Aug 02, 2025

🌐 SOP54v1_TGD_GenotypingSubmissionforCollaborators

DOI

dx.doi.org/10.17504/protocols.io.e6nvwk8jzvmk/v1

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Protocol status: Working
We use this protocol and it's working

Created: May 02, 2022

Last Modified: August 02, 2025

Protocol Integer ID: 61762

Keywords: sop54v1-tgd-genotypingsubmissionforcollaborator, collaborator sample, sample, protocol
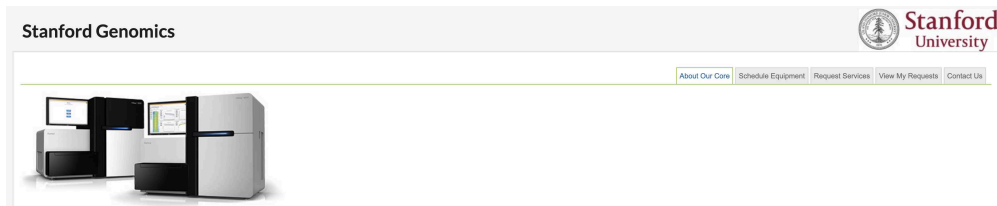
Abstract

This is the protocol to submit samples for genotyping for collaborator samples.

Before start

QC Template: 📗 Genotyping QC Template.xlsx

1   Go to Stanford ilabs: https://stanford.ilabsolutions.com/landing/7

2   Log in with your credentials, then select Core Facilities in the left hand side menu.

3   Select Stanford Genomics. Then select Request Services.

4   Select "**Whole Genome Genotyping Assay Service Request (Genotyping)"** in their list
         of services.

5

         Fill out the first part of the form like so:

6   Fill out the second part of the form like so:

6.1 In Project Title, write the correct batch number of this genotyping batch.
Upload the Genotyping QC file for the batch of samples you are submitting, in the "QC Results File" section. The template for this is here: **Genotyping QC Template.xlsx**
Fill out the sample information form - you can download an excel template and then reupload to make it easier.

7 In the payment section, fill out the PTA information. You will need to know the PTA breakdown and distribution for each sample type (each collaborator might require a different grant be used). Have that reflected here.

8 Click submit request to core.

9   Prepare your samples in a 96 well plate. Remember to indicate which sample went where in your QC spreadsheet, in plate layout.
Dilute samples to 50 ng/uL in 15 uL of elution buffer. If samples are very low in concentration (below 10 ng/uL), provide the entire sample in a tube to the Stanford Genomics core, and indicate that it needs speed vacuuming in the QC spreadsheet.