# Shipment Protocol Sequencing Services
# MedSeq V4

It is important to follow the criteria summarized below when sending DNA samples for MedSeq V4 Sequencing services to the Genomics Core Facility of Erasmus MC.

## DNA Purity, Format and Quality Guidelines

1. DNA concentrations (ng/uL) should be quantified using fluorescence (Quantafluor, Qbit).

   Using an optical based method (e.g. nanodrop), usually gives an overestimated concentration.

2. Minimum DNA sample volume to hand in is 10 uL.

3. The sample concentration should be >0.35 ng/uL, but >5.78 ng/uL will give best results.

   If the DNA sample concentration is lower than 0.35 ng/uL we might still able to perform the library prep, but only at your request and at your own risk.

4. Hand in your samples undiluted. If diluting is required, we'll do the dilution.
   Leftover intake sample volume, will be returned at your request

5. Please make sure the DNA is free of salts, metal ions, and organic solvents.

6. Do not use Fenol/Chloroform or Trizol based isolation methods, or a speedvac; this typically causes issues during prep.

7. It's recommended to do the DNA isolation using a kit (e.g. Qiagen). This typically gives a good results.

8. DNA samples should be aspirated in 1.5 ml LoBind safelock tubes.

   Make sure the identifiers on the tubes are clearly readable.

   Large quantities of samples are also accepted in plates. If the samples are handed in in a plate make sure the correct samplename and samplewell are linked in the "Sample Information File" (see below)

   Note: If your study design is a case control design or a follow up study, the samples should be randomized over the plates to minimize batch effect. So please randomize your samples.

## Sample Information File (SIF)

We'd like to receive an Excel Sample Information File (SIF) containing the following information for each sample:

1. The prep method (“Medseq V4”)
2. Analysis type (e.g. “NextSeq2000 PE50”, see contract for details)
3. Tube ID or PlateWell ID (if using a plate)
4. Sample name
5. Expected concentration (ng/uL)
6. Volume of the sample (uL)
7. Type of start material: gDNA or cfDNA
8. Species
9. Mapping reference (example: human (GRCh38); Mouse (GRCm38)
10. Methylation type: CpG or Dcm

**Please save this file with your contract number and prepmethod in the filename!**
**(e.g. SIF_S-2023-79_MeDSeqV4.xlxs)**

**Important considerations for sample IDs**

For efficient processing of your samples, we recommend you to keep a few guidelines in mind concerning sample IDs. Most genetic software are unable to handle sample IDs including these features and will generate errors. Also tracking systems and Excel might recode sample IDs with these features. It is fixable post data-generation but this is error prone. When making your sample IDs please avoid the following:

- Special characters in sample IDs (e.g., 12.34 or 12,34 or 12_34 should be 1234)
- Spaces in sample IDs (e.g., 12 34 should be 1234)
- Number IDs starting with one or multiple ‘0’s (e.g., 01234 should be either 1234 or a01234)
- Duplicate IDs. If a sample has been run twice please add an addition to the IDs (e.g., 1234a and 1234b)

In general we advise to use a combination of numbers and letters, and avoid special characters, symbols and spaces.

**Sample Shipping Guidelines**

**(external shipments)**

1. Before sending samples, please contact our lab and send Sample Information File to: genomics-sequencing@erasmusmc.nl.
2. Make sure the tubes/plates are labeled with an Tube ID or Plate ID . Preferably use stickers.
3. Accompany the samples by the following information :
    - Contract number
    - Which samples should be present in the box
    - Research Centre / study name

4. DNA samples should be ***securely sealed, wrapped*** and send by overnight courier. Do not ship samples on a Thursday, Friday or Saturday. Only ship samples after our lab has agreed on the moment of shipping.
5. Ship to the following address (open 7.30-16.30 hr):

   Erasmus MC
   Genomics Core Facility
   Att: Xander den Dekker / Zeliha Ozgur / Zakia Azmani / Edwin Oole
   Room Ee 691
   Westzeedijk 353
   3015 AA Rotterdam
   The Netherlands
6. Please keep close contact with our lab at (see Contact information) when shipping the samples. Report exact time, date, shipment number etc. before sending the samples. We will notify you upon receiving the samples.

**(internal shipments)**

1. Before sending samples, please return a copy of your signed contract to get a project number.
2. Go to the website and log in using your account: https://biomics.erasmusmc.nl/wordpress/login/illumina-intake-2/
3. Select the corresponding project and fill in the required details of your samples.
4. After the sample registration, your samples are assigned to:
   - An Intake ID (I25-xxxx-xx)
   - A storage box position.
5. Bring your samples to Ee691; here you can find the printed labels, add the matching labels onto your samples.
6. Place the samples in the box (at the indicated positions) located in the “Intake” drawer of freezer 211.

**Contact information**

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For general questions regarding projects, please contact the contract- and project manager dr. Gaby van Dijk (g.m.vandijk@erasmusmc.nl or genomics@erasmusmc.nl).