NCI Patient-Derived Models Repository (PDMR) Database User Help Guide

Effective Date: 6/3/2021

Please check for revision status of the SOP at

https://pdmr.cancer.gov/sops/

PDMR NCI Patient-Derived Models Repository
An NCI Precision Oncology Initiative℠ Resource

New samples are always being added to the Repository, even for existing patient IDs, so check the database often. For example, a PDC culture may develop after the PDX has been made public or a secondary tissue collection site might develop a PDX after one from a primary site has been developed.

Visit the PDMR database: https://pdmdb.cancer.gov/web/apex/f?p=101:1

Visit the PDMR website for more info: https://pdmr.cancer.gov/

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1.0 WHAT INFORMATION CAN I FIND IN THE PDMR DATABASE?

Patient → Patient Specimen(s) → Sample(s) → Distribution Lot

1.1 The PDMR database is structured in a nested fashion and includes information such as:

1.2 **Patient**: Patient ID, diagnosis, Grade/Stage and STR profiles of all distribution lots for the patient. The limited medical information tab (non PII) will include treatment history medical history (e.g., genetic screening, prior disease history), self-reported race/ethnicity, and inferred ancestry from sequencing data.

1.3 **Specimen**(s) - collected specimen tissue from the patient: specimen id, site of tumor collection, origin (primary vs metastatic), collection date, human pathogen status. Specimen notes. PDX Growth Curves of consecutive passages. Consensus WES of Genomic Variants. PDX mouse strain and implant site.

- Note: Not all specimens give rise to multiple types of distributable samples.

1.4 **Sample**(s) – representative information for generated models: type (PDX, PDC, PDOrg, CAF, originator), Pathology Data including H&E images and tumor/stromal content, individual NGS files (WES, RNASeq), Cancer Gene Panel mutational status.

1.5 **Distribution Lots**: type of material available (PDX, PDC, PDOrg, CAF), maximum passage of distributed material, Distribution Lot Name (for requests), and human pathogen status

2.0 HOW ARE THE MODELS CLASSIFIED?

2.1 Models are classified **first by Disease Body Location**

2.1.1 Link to NCI definitions: https://www.cancer.gov/types/by-body-location

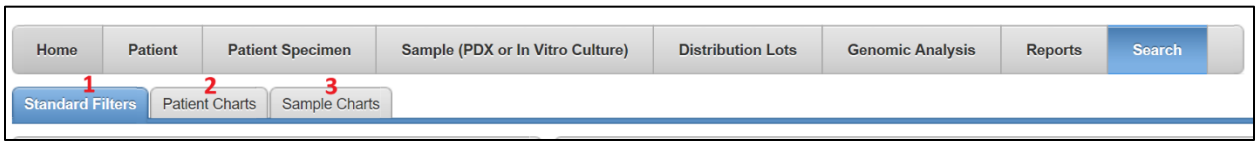
2.2 **Then by** CTEP Simplified Disease Classification (SDC) corresponding to the patient diagnosis

2.2.1 Link to the CTEP list: https://ctep.cancer.gov/protocolDevelopment/codes_values.htm#disease

2.2.2 This is a modified list of MedDRA disease codes for cancer provided by NCI's Cancer Therapy Evaluation Program (CTEP).

3.0 HOW TO SERACH

3.1 Option 1: SEARCH Tab



3.1.1 Standard Filters – apply filters across multiple categories

3.1.2 Patient Charts – Search with interactive pie chart by the following categories: (See SOP Section 4.1 - Example 1)

- Disease Body Location
- Tissue Type – e.g., biopsy, resection
- Therapy Regimen
- Gene – Known gene involved in cancer, can apply “AND Logic” or “OR Logic” to filter

3.1.3 Sample Charts – Search with interactive pie chart by sample types

- PDX
- PDC
- CAF
- PDOrg – organoids

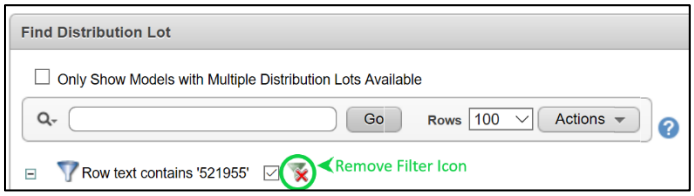
3.1.4 This mode/method of searching will retrieve all specimen records with associated search term and/or filters. You must still open the individual specimen pages to access available distribution models.

3.2 Option 2: DISTRIBUTION LOTS Tab

3.2.1 Search by Keyword/term in Distribution Lot sub-tabs.

- **Patient-Derived Xenograft Samples** only sub-tab
- **In Vitro Cultures** only sub-tab
- **All Distributed Material** sub-tab. Can check the 'Only Show Models with Multiple Distribution Lots Available' to display, for instance, models that have both a PDX and a PDC model.

3.2.2 Type in the search term and click Go. To remove filter, click on the "Remove Filter Icon."

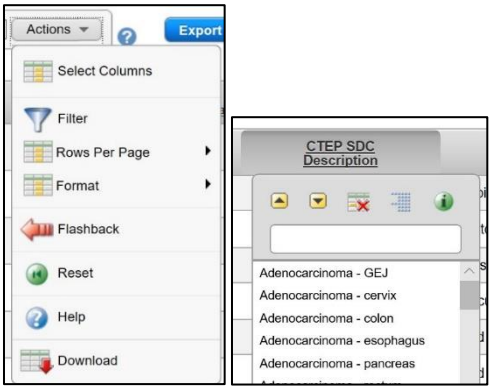


3.3 Advanced Users

3.3.1 Users can modify search outputs (customize report) by using the **Actions** pull-down menu.

- Select Column: used to modify (add, remove, reorder) data columns displayed.
- Filter: advanced filter (see online help)
- Format:
- Chart: displays the report data as a chart

3.3.2 Users can also easily search within, sort, or hide a column by clicking on individual column headings

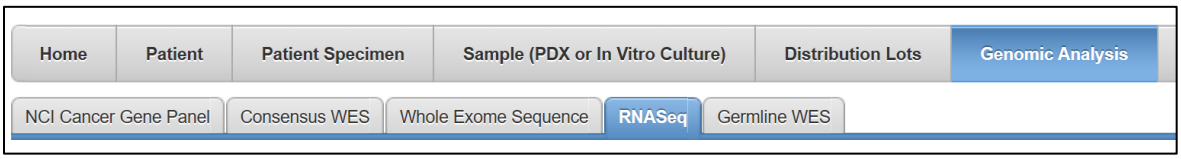


3.4 Search for Next-generation sequencing (NGS) Data

IMPORTANT: NGS files from multiple passages of PDXs are available. These datasets are representative of the models and may not exactly match the distributable PDX fragment.

3.4.1 NGS Data are available for ALL available patient and distribution material free of charge for originator/patient (where there was sufficient material), PDXs, PDOrg, PDC, and germline samples (PBMC or CAF origin; where there was sufficient material).

3.4.2 Users can easily search for NGS Data (RNASeq, WES, Gene mutations, etc) under the GENOMIC ANALYSIS tab and then choosing the sub-tab for the data type they wish to query.



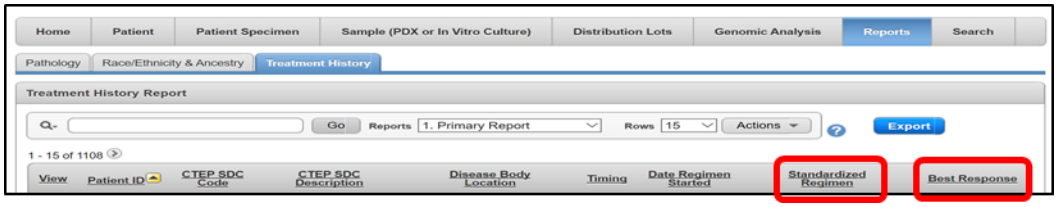
- RNASeq: Gene expression for individual samples (.fastq and .tpm).
- Whole Exome Sequence (WES): Sequence files for individual samples (.fastq and .vcf)
- Consensus WES: reports variants present in 100% of the sequenced PDX samples
- Cancer Gene Panel: Detailed list of variants in genes implicated in cancer

3.4.3 When using the search bar within the GENOMIC ANALYSIS sub-tab, you must first select the search criteria from the magnifying glass drop down list. Alternatively, use the column filter feature.

3.5 Search by Patient Treatment History

3.5.1 Users can easily search by treatment history under the REPORTS tab and then choosing the TREATMENT HISTORY sub-tab.

- Search for treatment – listed by generic drug name – or filter using the Standard Regimen column.
- Treatment response (if available) is reported under the BEST RESPONSE column.



4.0 STEP-BY-STEP GUIDE

4.1 EXAMPLE 1: Find Melanoma samples

4.1.1 Navigate to the **Patient Charts** sub-tab under Search tab.

4.1.2 Choose to plot data by Disease Body Location.

4.1.3 Melanoma affects the skin so we will click on the "Skin" pie are (Left image below).

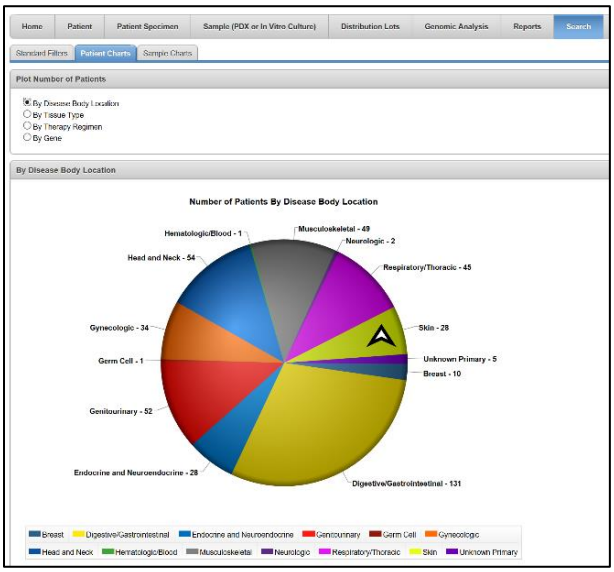
4.1.4 This brings us to a pie chart of different types of Skin cancer.

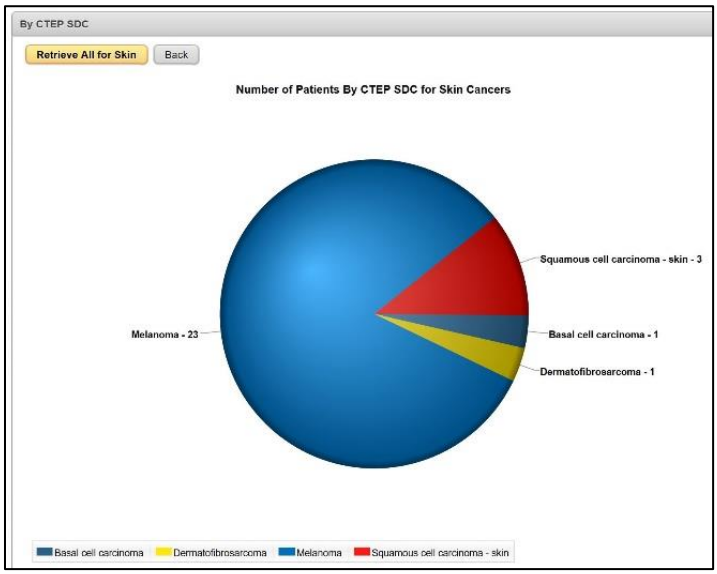
4.1.5 Click on the Melanoma pie area to retrieve records for only melanoma samples (Right image below).

4.1.6 Click the "Retrieve All for Skin" button at the top of the page to retrieve records for all skin cancer samples.

4.1.7 Click the "Back" button to return to the previous pie chart.

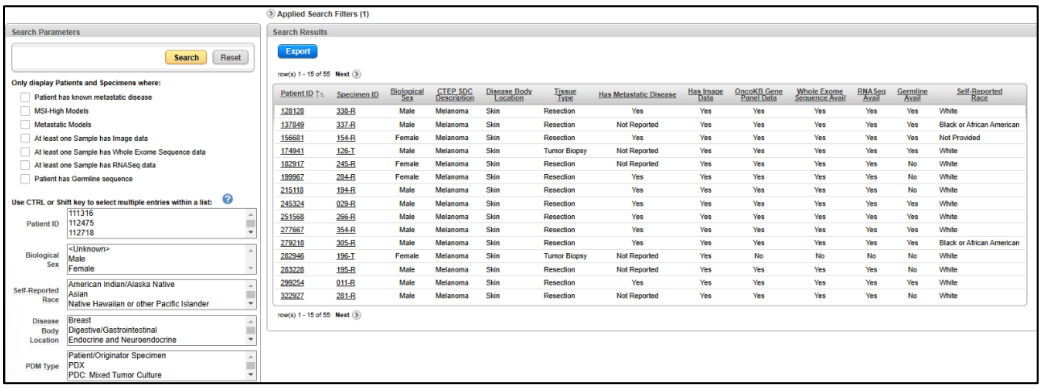
4.1.8 Since we are looking for melanoma samples, we will click on the Melanoma pie area





4.1.9 This brings us to a list of all available melanoma specimens. Click the Specimen ID link to take you to the Specimen record where you can find the type of Material Available for Distribution.

4.1.9.1 Apply additional filters using the Search Parameters on the Left



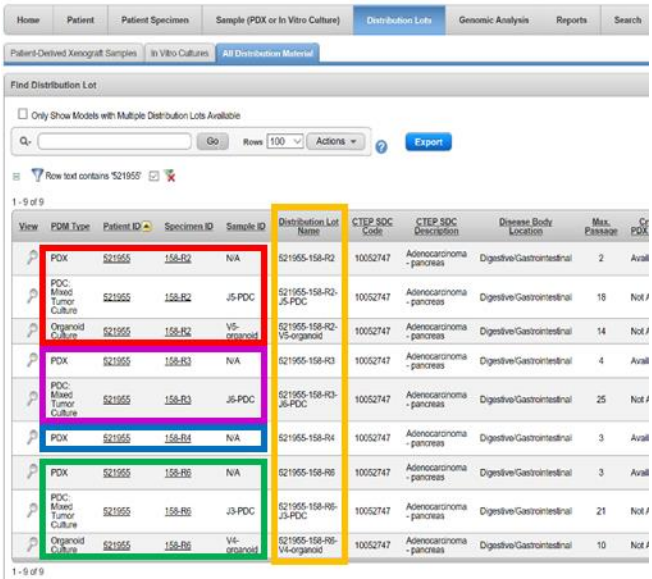
4.2 EXAMPLE 2: Navigating Patient Samples

4.2.1 Search for patient ID 521955 in the **All Distribution Material** sub-tab of the Distribution Lots tab.

4.2.1.1 This patient has 9 models for distribution. Each model has a unique Distribution Lot Name (used for requests).

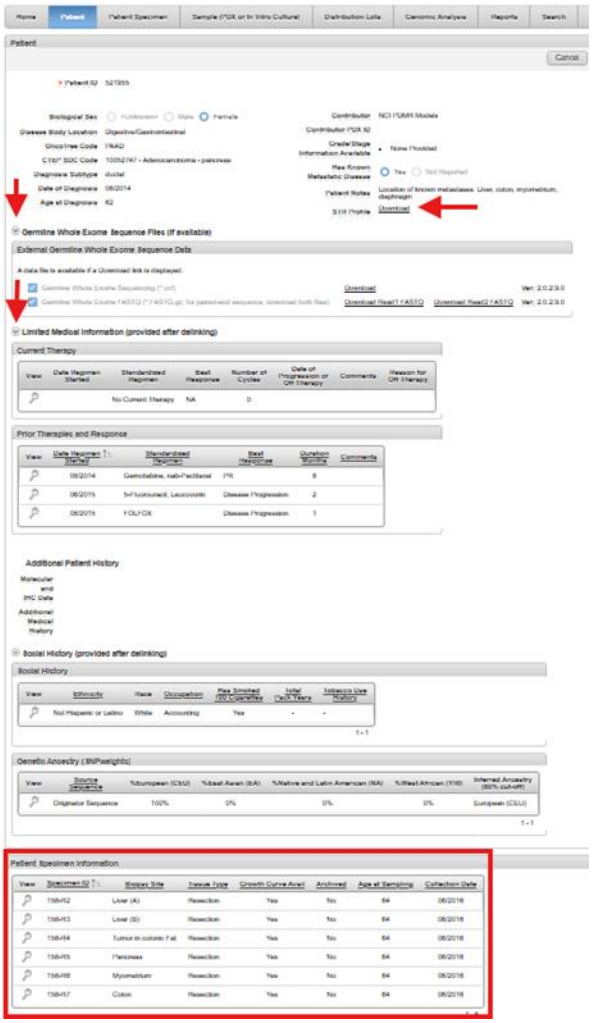
4.2.1.2 Four (4) SPECIMENS gave rise to the 9 models (e.g., specimen 158-R2 gave rise to 3 models – a PDX, PDC, and PDOrg model)

4.2.1.3 If we search for this patient ID under the 'Patient-Derived Xenograft Samples' or "in Vitro Cultures' sub-tab, only the specific sample types for the model would be retrieved.



4.2.2 If we click on the Patient ID 521955 (on any sample), the patient record is retrieved:

- Patient Info
- STR profile: Download link
- Germline WES (not available for this patient)
- Limited Medical Information: this patient did have therapy prior to tissue collection
- Social History: Self-reported Race and Ethnicity, Inferred Genetic Ancestry, Smoking History
- Patient Specimen Information: this patient had 4 collection sites with distributable material
    - Liver – site A
    - Liver – site B
    - Myometrium
    - Colonic Fat



4.2.3 Next, we will view the information for specimen 521955-158-R6. Clicking on the magnifier icon brings you to the specimen record.

4.2.3.1 Specimen Info: tissue origin, pathogen status, Mouse strain and implant site

4.2.3.2 Representative Growth Curve Data (see SOP Step 4.2.4)

4.2.3.3 Consensus WES data for Genomic Variants: is available

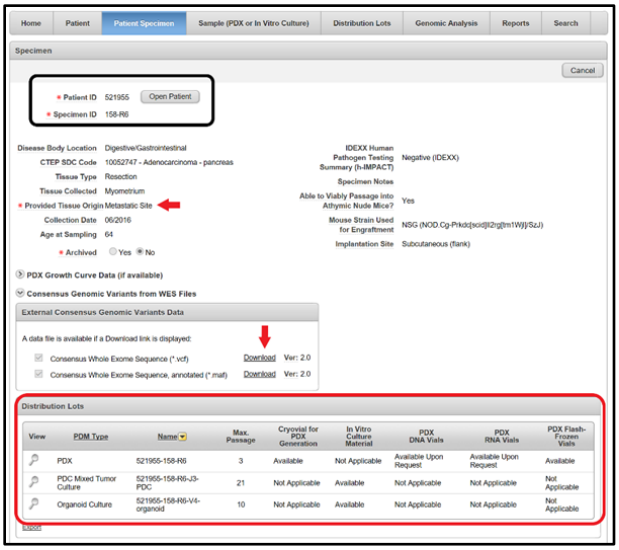
4.2.3.4 Distribution Lots: Material(s) available for request submission

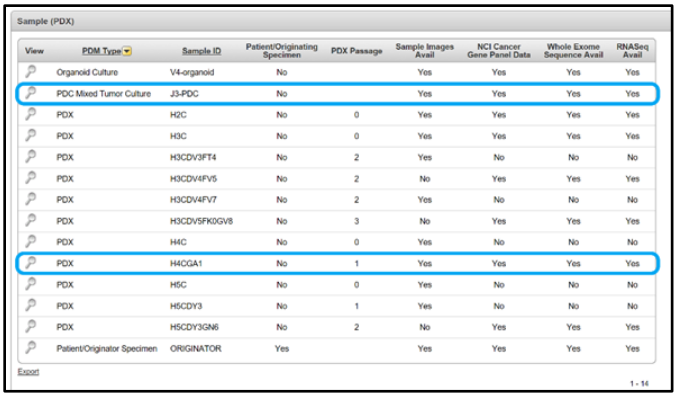
4.2.3.5 Links to data for representative sample generated from specimen 521955-158-R6:

- 11 PDXs from passage 0-3
- 1 PDC
- 1 PDOrg
- Originator

4.2.3.6 Navigate back to the patient info using the “Open Patient” button

IMPORTANT: Not every SPECIMEN will generate multiple types of material for distribution



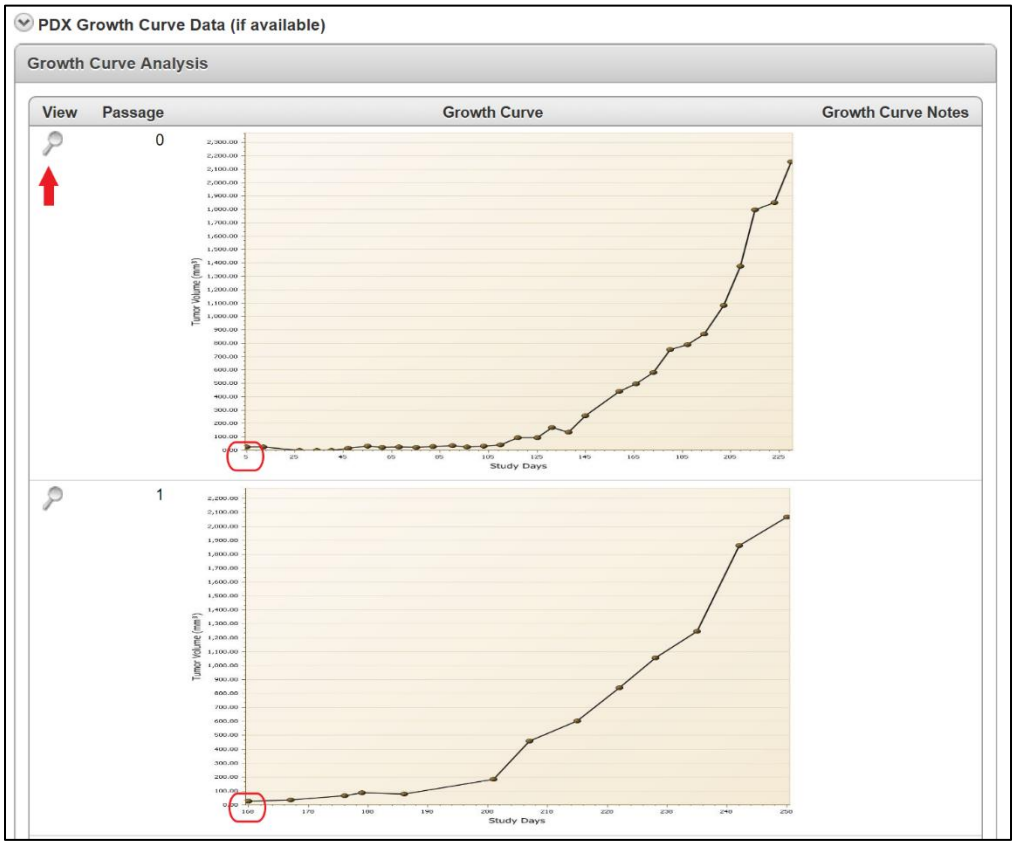


4.2.4 To view the representative Growth Curve Data for PDXs, expand the section

4.2.4.1 PDX Growth Curve Data: shows JPEGS of the Growth Curves for consecutive passages. These are provided to give researchers an idea of growth rate for models.

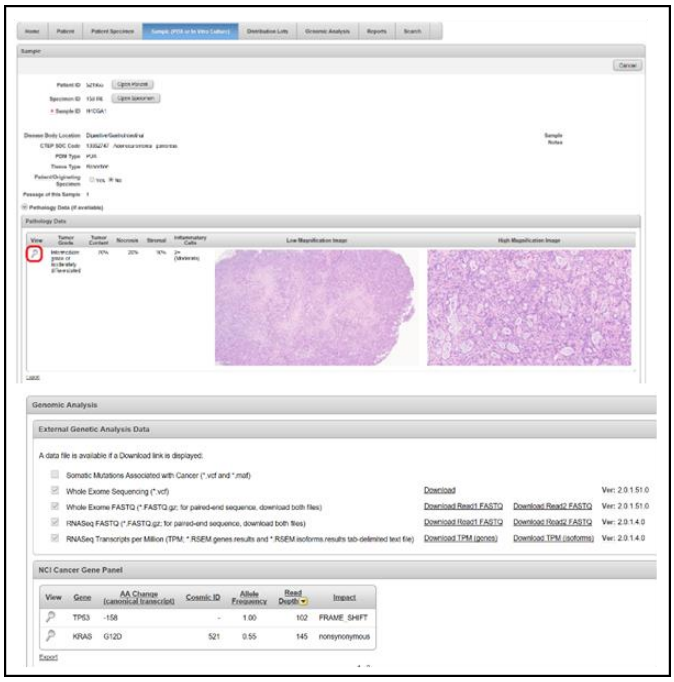
4.2.4.2 NOTE: Pay attention to the Study Days (x-axis) as it refers to the day of implant from passage 0

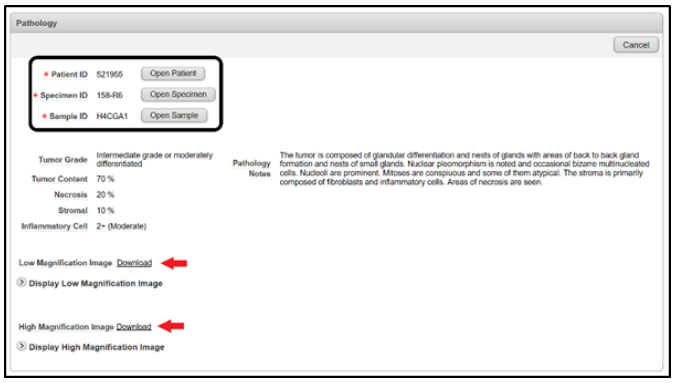
- In this example, passage 1 implant began at ~Day 170. Tumor volume reached 1000mg at ~ Day 230. So, passage 1 took 60 days to reach 1000mg.
- Passage 0 took 200 days to reach 1000mg.



4.2.5 Next, we will view the PDX sample information (blue box in SOP Step 4.2.3.6). Clicking on the magnifier icon will bring you to the Sample record.

- Sample Info
- WES and RNASeq: avaialble, download
- NCI Cancer Gene Panel: mutations
- Specimen notes (if available)
- Pathology Data: click on the magnifier for more info
    - Pathology Notes
    - Download images
    - Click on “Open Sample” to return to sample page





4.2.6 Finally, we will view the PDC sample (blue box in SOP Step 4.2.3.6). Clicking on the magnifier icon will bring you to the sample record.

- In vitro Culture Conditions and Characteristics
  - Derivation
  - Required Media
  - Proliferation rate
  - Sub-culture recommendations
- Images: expand for more info
- WES and RNASeq Data: available, download
- NCI Cancer Gene Panel: mutations detected
- Navigate back to Specimen or Patient page using the nested buttons