Nuclei EXtraction by SONication - NEXSON

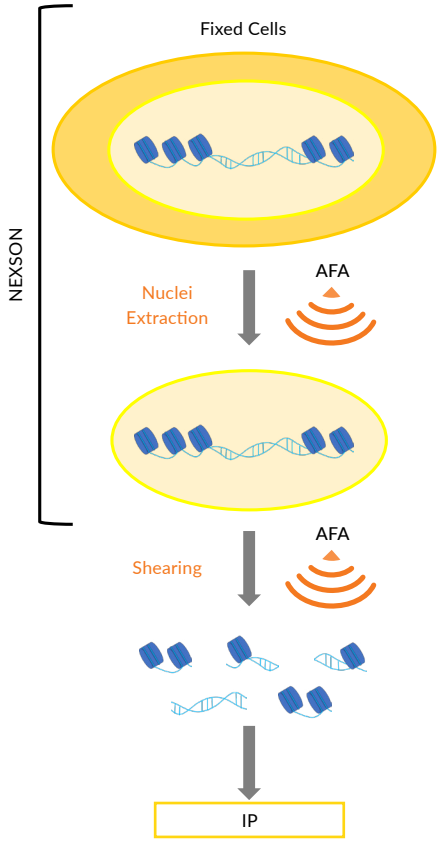
Scientific Relevance

- ChIP-Seq is a powerful tool to map DNA binding proteins as well as histone modifications across the genome (1,2)
- To allow the comparison of different studies and different input materials standardization of the sample preparation steps are required, which has been challenging (3,4)
- NEXSON provides a simple but highly reproducible technique for efficient nuclei isolation, ensuring the generation of comparable chromatin maps from different sample types (5)

Challenges

- Huge variations in sample preparation for ChIP make data comparison challenging
- In particular, the chromatin shearing step is tedious to optimize and standardize for different input materials and across different laboratories
- Insufficient chromatin shearing compromises the quality of chromatin and sequencing results
- Shearing optimization is labor-intensive, material-consuming, expensive, and especially difficult when working with precious samples such as clinical specimens

Workflow



Schematic representation of NEXSON workflow (6)
Nuclei from fixed cells are efficiently isolated applying tuneable AFA. Pure fractions of isolated nuclei are subjected to ChIP workflow. In brief, chromatin is sheared using AFA and subjected to IP for histone modifications or transcription factors of interest.

Advantages of Adaptive Focused Acoustics® (AFA®)

AFA technology is a very gentle, reproducible, and tuneable shearing method.

- The high efficiency of nuclei isolation allows the scale down of input material to 10,000 cells/histone ChIP and 100,000 cells/transcription factor ChIP
- Increased robustness permits comparison across different tissues, cell types, disease stages, and laboratories
- The highly reproducible and efficient isolation of nuclei allows for novel high throughput derivates of ChIP technology (7)

Suggested Covaris Products

- Covaris Focused-ultrasonicator
  (M-Series, S-Series, E-Series, or LE-Series)

Citations

- Arrigoni et al. Standardizing chromatin research: a simple and universal method for ChIP-seq. NAR. (2016)
- Durek et al. Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. Immunity. (2016)
- Castex et al. Inactivation of Lsd1 triggers senescence in trophoblast stem cells by induction of Sirt4. Cell Death & Disease. (2017)
- Ramirez et al. High-resolution TADs reveal DNA sequences underlying genome organization in flies. Nature Communications. (2018)

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