

Oct 01, 2024

SOP52v1_TGD_IIDP-HIGISampleProcessing

This protocol is a draft, published without a DOI.

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Protocol Citation: Varsha Rajesh 2024. SOP52v1_TGD_IIDP-HIGISampleProcessing. **protocols.io**

<https://protocols.io/view/sop52v1-tgd-iidp-higisampleprocessing-b4rhqv36>

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Protocol status: Working

We use this protocol and it's working

Created: February 06, 2022

Last Modified: October 01, 2024

Protocol Integer ID: 57865

Abstract

This workflow details the processing of acinar tissue obtained as part of the HIGI cohort (IIDP), by TGD Lab.



Receiving Samples

- 1 When acinar samples are received from the various isolation centers, match what is physically sent with sample info list sent with package and make sure all samples are accounted for. Take note of the condition of the samples.
- 2 Let isolation center know samples were received and in what condition.
- 3 Print QR barcodes for the acinar samples in this format and tape onto the tubes.

HIGI#ACIN (# being the next sequential number)
- 4 Store tubes in Yalow -80°C freezer in "IIDP - HIGI Acinar Samples" box.

Extracting DNA

- 5 Thaw acinar tubes on ice.
- 6 Use DNA extraction protocol for DNeasy Blood & Tissue Kit (<https://protocols.io/view/dna-extraction-qiagen-dneasy-blood-amp-tissue-kit-bjngkmbw>).

QC

- 7 After extraction, measure the concentration by nanodrop, taking account of 260/280 and 260/230 values as well. 260/280 value should be close to 1.8 and 260/230 should be around 1.8-2.0.
- 8 Take a portion of the sample to measure concentration by Qubit. Protocol can be found here: <https://protocols.io/view/qubit-dsdna-assays-bnstmeen>. For genotyping, Qubit concentration should be above 50 ng/uL and total DNA should be above 750 ng.
- 9 Create QR codes that include sample name in this format: HIGI#DNA. Label should also include nanodrop concentration and QC info.

Genotyping

- 10 Record sample info, nanodrop QC and qubit information in genotyping QC spreadsheet, which will be sent to the SFGF core whenever the entire batch is ready (follow this protocol: <https://www.protocols.io/edit/sop54v1-tgd-genotypingsubmissionforcollaborators-b8jaruie>).



- 11 As of 2023-12-01, samples were sent to be genotyped on Illumina's Infinium Omni Exome 2.5 arrays.