Sample preparation guidelines

Table of Contents:

Clinical Genomics

Sample Preparation Guidelines

- WGS:
  - 2ug of gDNA in 50ul 10mM Tris (8.0) or water.
  - DNA concentration MUST be determined by Qubit
  - DQN/DIN value greater than 7.5. If the Genome Center must perform the DQN/DIN analysis, please provide 2.1ug in 55ul. (The cost for this DQN analysis in 10CHF per sample)
  - Please provide 260/280 and 260/230 ratios. If the Genome Center must perform the ratio analysis, please provide 2.1 ug in 55ul. (The cost for this analysis in 10CHF per sample.)
- WES:
  - 500ng of gDNA in 50ul 10mM Tris (8.0) or water
  - DNA concentration MUST be determined by Qubit.
  - DQN/DIN value greater than 8. If the Genome Center must perform the DQN/DIN analysis, please provide 600ng in 60ul. (The cost for this DQN analysis in 10CHF per sample)
  - Please provide 260/280 and 260/230 ratios. If the Genome Center must perform the ratio analysis, please provide 600ng in 60ul. (The cost for this analysis in 10CHF per sample.)
- RNA-seq:
  - 500ng of total RNA in 50ul water or 10mM Tris (8.0)
  - RNA concentration MUST be determined by Qubit
  - RQN/RIN value greater than 7. If the Genome Center must perform this analysis, please provide 600ng in 60ul. (The cost for this analysis in 10CHF per sample)
  - Please provide 260/280 and 260/230 ratios. If the Genome Center must perform this analysis, please provide 600ng in 60ul. (The cost for this analysis in 10CHF per sample)

    Provide the nucleic acid samples in a 96-well plate – DO NOT PROVIDE THE gDNAs IN INDIVIDUAL TUBES. Load the plate by column – A1, B1, C1, D1…..H1, A2, B2, C2 etc., not by row.

    When naming samples, **use ONLY upper- and lower-case English letters from "a" to "z", numbers from 0 to 9 and the special character "_" (underscore)**. If you put other characters, you will be asked to reformat your sample names.

- Proteotyping:
  - Please provide frozen cell pellets of ~1e6 cells (or alternatively ~100 µg

protein) stored at -80 °C in 1.5 ml Eppendorf tubes. Prior to freezing, cells pellets **have to be washed at least 2-3times with PBS** to reduce contaminating proteins. The washing protocol might have to be adjusted according to sample preparation and expected sample contaminations.

Sample Quality

- See above for genomic samples
- For protein samples make sure that your cells were not apoptotic before freezing and did not go through freezing/thawing cycle

Sample Submission

- RNA samples should be shipped to the Genome Center on dry ice; gDNA samples are sequencing libraries should be shipped on -20 °C freezer packs.
- Pellets for protein extraction should be sent on dry ice.

Clinical Proteomics

Sample types and requirements

- Cells
    - **Frozen cell pellets (dry ice), washed 1x with PBS, collected by scraping**
    - Sample processing using the Preomics Kit (1-100 ug material),
        - **Minimal input requirement: 300 000 cells**
        - **one shot samples: 10 000 cells**
        - **pellet of 1x 6-well**

- Native Tissue
    - **Transfer frozen (dry ice)**
    - Sample processing: tissue homogenization (mixer, douncer), sonication in vial tweeter
    - Sample processing using the Preomics Kit (1-100 ug material),
        - **input requirement: 2 mm biopsy punch (lengths ca. 0.5-1 cm); biopsy slice (10-20 μm thickness of a tissue block, 1cmx1-2 cm)**
        - **for statistical data evaluation three punches/slices (biological replicates) are required**

- Formalin-fixed Tissue (FFPE)
    - **Transfer RT**
    - Sample processing: de-waxing using a series of Xylene/Heptane and Ethanol; tissue homogenization (mixer, douncer), sonication in vial tweeter
    - Sample processing using the Preomics Kit (1-100 ug material), protocol for FFPE tissue
        - **input requirement: 1 mm biopsy punch (lengths ca. 0.5-1 cm) or biopsy slice (10-20μm thickness of a tissue block, 1cm x 1.5 cm);~weight input material 0.5-1 mg**

Clinical Metabolomics

Sample types

- **Biofluids: serum, plasma, urine, CSF, saliva**
  - Requirements: 25 microL needed, 100 microL preferred
  - Sample preparation: done by us
  - Examples: DOI: 10.2337/db19-0131call_made
  - Example coverage: Plasma (ZIP, 1.6 MB)vertical_align_bottom
  -
- **Solid samples: biopsies, fecal samples**
  - Requirements: 1 mg needed, 50 mg preferred
  - Sample preparation: to be discussed
  - Examples: DOI: 10.1126/science.aad0189call_made DOI: 10.1186/s12864-017-3547- 3call_made
  - Example coverage: Muscle biopsy (ZIP, 1.4 MB)vertical_align_bottom
- **In vitro cell cultures, spheroids, organoids**
  - Requirements: 100'000 cells ok, more is advantageous for rare compounds
  - Sample preparation: to be discussed
  - Examples: DOI: 10.1016/j.cell.2016.09.031call_made DOI: 10.1016/j.ymben.2016.12.009call_made DOI: 10.1111/febs.14852call_made DOI: 10.1016/j.molcel.2015.06.017call_made
  - Example coverage: Cancer cell line (ZIP, 1.1 MB)vertical_align_bottom
- **Medium**
  - Requirements: 10 microL needed, 25 microL preferred)
  - Sample preparation: done by us
- **Dried blood spots**

Clinical Lipidomics

Sample types

- **Plasma**
  - Preferably EDTA but also other anti-coagulants (e.g., Citrate or Heparin) can be used
  - Requirements: 20 µl needed, 100 µl preferred
  - Sample preparation: done by us
- **Serum**
  - Requirements: 20 µl needed, 100 µl preferred
  - Sample preparation: done by us
- **Cerebrospinal fluid**
  - Requirements: 50 µl needed
  - Sample preparation: done by us
- **Tissues and biopsies**
  - Requirements: 10 mg wet weight needed
  - Sample preparation: done by us
- **Tissue cultures:**
  - Requirements: 50,000 cells needed, 1 Mio preferred.
  - Sample preparation: done by us
- **Lower organisms (bacteria, yeasts)**
  - Requirements: 1 OD*mL (frozen pellet) preferred
  - Sample preparation: done by us
- ***C. elegans, Drosophila, Zebrafish, ...***
  - Contact us