**TMT location:**

1. Log in to TMT (<http://vtest11.wustl.edu:8080/catissuetmt/Home.do>).
2. Select Test cases tab.
3. Expand caTissue product from the tree view.
4. Expand Mater List-v2.0 version
5. Expand Biospecimen Component
6. Expand Specimen test area
7. Select Test case ID 391 with short title Label\_Generation\_Tokens\_PPI\_SP\_TYPE\_PPI\_YOC\_UID\_YR\_OF\_COLL

**Purpose**:

**To ensure while collecting specimens for a protocol labels are generated as per the specified label format:**

**CP Details page:**

**Parent Specimen label format: Blank**

**Derivative label format: Blank**

**Aliquot label format: Blank**

**Specimen Requirements page:**

**Parent Specimen label format:   
GC\_%PPI%\_%SP\_TYPE%%PPI\_YOC\_UID%\_%YR\_OF\_COLL%  
Derivative label format:   
GC\_%PPI%\_%SP\_TYPE%%PPI\_YOC\_UID%\_%YR\_OF\_COLL%  
Aliquot label format:   
GC\_%PPI%\_%SP\_TYPE%%PPI\_YOC\_UID%\_%YR\_OF\_COLL%**

**Prerequisites**:

Import latest dump located at

Oracle: https://ncisvn.nci.nih.gov/svn/catissue\_persistent/caTissue Database Dump/v2.0/Oracle

MySQL: https://ncisvn.nci.nih.gov/svn/catissue\_persistent/caTissue Database Dump/v2.0/MySQL and deploy application.

Modify the label generator. Properties file located at caTISSUE\_HOME/catissuecore-properties/. Set the value of property specimenLabelGeneratorClass to specimenLabelGeneratorClass=edu.wustl.catissuecore.namegenerator.DefaultTemplateLabelGenerator.Redeploy the application and restart the application server.

Modify the PrintServiceImplementor.properties file located at caTISSUE\_HOME/catissuecore-properties for following.

PrintWebServiceEndPoint= http ://< ipaddress: portNo>/caTissuePrintWebService/Print? Wsdl>

(This is the URL of Print Web Service, where IP address and port is of the server where print web service is deployed.)

Specimen=edu.wustl.catissuecore.printservicemodule.WashuSpecimenLabelPrinterImpl

Specimencollectiongroup=edu.wustl.catissuecore.printservicemodule.WashuSpecimenCollectionGroupLabelPrinterImpl.

Note: Refer the page at <https://cabig-kc.nci.nih.gov/Biospecimen/KC/index.php/Label_Printing> for web-service deployment.

Place print\_rules.xls inside JBOSS-HOME (Print server)/print/printrules .Please use the print.xlsx located at https://ncisvn.nci.nih.gov/svn/catissue\_persistent/caTissueDocs/trunk/TestCases/Manual/print\_rules.xls

**Procedure:**

1. Login as site administrator ([admin\_gc@washu.com,Test123](mailto:admin_gc@washu.com,Test123)).
2. Navigate to Biospecimen Data🡪Collection Protocol Based view. Select collection protocol “***ADRC GC CP***” from the ***Collection protocol*** drop-down list.
3. Select participant “***Johnson, Johnson***” from the ***Participant*** (***Protocol ID***) drop-down. Refer the expected Output.
4. From the L.H.S>>***Specimen Details***>>Select the anticipated specimen collection group with study calendar event point as ***T0.0; Blood Draw***. Refer the expected Output.
5. On R.H.S🡪***Edit Specimen Collection Group page***🡪Enter ***collection site*** as ***ADRC Genetics Core*** and ***collection status*** as ***Complete***. Click on Submit. Refer the expected Output.
6. On ***Specimen Details*** page, check the check-boxes next to ***Coll?*** and ***Print*** for all the parent and child specimens. Click on Submit. Refer the expected Output.
7. Repeat the steps 4-6 for the study calendar event point ***T5.0; Post Blood Draw.*** Refer the expected output.
8. From the Edit Specimen Collection group page, uncheck the check-box for Specimen entry based on collection protocol. Enter number of specimens as 5. Click on Add multiple specimens. Refer the expected Output.
9. Enter specimen labels as ABC\_1, ABC\_2, ABC\_3, ABC\_4, and ABC\_5.Click on Submit.
10. From the Edit Specimen Collection group page, uncheck the check-box for Specimen entry based on collection protocol. Click on Add specimen. Refer the expected Output.
11. Enter specimen labels as ABC\_6. Click on Submit.
12. Navigate to Biospecimen Data-🡪Specimen🡪Aliquot page. Enter parent specimen label as GC\_181\_322\_WB1\_2011 (collected in step6) .Enter count as 2, quantity as 0.1. Refer the expected Output.
13. Enter specimen labels as GC\_181\_322\_WB1\_2011\_1 and GC\_181\_322\_WB1\_2011\_2 .Click on Submit.
14. Navigate to Biospecimen Data-🡪Specimen🡪Derive page. Enter parent specimen label as GC\_181\_322\_WB1\_2011 (collected in step 6). Refer the expected Output.
15. Enter specimen labels as GC\_181\_322\_WB1\_2011\_3. Click on Submit.

**Expected Output:**

3 Edit participant page should be displayed on R.H.S and Specimen Details tree on L.H.S should display event points as:

* ***T0.0; Blood Draw***
* ***T5.0; Post Blood Draw***

4 Edit Specimen Collection group page should be displayed on R.H.S.

5 “***Specimen Collection Group successfully updated***.” message should be displayed at the top of the page and Specimen Details page should be displayed with Specimen Details, Derivative Details and the Aliquot Section. The label text-boxes for parent, derivatives and aliquots should be shown as “***AUTO-GENERATED***”. The event icon for ***T0.0; Blood Draw*** should turn golden-brown.

6 Edit specimen collection Group page should be displayed, a message should be shown as “***Printed successfully***”. The specimen icon for collected specimens should turn pink. From the specimen details section on L.H.S Verify the labels generated for the specimens. Unique labels should be generated for all the specimens. Refer the table below for the tokens used:

|  |  |
| --- | --- |
| **Tokens** |  |
| **%PPI%** | For adding participant protocol id in specimen label. |
| **%SP\_TYPE%** | For adding specimen type abbreviation. The abbreviations are picked up from “Abbreviations.xml” present in JBOSS\_HOME/servers/default /catissuecore-properties folder |
| **% PPI\_YOC\_UID%** | For adding a unique sequence number related to specific PPI and year of collection. |
| **% YR\_OF\_COLL%** | For adding year of collection of specimen |
| **Labels for specimens collected as per CP definition** | In case Participant Protocol Identifier (PPID)is 181\_322, Specimen type collected (SP\_TYPE) is whole blood , unique sequence number (PPI\_YOC\_UID) is 1 and collection year (YR\_OF\_COLL )is 2011, label would be GC\_181\_322\_WB1\_2011 |
| **Labels for specimens collected not as per CP definition** | User should be able to provide the specimen labels. |
| **Labels for the specimens collected for event point T0.0; Blood Draw** | GC\_181\_322\_WB1\_2011,GC\_181\_322\_PL2\_2011,GC\_181\_322\_PL3\_2011,GC\_181\_322\_PL4\_2011,  GC\_181\_322\_PL5\_2011, GC\_181\_322\_PL6\_2011, GC\_181\_322\_WB7\_2011, GC\_181\_322\_SE8\_2011, GC\_181\_322\_SE9\_2011….. |
| **Labels for the specimens collected for event point T5.0; Post Blood Draw** | GC\_181\_322\_WB22\_2011,GC\_181\_322\_WB23\_2011,GC\_181\_322\_WB24\_2011 |

Verify the .cmd files generated at JBOSS-HOME (Print server)/bin/print/printer. The .cmd file should show details as per the configured print.xlsx. The specimen labels in the .cmd files should be as per the table above.

8 Empty Label edit boxes should be displayed; User should be able to enter specimen labels.

9 A message should be displayed as “Specimens created successfully”.

10 Empty Label edit boxes should be displayed; User should be able to enter specimen labels.

11 A message should be displayed as “Specimens created successfully”.

12 System should auto-generate specimen labels, labels generated should be PSPECIMEN\_LABEL\_1, PSPECIMEN\_LABEL\_2.

13 A message should be displayed as “Aliquots created successfully”.

14 Empty Label edit boxes should be displayed; User should be able to enter specimen labels.

15 A message should be displayed as “Derivatives created successfully”.