is advisable to first save the scanned text locally (e.g. in a Word document), and then copy and paste the label string(s) into the Biorepository system’s barcode text box rather than scanning directly into the Biorepository system.
2. Using your scan gun, scan the samples contained in a box. Samples should be scanned in the same order in which they are placed in the box.
3. Review the string(s) that were scanned for any issues and help catch errors before they are saved in the system.
4. Enter the Box information as described in the previous section.
5. Paste the string in your word document into the Barcode textbox and click “Save”.
6. At this point, the system will parse the string and evaluate it for any errors. You may also check the text for errors by clicking the icon  next to barcode text box to the right of the text.
7. If the system does not detect any errors in the barcode, the “String has been saved” popup will appear, as below. Click “OK”.



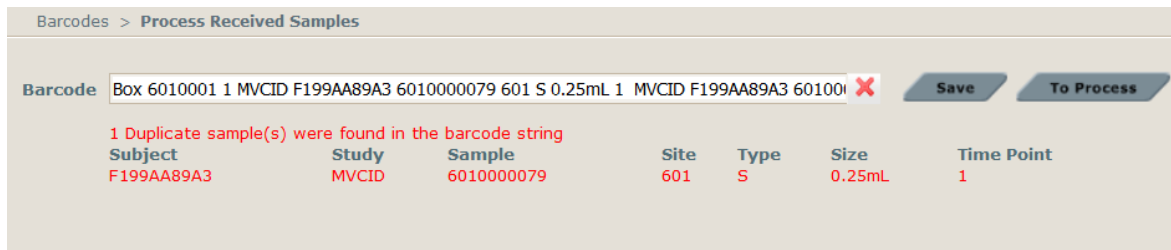
Note: Configure your scanner to leave a space between each scanned string. For code scanners, a configuration guide is available at <http://www.codecorp.com/ConfigGuide/>.

Ensure there is no space before the word 'Box' when you enter strings in the Barcode textbox. For example:



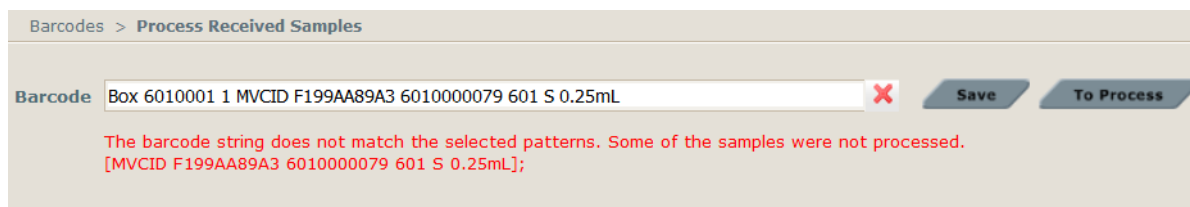
The following are the potential errors when receiving samples and how to troubleshoot them:

1. You have a duplicate vial. This means you scanned and/or entered the same vial more than once. You will see the screen below.

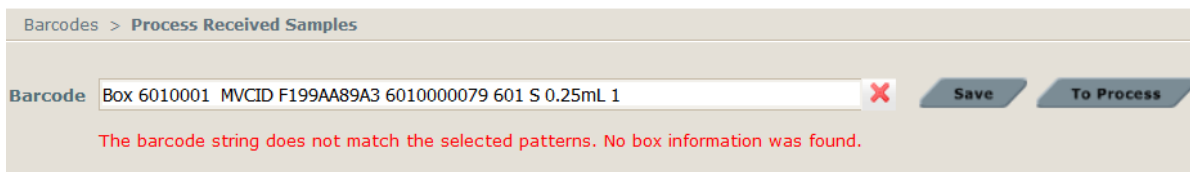


2. A portion of your string for a box or sample does not match the barcode pattern used by the system.

In this example, the time point is missing.



In this example, the box information is missing.



Once the string is saved, the system will provide a summary of the box and specimen data it extracted from the saved text. For more information about the fields shown below, refer to the previous section reviewing the various data types contained in box and biospecimen labels. You will also see two empty fields per *box*, “*Row #*” and “*Column #*” that identify a cell in the corresponding box into which the first vial of the batch is placed.

Barcodes > Process Received Samples

Barcode: Save

Box:6010001 Type:1 Subject:F199AA89A3 Study:MVCID Sample:6010000079 Site:601 Type:S Size:0.25mL Time Point:1

Boxes						
ID	Type	Samples	Row #	Column #	Status	Action
6010001	1	1			Processing	<input type="button" value="Validate"/>

Enter for each box, “*Row #*” and “*Column #*” of the cell in which you placed your first vial of that batch of sequentially placed vials. The system will then automatically fill subsequent empty cells in the specified box with the scanned specimens from left to right, moving down once the end of a row is reached.

For example, if the first thirteen cells of the box are already taken by a previously processed batch of vials, you would place your first vial of this batch into the cell located in the second row and fifth column. In this case, you would type “2” in *Row #* and “5” in *Column #*.

	1	2	3	4	5	6	7	8	9
1	c	c	c	c	p	p	p	p	p
2	c	p	c	c	#	#	#	#	
3									
4									
5									
6									
7									
8									
9									

Barcodes > Process Received Samples

Barcode: Save

Box:6010001 Type:1 Subject:007F199AA89A3 Study:MVCID Sample:6010000079 Site:601 Type:S Size:0.25mL Time Point:1

Boxes						
ID	Type	Samples	Row #	Column #	Status	Action
6010001	1	1	2	5	Processing	<input type="button" value="Validate"/>

As mentioned above, if you have more than one box listed, then specify the batch’s first cell for each box.

Barcodes > Process Received Samples

Barcode Save To Process

Box:6010001 Type:1 Subject:007F199AA89A3 Study:MVCID Sample:6010000079 Site:601 Type:S Size:0.25mL Time Point:1

Boxes						
ID	Type	Samples	Row #	Column #	Status	Action
6010001	1	1	1	1	Processing	Validate
6010002	1	1	1	1	Processing	Validate

Next, click “Validate” for the box. The system will check that the cells that you indicated are empty in the Biorepository’s inventory for the specified box. If the system attempts to place a specimen in an occupied cell, it will return an error message. Such an error typically means one of four things:

1. (Most commonly) Someone shipped out a sample from the box but did not inform the System, i.e. has not used the “Processed Shipped Samples” page to indicate that the specimens are no longer in their former location.
2. The entered box’s “Row #” and “Column #” values do not correspond to the box’s cell in which you placed your first vial.
3. The entered box’s “Row #” and “Column #” fields’ values were meant for a different box.
4. Incorrect values were entered and processed by the System for a previous set of imported labels.

If the system finds no problems with entered values, a “Box has been validated” message will pop up. Acknowledge this message by clicking “OK”. The “Status” will then say “Processing” and the “Action” button will change its value from “Validate” to “Import”.

Barcodes > Process Received Samples

Barcode Save To Process

Box:6010001 Type:1 Subject:F199AA89A3 Study:MVCID Sample:6010000079 Site:601 Type:S Size:0.25mL Time Point:1

Boxes						
ID	Type	Samples	Row #	Column #	Status	Action
6010001	1	1	1	1	Processing	Import

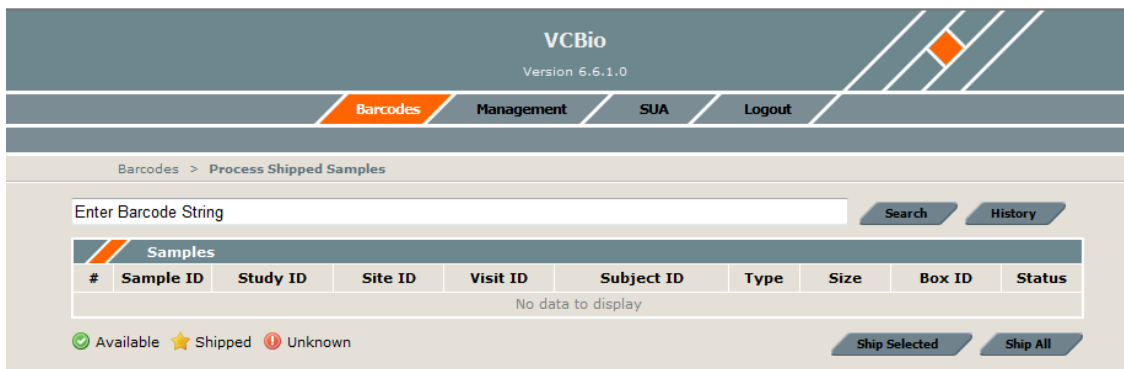
Click “Import” to save the samples in the MarkVCID Virtual Biorepository system.

Processing Shipped Samples (or samples that have been used)

The MarkVCID Virtual Biorepository system must be notified when a sample or set of samples no longer resides in the originally indicated site location. This process will be necessary whenever samples are either consumed at a site or sent from one site to another. To scan biospecimens for shipping, select “Process Shipped Samples” under the “Barcodes” tab.



The screen will appear as below:



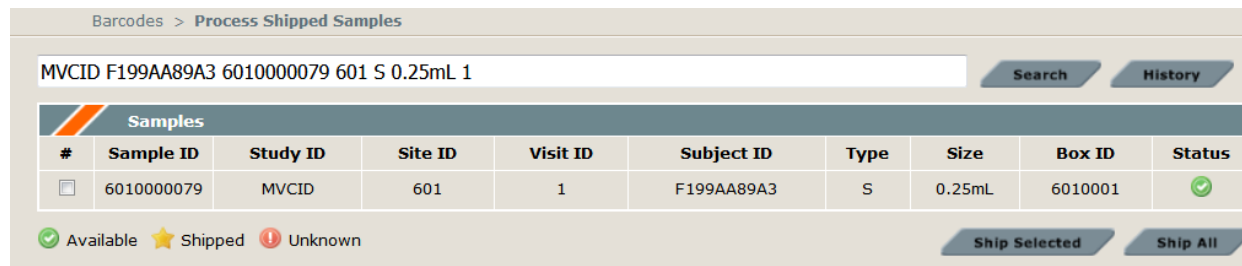
Using a scan gun, collect the barcode text from all the specimens you wish to use/ship in a separate document. Note that using/shipping specimens does not require a box barcode to be scanned, as the system will already know the box in which each of the scanned samples was being stored.

Click into the “Enter Barcode String” field and copy the scanned text into the text box.

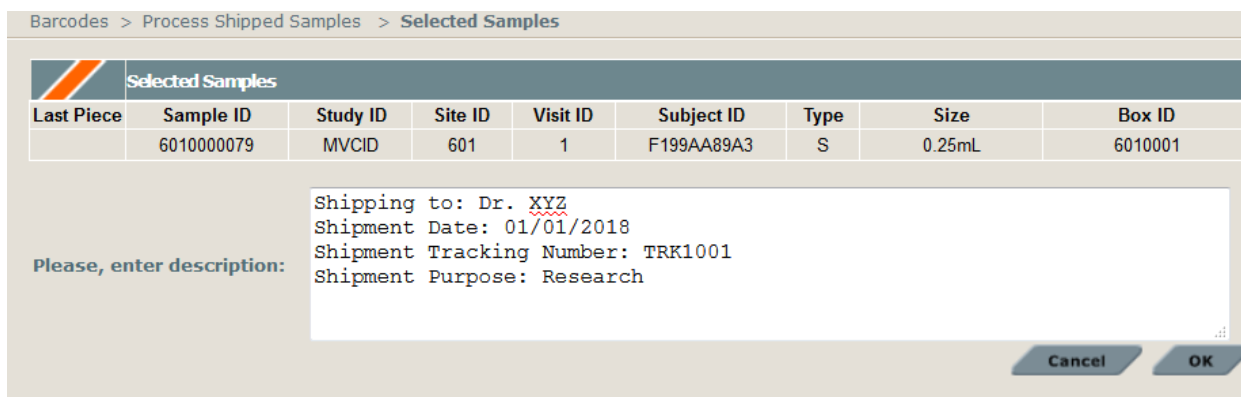
Click “Search”.

Assuming the text correctly corresponds to vials already existing in the MarkVCID Virtual Biorepository, the system will generate a list of biospecimens from the entered batch along with additional information about each sample. There will be one row per processed sample in the *Samples* table. A green check mark in the *status* column indicates that the sample is available for shipping.

You may select all or a subset of the samples in the list, then click *Ship Selected* button. If you would like to confirm that all biospecimens from the table are being shipped/utilized, then click “Ship All”.



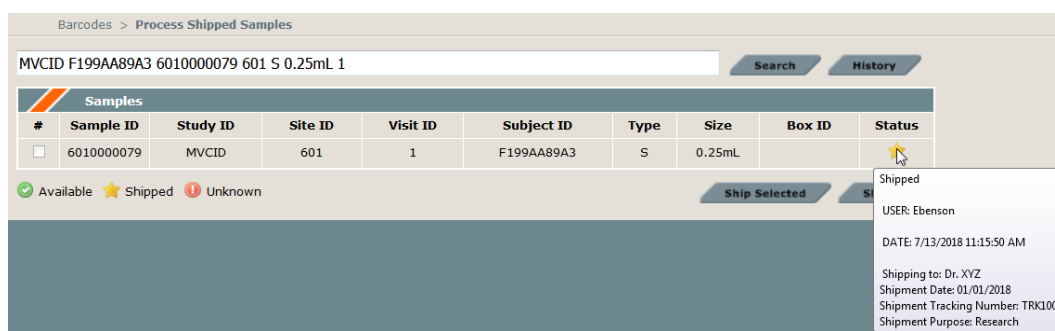
The system then asks for a description of the shipment. While this information is not required, it is highly recommended to enter some meaningful information into that box for later reference. An example of this information can be seen in the screenshot below. Click “OK”.



The samples will be removed from the inventory once you ship the samples and the actual inventory number will be updated.

Confirming a Sample has Been Checked Out of Inventory

To double-check that the system checked out shipped/used samples from its inventory, you can enter the barcode string in the barcode text box and click search. The icon in the *Status* column will change its shape to a yellow star if it was successfully removed from inventory. You can also view the shipment history by clicking “History” button on the “Process Shipped Samples” page.



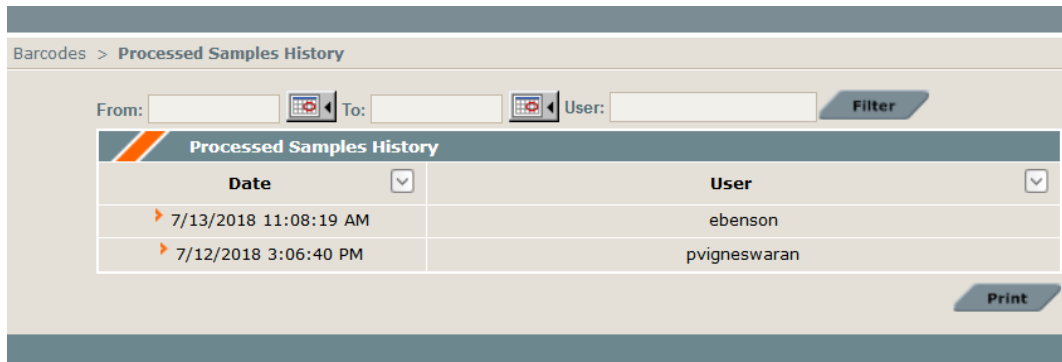
Processed Samples History

The “Processed Samples History” page can be selected under the “Barcodes” tab.

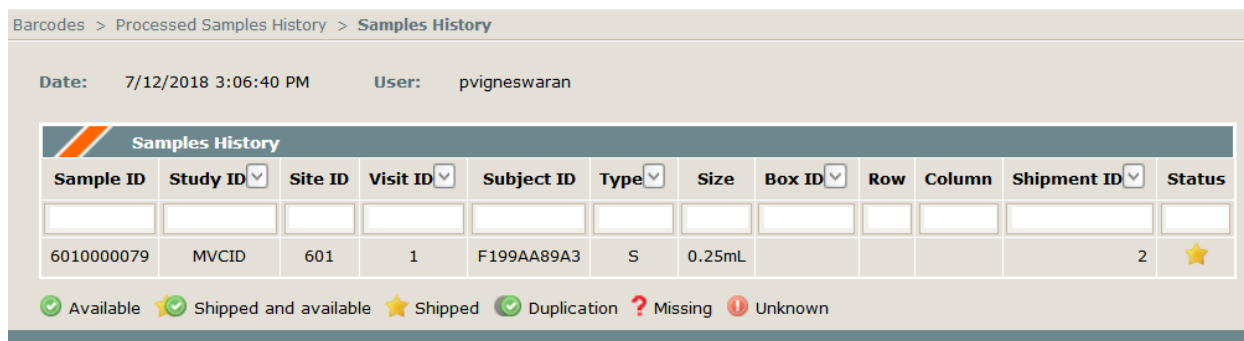


The “Processed Samples History” page maintains records of all sample batches entered into the biorepository. A new record is added here each time a batch of samples is successfully processed. Each table record displays the name of the user who processed the batch of samples and the date and time of the processing.

To review information on a specific batch, click on its “Date” value to be taken to its “Samples History” page.



The top of the “Samples History” page displays the original date and time this batch was scanned and the name of the user who scanned it. The Samples History table displays each batch’s sample values and its current status. The table can be browsed, sorted, filtered, and searched.



Questions or Need Help?

If you have any questions, please contact:

NCRI Help Desk Support

NCRISupport@partners.org

1-855-ASK-NEUR (1-855-275-6387)