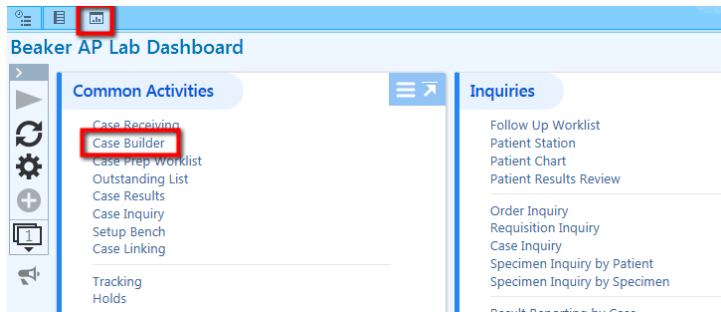# Gyn Cyto Beaker AP Guide:

Gynocology Specimens:

Create and Accession a Case in Case Builder:

1. To create a case, you need to enter **Case Builder**. Click on the **Case Builder** link on the Dashboard.
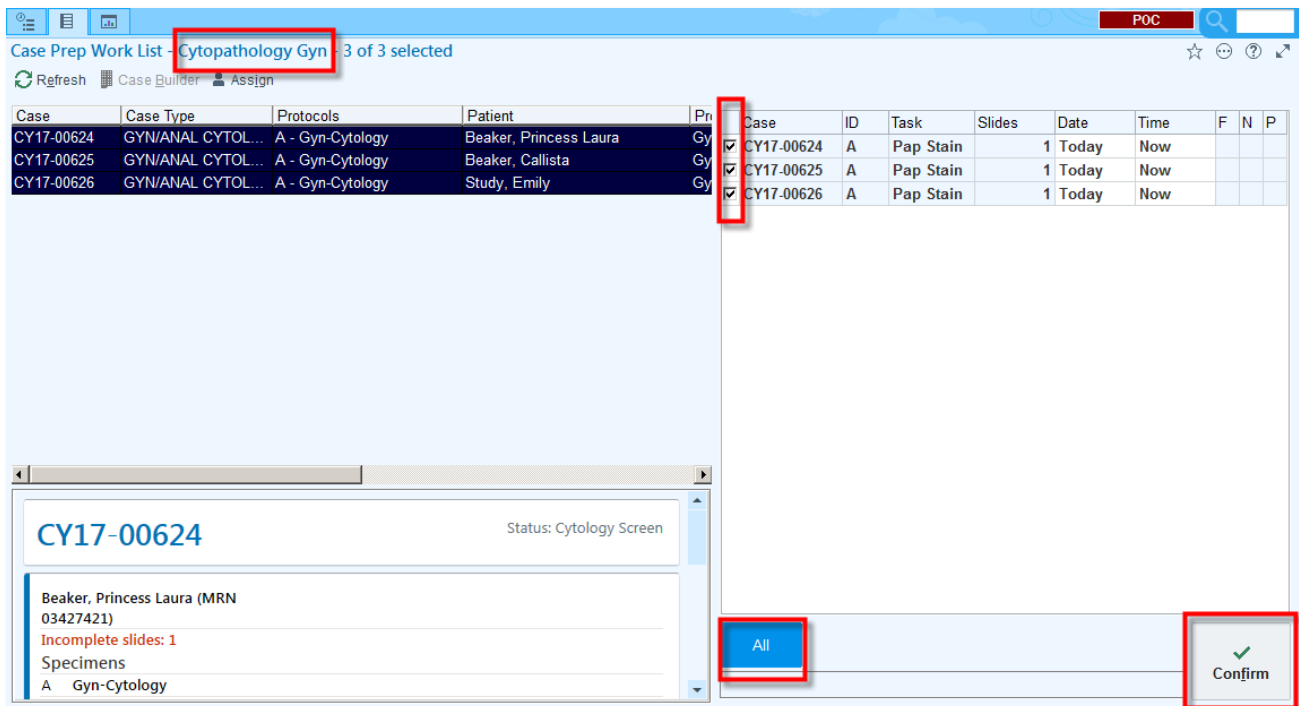
2. Scan in the specimen using the barcode reader or type the specimen ID# manually. Click the **Accept** button. If this specimen does not have a case assigned previously, it will start a new case.

3. Once you are in **Case Builder**, make sure that the **Protocol** is "**Gyn-Cytology**" and the **Task** is a Pap Stain. **Collection Date**, **Collection Time** and **Collector** should already be filled out.
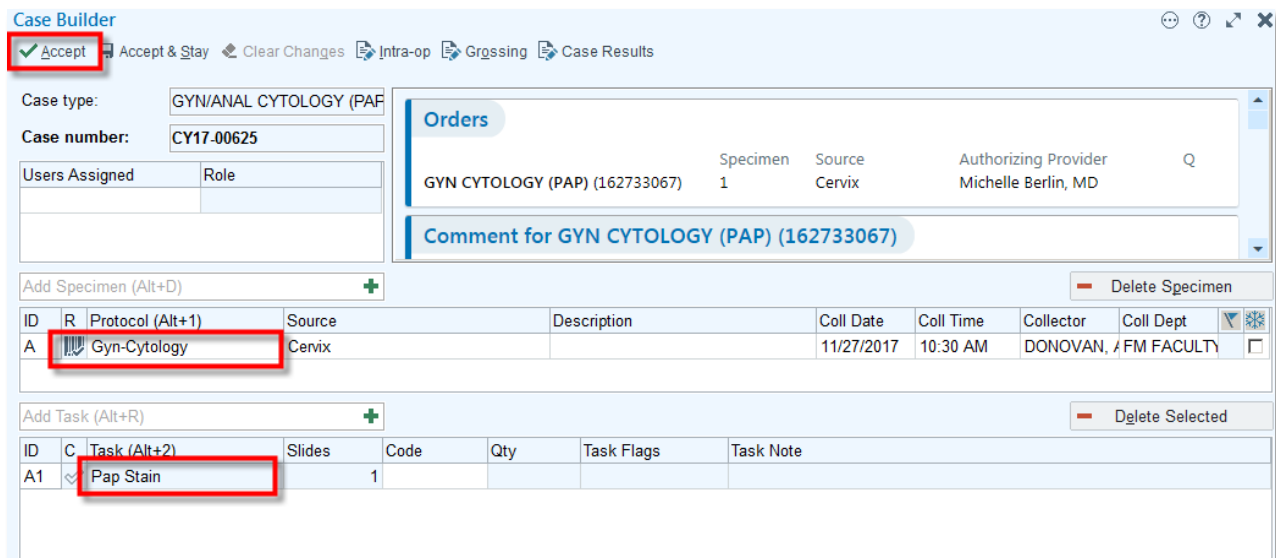
4. When you are done, click ✔ **Accept** to accession the case and close the **Case Builder** activity.

Confirm Tasks in Case Prep Work List:

1. Click the 🗐 tab to open the **Case Prep Work List**. You can also find a link to it from your Beaker AP Lab Dashboard.

2. Make sure you are viewing the **Cytopathology Gyn** view. To change your view, click on the 😊 **Actions** button and choose 🛠 **Views** and pick the view you want. You can use the column headers for "Case Status" to sort and filter the list.

3. Select the cases you want to confirm on the left side of the window. You can hold down the CTRL key to select multiple cases. The tasks for all the selected cases appear on the right.

4. Click the **All** button to confirm all of the tasks for the selected cases. The current date and time appear by default. If necessary, update the completion date and time to reflect the actual time a task was completed.

5. Click ✔ **Confirm**. The slide labels print and the selected cases will drop off the work list.
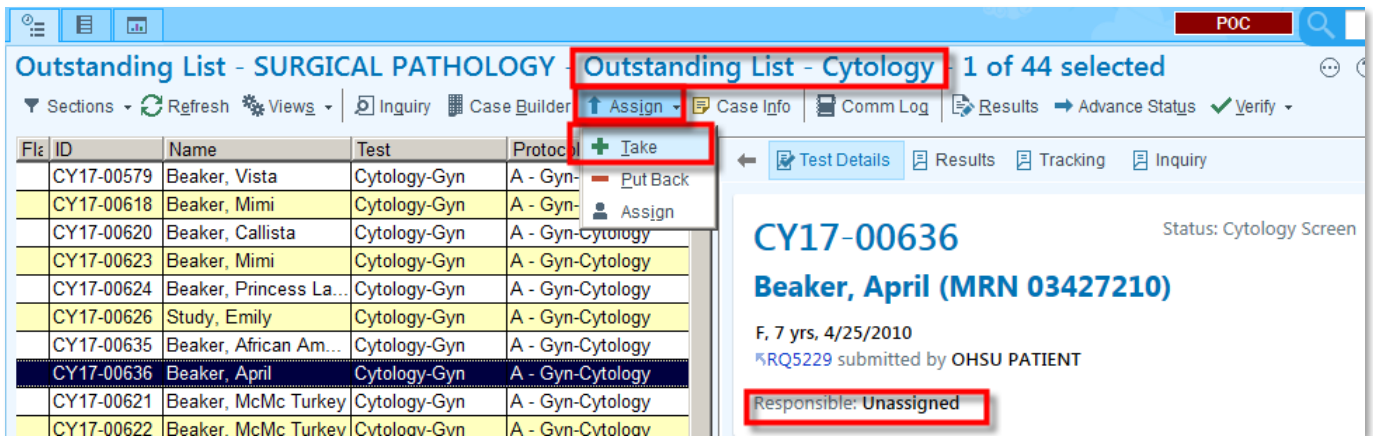
Cytotech – Assign Cases to Yourself before Resulting

1. **Before you can result cases in Case Results, you NEED to assign the case to yourself.** The best way to select cases is the **Outstanding List**.

2. Go to the **Outstanding List** by clicking on the first tab ⌐☰ of your startup activities or clicking the **Outstanding List** link from your Dashboard.

3. Make sure you are viewing the **Outstanding List-Cytology** view. To change your view, click on the ✤ **Views** and selecting a view from the list.

4. Select the cases from the **Outstanding List** and click the arrow next to ⬆ **Assign**, and select ✚ **Take**.

   a. To assign responsibility to another cytotech, click 👤 **Assign** and enter the person's name in the **User** field.

Resulting a Case:

1. Cases that need to be resulted or reviewed before signout appear on the **Outstanding List**. To enter results for a case, double-click the case in the **Outstanding List**.

   a. You can get to the **Outstanding List** by clicking on the ⏱ of your startup activities or clicking the **Outstanding List** link from your Dashboard.

   b. Make sure you are viewing the **Outstanding List-Cytology** view. To change your view, click on the ✳ **Views** and select a view from the list. The cases that are abnormal should be assigned to you.
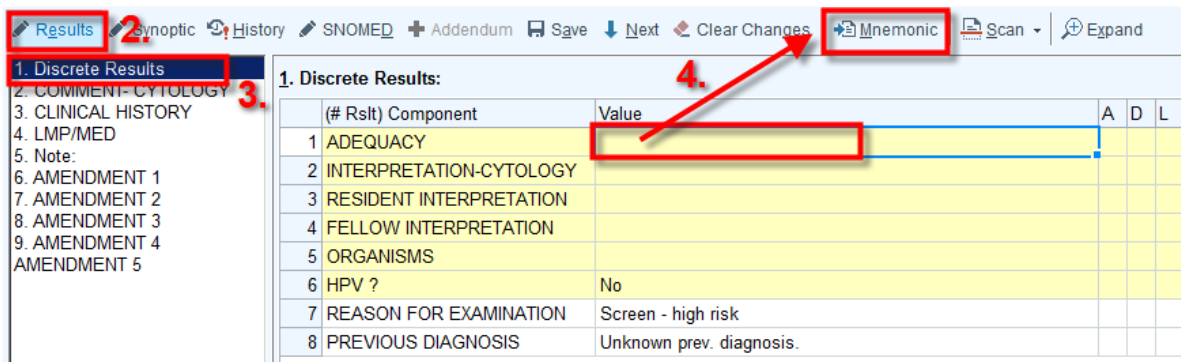
ℹ Switch to another work list by clicking ✳ **Views** and selecting a view from the list.

ℹ Click **CTRL+F** to search the Outstanding List for a test or patient.

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2. To enter cytology results, click on the **Results** button on the middle toolbar.

3. Click on the **1. Discrete Results** component on the left side of the screen. The result fields for this component come up on the right side.

4. Click in the **Value** field for the **ADEQUACY** row. Click on the **Mnemonic** button. (Powerpath called these macros.) It will bring up the following window. Click on the **magnifying glass** icon.

5. Choose the appropriate result and press the **Accept** button. Choosing one of these options will pull in results for the Adequacy and Interpretation-Cytology fields.

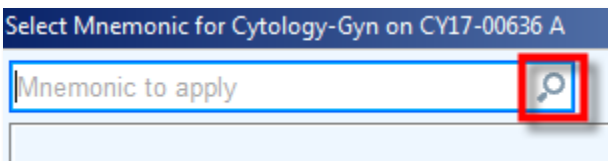| Mnemonic Name	Mnemonic ID
AGUS TZ PRESENT	737
ASCH TZ ABSENT	738
ASCH TZ PRESENT	701
ASCUS TZ ABSENT	727
ASCUS TZ PRESENT	726
GYN CYTOLOGY NOTE	748
HSIL TZ ABSENT	731
HSIL TZ PRESENT	730
LAB GYN CYTOLOGY CASE SEEN BY	862
LSIL TZ ABSENT	729
LSIL TZ PRESENT	728
NIL ATROPHIC	725
NIL TZ ABSENT	724
NIL TZ PRESENT	723
UNSAT ACELLULAR	733
UNSAT NO DX	734

6. Note that some of the mnemonics will have a **Comment** associated with the **Interpretation-Cytology** row. If a comment exists, the Comment icon is filled. Hovering over the icon will tell you what the comment says. By clicking on that icon, you can change the comment text.

1. Discrete Results:

(# Rslt) Component	Value	A	D	L	R	Units	Ref. Range	Method	C
1 ADEQUACY	Satisfactory for evaluation. Transfor								
2 INTERPRETATION-CYTOLOGY	Negative for Intraepithelial Lesion or								
3 RESIDENT INTERPRETATION									
4 FELLOW INTERPRETATION									
5 ORGANISMS									
6 HPV ?	No								
7 REASON FOR EXAMINATION	Screen - high risk								
8 PREVIOUS DIAGNOSIS	Unknown prev. diagnosis.								

> **!** If you change mnemonics, the old comment in the Interpretation-Cytology is not deleted! Click on the Comment icon and delete the comment text from the first mnemonic you used.

7. You can also add information to the Organisms field either by clicking on that field and pressing F5 or clicking the magnifying glass icon. A Organisms values window will appear, click on the first row and click the magnifying glass. Choose from one of these options. If you need to add another choice, click on the second row and click on the magnifying glass icon to add another option to the list.

| Title	Number
Fungal organisms morphologically consistent with Candida species.	1
Shift in flora suggestive of bacterial vaginosis.	2
Cellular changes associated with Herpes simplex virus.	3
Bacteria morphologically consistent with Actinomyces spp.	4
Trichomonas vaginalis	5

8. When you are finished resulting the case, click the **Save** button.

9. If it is a normal pap smear, then you can click the **Verify** button to verify the results and release the result to the patient chart. This will bring you to the Verification window which will force you to scroll through the case for review. When you get to the bottom, the **Final Verify** button will be active and you can click on that button to verify the case.

Sending a Normal Pap for Pathologist Review:

Sometimes you may need to send a normal pap for pathologist review.
Click on ⊙ **Actions** and select **Advance Status.**

1. Click on the magnifying glass on the **New Status** line **(1)**
2. Choose **Cytopathologist Review (2)** and **Click Accept (3)**
3. Scroll to the bottom of the screen and click **Advance Status (4)**

NOTE: If **Cytology Rescreen** is picked in error, the case must be reviewed by another cytotechnologist. This is the only way to advance the case to **Cytopathologist Review**.
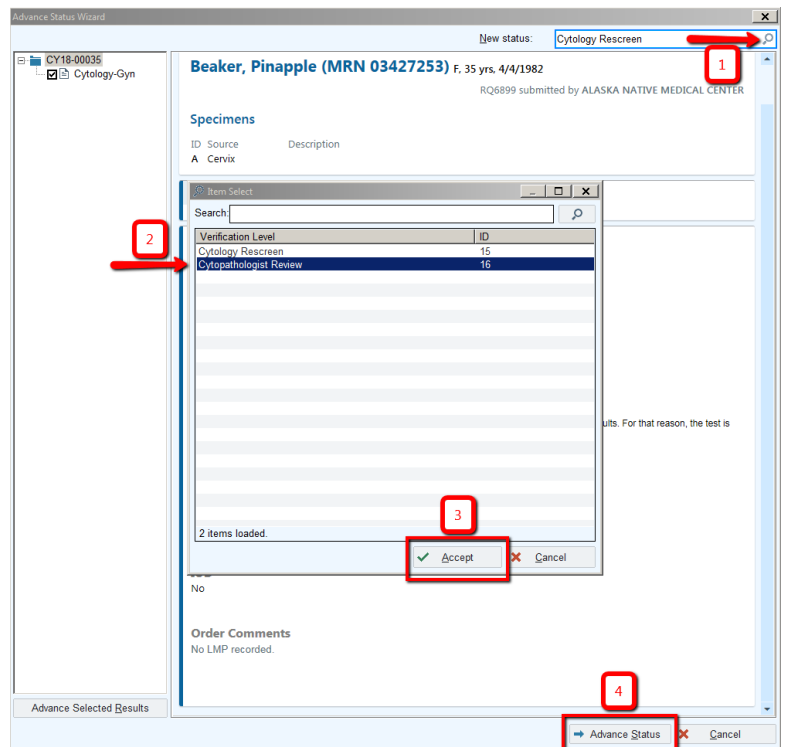

Rescreens:

10. Beaker is set to choose 10% of normal case results for rescreens by another cytotech. These cases will return to the Outstanding List with the case status of **Rescreen**. Another cytotech should go to **Case Builder** and add themselves to the list of **Assigned Users**. They should read the slides and enter results as outlined above.

Reassigning Abnormal Results:

11. If this is not a normal pap smear, an exclamation point will signify an abnormal result. When you click the **Save** button, the case will automatically change status to **Cytopathologist Review**. An abnormal test result will reflex a HPV test.

12. Click the ⬆ **Assign** button and choose the pathologist's name for the **User** field and Staff Pathologist for the **Role** field.

    a. If there is resident and/or a fellow who will be working on the case, then click on the ⬆ **Assign button** multiple times and choose a resident and/or fellow to be assigned. If there is no resident or fellow on the case, the Staff Pathologist assignment is all you need to do.
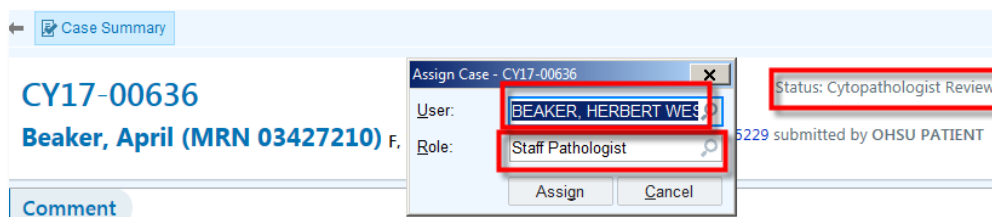
Sending Out Specimens:

A HPV label will print at the accessioner's area. The specimens are labeled and the specimens need to be added to a packing list in Beaker. Samples can either be added to the packing list by scanning the barcode labeled specimens into the created packing list or using the **Sendout Bench** to see all the samples that are waiting to be sent out and adding them from that list

Creating a Packing List:

1. Click on the **Packing List Editor** link on your Dashboard.
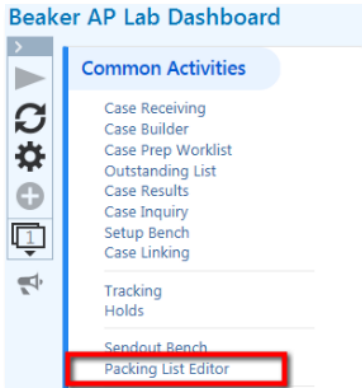

	NOTE: The first time you run it, it may ask what **Available Settings** view you would like to pick. Choose **Packing List Creation[2759704]** and check off the **My Default Report check box** in the top right corner. Click **Accept** Button.)

2. The following **Packing List Lookup** window will appear. Choose the ⊙ **Create** option and make sure the **List Type** field is OHSU INTER-LAB TRANSFER PACKING LIST. Click the ✔ **Accept** button.
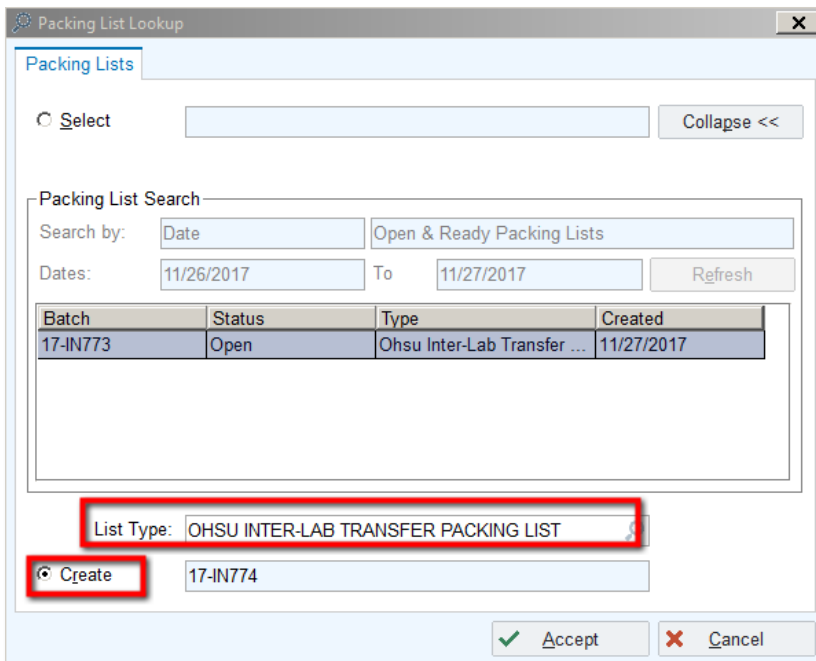
3. The **Packing List Editor** activity will open. Choose a destination in the **Destination** field. In this case, you would choose **Knight Diagnostic Lab**.
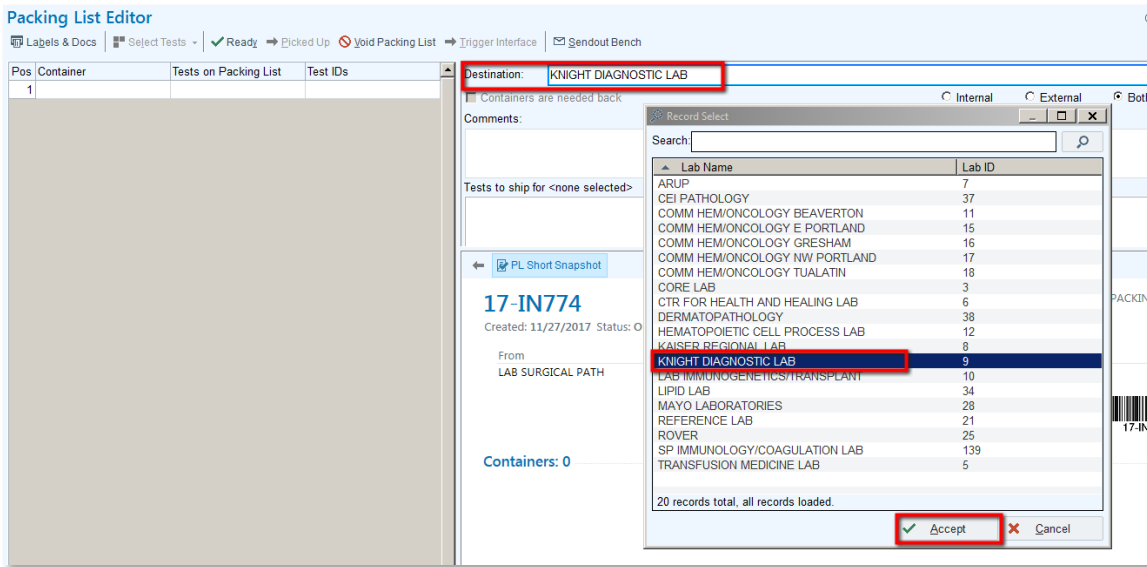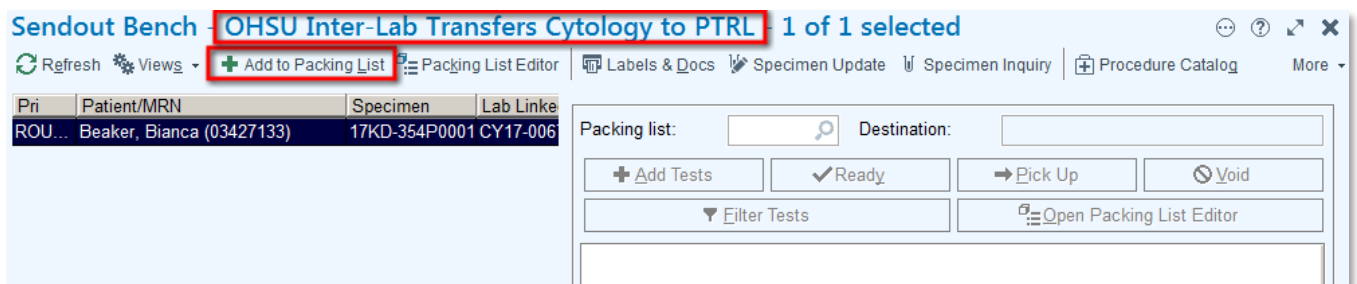

Adding Specimens to the Packing List:

4. The Packing List is now created, you can add specimens by either scanning them directly into the Packing List Editor right now or using the **Sendout Bench** list (Make note of the Packing List ID).

   a. Scan your specimen barcodes or enter the Specimen ID#'s in the **Container** field (be sure to include the **–A** of the ID). Once they are entered, the specimen information should populate the left side of the window.

   b. To use the **Sendout Bench**, click on the **Sendout Bench** link from the Beaker AP Lab Dashboard.

> **(i)** **NOTE:** The first time you run the Sendout Bench, it may ask what **Available Settings** view you would like to pick. Choose **OHSU Inter-Lab Transfers Cytology to PTRL [5230894]** and check off the **My Default Report check box** in the top right corner. Click **Accept** Button.)
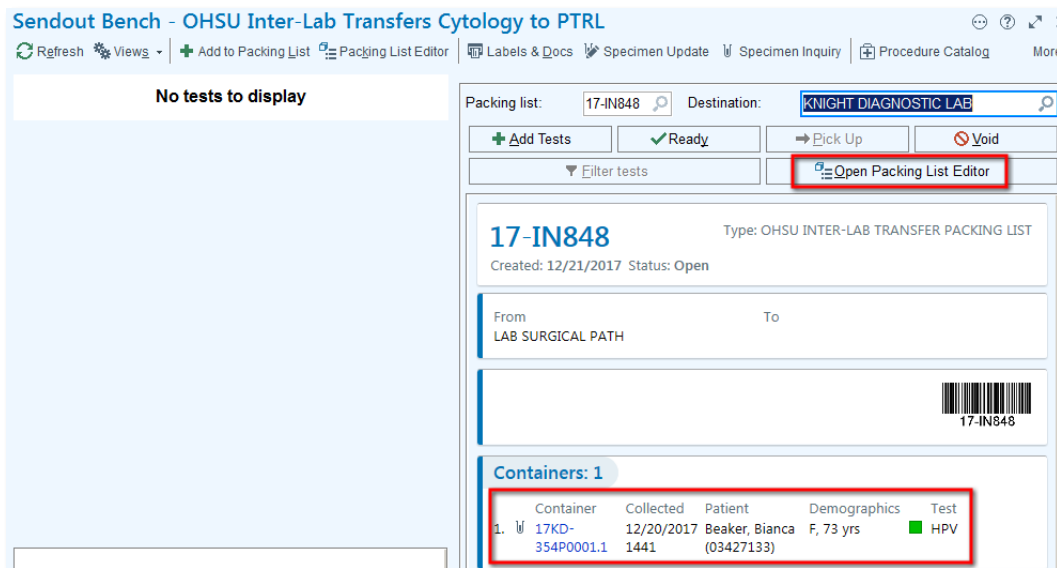

   i. Select the specimens on the left you want to add to a packing list and click on the **Add to Packing List** button.

   ii. Choose the packing list you created earlier and click the **Accept** button.
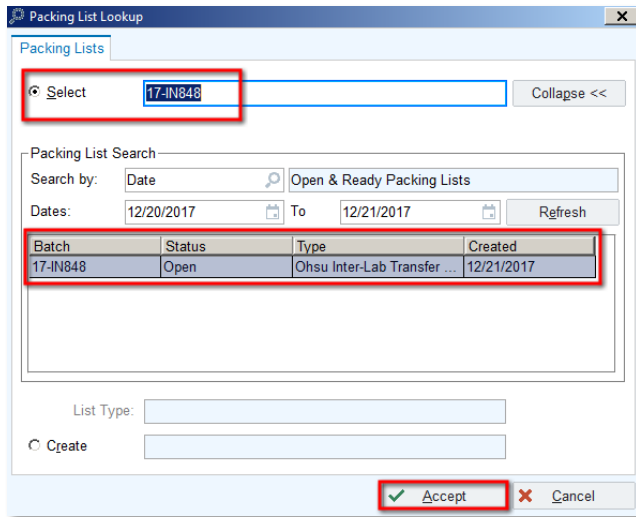
iii. The selected tests will be removed from the Sendout Bench list, and added to the Packing List. Click the **Open Packing List Editor** button to continue.

Closing the Packing List to Send Specimens:

5. When you are finished adding specimens, you can click the ✔ **Ready** button. When you click Ready, the following things happen.

    a. The list is locked, so that no more containers can be added to it. It is not a permanent lock. You can click the ✔ **Unready** button to unlock it.

    b. The ➡ **Picked Up** button is enabled.

c. Then the packing list **Status** changes from **Open** to **Ready**.
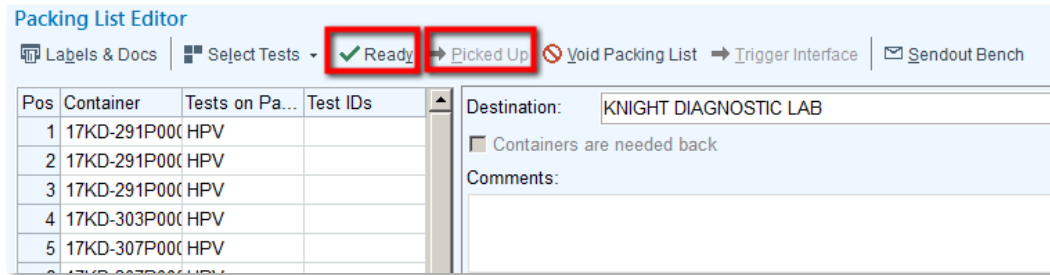
6. When someone comes to pick up the samples, go into the Sendout Bench or Packing List Editor and open the current packing list. Click the ➡ **Picked Up** button. At this point, the list is closed and you can no longer edit it. The packing list **Status** changes from **Ready** to **In Transit**.