

ADDING SAMPLES

This document will guide the user to add new Sample records to an existing Donor/Participant. Please consult the document 'Donor Management' if you need to add a Donor/Participant record first.

Samples may be added individually or in bulk. They can be created in isolation or as a child of a parent sample, either through creating aliquots or creating a new derivative of an existing sample. For example extracting plasma and serum from an existing whole blood sample.

ADDING A SINGLE SAMPLE

- Navigate to the Collection in which the Sample record will be created
- Open the Participants navigation option to view the Participant grid
- Find the necessary Participant record and open it by clicking on the hyperlink within the Participant ID column
- In the Participant record, open the Samples navigation option to view any existing Sample records
- Select the *Insert New Sample* workflow option from the Samples grid
- This will directly open a new Sample record
- Mandatory fields include *Sample Form*, *Tissue Type* and *Derivative*
- Upon saving the record, unless populated the *Internal Reference* field will have an automatically generated value inserted
- Save & Close
- NB The new Sample record will be flagged as *Checked Out* as it currently has no location information associated with it. Follow the *Check In/Move Location* workflow to place the Sample record into storage (see Checking In samples document for further guidance)

ADDING SAMPLES IN BULK

Achiever is able to add many samples to a Participant record in a single workflow. The user decides how many *types* of sample are to be created, for example Blood, CSF and Bone Marrow would be 3. Following this the user selects the quantity of samples to be created for each derivative. This workflow creates samples with no parent.

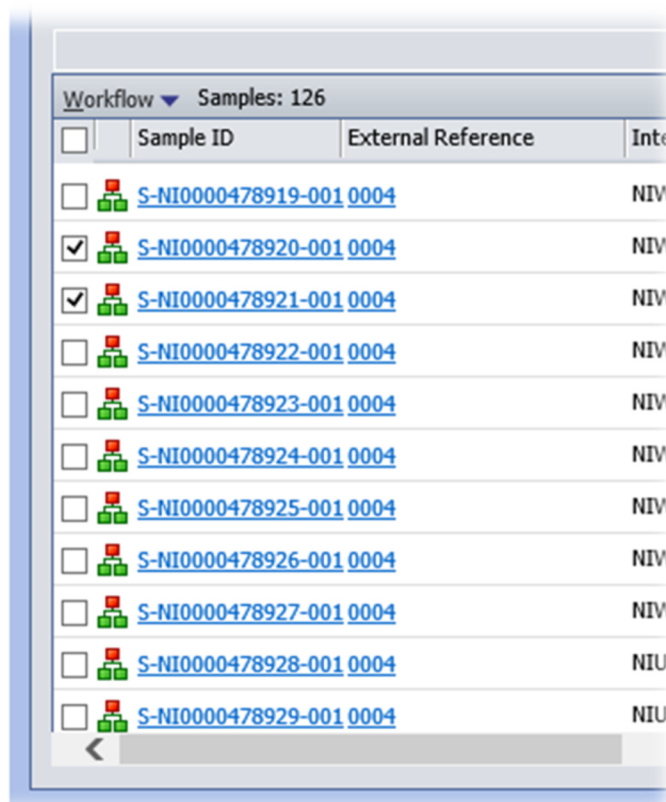
- As above, navigate to the required Participant record and open its Samples grid
- Select the *Insert New Sample Group* workflow
- The user is asked to pick the Number of Tissue Types – this does not reflect the resulting number of samples but how many different derivatives you need. For example to create 10 whole blood samples the value would be 1
- The optional *Date Taken* field will apply that value to each sample created
- Click continue
- The following form will allow the user to choose *Sample Form*, *Tissue Type*, *Derivative* and *Quantity* for the number of derivatives chosen in the previous step
 - Some teams may also have the option to choose *Sample Site*, or *Visit Number* on this screen
- Clicking *Create Samples* will create all of the Sample records and display them in a summary grid to the user
- This summary grid is very useful as it provides an isolated 'working group' of samples which can be opened, edited, and have workflows run on them without having to search/select the samples at the Participant or Collection level where they may be mixed among many other samples. It also offers *edit-in-place* fields which can be updated without opening each Sample record in a similar way to an












Excel spreadsheet. If a mistake is made and samples are created in error, the summary grid also provides a bulk delete workflow.

CREATING ALIQUOTS

Achiever allows a Sample record to be split, creating new Sample records with the same Tissue Type/Derivative while maintaining a parent/child relationship to the original Sample record. Optionally, the parent Sample record can be marked as used up within the same workflow.

- Find the Sample record(s) to be split from either the Collection-level or Participant-level Samples grid, and select them
 - Multiple samples may be split at the same time, they will have exactly the same operation performed on them



Workflow ▾ Samples: 126			
<input type="checkbox"/>	Sample ID	External Reference	Inter
<input type="checkbox"/>	 S-NI0000478919-001 0004		NIWI
<input checked="" type="checkbox"/>	 S-NI0000478920-001 0004		NIWI
<input checked="" type="checkbox"/>	 S-NI0000478921-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478922-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478923-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478924-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478925-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478926-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478927-001 0004		NIWI
<input type="checkbox"/>	 S-NI0000478928-001 0004		NIUR
<input type="checkbox"/>	 S-NI0000478929-001 0004		NIUR

- Select the Split Sample(s) (Simple Aliquots) workflow



Simple Sample Split

 Save & Continue

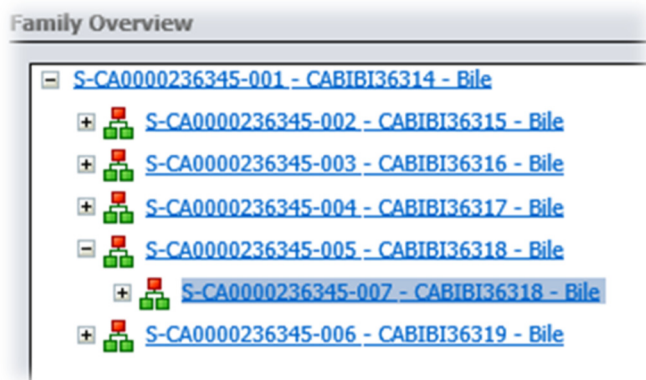
Number of Aliquots

Mark Parent as Used Up? ☐

Copy Internal Reference? ☐

- The only mandatory field is *Number of Aliquots* – this is the number of new Sample records that need to be created
 - Mark Parent as Used Up?* Will also flag the selected Sample record(s) as used up during the workflow. Any storage location details will be removed from the parent record

- *Copy Internal Reference* will apply the selected Sample record's *Internal Reference* value to each newly created Sample record. This is useful as the user can then simply update the newly created records by appending a suffix to each record on the resulting summary grid
- Click *Save & Continue* to create the samples. A summary grid will be shown with the newly added Sample records
- Sample records created in this way will have a new navigation option available *Family Overview*
 - Navigating to this screen will display the a history of this Sample record in a hierarchy, displaying parent/child and sibling Sample records



- The currently selected Sample record will be highlighted, and each other record can be opened by following the links

CREATING NEW DERIVATIVE SAMPLES

Using this workflow a user can create child Sample records in a similar way to the simple aliquot workflow however they can also change the type of Sample record which is created. This is useful to show when eg serum is extracted from whole blood while maintaining the parent/child relationship.

- Find the Sample record(s) to be split from either the Collection-level or Participant-level Samples grid, and select them
 - Multiple samples may be split at the same time, they will have exactly the same operation performed on them
- Select the Split Sample(s) workflow
- Similarly to when adding samples in bulk (see above) the user must select the number of derivatives to be created. For example if extracting plasma and serum from an existing whole blood Sample record this would be 2
 - *Mark Parent as Used Up?* Will also flag the selected Sample record(s) as used up during the workflow. Any storage location details will be removed from the parent record
 - *Copy Internal Reference* will apply the selected Sample record's *Internal Reference* value to each newly created Sample record. This is useful as the user can then simply update the newly created records by appending a suffix to each record on the resulting summary grid
- Click *Continue*
- Again, in the same way as when performing the *Insert New Sample Group* workflow, the user must select the appropriate *Sample Form*, *Tissue Type* and *Derivative* for each derivative type chosen as well as a quantity of samples to be created
- Click the *Create Samples* button to add the new Sample records and view them within a sample summary grid

ADDITIONAL FIELDS

When creating samples for the first time, it is useful to view what additional fields are available to store useful data. All fields are searchable within Achiever. Commonly used additional fields include:

- Sample – free text used for any purpose
- Site/Subsite – Allows further specificity of sample eg Shoulder/Skin vs Right Breast/Skin
- Time Point – includes unit field and value
- Taken/Received/Processed/Frozen fields – Ability to assign a date and time and/or a name against common processes
- Additive – picklist including EDTA, Heparin and other commonly used additives/reagents

Users are encouraged to view a sample record and browse the fields available