

Applying for CGF Genotyping Services

-- *Descriptive information*

1. Enter the **title** of the genotyping request, for example:
[PLCO Prostate Cancer Study: Obesity/Insulin Signaling Pathway](#)
2. Enter the **Investigator name**, first name then last name, for example:
[Jane Doe](#)
3. Enter the investigator's **Email address**, for example:
jane.doe@abcd.edu
4. Enter the investigator's **Street address**, up to three lines.
5. Enter the **Application source**, either NCI grantee or NIH external.
6. If you are an NCI grantee, enter the **NCI grant number**.
7. Enter the **Project Goals**. This is a textual description of the scientific goals of the project.
8. Enter the **Number of Samples** – the number of DNA samples to be genotyped.
9. Enter the **Date extracted**.
10. Describe the **Biomaterial source** from which the DNA was extracted.
11. Describe the **Extraction/quantification method** used to extract and quantify/aliquot the DNA.
12. Enter the **Sample amount** - total ug available to CGF for genotyping.
13. Enter the **Sample concentration**.
14. Enter the **Date available** – the date samples would be available to ship to the CGF.

-- SNPs to be genotyped

When submitting a genotyping request to the CGF, you need to know the status of the SNP assays. Each SNP must be placed in the correct section of the form, depending on its sequencing and genotype assay status. Each SNP is identified by its **SNP500Cancer ID**, comprised of the gene symbol followed by a sequence number, e.g. BRCA1-03.

To check the status of a SNP, go to the SNP500Cancer web site, <http://snp500cancer.nci.nih.gov>, or click the link on the task bar.

- To search for the SNP, enter its SNP500Cancer ID.
- On the SNP page, scroll down to the “Assays” section, and note the assays that have been validated.
- If there are no results, the SNP has not yet been sequenced.
- If there is an “Assays” section, but there are no genotyping platforms listed (Taqman, MGB Eclipse, Sequenom), the SNP does not yet have a valid genotyping assay.

You can also check the SNP Assay List at http://snp500cancer.nci.nih.gov/assay_list.cfm

Section 1: Genotyping assay work request

The SNPs in Section 1 must have at least one validated genotyping assay (Taqman, MGB Eclipse, or Sequenom). **Enter the SNP500Cancer IDs, one per line.**

Section 2: CGF assay development request

The SNPs in Section 2 must have validated sequencing but no valid genotyping assays. **Enter the SNP500Cancer IDs, one per line.**

Section 3a: Request for sequencing existing CGF SNPs

The SNPs in Section 3a must be in the SNP500Cancer database, but not yet sequenced. These SNPs will have a status of “No results yet” or “Sequencing in progress”. **Enter the SNP500Cancer IDs, one per line.**

Section 3b: Request for sequencing Genes or SNPs not in CGF pipeline

If you are interested in genes or SNPs that are not in the CGF pipeline, enter them as free text in Section 3b. You can also include SNPs with no variation in this section – enter the SNP ID, followed by a comment, for example:

BRCA2-07: we know this has no variation, but we want to see it genotyped in our population

-- Saving the genotyping request

1. To submit the application, click **Submit Application**
2. If a SNP was entered into the wrong section, you will get an error message. To correct the problem, follow the instructions.
3. To view assay development status for a SNP in Section 2 or Section 3a, click on the SNP.