



iMLGAM: integrated Machine Learning and Genetic Algorithm-driven Multiomics analysis for pan-cancer immunotherapy response prediction

Bicheng Ye^{1#}, Jun Fan^{2#}, Lei Xue^{2#}, Yu Zhuang^{3#}, Peng Luo⁴, Aimin Jiang⁵,
Wenhang Zhou^{6*}, Chuanli Ren^{7*}, Haoran Lin^{2*}, Pengpeng Zhang^{8*}

¹Zhongda Hospital, Medical School, Southeast University,

²The First Affiliated Hospital of Nanjing Medical University,

³Nanjing Chest Hospital, ⁴Zhujiang Hospital, Southern Medical University,

⁵Changhai Hospital, ⁶The Affiliated Huai'an Hospital of Xuzhou Medical University,

⁷Northern Jiangsu People's Hospital Affiliated to Yangzhou University,

⁸Tianjin Medical University Cancer Institute and Hospital

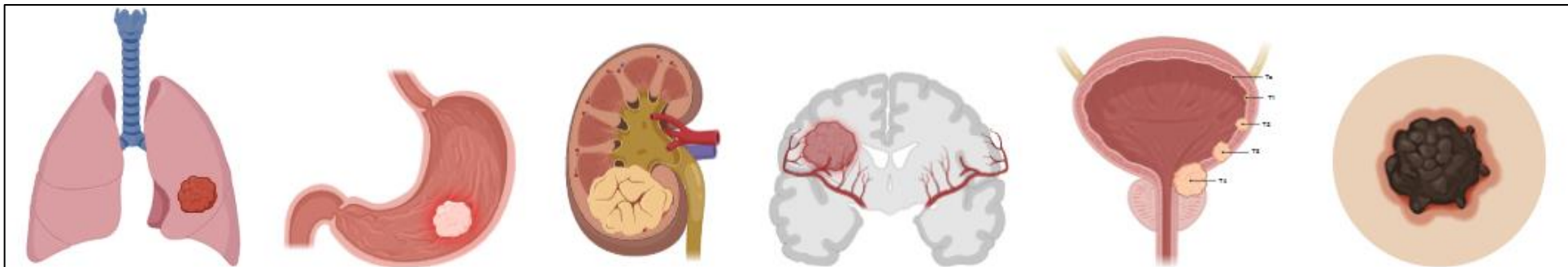


Bicheng Ye, Jun Fan, Lei Xue, Yu Zhuang, Peng Luo, Aimin Jiang, et al. 2025. iMLGAM: integrated Machine Learning and Genetic Algorithm-driven Multiomics analysis for pan-cancer immunotherapy response prediction. *iMeta* 4: e70011.

<https://doi.org/10.1002/imt2.70011>



Introduction



iMLGAM: integrated Machine Learning and Genetic Algorithm-driven Multiomics analysis for pan-Cancer immunotherapy response prediction

Overview

This repository contains data and code related to the study of predictive models for pan-cancer immunotherapy. The purpose of this study is to construct a signature based on RNA sequencing data to predict the outcomes of immunotherapy in patients with pan-cancer.

Directory Structure

- `Figure1`, `Figure2`, ...: Data and original code for saving generated figures.
- The source code of the iMLAGA package.

Prerequisites

Make sure you have R and the following packages installed: iMLAGA. Install "iMLAGA" via this [GitHub page](#) or by running the code.

```
devtools::install_github("Yelab1994/iMLGAM")
```

Calculate iMLGAM Score for Guiding ICI Therapy

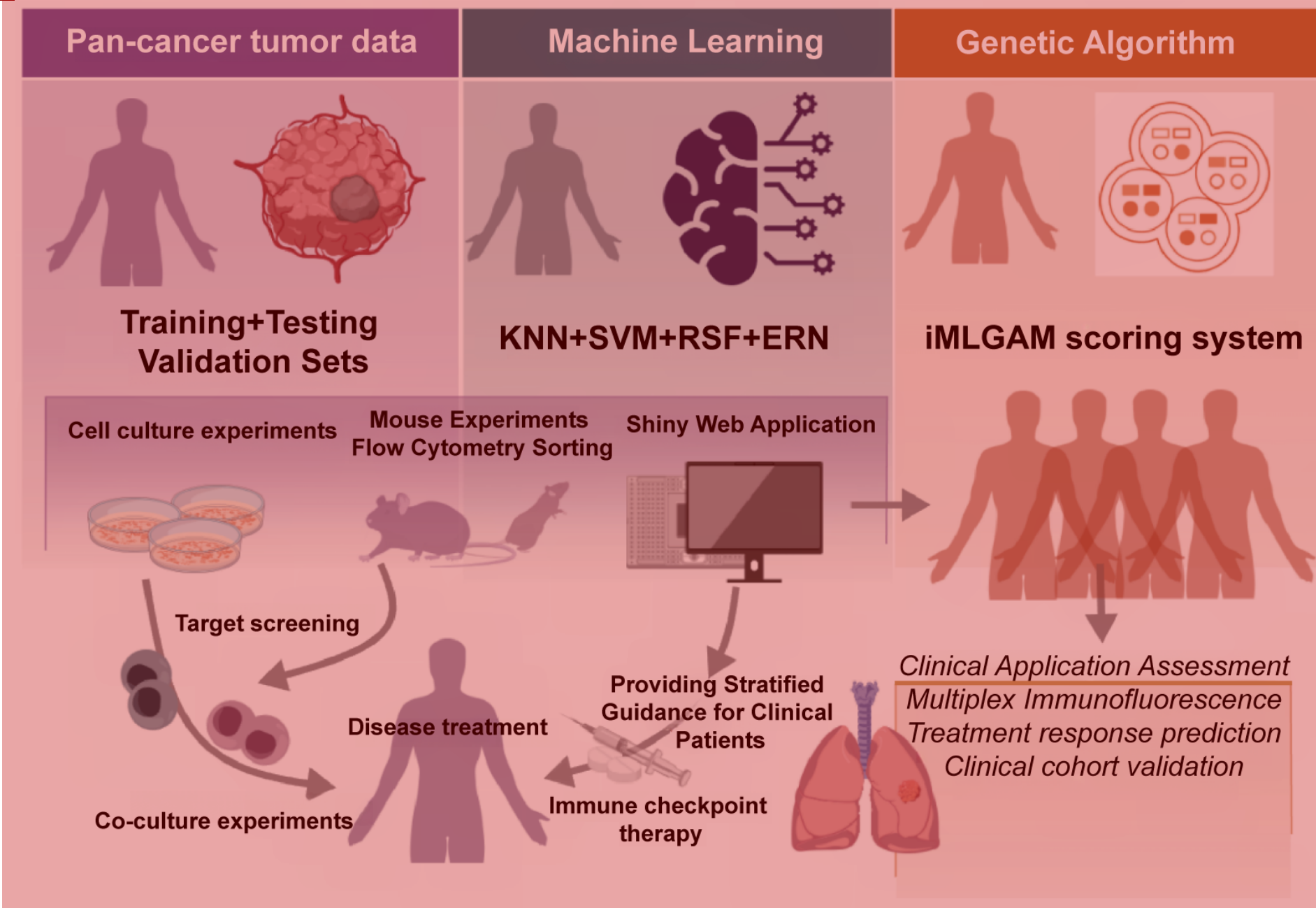
If the iMLGAM score is lower than 0.966, it may benefit from ICI therapy.

Expression	
BMP2	SELE
<input type="text" value="0"/>	<input type="text" value="0"/>
CD274	SH3TC1
<input type="text" value="0"/>	<input type="text" value="0"/>
CHST15	LAG3
<input type="text" value="0"/>	<input type="text" value="0"/>
CKLF	TLR7
<input type="text" value="0"/>	<input type="text" value="0"/>
ESCO2	RXRA
<input type="text" value="0"/>	<input type="text" value="0"/>
<input type="button" value="Submit"/>	

<https://github.com/Yelab1994/iMLGAM>

https://ici-theaphy-gms.shinyapps.io/my_shiny_app/

Highlights



Development of iMLGAM Scoring System

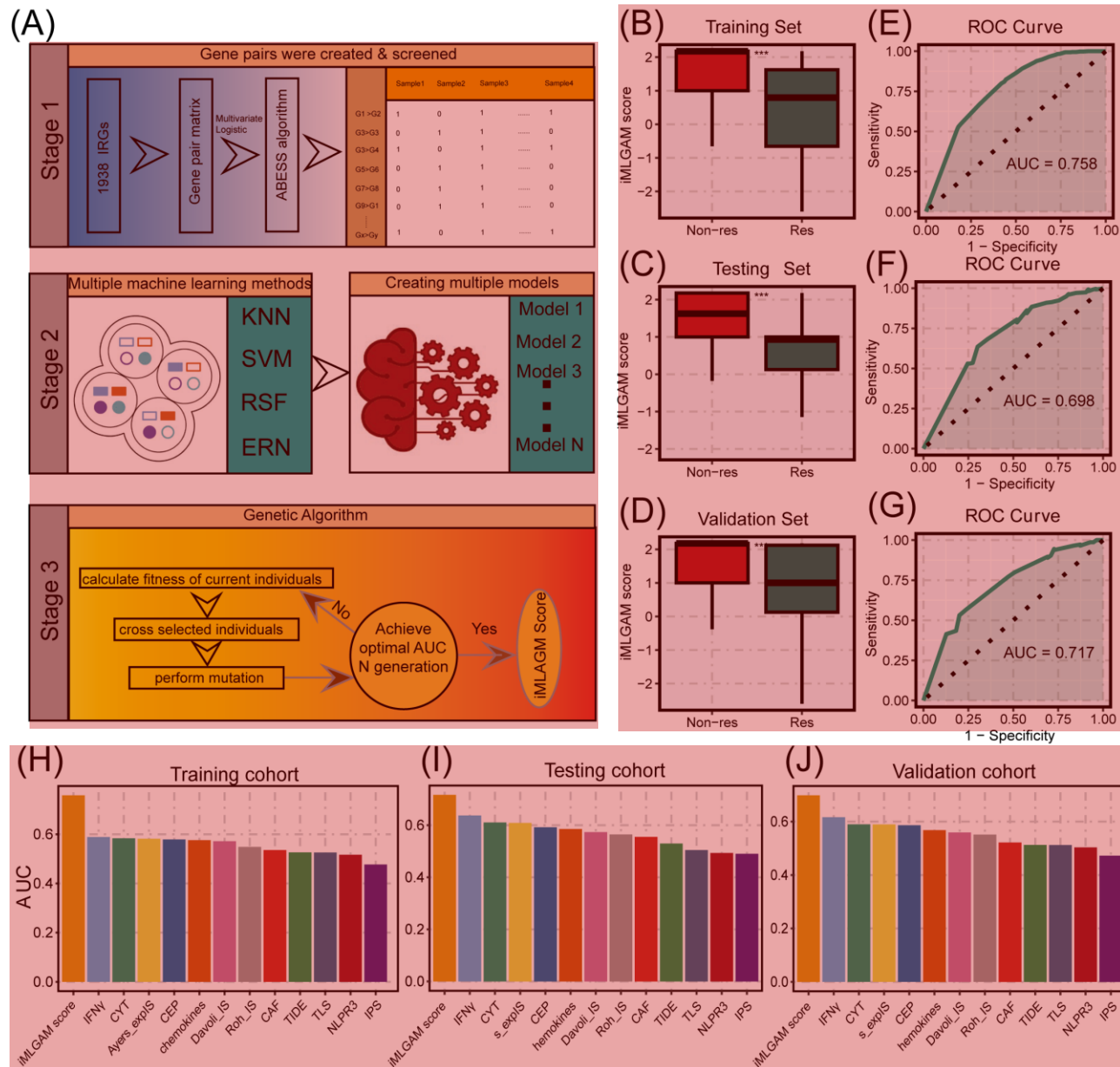


Figure 1. Construction and Validation of the iMLGAM Scoring System

iMLGAM Score Website Development and Pathway Analysis

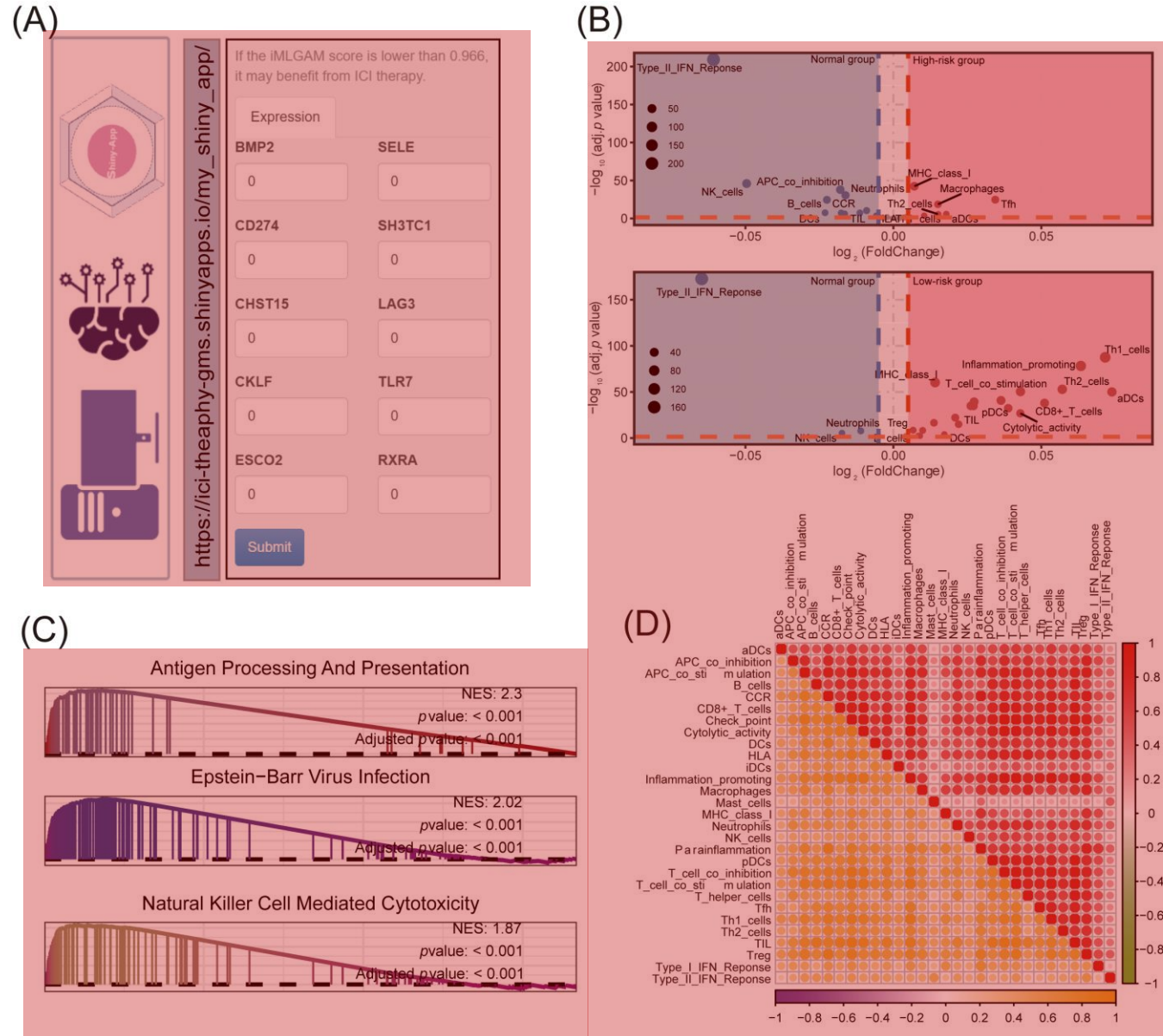


Figure 2. Correlation Analysis of iMLGAM Score with Immune Features and Molecular Pathways

Clinical Validation of iMLGAM Score

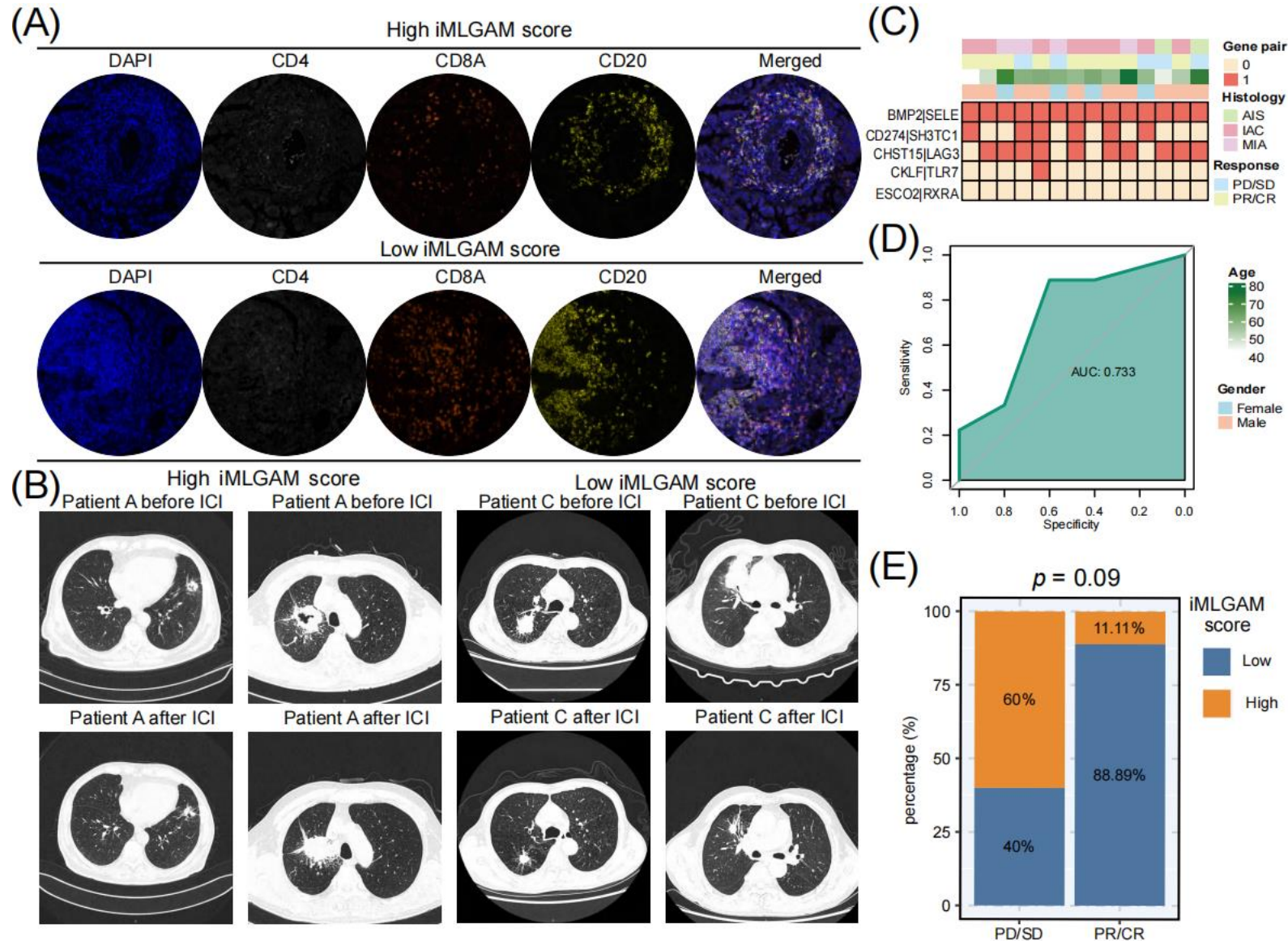
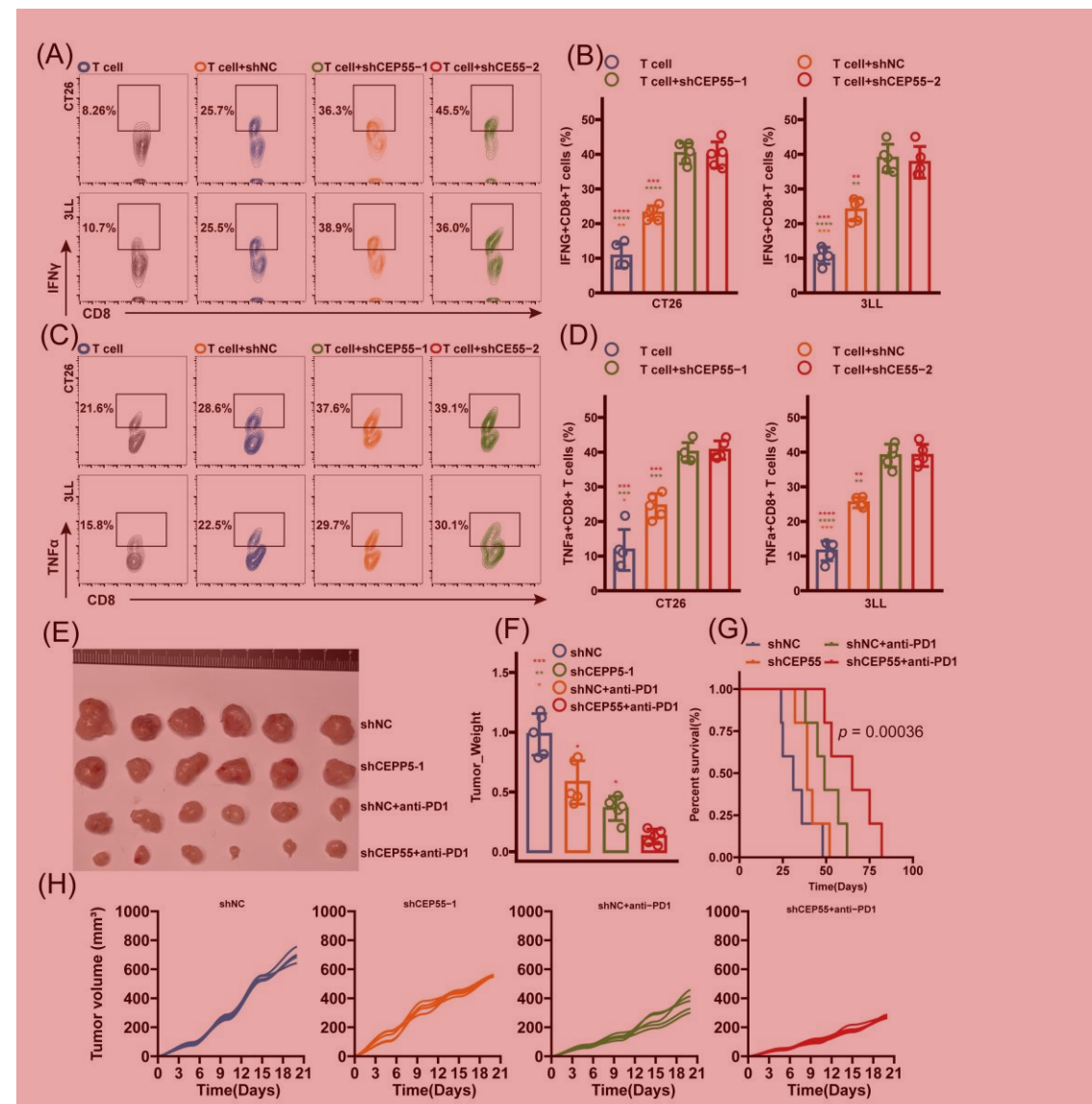
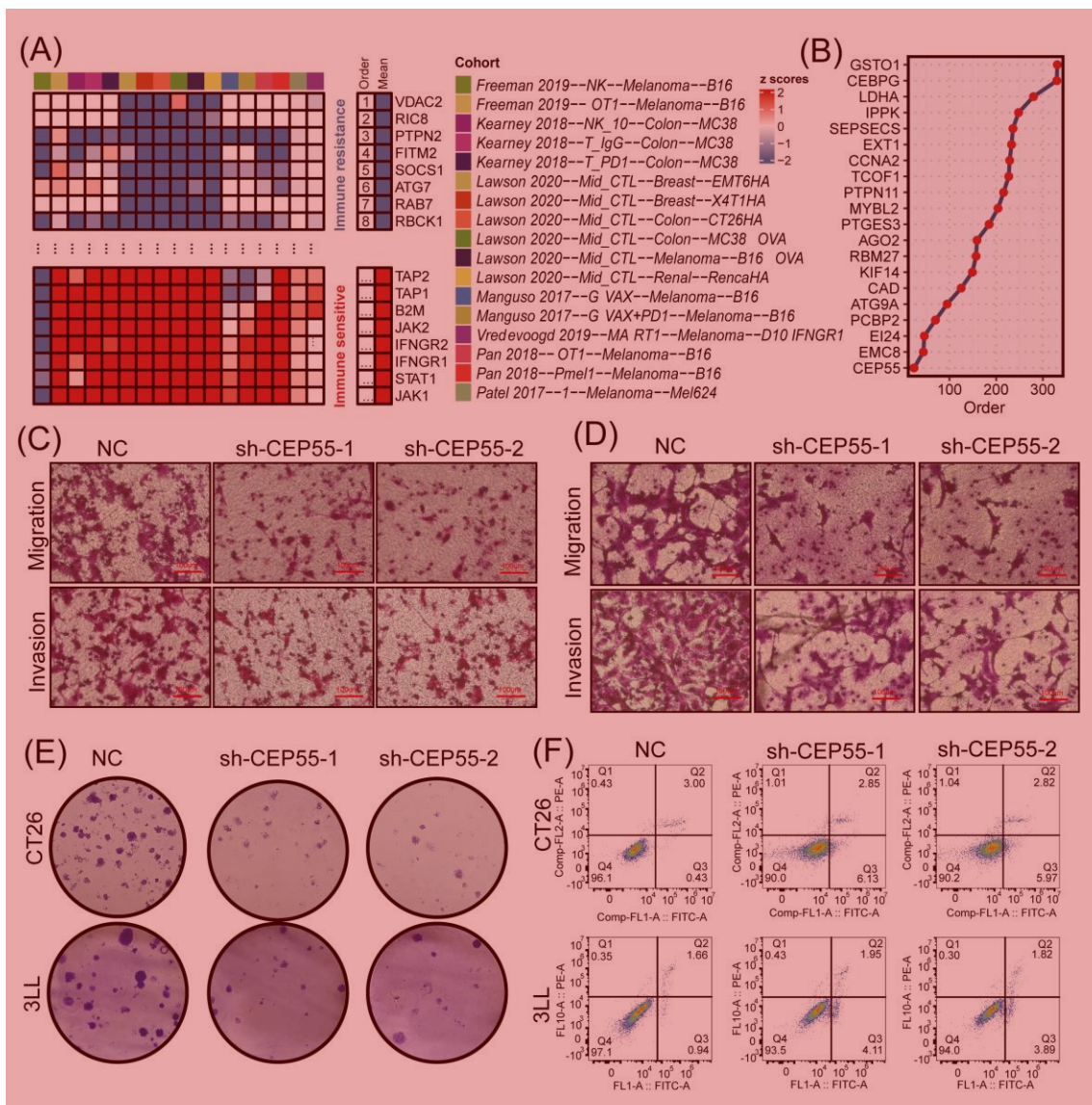


Figure 3. Clinical Validation of iMLGAM Score in House-Based Cohort



CRISPR Screening and Functional Analysis of CEP55



Figures 4 and 5. CRISPR Screening and Functional Analysis of CEP55 Based on iMLGAM Score



Summary

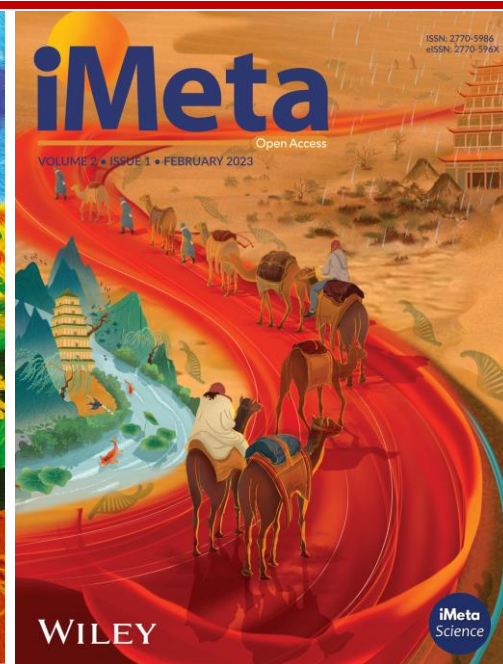
- ❑ In this study, we developed the iMLGAM scoring system, a multi-omics analysis tool that integrates machine learning and genetic algorithms to predict tumor patients' response to immunotherapy;
- ❑ Through multi-cohort validation, we found that the iMLGAM score could effectively predict the efficacy of immune checkpoint blockade (ICB) therapy;
- ❑ For user convenience, we developed an online analysis tool that can be directly accessed through a web interface:
https://ici-theaphy-gms.shinyapps.io/my_shiny_app;
- ❑ The R package version of iMLGAM has been open-sourced on GitHub, and researchers can access it at <https://github.com/Yelab1994/iMLGAM>

Bicheng Ye, Jun Fan, Lei Xue, Yu Zhuang, Peng Luo, Aimin Jiang, et al. 2025. iMLGAM: integrated Machine Learning and Genetic Algorithm-driven Multiomics analysis for pan-cancer immunotherapy response prediction. *iMeta* 4: e70011.

<https://doi.org/10.1002/imt2.70011>




iMeta: Integrated meta-omics to change the understanding of the biology and environment

WILEY



“***iMeta***” is a Wiley partner journal launched by iMeta Science Society in 2022, first **impact factor (IF) 23.8 in 2024, ranking top 107/21973 in world and 2/161 in the microbiology**. It aims to publish innovative and high-quality papers with broad and diverse audiences. **Its scope is similar to *Nature, Cell, Nature Biotechnology/Methods/Microbiology/Medicine/Food* etc.** Its unique features include video abstract, bilingual publication, and social media dissemination, with more than 600,000 followers. Indexed by **SCIE, PubMed, Google Scholar** etc.

“***iMetaOmics***” launched in 2024 and ***iMetaMed*** in 2025, with a **target IF>10, and its scope is similar to *Nature Communications, Cell Reports, Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics*, etc.** All contributes are welcome!

 Society: <http://www.imeta.science>
 Publisher: <https://wileyonlinelibrary.com/journal/imeta>
 Submission: <https://wiley.atyponrex.com/journal/IMT2>
<https://wiley.atyponrex.com/journal/IMO2>

 office@imeta.science
imetaomics@imeta.science

 [Promotion Video](#)

 [iMetaScience](#)

 [iMetaScience](#)