

User Manual of Multi-omic Acra Melanoma Atlas

1. Overview	2
2. Home Page	3
3. Pathology Sections	3
4. Clonal Evolution	3
5. Single-cell RNA-seq	4
6. Spatial Omics	5
7. Molecular Subtypes	5
8. Documents	6
9. About	6

MAMA (Multi-omic Acral Melanoma Atlas) is an interactive web server based on R package *shiny*. It is developed to showing the multi-omic analyze of Acral Melanoma in our research. We hope that our research will inspire future studies on acral melanoma by providing novel multi-omic perspectives.

1. Overview

First let's take an overview of our website, which consists of **4** parts. Utilizing the **Menu bar**, users have the ability to switch to different pages. In the **Functional area**, you can interact with the server by modifying parameters or uploading data, finally controlling the Display area's figure. Furthermore, the abstract of the page is sometimes displayed in this section as supplement. Provided figures or texts are displayed in **Display area**, which helps get an in-depth understanding of our research.



Besides, via clicking this button, users can hide the Menu bar and the name of website. This function provides a better perspective for figure display.

We also realize the function that any functional module could be minimized by clicking the “-”.



2. Home Page

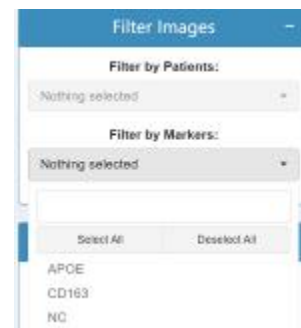


Users should choose a wanted page, then fill in your target genes. By clicking the **“Search”** button, you will skip to the target page and our server will plot the corresponding figure for you.

Attention! You can and only can split genes with **comma(“,”)**, **space(“ ”)**, and **newline**. Please don't use other ways

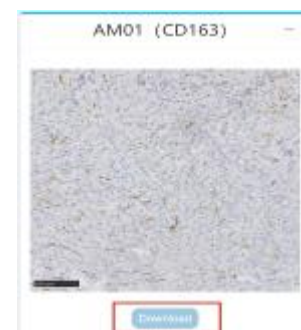
3. Pathology Sections

Users can filter the pictures via patients or markers. Users can view and download images.



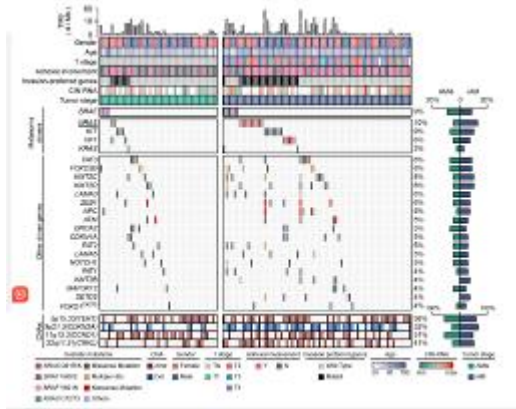
Besides, we allow users to upload their own picture to contract with ours.

Filter or not, immunohistochemical pictures will be shown on the Display area. By clicking the **“Download”** button below a picture, users could download it. **All** of our pictures are **downloadable** for academic.



4. Genomic Profiling

In the context of cancer, clonal evolution describes how tumor cells accumulate genetic alterations over time, leading to the formation of multiple subclones with differing genomic profiles. These subclones may have different



growth rates, responses to therapy, and metastatic potentials, contributing to the complexity and heterogeneity of cancer and posing challenges for effective treatment. Clonal evolution can be analyzed using techniques such as single-cell sequencing, multi-region

sampling, and phylogenetic analysis to reconstruct the evolutionary history of the tumor and identify the genetic alterations and evolutionary trajectories that give rise to different cellular subpopulations.

We provide our ComplexHeatMap figure in this page. Users can refer to it to decide the inputted genes in the functional area. In this way you can customize a heatmap you want about clonal evolution. Please pay attention to the way you split genes. **Only** comma(“,”), space(“ ”), and newline can be used.

5. Single-cell RNA-seq

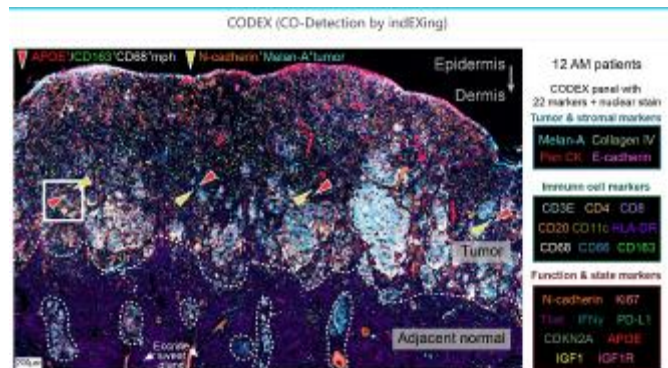
Users can visualize gene expression features in single-cell RNA sequencing data by clicking the **“Plot”** button to submit your target genes. We’ll provide the **Featureplot** figures and **expression** across subclusters in the corresponding dataset. (This function will be implemented in future website updates.) It allows researchers to quickly and intuitively view the

expression levels of different genes within individual cells, and can associate this information with cell clustering, subgroups, etc. Below the Image Generate Area, users can find provided reference marker genes and subclusters annotation, which can guide to choose the target genes. If you input

unrecognized genes, our server will return **“No data”** rather than Feature plot figures. **Only** comma(“,”), space(“ ”) and newline are allowed. It will also influence our feedback.

6. Spatial Omics

The conventional approach to studying tissue transcriptomes involves RNA-sequencing (RNA-seq) of homogenized biopsies, resulting in an averaged transcriptome and the loss of spatial information. Spatial omics refers to a group of techniques that integrate traditional omics approaches, such as genomics, transcriptomics, proteomics, and metabolomics, with spatial information within biological systems. These technologies enable the characterization and analysis of biomolecules within the context of their precise location in tissues and cells.



Input Gene(s)

Input Genes
Upload Gene List

Enter multiple genes (split by newline, space, or comma)

CD163 CD4

Plot

The same as Molecular Subtypes, we allow users to input or upload genes, resulting in corresponding Spatial Transcriptomics figures. Splitting by comma(“,”), space(“ ”) and newline is still a **must**. Reference spatial areas are also provided.

7. Molecular Subtypes

Select Patient

Input Genes
Upload Gene List

Enter genes (split by newline, space, or comma)

CD4
 CD3E APOE, CSF3R CD163

Plot Survival

By inputting or uploading genes, users could get the corresponding Patient Survival Plot Regions. **Only** comma(“,”), space(“ ”), and newline are allowed to use.

8. Document

Just read this.

9. About

We provide the used R package, citation, contact way. All resources are allowed to be used for academic. If you have any problems, please contact Hengkang Liu (liuhengkang@pku.edu.cn).