Complex Heatmap Visualization

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Introduction

Heatmap has been a standard tool for visualizing omics-level data.

We have previously developed an R/Bioconductor package named "*ComplexHeatmap*":

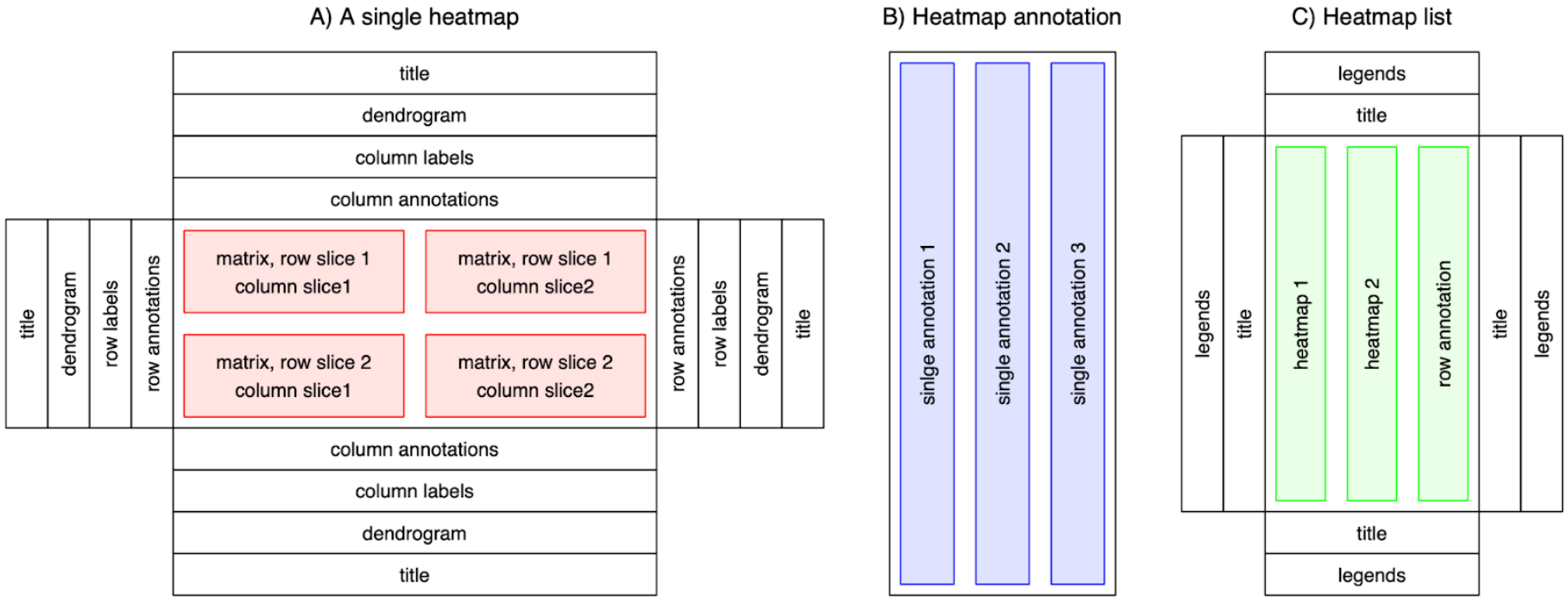
- > 500K downloads.
- 104 other R/Bioconductor packages have direct dependency on it.
- > 3000 Google Scholar citations.

In this article, we will give a comprehensive introduction on the current state of *ComplexHeatmap*, including its modular design, its rich functionalities and its broad applications.

Modular design

There are three main classes defined for heatmaps:

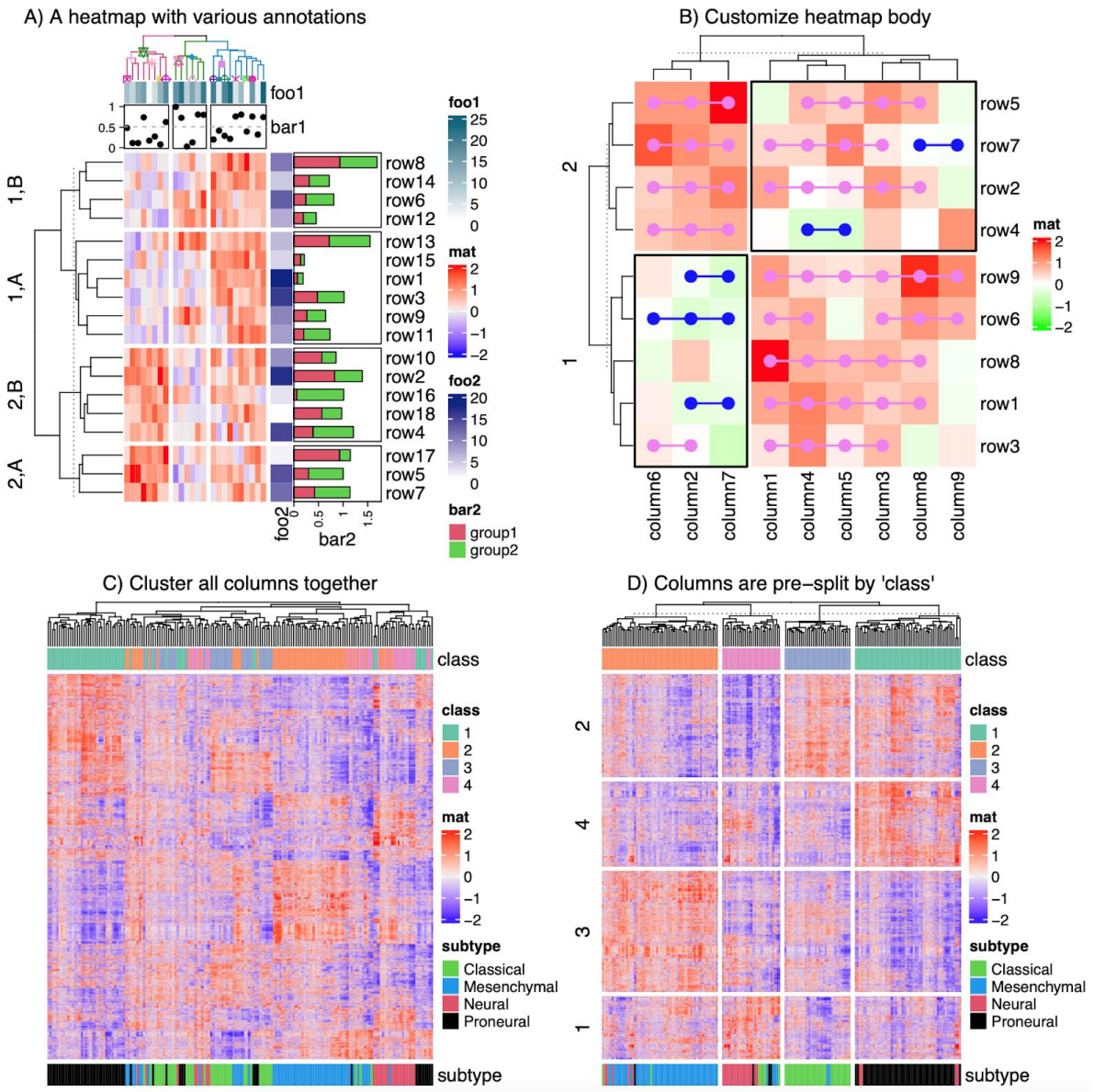
- *Heatmap* class
- *HeatmapAnnotation* class
- *HeatmapList* class



A single heatmap

A single heatmap is made by the function `Heatmap()`. It has the following unique features:

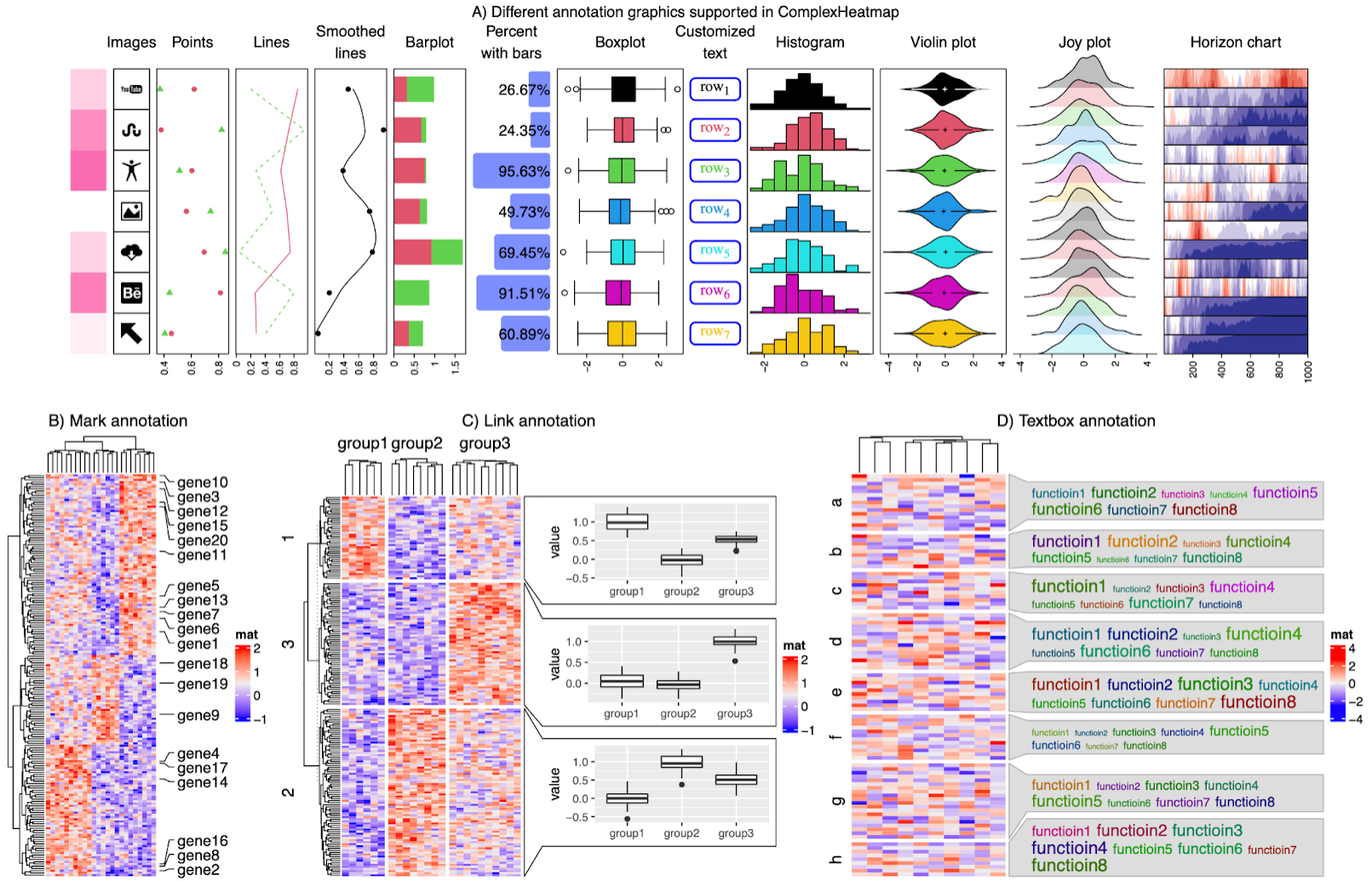
- flexible controls of clustering and reordering
- split heatmap
- render heatmap body as raster images
- customize heatmap
- flexible controls of colors and legends



Heatmap annotations

There are the following annotation graphics supported:

- Heatmap-like annotation
- Image annotation
- Points annotation
- Lines annotation
- Barplot annotation
- Boxplot annotation
- Text annotation
- Histogram annotation
- Violin annotation
- Joy plot annotation
- Horizon annotation
- Mark annotation
- Textbox annotation
- self-defined annotation graphics



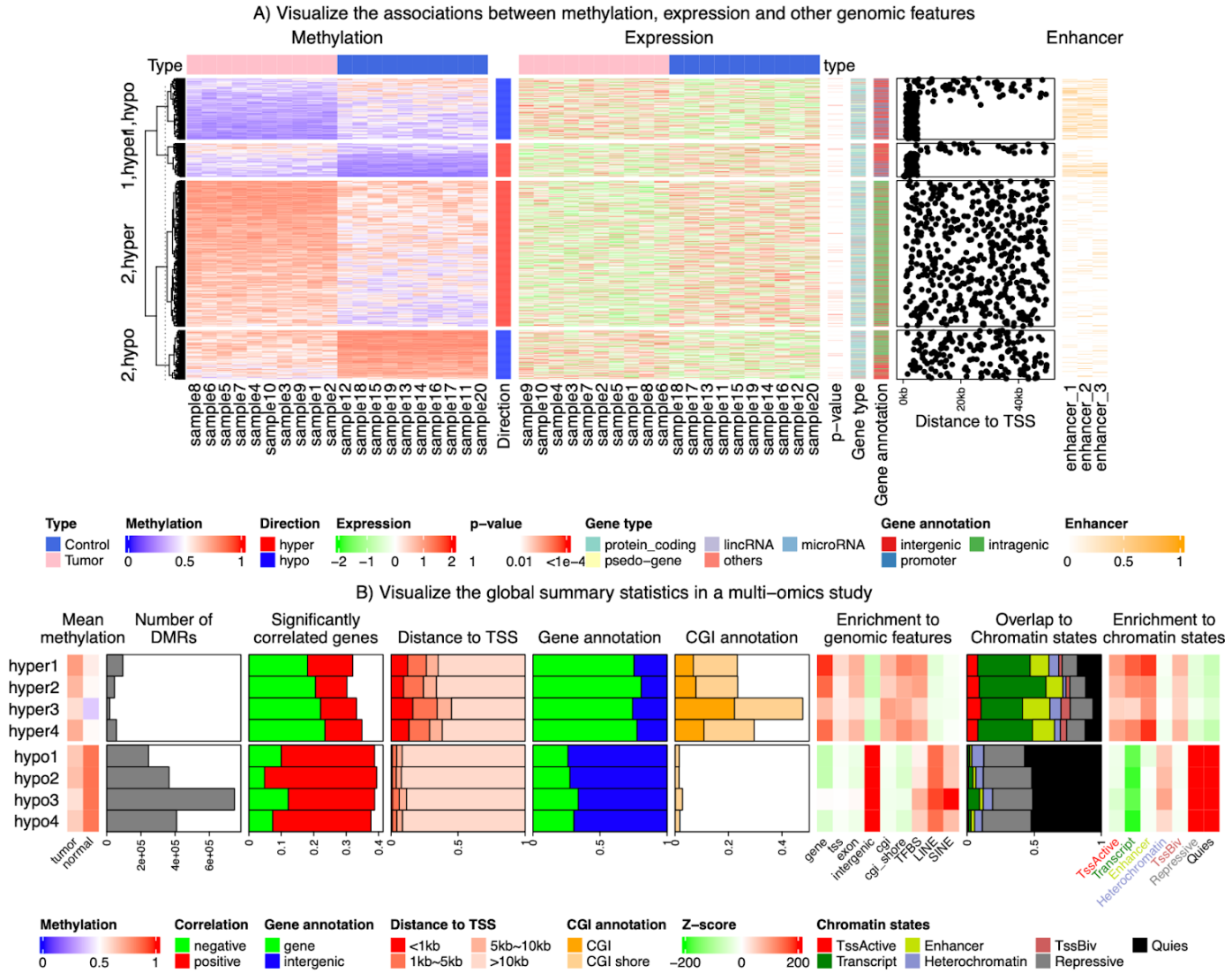
A list of heatmaps

ComplexHeatmap provides a simple syntax for concatenating multiple heatmaps with the operator + or `%v%`.

```
Heatmap(...) +
    Heatmap(...) +
    rowAnnotation(...)
```

Two examples:

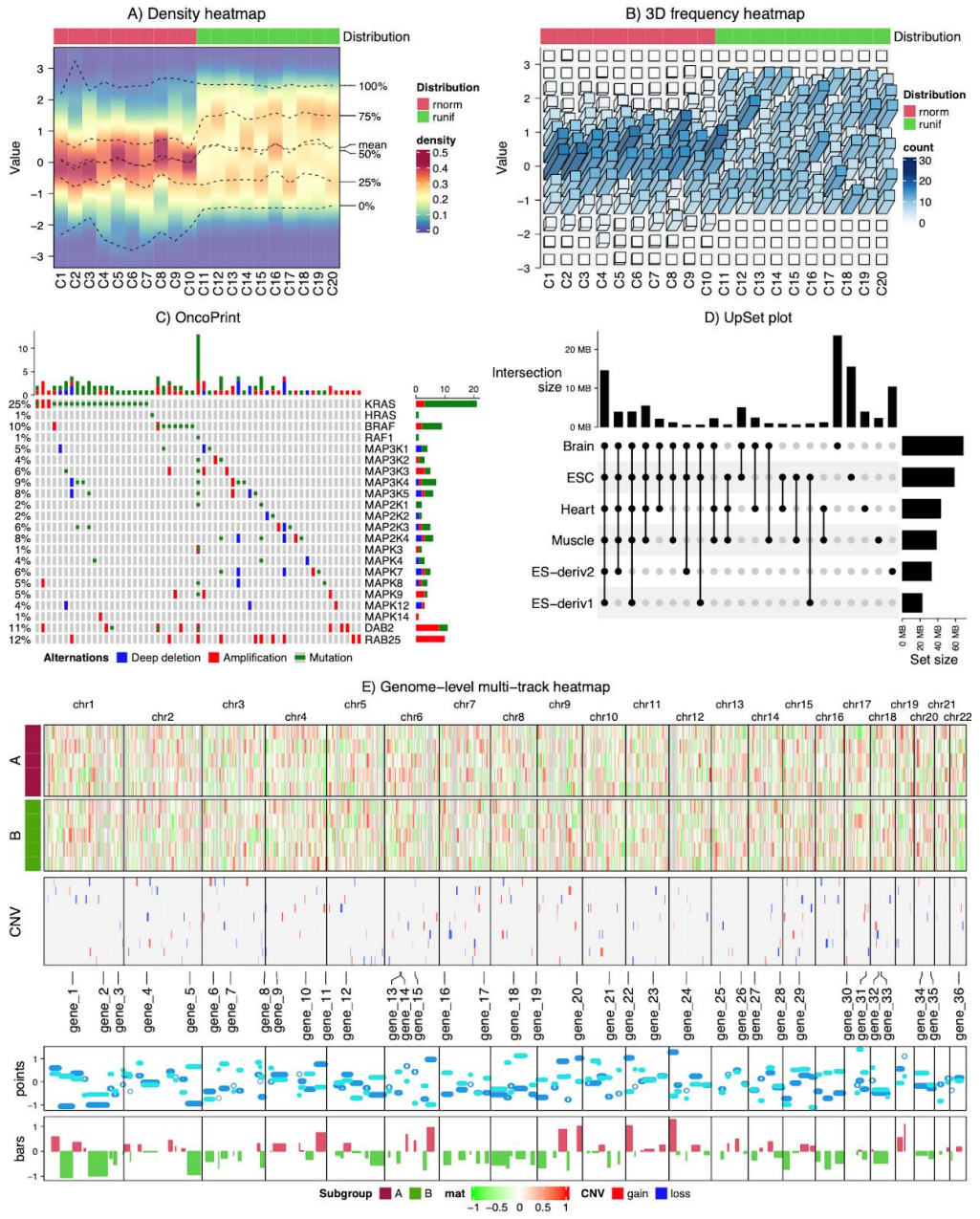
- Visualize associations between DNA methylation and gene expression
- Visualize global summary statistics in multi-omics studies



High-level plots

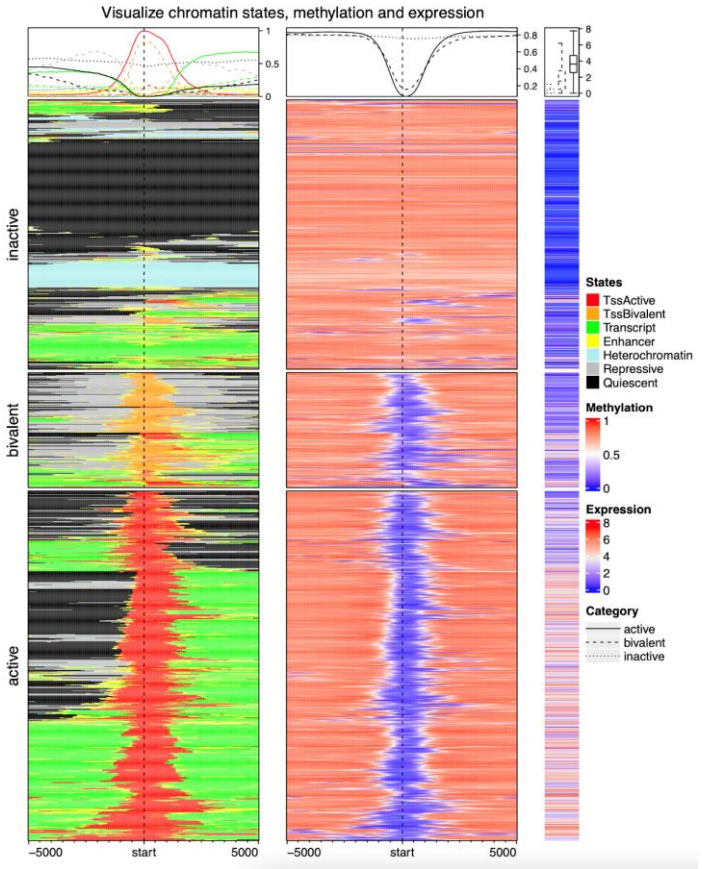
ComplexHeatmap has already implemented some high-level graphics functions:

- Density heatmap
- 3D heatmap
- oncoPrint
- UpSet plot
- Genome-level plots



Integrated in other packages

- *EnrichedHeatmap*
- *InteractiveComplexHeatmap*



Conclusion

- Complex heatmap visualization is a powerful way to associate multiple sources of information.
- We believe *ComplexHeatmap* will continually be a useful tool for bioinformatics and the general data science field for revealing hidden structures in the data.

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