

Current Rules for Sample Receipt

For Samples Coming to the CGF:

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. If samples are to be shipped, the investigator must notify the CGF at CGFreceipt@mail.nih.gov. This should be done before the repository begins to pull the samples for shipment.
 - Samples will only be accepted if a fully actionable genotyping request is in place to complete once the samples have been received and handled.
 - 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.
3. After the genotyping project is in place at the CGF, the investigator will notify the repository to ship the samples needed according to the guidelines set by the CGF:
 - 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.
 - The following are the minimum acceptable volumes and concentrations for samples according to the proposed work. **Please note:** These requirements are for samples to enter the sample handling pipeline. Specific material requirements for the genotyping platform(s) requested are available on the CGF website (<http://cgf.nci.nih.gov/>).
 - Genotyping assays: Minimum volume of 50µl* of DNA at a concentration greater than 25 ng/µl via NanoDrop micro-volume OD.
 - Samples received for WGA: minimum volume of 10µl of DNA at a concentration greater than 5 ng/µl via NanoDrop micro-volume OD. This is the requirement for any sample for which WGA is to be done at the CGF, which includes samples submitted for WGA only or samples that fail above requirements (if WGA is requested by the investigator).

***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.**

- 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.
 - The CGF will also cease combining DNA from different vials; each sample vial received 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
8717 Grovemont Circle
Advanced Technology Center, Room 149
Gaithersburg, MD 20877-4117
4. 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 of 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. fully actionable genotyping request not currently in place 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.
 5. The shipment should be accompanied by a hard copy manifest for confirmation.
 6. As part of CGF's commitment to quality control, we are also requiring 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 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.