guidelines v1.01

ATACed gDNA submission guidelines for library prep

IN SHORT: Prepare your DNAs according to these guidelines and put them in our submission drawer at -20°, in minimum 5ul (more is better). In parallel, send the ATACed gDNA submission excel form to gecf@epfl.ch . No info should be transmitted only orally.

How to submit your ATACed DNA samples?

- Fill in the **ATACed DNA submission excel form** found on our website and email it to us. All relevant information should be included in this form, nothing should be communicated only orally.

- The GECF is an open access facility, therefore we cannot give guarantee regarding the confidentiality of data. If this is an issue, the easiest solution is to code your sample names.

- In parallel to submitting the form, please bring DNAs during regular office hours, on ice, in DNase-free PCR-grade 0.5ml-2ml microtubes, but not in PCR tubes/strips/PCR plates. Leave some space on the side of tubes for GECF codes.

- Indicated tube labels must match exactly the ones on your physical tubes. If available, labels of profiles must also match perfectly either tube labels or sample names.

- Avoid using “S1”, “S2” and “R1”, “R2” … in your samples name, as these codes are already appended by the sequencer to fastq files.

- If you need to **modify** or comment on your submission in any way, do it by email, even when you have already told us orally.

- Concentration or total ng amount submitted don’t need to be normalized/identical across samples.

- There are no strong constraints on volume to submit, but a reasonable amount is between 10ul and 50 ul.

- Most people don’t measure concentration of the ATACed gDNA before the library prep, so we don’t make it mandatory. We will not measure or normalize the gDNA concentration on our side, so let us know in case some samples were tagmented from more cells.

ATACed gDNA preparation

- We assume you follow a standard ATAC protocol for tagmentation, let us know if not the case in the submission form.

- **DNA elution** should ideally be done in 10mM Tris, pH8 (=EB buffer), but can also be done in PCR-grade H2O, or “low-EDTA TE”.

- **DNA storage** should be done at -20°.

Determining sequencing parameters

- The consensus for ATAC-seq is PE50-PE75, we thus use these parameters by default. Let us know if a longer read length is needed (rarely relevant for ATAC).

- Mio reads/sample? For broad profiling, 40-50 mio reads are typically used. For footprinting, 100-200 mio reads.

Bioinformatics

- We do not offer in depth bioinformatics analysis. If needed contact the EPFL bioinformatics facility.

Versions log

- v1.01 (17.08.2026): Initial release.