Medical College of Wisconsin

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Assay for Transposase Accessible Chromatin Sequencing (ATAC-Seq)

Test Description

Assay for Transposase Accessible Chromatin sequencing (ATAC-Seq) is used to understand and map the epigenetic landscape of DNA in the cell. Histones and other proteins package and regulate DNA through open (euchromatin) or closed (heterochromatin) conformations. Changes in accessibility can be assessed through ATAC-Seq and comparisons made to map out the genomic location and associated genes changing during disease progression, drug treatments, or other experimental conditions. Pairing ATAC-seq data with transcriptomics data can reinforce and reveal novel mechanisms by which cellular phenotypes are regulated by epigenetic systems.

Sample Types and Requirements

Live Cells: Approximately 50,000-100,000 cells
Prepared Libraries: Completed library prep, fragment size 200-1000 base pair (bp)

Recommended Sequencing Depth

Greater than 25 million unique reads, paired end, 2x100 bp sequencing

Submission Requirements

Sample Intake Form and iLabs request. Adaptor sequences and index kit part number must be included if submitting completed libraries. Contact lab for drop off or shipping requirements.

Turnaround Time

4-6 weeks for fastq files only
2-3 additional weeks for bioinformatics analysis

Deliverables

Library quality control (PDF)
ATAC-seq report (html with linked documents)
BAM, fastq.gz files
All annotated NGS data files will be delivered via Mellowes Center portal

Test Methodology

ATAC libraries are prepared using the Active Motif ATAC-Seq kit. Nuclei are isolated from recently harvested, live cells and incubated with hyperactive Tn5 transposase for DNA fragmentation and tagging with adapter for sequencing. After DNA isolation and PCR amplification with indexed Illumina adapters, libraries are size selected to enrich for 200-1000bp fragments. The quality and quantity of the DNA library is checked by fragment analysis and qPCR respectively. Libraries are then pooled, and distribution confirmed on the Illumina MiSeq before sequencing is completed on the Illumina NovaSeq.

Bioinformatic Core Analysis

ATAC-seq report includes:

- Quality control and sequencing metrics (insert length, peak call numbers, fragment distribution around TSS)
- Distribution of peak annotations (to nearest gene or genome feature)
- Differentially bound and accessible regions of the genome
- Volcano plots, Venn diagrams, and gene associations with significant peaks
- Pathway and GO term enrichment analysis
- Additional analysis can identify overrepresented DNA motifs, integrate analysis with RNA-seq and more

Contact & Submission

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