ATAC METHOD

♦ Cell preperation and treatment

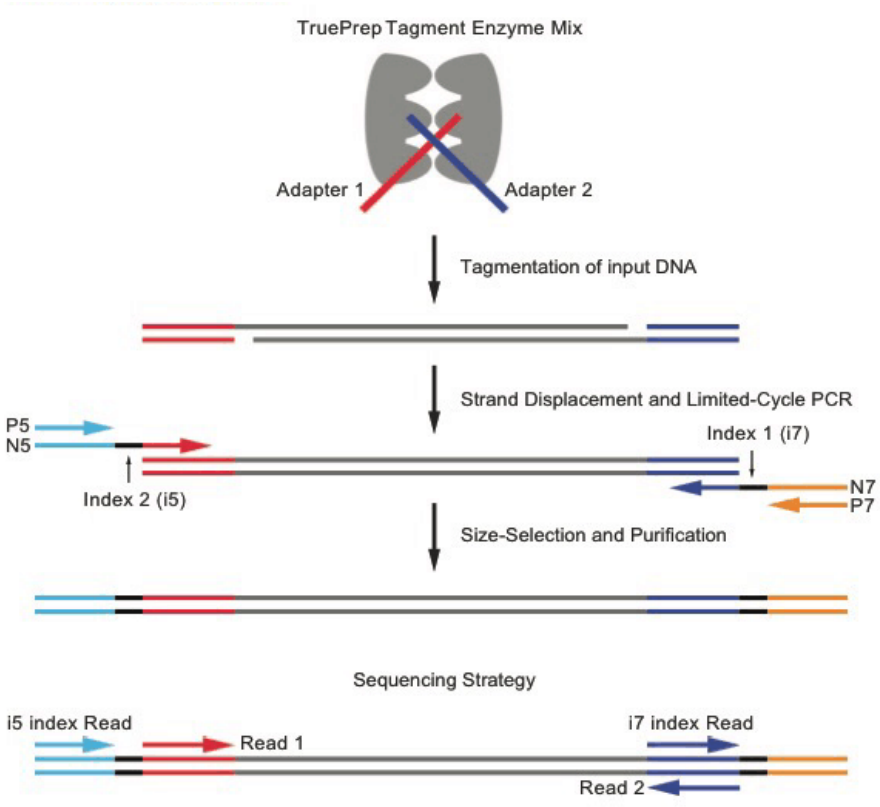
1. Cell activity assay

Cell acitivity was detected with Trypan blue assay and counted. (for cell samples)

2. ATAC-seq protocol

ATAC-seq was performed as previously reported (Buenrostro et al. 2013;Corces et al. 2017; Bajic M et al. 2018). Briefly, nuclei was extracted from samples, and the nuclei pellet was resuspended in the Tn5 transposase reaction mix. The transposition reaction was incubated at 37°C for 30 min.

Equimolar Adapter1 and Adatper 2 were added after transposition, PCR was then performed to amplify the library. After the PCR reaction, libraries were purified with the AMPure beads and library quality was assessed with Qubit.



♦ Clustering and sequencing

The clustering of the index-coded samples was performed on a cBot Cluster Generation System using TruSeq PE Cluster Kit v3-cBot-HS (Illumina) according to the manufactuer's instructions. After cluster generation, the library preparations were

sequenced on an Illumina Hiseq platform and 150 bp paired-end reads were generated.

♦ Data analysis

Nextera adaptor sequences were firstly trimmed from the reads using skewer (0.2.2). These reads were aligned to a reference genome using BWA, with standard parameters. These reads were then filtered for high quality (MAPQ ⩾ 13), non mitochondrial chromosome, and properly paired reads (longer than 18 nt).

♦ Peak calling and peak scores.

All peak calling was performed with macs2 using 'macs2 callpeak --nomodel --keepdup all --call-summits'. For simulations of peaks called per input read, aligned and de-duplicated BAM files were used without any additional filtering.

Reference:

- Buenrostro J.D., Giresi P. G., Zaba L.C., Chang H. Y., Greenleaf W.J. (2013) Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. Nature Methods. 10:1213-1218. **(for cell samples)**
- Corces MR., Trevino AE., Hamilton EG., Greenside PG., et al. (2017) An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods. 14:959-962. **(for animal tissues)**
- Bajic M., Maher KA., Deal RB. (2018) Identification of open chromatin regions in plant genomes using ATAC-Seq. chapter in Methods in Molecular Biology in book: Plant Chromatin Dynamics,pp 183-201. **(for plant tissues)**