

New Strategies

The CGF is piloting some activities that we hope will smooth specimen flow from the DCEG repositories and extraction facilities to the CGF. Utilizing this new workflow, we are confident we can both simplify and increase efficiency of the process. We are running a test project in which all samples are quantified and plated/prepared (“staged”) in the appropriate format for the genotyping work to be done prior to arriving at CGF’s door. 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 CGF receives just the amount that it needs to complete the genotyping project. 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 possible. We also believe this will reduce the actual amounts of DNA needed.

Updates on the pilot project will be available soon.

Current Rules for Sample Receipt

1. The investigator must notify the CGF at CGFreceipt@mail.nih.gov that samples are being sent and what genotyping activities are intended. This should be done before the repository begins to pull the samples for shipment.
 - Samples will be accepted only if the CGF has received approval from the DCEG Genotyping Review Committee (GRC) to conduct a genotyping project for these samples.
 - An estimated cost will be sent via email to the PI and branch head for the total cost of handling and genotyping of the project requested.
2. The investigator will notify the repository to ship the samples according to the guidelines set by the CGF:
 - Minimum volume and concentrations for samples according to the proposed work:
 - Uniplex assays (TaqMan / MGB Eclipse): minimum volume of 50µl of DNA concentration greater than 30 µg/ml concentration*.
 - Array assays (Illumina): minimum volume of 60µl of DNA concentration greater than 75 µg/ml concentration*.
 - Samples received for WGA: minimum volume of 10µl of DNA concentration greater than 5 µg/ml concentration.

***Any sample containing below 50µl of volume will be increased to 50µl during initial sample handling, unless the sample is being directed to WGA. After volume calibration, if the concentration of the sample is less than 25 ng/µl based on NanoDrop optical density readings, the sample will be removed from the sample handling process.**

- Samples should be shipped in cryovials in freezer boxes to the CGF, if samples are already at the repository in another format, exceptions may be made at the discretion of CGF management.
 - CGF laboratory staff will perform a pre-processing procedure on all samples; any samples that do not meet the above criteria may be returned to the repository. Samples currently at the CGF that do not meet these criteria will not be added to a current genotyping project, and the investigator will be notified that replacement vials will be needed in order for the CGF to genotype those samples at a later date. The CGF will not combine DNA from different vials; each sample vial will be handled independently.
 - Samples that do not meet the CGF handling requirements may be subject to a higher sample handling fee.
 - All shipments should be delivered to:
Core Genotyping Facility, ATC
8717 Grovemont Circle, Room 149
Gaithersburg, MD 20877-4117
3. The repository must notify the CGF 24 hours prior to sample shipment and email the sample manifest to the project coordinator of the CGF. The electronic manifest should include: study, vial ID, sample volume, and concentration for all samples. The manifest should list samples reflective of the ordering within the freezer boxes. The CGF will respond to the repository that they will accept the shipment, or if problems exist such that the shipment will not be accepted (e.g. DCEG GRC Approval not granted for the samples). There should be no shipment of samples without prior CGF approval of the shipment. Shipments may be returned if approval has not been given or the shipment is received in an unacceptable format.
 4. The shipment should be accompanied by a hard copy manifest for confirmation.
 5. As part of CGF's commitment to quality control, we also require a basic phenotype file for all samples received for genotyping. This data will be used by QC/QA and analysts to appropriately check data for inconsistencies prior to any genotyping work. The laboratory staff continues to be blinded to all of this information. Please see **Investigator Documents**, at http://cgf.nci.nih.gov/investigator_menu.cfm, then select **Data Input Requirements for Sample Submission** for the instructions and template for this file.