



# A Hiplot-based web service for cold atmospheric plasma high-throughput data integration and analysis on breast cancer

Xiaofeng Dai<sup>1\*#</sup>, Mingjie Wang<sup>2#</sup>, Yang Liu<sup>1</sup>

<sup>1</sup>National Local Joint Engineering Research Center for Precision Surgery & Regenerative Medicine, Shaanxi Provincial Center for Regenerative Medicine and Surgical Engineering, The First Affiliated Hospital of Xi'an Jiaotong University, Xi'an Jiaotong University, Xi'an 710061, China

<sup>2</sup>Department of Gastroenterology, Ruijin Hospital, Shanghai Jiaotong University, School of Medicine, Shanghai 200025, China

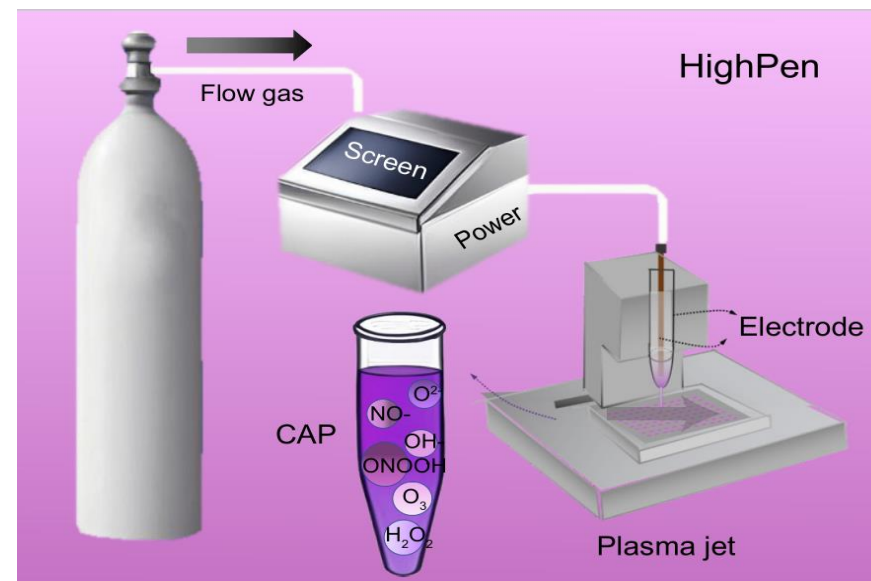
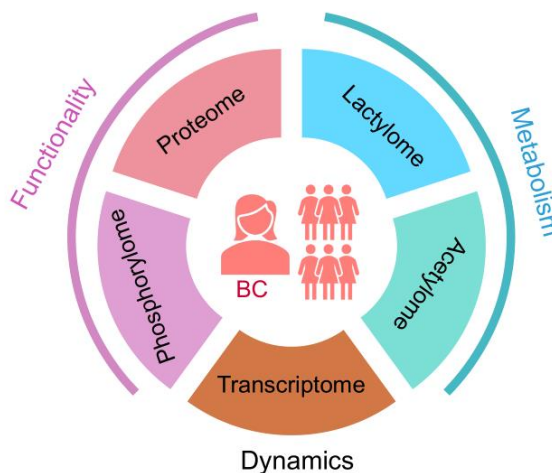
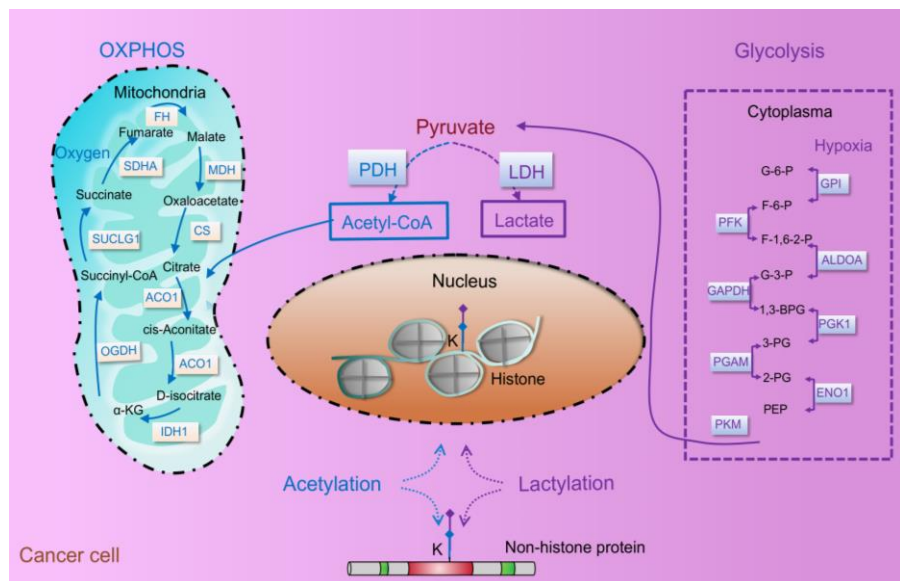


Xiaofeng Dai, Mingjie Wang, Yang Liu. 2025. A Hiplot-based web service for cold atmospheric plasma high-throughput data integration and analysis on breast cancer. *iMeta* 4: e70045. <https://doi.org/10.1002/imt2.70045>



# Introduction

Hiplot-based center for cold atmospheric plasma (CAP) omics data integration and analysis on breast cancer (BC)



**Figure 1.** Illustrative diagram showing the rationale for gaining metabolic clues from combining the acetylome and lactylome using cold atmospheric plasma medicine in breast cancer (CAPmed-BC).

**Figure 2.** Illustrative diagram showing the infrastructure of HighPen and the procedure of CAP preparation.



# Highlights

- ❑ CAP, short for cold atmospheric plasma, represents an emerging onco-therapeutics that can specifically ablate cancer cells without harming their healthy peers via redox perturbation.
- ❑ CAPmed-BC, CAP medicine in breast cancer, is the first reservoir of multi-level omics data including whole transcriptome, acetylome, lactylome, proteome, phosphorylome recording the responses of different types of breast cancer cells to CAP treatment.
- ❑ CAPmed-BC can be used to capture the dynamics, functionality and metabolism of triple negative breast cancer (TNBC) cells in response to CAP treatment.
- ❑ CAPmed-BC is unique in interrogating cell metabolic alterations through coupled analysis of acetylome and lactylome.



# Case 1: Multi-omics data analysis using the database

**CAPmed-BC**

1. <https://hiplot.com.cn>

Tools → Data analysis

2. <https://capbc.hiplot.com.cn>

Omics data: Whole transcriptome

Cancer Subtype	TNBC		Non-TNBC		
	Group	CAP treatment	Control	CAP treatment	Control
Whole transcriptome, CAP 1h	Available	Available	Available	Available	Available
Whole transcriptome, CAP 8h	Available	Available	Available	Available	Available
Acetylation	Available	Available	Available	NA	NA
Lactylation	Available	Available	Available	NA	NA
Protome	Available	Available	NA	NA	NA
Phosphorylome	Available	Available	NA	NA	NA

3. mRNA

Differential expression | Single gene expression | GO\_KEGG | GSEA | PPI network

Group 1: TNBC\_CAP\_1h  
Group 2: TNBC\_Control

P Cutoff: 0.05  
LogFC Cutoff: 2.00

Start analysis

↓ Figure1 | ↓ Figure2 | ↓ Table

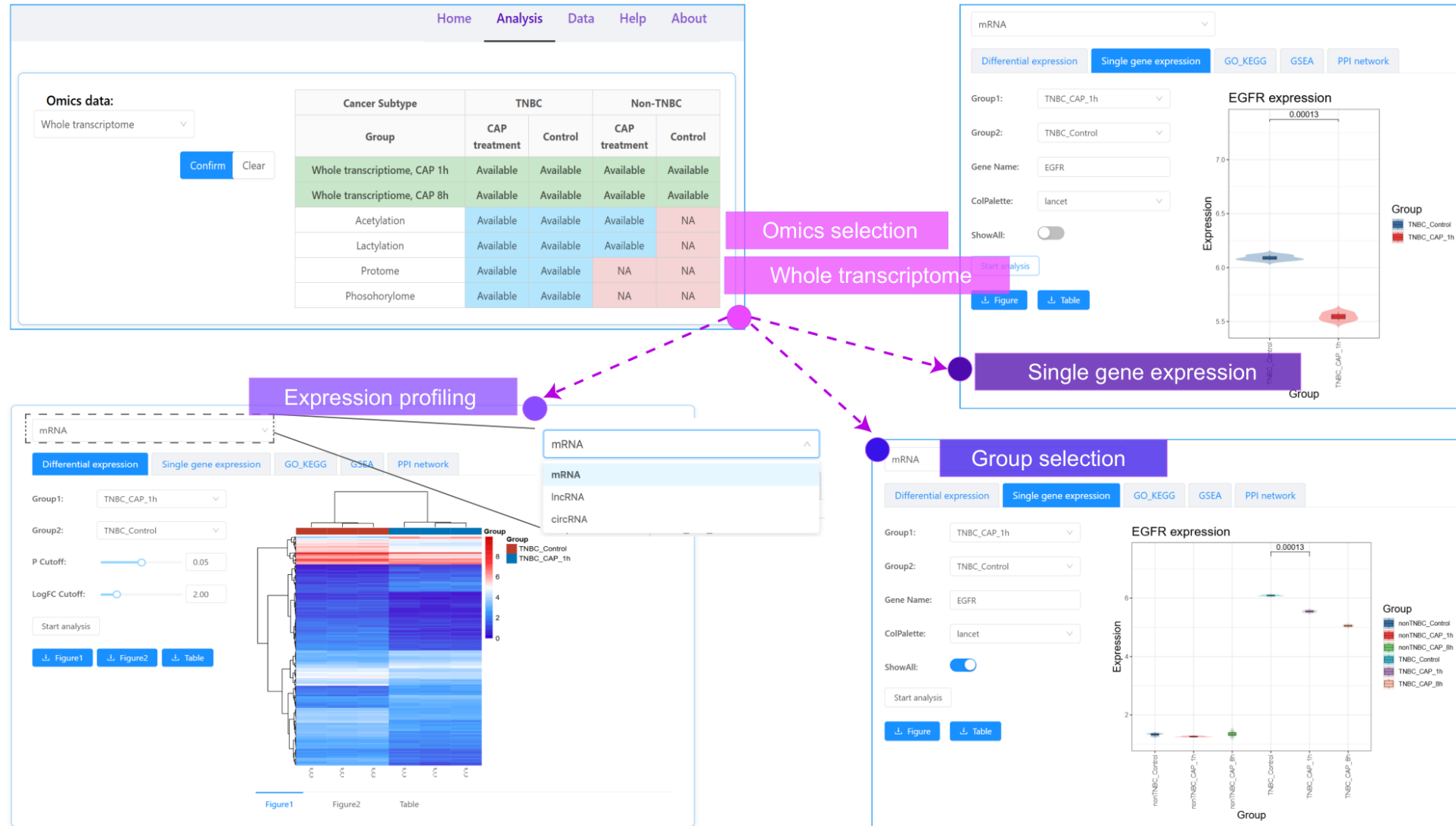
GeneName	logFC	AveExpr	t	PValue	adj.PVal	B
MIR3648-1	3.445067734858 82	4.633564534713 69	8.976010890993	0.000459634224 271983	0.006892536176 66039	0.264 91
RNU1-1	2.922062231531 85	2.566176536291 37	23.16527667607 08	0.000006711988 18056137	0.001078512049 28457	4.974
RNU1-2	2.279803322986 55	5.003509819722 08	20.57331235303 66	0.000011470398 2442312	0.001194484494 02774	4.421 69
LINC00506	-2.22492695346 297	6.465302665018 14	-14.0372801163 265	0.00063861341 3781854	0.002688537029 25612	2.541 32
LOC100129434	-2.20423812761 214	5.817692928784 32	-15.9616192690 527	0.00035935938 8777548	0.001983479692 30381	3.184 75
RNVU1-7	2.168553271195 08	1.540217498782 73	10.51290512015 6	0.000230235942 95233	0.004861391026 94075	1.071 26

Figure1 | Figure2 | Table

4. Heatmap, Volcano plot, GSEA, KEGG, Gene Ontology, Network

Figure 3. A demonstration of data analysis workflow in CAPmed-BC.

# Case 2: Single Gene Expression Analysis



**Figure 4.** A demonstration of single gene expression analysis using whole transcriptome data in CAPmed-BC.

# Case 3: Proteome and Phosphoproteome Combined Analysis



**Figure 5.** A demonstration of combinatorial analysis using proteome and phosphoproteome data in CAPmed-BC



# Case 4: Metabolic Reprogramming Clues Identification

## Acetylome

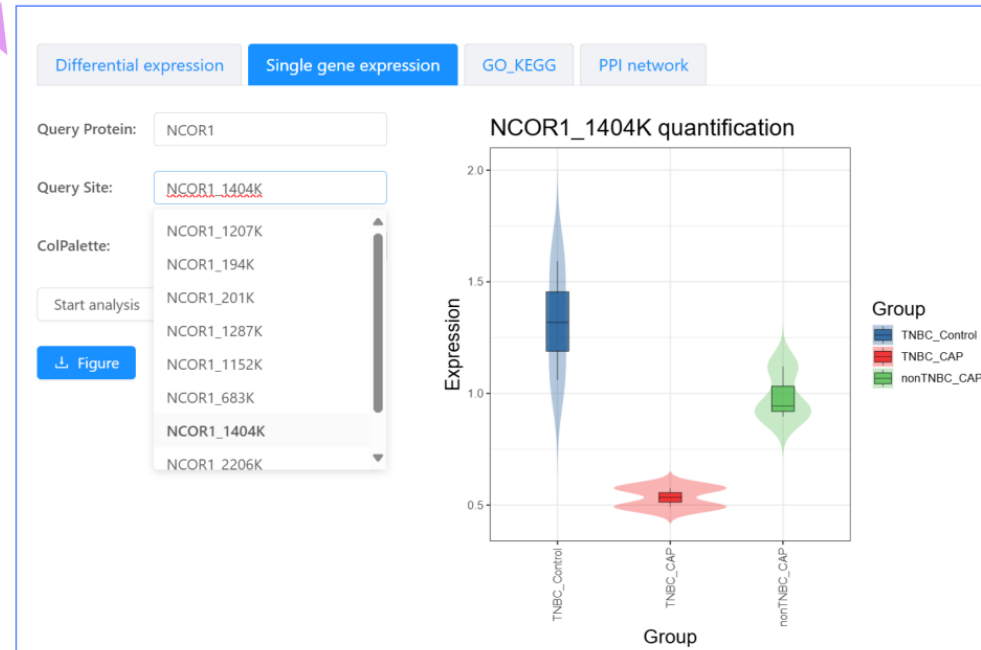
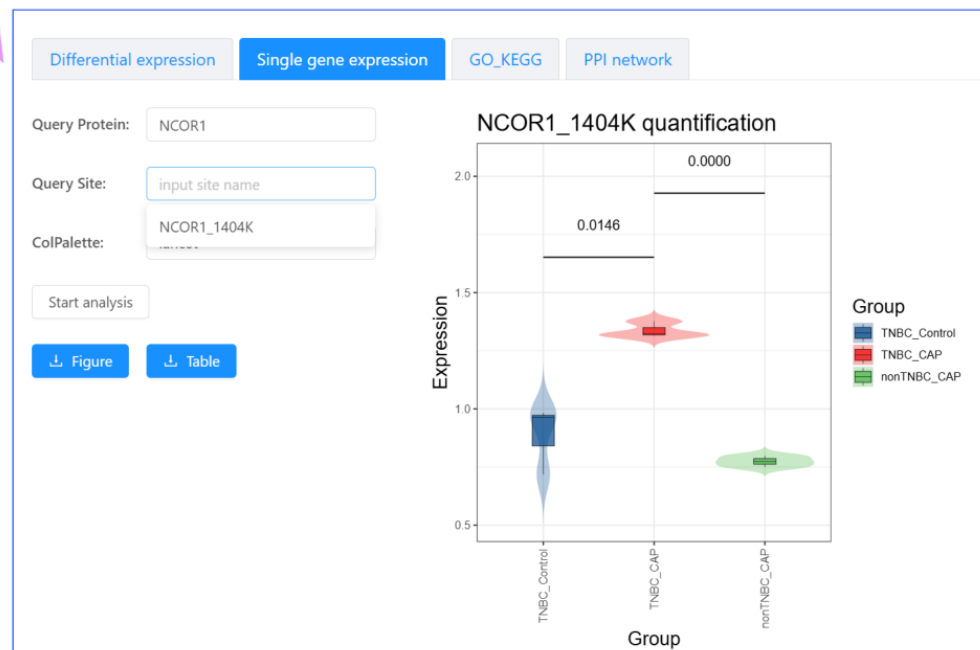
Omics data:

Cancer Subtype	TNBC		Non-TNBC	
	CAP treatment	Control	CAP treatment	Control
Whole transcriptome, CAP 1h	Available	Available	Available	Available
Whole transcriptome, CAP 8h	Available	Available	Available	Available
Acetylation	Available	Available	Available	NA
Lactylation	Available	Available	Available	NA
Protome	Available	Available	NA	NA
Phosphorylome	Available	Available	NA	NA

## Lactylome

Omics data:

Cancer Subtype	TNBC		Non-TNBC	
	CAP treatment	Control	CAP treatment	Control
Whole transcriptome, CAP 1h	Available	Available	Available	Available
Whole transcriptome, CAP 8h	Available	Available	Available	Available
Acetylation	Available	Available	Available	NA
Lactylation	Available	Available	Available	NA
Protome	Available	Available	NA	NA
Phosphorylome	Available	Available	NA	NA



**Figure 6.** A demonstration of combinatorial analysis using acetylome and lactylome data in CAPmed-BC.



# Summary

- ❑ We introduced CAPmed-BC, a platform for analyzing breast cancer responses to CAP through multi-omics data integration.
- ❑ The platform integrates transcriptome, proteome, phosphorylome, acetylome, and lactylome data, and is equipped with various analytical tools such as differential expression analysis, GSEA, and protein-protein interaction (PPI) network analysis to meet the research needs.
- ❑ CAPmed-BC enables in-depth exploration of the dynamic changes, functional activities, and metabolic reprogramming of TNBC cells following CAP treatment, facilitating a comprehensive understanding of the molecular mechanisms and promoting research progress in plasma oncology.
- ❑ Website : <https://capbc.hiplot.com.cn>

Xiaofeng Dai, Mingjie Wang, Yang Liu. 2025. A Hiplot-based web service for cold atmospheric plasma high-throughput data integration and analysis on breast cancer. *iMeta* 4: e70045. <https://doi.org/10.1002/imt2.70045>



“**iMeta**” launched by iMeta Science Society in 2022, **impact factor (IF) 23.8**, 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 Cell, Nature, Science, Nature Biotechnology/Methods/Microbiology/Medicine/Food**. Its unique features include video abstract, bilingual publication, and social media with 600,000 followers. Indexed by **SCIE/ESI, PubMed, Google Scholar** etc.

“**iMetaOmics**” launched in 2024, 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.

“**iMetaMed**” launched in 2025, with a **target IF>15**, similar to **Med, Cell Reports Medicine, eBioMedicine, eClinicalMedicine** etc.



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

Submission: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



[iMetaScience](#)



[iMetaScience](#)



[office@imeta.science](mailto:office@imeta.science)  
[imetaomics@imeta.science](mailto:imetaomics@imeta.science)



[Promotion Video](#)

Update  
2025/5/21