Working in the Primary Tumor Archive Team at Novartis Institute for Biomedical Research

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Introduction

I worked at Novartis Institute for Biomedical Research (NIBR) in the Oncology-Pharmacology Department from July through December 2014. I was a member of the Primary Tumor Archive Team as well as participating in running a clinical trial (MCT). My main duties within the team were culturing of a tumor bank, genomics work concerning DNA and RNA extraction, testing, and coordination of these projects with outside teams, and sample and data management.

Primary Team and MCT

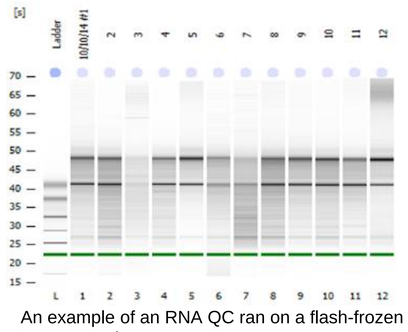
I assisted with general work as well as my own personal projects in the teams I assisted during my co-op.
For the primary team, this included the upkeep according to protocol and IACUC standards of a colony of tumor-bearing mice from 11 different cancer indications for a bank of viably stored tumors for later implantation or testing. This included passaging and collecting samples from tumors, marking which models could be transferred to the trial, body weight and tumor size monitoring, lineage verification, and storage of samples.
For the MCT, this included the expanding of lineages for enrollment into the trial, verification of lineages, and assisting with identifying and locating models and samples for reimplantation and enrollment.

Acknowledgments

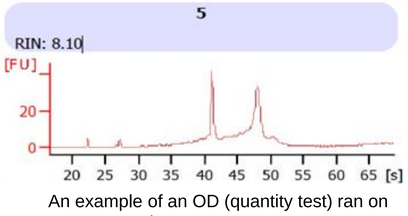
I would like to thank Northeastern and Dave Merry for the assistance in finding a coop, and the Primary Team at NIBR:
Hui Gao, Guizhi Yang, Jack Green, Alice Loo, Colleen Kowal, Julie Goldovitz, Kate Cosgrove, Thomas Hofstetter, and J. Allen

Genomics

I worked largely on the genomics team within my team, assisting in identifying unverified models (testing for species purity and consistency within a lineage) and extracting DNA and/or RNA for testing either in-house or for sending to outside teams for further or different testing. I extracted DNA and/or RNA from approximately 130 tumor fragments and ran quality and quantity checks on the extractions.
Related to this was the identification, extraction, collection, and organization of over 200 samples of hundreds of models to send of previously validated models for pathology analysis. This assured the quality and purity of our lines and helped ensure the safety of the people working with the tumors that they were not exposed to further pathogens.



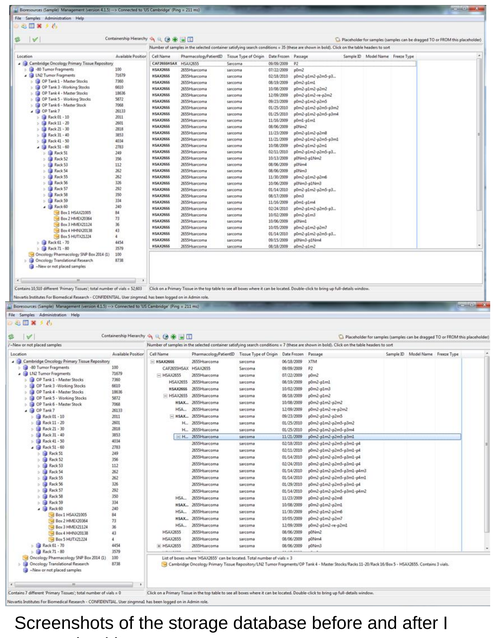
An example of an RNA QC ran on a flash-frozen tumor sample



An example of an OD (quantity test) ran on a DNA sample

Sample Curation and Management

I ran and/or assisted with much of the sample management within the team and coordinated the storage of all of our untreated samples. I also assisted with transferring all of the team's historical samples from unorganized storage into computerized storage.
For the historical samples, I transferred over 2,000 previously-extracted samples of DNA or RNA from tubes with readable labels to computer-readable barcoded tubes. This ensured more efficient use of our storage space, more efficient sample removal, and higher sample integrity.
For the teams' untreated samples, I first had to catuch up with the over-1,000 vial backlog of samples, leading to the storage of over 2,000 viably frozen samples collected throughout the entirety of 2014. This enabled the storage of surplus samples for established models. This required a reorganization of some of the team's freezer storage space, which consisted of consolidating historical samples and creating new spaces for newly established models.

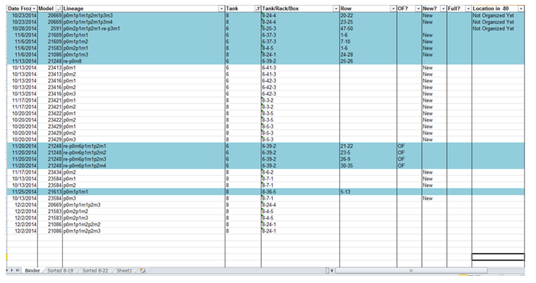


Screenshots of the storage database before and after I reorganized it

Data Curation and Management

Alongside my sample management, I worked to streamline the team's data management due to the high volume of samples we worked with, largely working with reorganizing and/or digitizing our databases. I also ran a few data curation projects concerning pure data or samples that had been sent to our team.
For the transferring of historical samples, I created a digitized log of historical, current, and MCT RNA and DNA samples that had or would be stored in the computerized freezer.

I transferred the data for the backlog from a paper binder to an easily searchable and editable digital notebook that listed where collected samples were supposed to go. This enabled faster location of samples for MCT, reimplantation, lineage verification, and general full knowledge of what and where our samples were. I was also able to assign new storage space to recently established models.



A screenshot of the digitized notebook I created for catching up with the backlog and efficient storage of future samples

Coordinated to this storage was the reorginization of a preexisting database to create collapsible family trees that listed the exact locations of every vial in our storage tanks. This reorganization also allowed for noting any linage breaks or other inconsistencies.

Lastly, the team was sent over 90 boxes of historical and recent samples from a recently closed site that needed updated and accurate digital box maps for them to be transferred into storage. I worked with other team members to log the contents of the boxes, and digitized the maps in a format that could be uploaded to the company's online database.