

# WSB316\_ATAC

For guidance, please consult ["Interpreting Cell Ranger ATAC Web Summary Files"](#) or contact 10x Genomics Support ([support@10xgenomics.com](mailto:support@10xgenomics.com))

## 7,711

Estimated number of cells

## 6,338

Median fragments per cell

## 74.9%

Fraction of fragments overlapping any targeted region

## 54.4%

Fraction of transposition events in peaks in cell barcodes

## Sample

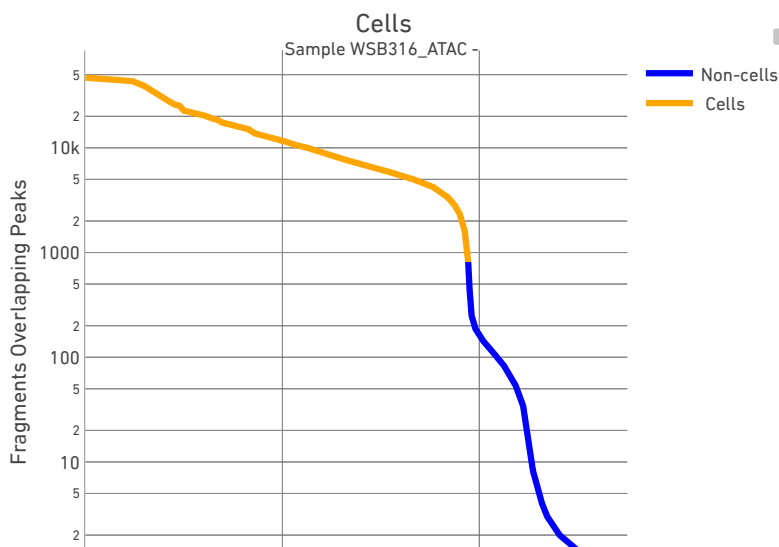
Sample ID	WSB316_ATAC
Sample description	
FASTQ path	...200508/ATAC/WSB316_ATAC
Pipeline version	1.2.0
Reference path	...abase/ATAC/Homo_sapiens
Organism	Homo_sapiens
Assembly	custom
Annotation	custom

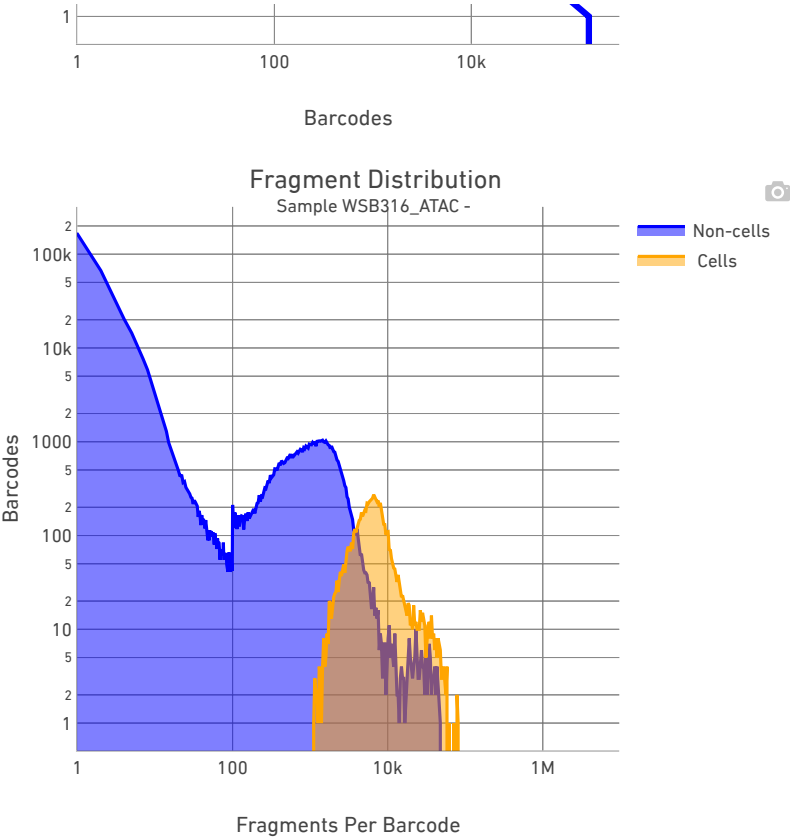
## Sequencing ?

Total number of read pairs	375,019,150
Fraction of read pairs with a valid barcode	98.1%
Q30 bases in Read 1	92.9%
Q30 bases in Read 2	92.8%
Q30 bases in Barcode	90.3%
Q30 bases in Sample Index	91.2%

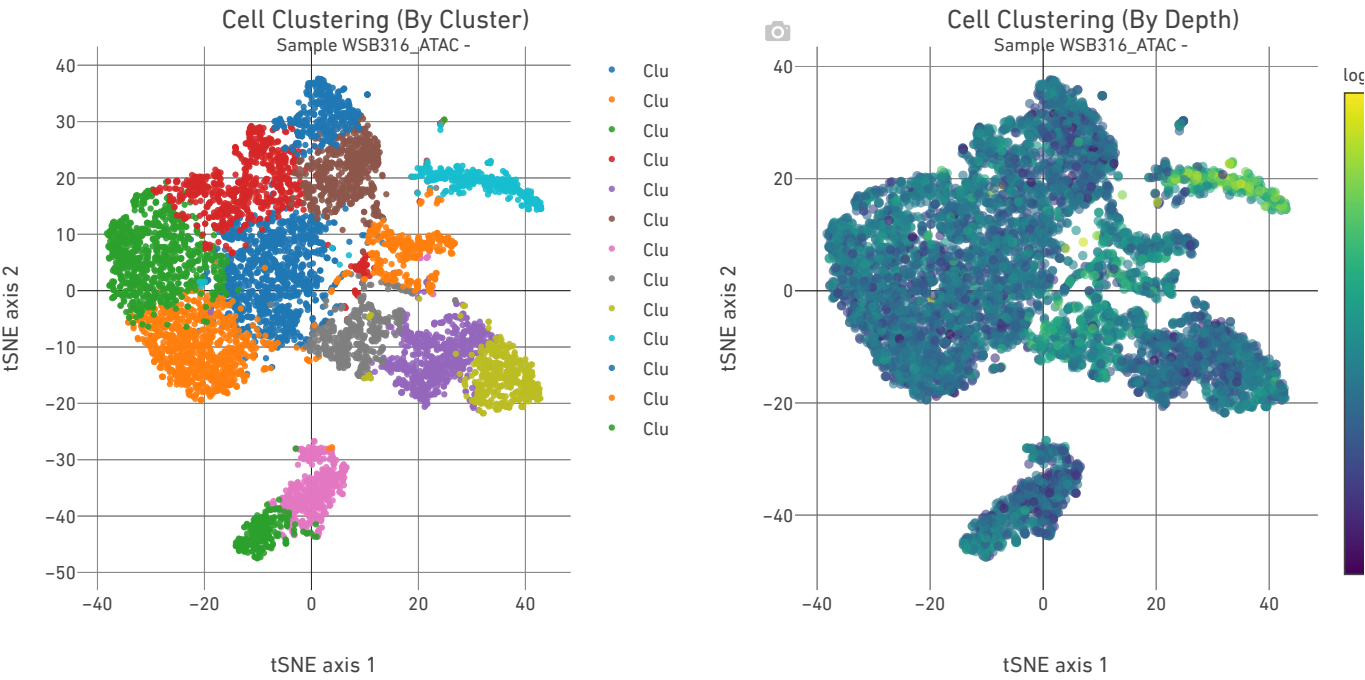
## Cells ?

Estimated number of cells	7,711
Lower threshold on the number of fragments overlapping peaks per barcode to annotate barcode as cell	815.00
Median fragments per cell	6,338
Median fragments per non-cell barcode	1



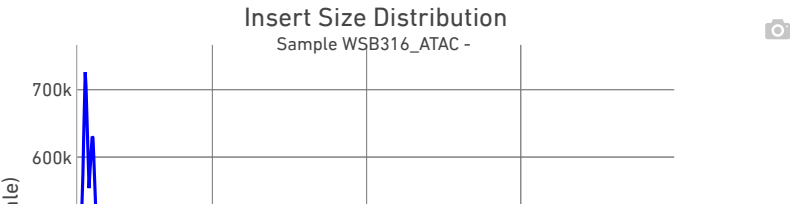


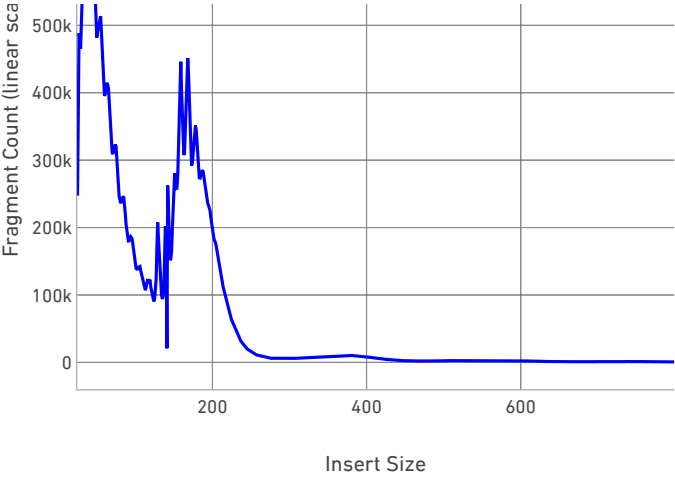
Cell Clustering ?



Insert Sizes ?

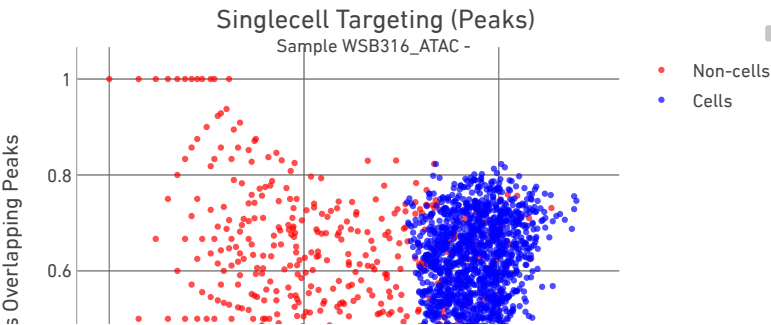
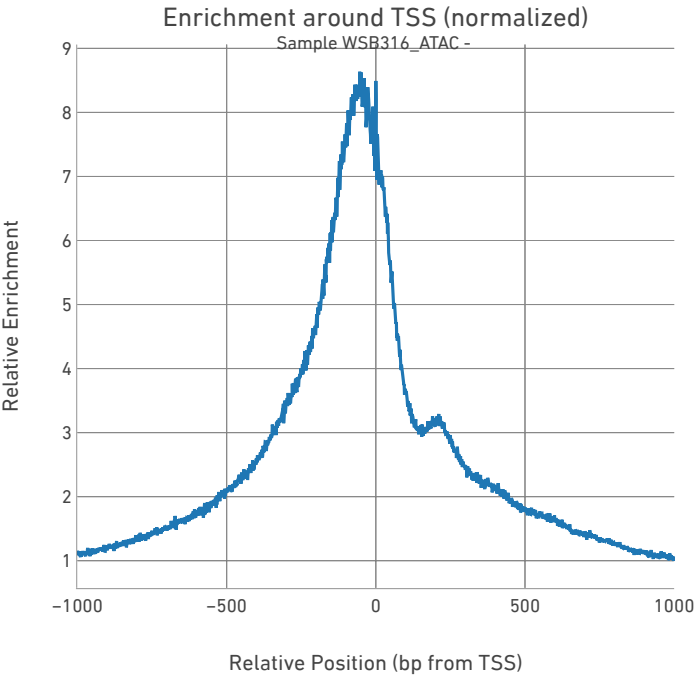
Fragments in nucleosome-free regions	56.8%
Fragments flanking a single nucleosome	40.7%

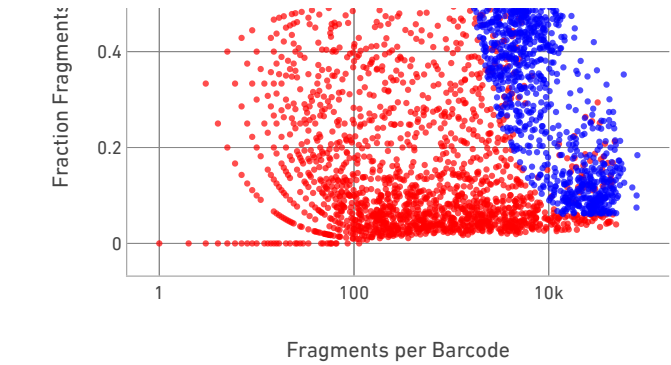




Targeting ?

Enrichment score of transcription start sites	8.64
Fraction of fragments overlapping TSS	49.5%
Fraction of fragments overlapping called peaks	55.4%
Fraction of transposition events in peaks in cell barcodes	54.4%
Fraction of fragments overlapping any targeted region	74.9%
Fraction of total read pairs mapped confidently to genome (>30 mapq)	83.8%
Fraction of total read pairs that are unmapped and in cell barcodes	0.2%
Fraction of total read pairs in mitochondria and in cell barcodes	0.1%





Library Complexity ?

Percent duplicates	12.9%
Sequencing saturation	58.7%
Estimated bulk library complexity	231,609,107

