TACG Azrieli
AACCC Technion
CTAT Genomics
GTTTT Center

Technion
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DNA-seq sample requirements

Note that the user is responsible for the results in case the samples submitted do not match the specifications below or do not meet the criteria of the chosen lab procedure.

- DNA should be submitted at the following concentration and volume-

Library prep	Concentration [ng/ul]	Volume [ul]
NEBNext DNA library prep	20	20
16S	0.5 or 5	20
Amplicon-seq	PCR reaction- no need to measure*	25
RRBS	50-80	20
Exome-seq	100	20
ChIP-seq	Input- 20 ; IP- 1-2	20

For samples outside the recommended concentration and/or volume, please contact us.
* Please indicate in the Submission Form if a sample has a **low concentration**.
* Please indicate in the Submission Form if there are **non-specific PCR products**.

- Concentration, 260/280 & 260/230 values should be determined using the NanoDrop. Measure DNA concentration with Qubit or NanoDrop. Please note that NanoDrop is reliable only if DNA concentration is >10 ng/µl (if lower – use Qubit).
  Pure DNA samples should be in the following range: 260/280 ≥ 1.8, 260/230 ≥ 2.0.
- DNA samples should be suspended in DDW or Tris buffer, with no EDTA.
- DNA samples should be submitted as follows:
  - in 1.7 ml Eppendorf tubes (<12 samples) or in PCR strip/96 well plate with an aluminum seal (>12 samples).
  - Tubes must be clearly marked with a serial number on the top and the side of the tube (not sample name), corresponding to the sample's number in the Sample Information Form. In the matching electronic sample information form, write the number and a meaningful name (this name will be used as the sample name in your fastq files and subsequent data analysis). Ensure that the number on the tube is identical to the serial number of the sample in the electronic Sample Submission Form.
  - Arrange samples in the correct order in a box. We cannot accept samples in plastic bags or randomly place on ice. Mark the box with your name and date.
- An electronic Sample Submission Form should be filled out and sent by email to linde@technion.ac.il.
  It is important to accurately fill out the Sample Submission Form. The information on the form is obligatory and the TGC will process the samples according to this information.
  For **Amplicon-seq**, it is important to indicate the amplicon size including the length of the primers!

Recommendations-

1. DNA extraction methods that are based on spin columns are preferred
2. If needed, re-check the DNA concentration after the initial dilution, to ensure the final concentration matches our requirements.
3. Please perform genomic DNA quality control prior to sample delivery, such as electrophoresis on agarose gel (load 500 ng DNA) and send us a copy of the results.
4. For **Amplicon-seq**, we recommend performing amplicon validation prior to sending your samples. The amplicon should be a single fragment at the expected length. There is no size-selection during library prep and all fragments in the sample will be sequenced (which will reduce the coverage of the target amplicon).
5. For **ChIP-seq**, we recommend performing qPCR validation of your IP samples with positive control primers against input and negative control samples, to make sure the IP protocol has worked successfully.