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OmicsCanvas: A multi-omics platform for integration and visualization of epigenetic regulation[FA]

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Epigenetic regulation including chromatin accessibility, histone modifications, DNA methylation, and RNA modifications plays a pivotal role in controlling gene expression (Hwang and Seo, 2026). These regulatory layers have been profiled genome-wide using complementary sequencing assays such as ATAC-seq, ChIP-seq, and m^{6}A-seq (Shim et al., 2020). Collectively, these approaches can be viewed as "peak-centric" epigenomic methods, in which regulatory activity is inferred computationally as statistically enriched genomic regions. In contrast, whole-genome bisulfite sequencing (WGBS; BS-seq) provides base-resolution DNA methylomes (Zhang et al., 2026), and Bismark is a widely used workflow for methylation calling (Krueger and Andrews, 2011).

Integrating transcriptomic data with epigenomic profiles (e.g., ATAC-seq, ChIP-seq, and BS-seq) is essential for dissecting the interplay between gene expression and epigenetic regulation. However, a major challenge in multi-omics studies is the lack of a unified framework that can cohesively analyze and visualize diverse data types in the context of gene architecture, which remains a bottleneck for biological discovery. Although numerous tools exist for next-generation sequencing (NGS) data analysis (Li et al., 2026) and visualization (Goecks et al., 2012), an integrated framework that explicitly links gene expression with epigenomic profiling is still lacking. Key unmet needs include consistent signal normalization across genes within a unified coordinate system, interpretable clustering of multi-omics patterns, and streamlined generation of publication-ready vector graphics for integrated visualizations.

To address these needs, we developed OmicsCanvas (Figure 1A), a toolkit that accepts standard inputs, including BAM, GFF/BED, and Bismark CX reports. OmicsCanvas maps multi-omics signals onto a unified coordinate system, thereby enabling cross-omics normalization and clustering within a consistent analytical framework. In addition, it provides a suite of publication-ready visualizations ranging from genome-wide overviews to single-gene displays, lowering the barrier to generating high-quality, interpretable multi-omics results.

OmicsCanvas is a Python (v3.9) software package designed for multi-omics integration and high-quality visualization. Built around BAM-centric inputs, it aligns heterogeneous sequencing signals to a shared genomic coordinate system using a unified binning framework and gene-centric analytical design, and directly generates publication-grade vector figures (SVG and PDF), with an emphasis on interpretability (Figure 1A). At the input layer, the pipeline accepts sorted and indexed BAM files from diverse libraries, including RNA-seq, ChIP-seq, ATAC-seq, and m^{6}A-seq (Dominissini et al., 2012), along with gene annotations in GFF or BED format. To demonstrate the utility of OmicsCanvas for multi-omics analysis, we used a *Populus trichocarpa* data set comprising DNA methylation (Hofmeister et al., 2020) and histone modification data (Lu et al., 2019) as an example.

For feature construction, each genomic element is partitioned into the gene body and flanking regions (Figure 1B), which are discretized into equally spaced bins (default: 300; user-configurable). For BAM-based tracks, signals are aggregated across bins as coverage values, with optional library-size normalization. To improve comparability across samples and tracks, OmicsCanvas provides normalization strategies and generates unified "element × bin" signal matrices. The toolkit also supports expression–epigenome integration (Figure 1C, D) by generating gene expression matrices (TPM/FPKM/counts). For BS-seq data, OmicsCanvas directly parses Bismark (Krueger and Andrews, 2011) CX output files and, together with BED annotations, computes gene-level methylation coverage and ratios. CG, CHG, and CHH methylation ratios are calculated at the bin level to generate metaplots (Figure 1E), heatmaps (Figure 1F), single-gene visualizations (Figure S1), and a genome-wide Circos view (Figure S2). OmicsCanvas also generates correlation heatmaps of genome-wide DNA methylation across samples (Figure S3).

Additionally, OmicsCanvas includes a differential expression module. For raw counts, it uses the median-of-ratios method from PyDESeq. 2 (Muzellec et al., 2023) to estimate size factors, followed by fitting a negative binomial regression model for each gene. *P*-values are adjusted using the Benjamini–Hochberg correction to control the false discovery rate (FDR; padj), and the outputs include Log_2 fold change, FDR, and other key metrics. When transposable element (TE) annotations (GFF or BED) are provided, OmicsCanvas quantifies TE expression, enabling joint assessment of TE-associated histone modifications, chromatin accessibility, and TE expression. OmicsCanvas also supports unsupervised learning (e.g., *K*-means) to identify coordinated multi-track signal patterns across genomic elements (Figure S4), generating clustered heatmaps and spatial profile plots along element structures, together with corresponding expression distributions. To facilitate GO enrichment analysis of the resulting clusters and streamline interpretation, we implemented an integrated GO enrichment module. This module performs Over-Representation Analysis (ORA) using a hypergeometric right-tailed test, with p-values adjusted by the Benjamini–Hochberg method (BH-FDR). It outputs enrichment tables and directly generates bubble/scatter plots.

For visualization, OmicsCanvas produces publication-grade genome-wide profiles (Figure 1B, E) as well as single-gene figures (Figure 1G, H). In the circular layout, the same genomic window is mapped onto angular coordinates (0–2π), with gene structure serving as the reference ring and peak coverage or methylation signals displayed as concentric outer rings (Figure 1G). This layout supports group-wise shared y-axis limits (via the --bam-group-ylims parameter) to maintain consistent scaling across tracks. In the linear layout, 2D or pseudo-3D multi-track plots stack multi-omics signals within a user-defined window (Figure 1H), and group-wise shared y-axes provide consistent scaling across samples. Both linear and circular plotting support batch execution, facilitating efficient generation of case-specific visualizations.

OmicsCanvas is implemented in Python 3.9 following a minimal-dependency design philosophy. Core functionalities rely on widely used scientific libraries, including pysam, NumPy, SciPy, scikit-learn, pandas, and Matplotlib (with Seaborn optionally available for enhanced plotting styles). The package is distributed with a command-line interface, comprehensive parameter documentation, example data sets, and workflow scripts. It supports batch execution on Linux servers and exports both intermediate data matrices and publication-ready figures. We also implemented a graphical user interface (GUI) for OmicsCanvas using Python/PySide6 (Qt), which organizes the command-line scripts into modular workflows (Figure S5). Built on the Qt backend, the GUI is cross-platform and can be deployed on both Windows and Linux desktop environments, subject to standard Python dependencies and

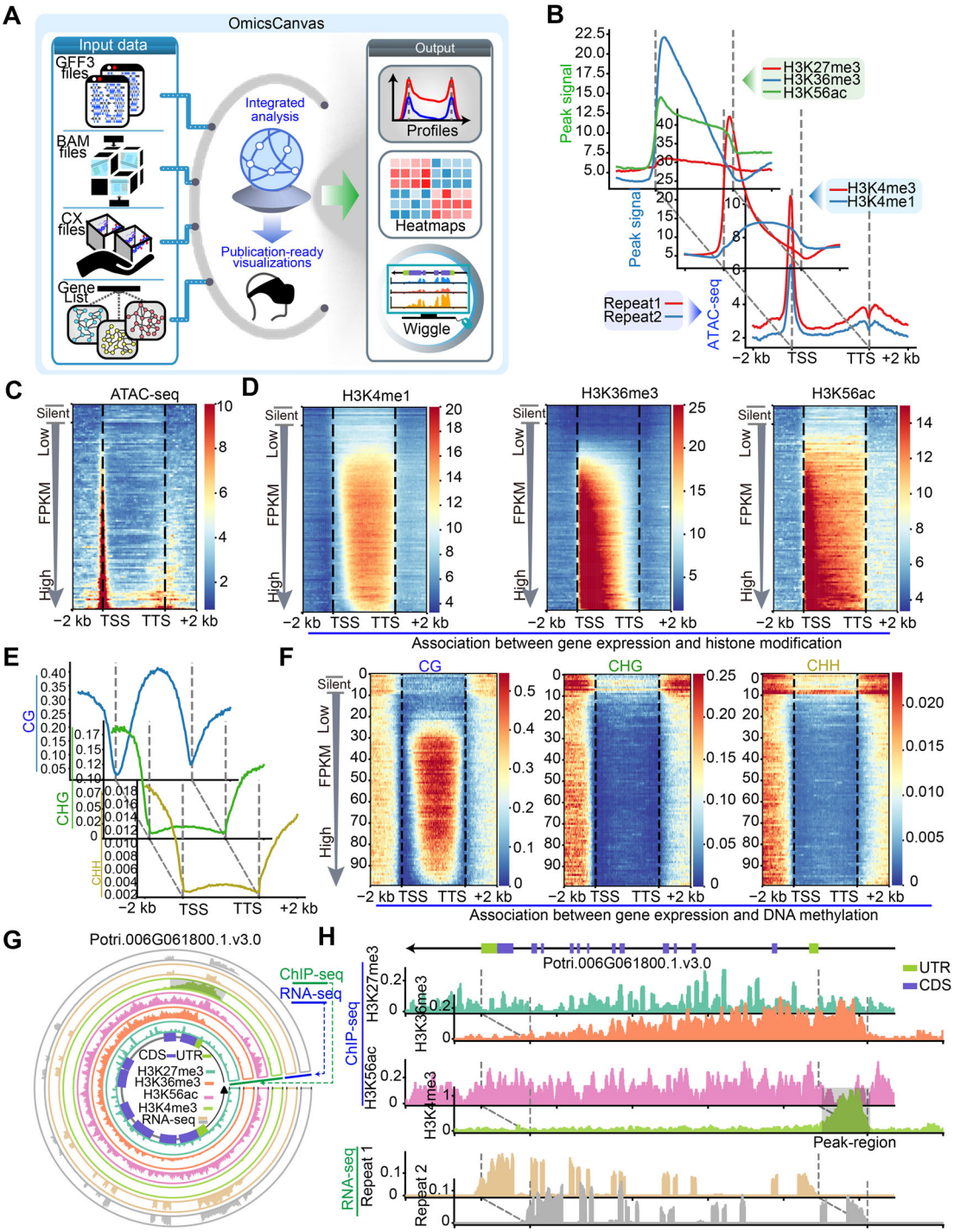

Figure 1. Workflow of OmicsCanvas and integrated visualization of epigenetic, transcriptomic, and DNA methylation profiles

(A) Flow chart of OmicsCanvas. **(B)** Metaplots showing the genome-wide distribution of five histone modifications and chromatin accessibility in leaves across ±2 kb flanking annotated gene bodies. **(C)** Heatmap depicting the association between chromatin accessibility and gene expression. Genes were stratified into non-expressed and expressed groups, with expressed genes sorted by expression level from low to high. ATAC-seq signals across gene bodies and ±2 kb of flanking regions are plotted. **(D)** Heatmap showing the association between histone marks (H3K4me1, H3K36me3, and H3K56ac) and gene expression. Genes were divided into non-expressed and expressed groups, with expressed genes sorted from low to high expression. The enrichment profiles of the three marks across gene bodies and ±2 kb flanking region are shown accordingly. TSS and TTS denote the transcription start site and the transcription termination site, respectively. **(E)** Metaplots showing the distribution of CG, CHG, and CHH methylation across gene bodies and ±2 kb gene-flanking regions. Tracks are shown from top to bottom as CG, CHG, and CHH methylation, respectively. **(F)** Heatmap representing the association between DNA methylation and gene expression. Genes were separated into non-expressed and expressed categories. The first 10 bins represent non-expressed genes, whereas the remaining 90 bins correspond to expressed genes ranked from low to high expression (top to bottom). Heatmaps are arranged from left to right for CG, CHG, and CHH methylation. **(G)** Circular track plot generated for a ±2 kb genomic window. From inner to outer rings, tracks represent H3K27me3, H3K36me3, H3K56ac, H3K4me3, and RNA-seq (two replicates). **(H)** Linear wiggle plot rendered in a modular pseudo-3D layout. Tracks are displayed from top to bottom as H3K27me3, H3K36me3, H3K4me3, H3K56ac, and RNA-seq. Semi-transparent shaded regions indicate H3K4me3 peak regions called from MACS2.

the required Qt runtime libraries. OmicsCanvas is available at https://github.com/zeyubio/OmicsCanvas.

In summary, OmicsCanvas provides an integrative solution that renders complex multi-omics relationships interpretable and visually accessible to the broad research community, while streamlining the delivery of publication-ready figures. Under a unified binning framework, the tool aligns and quantifies multiple track types, including RNA-seq, ChIP-seq, ATAC-seq, BS-seq, and m^6A-seq. This enables interpretable clustering and expression-linked analyses. OmicsCanvas supports both gene-centric and TE-centric quantification. The toolkit generates global heatmaps as well as single-gene or single-element visualizations in 2D, pseudo-3D, and circular layouts, with group-wise *y*-axis scaling to maintain consistent visual comparisons across tracks, and exports directly to publication-ready vector figures. Overall, OmicsCanvas delivers a reusable, interpretable, and reproducible pipeline for integrated multi-omics analysis and figure generation with minimal dependencies, substantially lowering the barrier to conducting multi-omics studies.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

Z.Z. and L.G. conceived and designed the research. Z.Z., Z.M., T.H., X.L., and S.X. performed data analysis. Z.Z. and L.G. wrote and revised the manuscript. All authors have read and approved the contents of this paper.

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