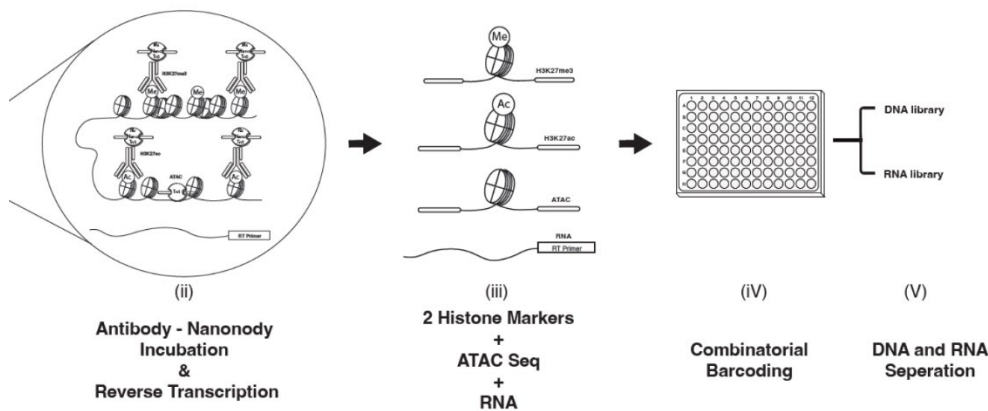


Decoding Epigenetic and Transcriptome in Single cells / TrES-seq



Ref. Nr

6.2708

Keywords

histone; high throughput; transcriptome profiling

Intellectual Property

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Description

Available multimodal technologies to study histone modifications (such as PAIRED Tag and uCoTargetX) are not efficiently allowing the exploration of the multiple histone modification without cross contamination and transcriptomic information simultaneously from same cell. This limitation hinders our ability to fully understand the connection between histone modifications and gene expression.

Designed multimodal single-cell high throughput allowing detecting two histone markers by using species specific nanobodies to avoid cross contamination (TrES-seq).

Advantages

Enable simultaneous detection of histone modifications, markers, transcription factors, proteins of interest, and transcriptome profiles within the same cell
 sensitive and cost effective.

Applications

Research tool