

Current Rules for Sample Receipt

Staging Lab Update and Information

In concert with the SAIC-Frederick Extraction Lab, the Core Genotyping Facility has piloted several projects using the new “Staging Laboratory” approach. While the studies to date have been limited, we have seen success such that we feel confident in beginning to utilize the new method. Below is a summary of the process we have developed into a Staging Laboratory workflow.

In the new process, all samples for a study are quantified (via approved CGF protocols). Equal amounts of material are then “staged” in 96-well format for any bio-assay work. By staging a set DNA amount for all samples in the study, the constant replenishment of samples and piece-meal genotyping will be eliminated. Any samples that do not have enough DNA, or have DNA that is at a concentration unsuitable for a particular platform, can be adjusted prior to its arrival at the CGF.

The assigned project manager and the quality control division will work with the investigators to ensure that the appropriate subjects meet the criteria for genotyping. In this way, the CGF receives only the amount of material that it needs to complete the genotyping project in a pre-plated fashion specifically designed for the platform to be used. This allows the project to begin quickly without additional sample handling and without leftover DNA that requires storage. In this way, all samples will be received at the CGF at one time and assay work can be done quickly and generate the most informative data set possible. We also believe this will reduce the actual amounts of DNA consumed.

Beginning with the DCEG Rare Cancer iSelect genotyping project, we have begun implementing the Staging Lab process.

As a rule of thumb, if your study does not currently have samples that exist at the CGF it should be handled through the new Staging Lab pipeline. However, if you are adding/replacing samples for a study at the CGF it is likely you should continue to ship samples to us. Before sending samples to any location, please check with CGF to be directed to the appropriate laboratory facility for sample handling.

For Samples Going to the Staging Lab:

1. All genotyping projects must be approved by the DCEG Genotyping Review Committee (GRC) prior to samples arriving at the CGF. For information and instructions please see: <http://intranet.dceg.cancer.gov/committees/genotyping-review-committee/genotyping-review-committee/>
2. All projects need to have a submitted and approved yellow task outlining the scope of work before any work can begin. This includes information about the number of samples, their location, if extractions are needed, and the amount of material to be staged.
3. All samples coming to the Staging Lab must be transferred to the CSP DNA Repository within BSI. Samples must have a BSI ID assigned to them prior to their transfer to the Lab. Samples may arrive in the form of plates, robot tubes (cluster racks) or vials (volumes from

0.5mL through 15mL). If the samples are in another format (filter paper, gels, etc.) the investigator/study manager must call prior to initiating the sample transfer.

4. The Staging Lab will coordinate the actual sample delivery with the appropriate repository transferring the samples.
5. Samples should be shipped to the following location:

Until the completion of the new DNA Extraction/Staging Laboratory is complete (at which time the address will be updated) all shipments should be delivered to:

DNA Extraction Laboratory
1050 Boyles Street
Bldg 560, Rm 11-23
Frederick, MD 21702

6. As part of our commitment to quality control, we are also requiring a basic phenotype file for all samples received for genotyping. This data will be used by project managers, QC/QA and analysts to appropriately check data for inconsistencies prior to reporting. The laboratory staff continues to be blinded to all of this information. Please see the CGF website for instructions and the file template: http://cgf.nci.nih.gov/docs/CGF_Phenotype_Manifest.xls.