MobiVision v4.1 Release Notes

Release Date: September 2025

1. New Features

   (1) Added ATAC-seq analysis module, supporting the processing of MobiCube ATAC-seq data.

   New subcommand: mobivision atac – dedicated ATAC-seq analysis pipeline.

   (2) Logging Module: More clear and comprehensive logging system.

   (3) BAM Conversion: Added BAM to FASTQ conversion functionality.

   (4) ChIP Resumption Analysis: Resume analysis from interrupted steps, saving time on repetitive processes and reducing resource waste.

2. Optimizations and Fixes

   (1) ChIP-seq Optimizations:

- ChIP-seq insert size plot now displays up to 1,000 bp.
- Replaced UMAP with t-SNE for ChIP-seq data visualization.
- Added visualization for ChIP-seq peak annotation analysis.
- Added histone modification names in ChIP-seq HTML reports.

(2) Transcriptome Optimizations:

- Improved adapter trimming algorithm.
- Enhanced mitochondrial violin plot recognition module for non-model species.
- Added noBam functionality.

(3) QC Metrics:

- Added cell and UMI counts to omics background information.

(4) Code Refactoring:

- Comprehensive framework refactoring to improve runtime efficiency.

(5) Memory Optimization:

- Enhanced large-scale data resource management.

(6) Error Prevention:

- Added 6-column GTF file format validation.
- Added reference.json verification to prevent late-stage errors and save time.

(7) Thread Management:

- Resolved pthread_create resource limitation issues.

MobiVision v3.2 Release Notes
Release Date: March 2025

1. New Features
   (1) mobivision integrate – New subcommand for integrated data analysis.
2. Optimizations and Fixes
   (1) Transcriptome Optimizations:

- New result file: cell_metrics.csv – more detailed cell-level QC metrics.
- Adjusted result files: h5ad files now retain complete information corresponding to the filtered-cell-gene-matrix.
- Added "Total Detected Genes" metric in summary.csv.
- Adjusted BAM file fields: Added UR, CR, UY, CY tags and unaligned reads.
- Report display adjustments: Modified UMAP dimensionality reduction algorithm.
- Updated help information.

(2) ChIP Module Updates:

- Removed result file: filtered.h5ad.
- Added result files: peaks_annotation.tsv.gz, index fragment files (.tbi).
- Added new QC metrics in reports: fraction of reads overlapping intergenic region, fraction of reads overlapping distal region, fraction of reads overlapping promoter region, TSS enrichment score.
- Visualization updates: Replaced PCA with LSA for dimensionality reduction in t-SNE projection.

(3) mk_chip_ref Module Updates:

- New required parameter: -g/--gtffile to specify genome annotation.

- New output files: tss.bed, transcripts.bed, genome.gtf.

(4) mtx2csv Module Updates:

- Now compatible with filtered-cell-gene-matrix from quantify output and filtered-cell-peaks-matrix from chip output.

(5) re_call_cell Module Updates:

- Fixed issue where HTML QC reports could not be generated.

(6) CITE Module Updates:

- CITE module analysis result files now retain transcriptome BAM files, with BAM tag information including barcode and UMI sequences along with quality values.

(7) VDJ Module Fixes:

- Fixed issue where HTML reports were not generated properly in the absence of cells/pairing.