

AAT C-Seq

Library Prep Kit for
Illumina Sequencer

TransNGS[®] ATAC-Seq Library Prep Kit for Illumina[®]

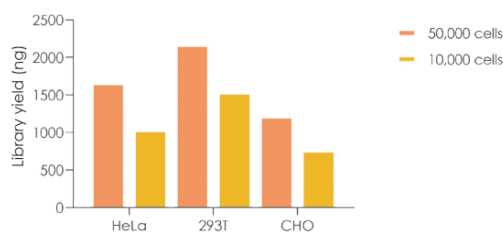
(KP171)

Product Features

- Low number of cells: High-resolution sequencing maps can be obtained for the initial volume of 50-50,000 cells.
- Short time: For 5000 cells and below, the library preparation time can be shortened to less than 2 h.
- High library yield: High library quality and good peak shape.
- Good library peak shape: library peak shape 200-2000 bp, no obvious joint peak.
- No sorting: If there are no special requirements for the length distribution of the library, you can skip sorting.

Experiment Data

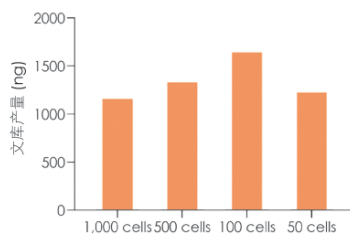
High library yield



ATAC library construction was performed on 3 mammalian cells starting at 50,000, 10,000 cells. The results showed that TransGen products could construct high-yield libraries for different cells and inputs.

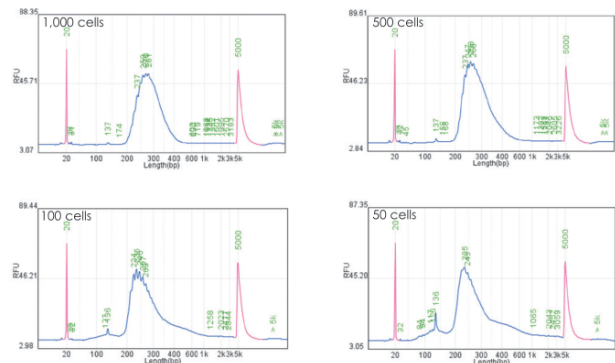
Low cell input

Library yield



Cell input	1,000	500	100	50
Cycles	20		25	

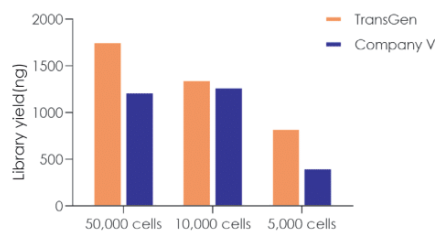
Library peak shape



ATAC libraries were constructed for HeLa cells with different cell inputs (50-1,000 cells), and the number of amplification cycles for different cell inputs was shown in the table above. The results showed that TransGen products could be used to construct ATAC libraries with low input (50 cells), high yield and good peak shape.

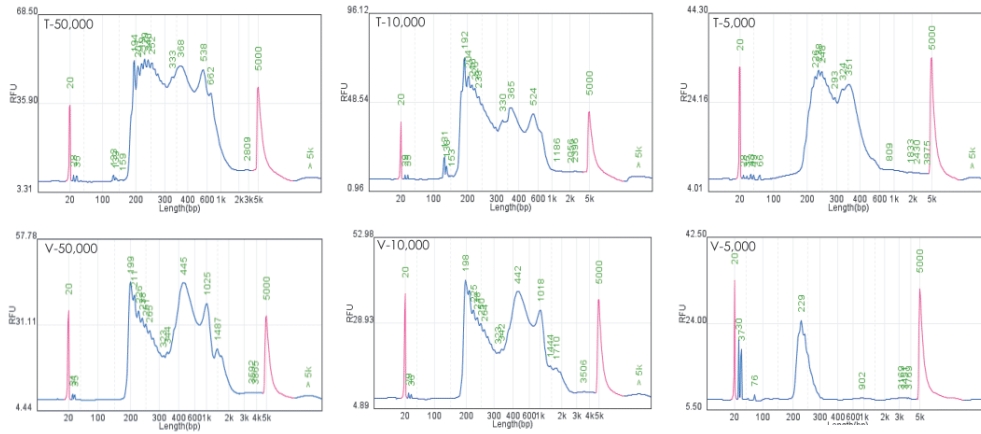
Compare with Competitor

Library yield



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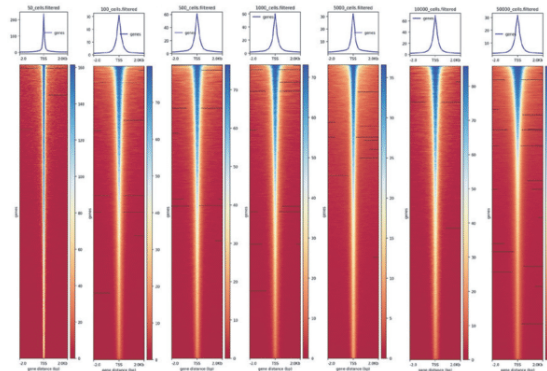
Library peak shape



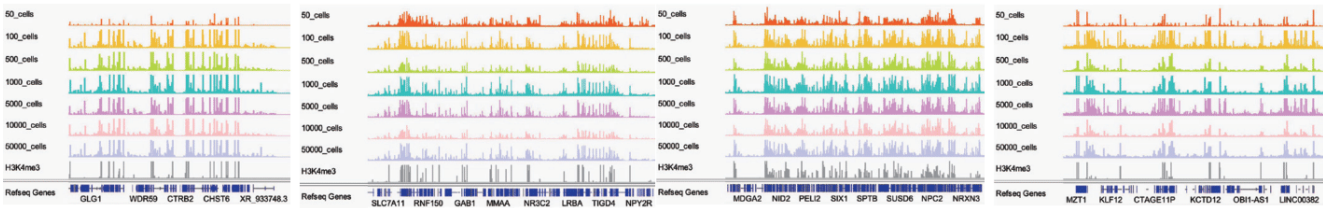
ATAC libraries were constructed for HeLa cells with different cell inputs (5,000-50,000 cells) using TransGen and Company V products, respectively. The results showed that the library yield and library peak shape of TransGen product were better than competitor.

Good Data

View of TSS at different cell inputs



IGV view at different cell inputs



Note: Four chromatin regions were randomly selected throughout the genome

ATAC libraries were constructed for HeLa cells with different cell inputs (50-50,000 cells), the libraries were sequenced, and biogenic analysis was performed. The results showed that the TSS enrichment map showed obvious enrichment around the transcription start site of the gene, and the IGV view showed that the ATAC at the key site was consistent with the ChIP-seq results of H3K4me3 gene, and the experimental results were real and reliable.

Product Information

Product Name	Cat. No.	Specification
TransNGS® ATAC-Seq Library Prep Kit for Illumina®	KP171-01	12 rxns
	KP171-02	96 rxns

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