



Ragomics-Meta: 面向代谢研究的多组学一体化分析 workflow 平台

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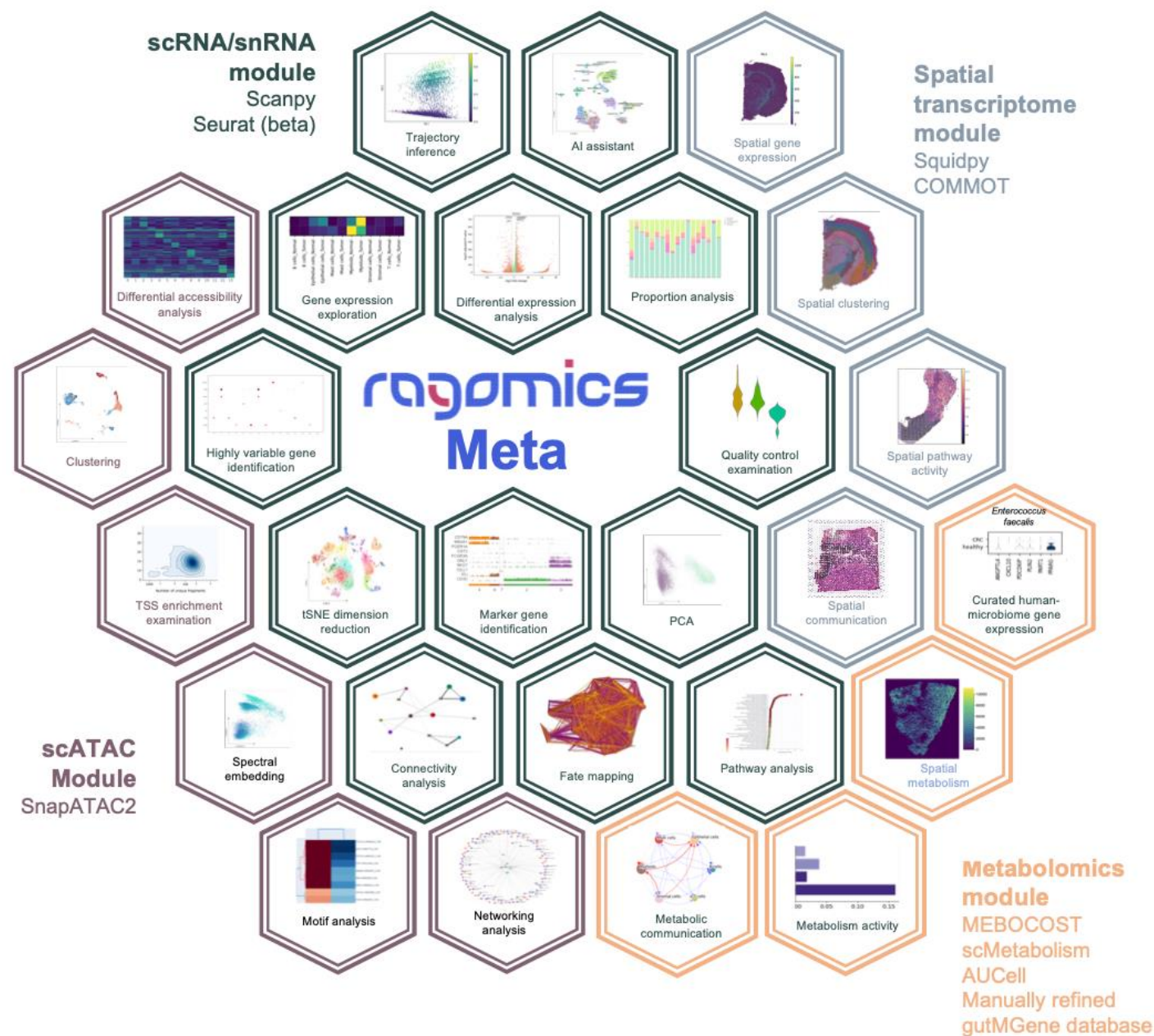


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Ragomics-Meta: An Open-Source, Scalable, Reproducible, and Extensible Multi-Omics Analysis Workflow.

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从单细胞到空间组学：Ragomics-Meta构建代谢研究一体化

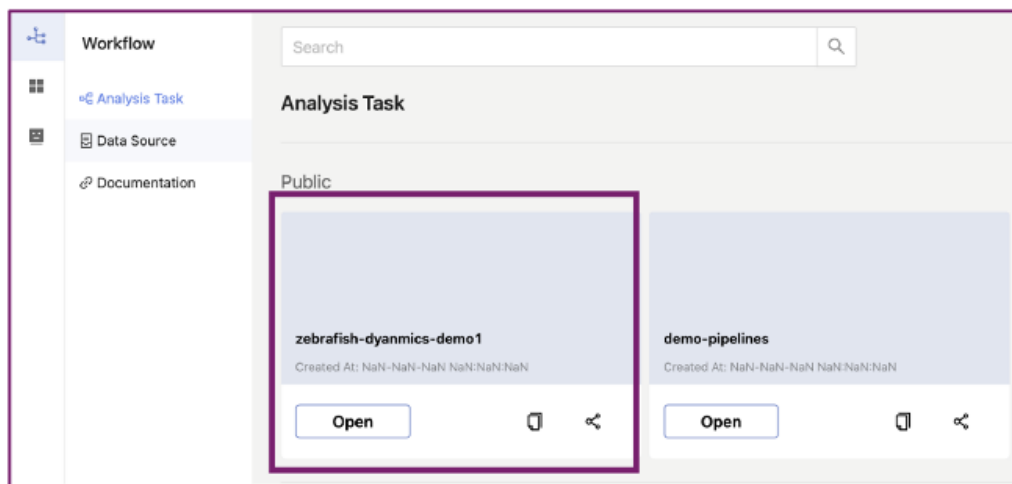


本研究开发了一个面向单细胞、多组学和空间组学的开放式分析工作流 **Ragomics-Meta**。该平台整合了scRNA/snRNA-seq、scATAC-seq、空间转录组和空间代谢组等数据分析模块，支持质量控制、降维聚类、差异表达、染色质可及性分析、代谢通路活性评分、细胞间通讯、转录因子调控网络、空间代谢可视化以及宿主-微生物互作探索。

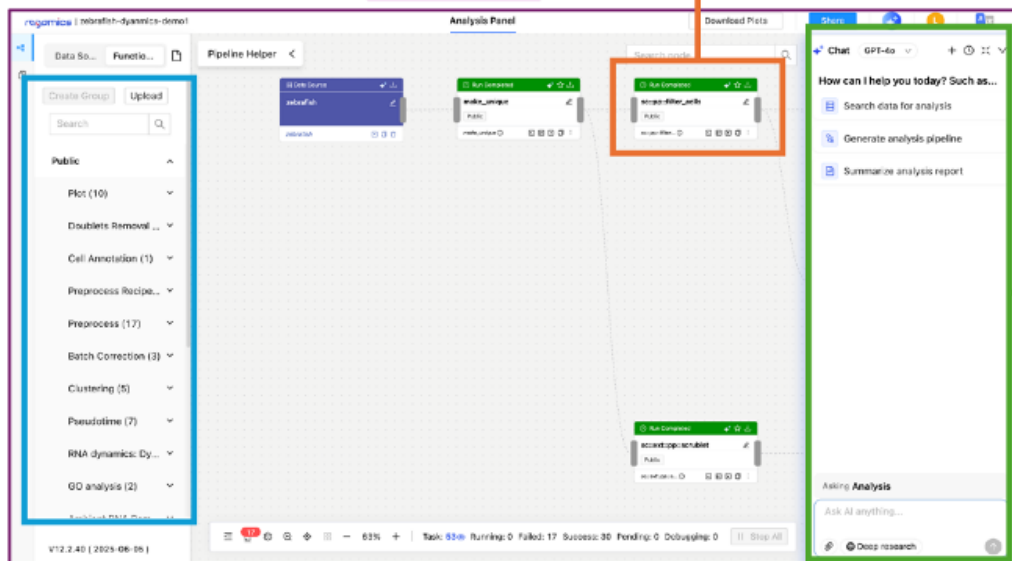


任务式云平台设计

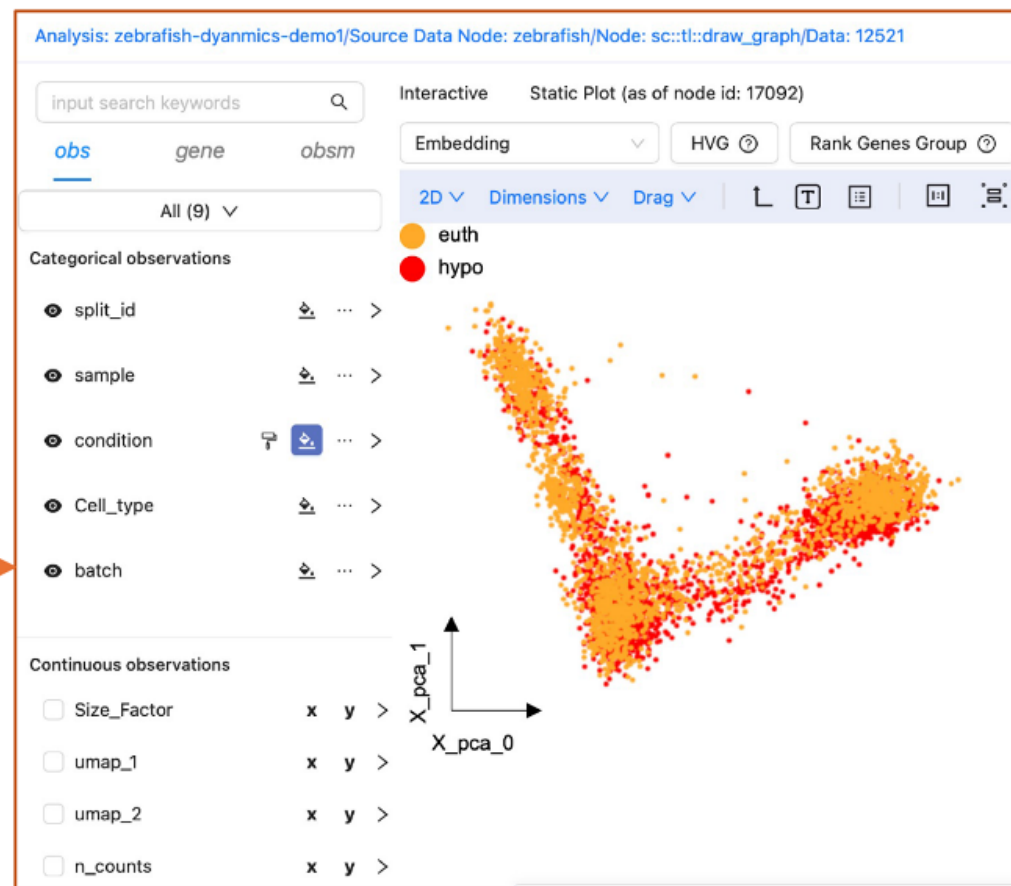
(A) Task panel



(B) Analysis panel



(C) Visualization panel

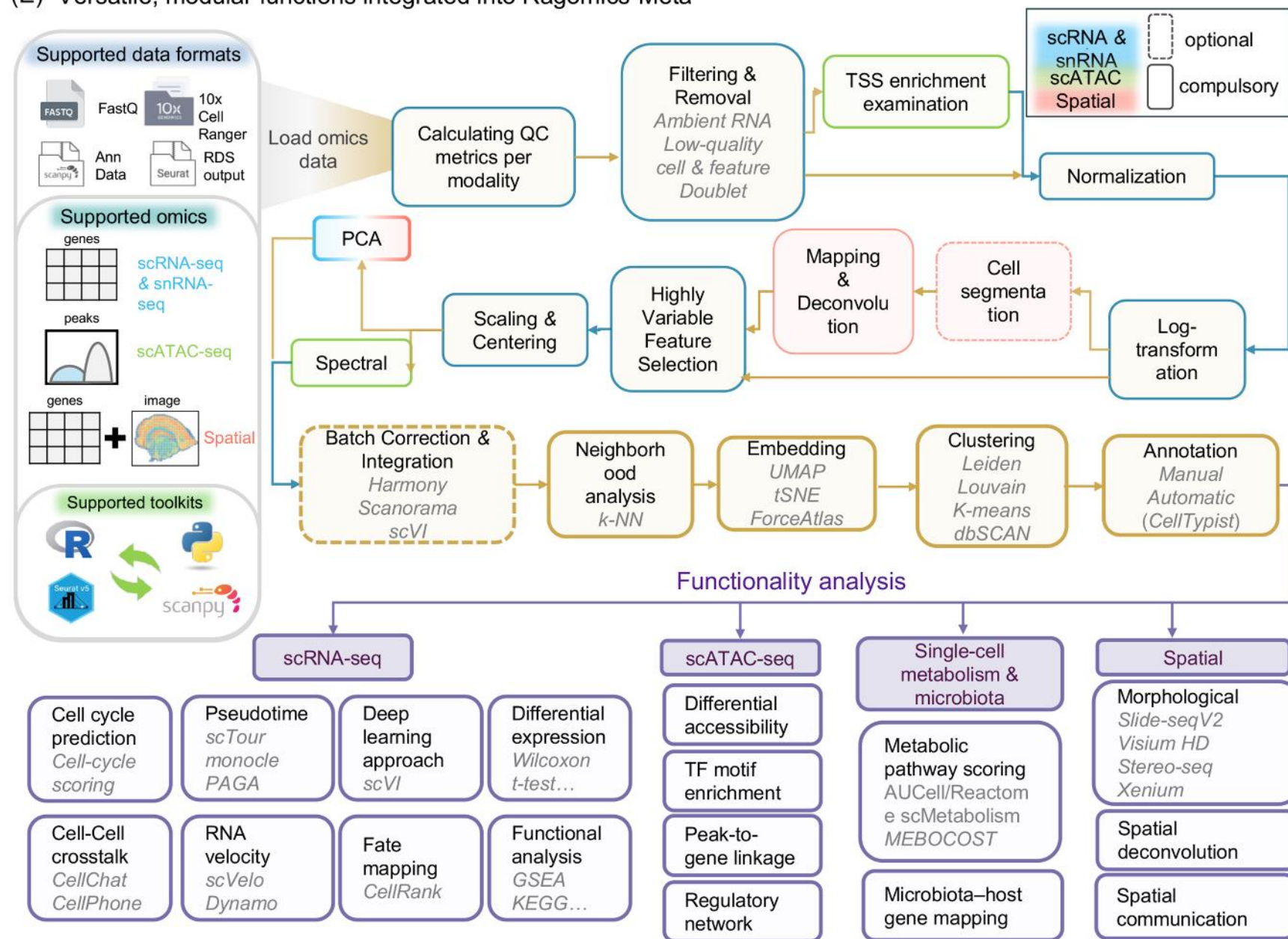


(D) Supported AI assistants



模块化 workflows: 覆盖质控、注释、通讯、代谢与空间解析

(E) Versatile, modular functions integrated into Ragoomics-Meta





云工具：AI辅助解读

Chat List

New Chat

Hello, I have a list of genes involving the interaction between human and gut microbiome, can you pinpoint which pathways are related for these genes? Here is the genelist: CCL20 DUOX2 IL10 IL12B IL12A TNF TLR2 TLR4 CXCL8 IL6 MAPK1 CCR6 CXCR6 CXCR3 TJP2 PRKCZ IL1B TLR5 TJP1 CLDN1 OCLN CGN DEFB4A CLDN4 F11R TGFB1 FOXP3 MAPK14 IKBKE MIR146A MIR155 CXCL10 PDCD6IP FFAR2 NFKB1 IL1A IL2 IL5 MYD88 RORA CXCL1 CXCL5 IL17A ANGPTL4 PLIN2 PPARG NR1H4 GLP1R VEGFA ACTB PARD6B ACTC1 ITCH JUP CNKSR3 SNAI1 HNF4A CD2AP VCL MAGI3 PALS1 CPSF2 CDK4 IFNG LEP CYP7A1 GPBAR1 TLR6 CLGN TJP3 CLDN14 IL4 SLC5A8 MUC1 MUC2 MGAT3 B4GALT1 ST6GAL1 FOS JUN PGP SLC19A2 SLC19A3 SLC9A3 RELA BCL10 SLC26A3 MGAT4B MGAT4A IL22RA2 PTGS2 IL18 HDAC3 HCAR2 CDKN1A Htr1a NBPFL13P RMRP RNR1 APOE CCL2 COX1 FABP2 HK2 LDHA ENO1 ENO1-IT1 IRAK1 IRAK4 TAB2 PTGER3 LPA GOT1 GPT IL11 IL24

To identify the related pathways for the genes involved in human-gut microbiome interactions, databases such as KEGG, Reactome, BioCarta, or pathway analysis tools could be used. Here is a list of some well-known pathways potentially associated with the provided genelist. Please further verify using specific databases or pathway analysis tools for precise mappings: 1. **CCL20, CXCL8, CXCL1, CXCL5, CXCL10, CCL2** – Chemokine signaling pathway. 2. **DUOX2, NOX family members** – Reactive Oxygen Species (ROS) generation and regulation. 3. **IL10, IL12B, IL12A, IL6, IL1B, IL1A, IL2, IL5, IL4, IL17A, IL24, IL22RA2** – Cytokine-cytokine receptor interaction pathways. 4. **TNF, IL10, IL6, CXCL8, TLR pathways** – TNF signaling pathway. 5. **TLR2, TLR4, TLR5, MYD88, IRAK1, IRAK4** – Toll-like receptor signaling pathway. 6. **MAPK1, MAPK14, JUN, FOS** – MAPK signaling pathway. 7. **FOXP3** – T cell receptor signaling pathway and regulation of immune response. 8. **TGFB1, FOXP3** – TGF-beta signaling pathway. 9. **PPARG, RORA, NR1H4, HNF4A** – Nuclear Receptor signaling pathways. 10. **NFKB1, MIR146A, MIR155, BCL10, RELA** – NF-kappa B signaling pathway. 11. **PLIN2, FABP2** – Lipid metabolic pathways. 12. **LEP, VEGFA** – PI3K-Akt signaling pathway. 13. **ITCH, JUP, SNAI1** – Wnt signaling pathway. 14. **CDK4** – Cell cycle regulation. 15. **ANGPTL4, VEGFA** – Angiogenesis. 16. **COX1, PTGS2** – Inflammatory response and Prostaglandin synthesis. 17. **APOE** – Cholesterol metabolism and transport. 18. **ENO1, LDHA, HK2, GOT1, GPT** – Glycolysis/Gluconeogenesis pathways. 19. **MGAT3, MGAT4A, MGAT4B, B4GALT1, ST6GAL1** – N-Glycan biosynthesis. Note that the actual involvement in these pathways can vary based on species and tissue type, and cross-referencing with specific pathway databases is recommended for research-specific accuracy.

Input your question there to get answer

AI Interpretation

Regenerate

Interpretation of Function Block Output:

- Biological Significance of Motif Enrichment:**
 - The heatmap illustrates motif enrichment analysis results showing differential enrichment of transcription factor binding motifs between two groups: CRC (colorectal cancer) and healthy cells.
 - The y-axis lists motif names along with identifiers, with colors representing the significance level of enrichment (log-transformed p-values).
 - Dark red represents significant enrichment in CRC samples, whereas blue indicates significant enrichment in healthy samples.
 - Motifs such as TCF7L2 and LEF1 are highly enriched in CRC, suggesting potential regulatory roles in cancer pathogenesis.
- Dataset Changes:**
 - The computation used differentially accessible regions (peaks) identified in previous steps, separating them into CRC and healthy groups based on log2 fold changes.
 - No major changes in sparsity or structure of the dataset are noted post-execution, indicating focus on interpretative analysis rather than data transformation.
- Historical Context:**
 - Previous clustering and differential testing identified groups and peaks underlying this analysis.
 - The analysis follows differential expression with motif enrichment, a critical step for understanding transcriptional regulatory mechanisms.
- Potential Next Steps:**
 - Validate findings with experimental methods, such as ChIP-seq, to confirm motif activity.
 - Integrate data with additional omics layers (e.g., proteomics) for a comprehensive view of molecular differences.
 - Explore motif enrichment in other conditions or cell types for broader insights into regulatory networks.

These interpretations provide insights into the transcriptional landscape differences between CRC and healthy cells, offering a pathway for further investigation into cancer biology.



案例一：大规模ALL单细胞数据验证平台可复现性

(F)

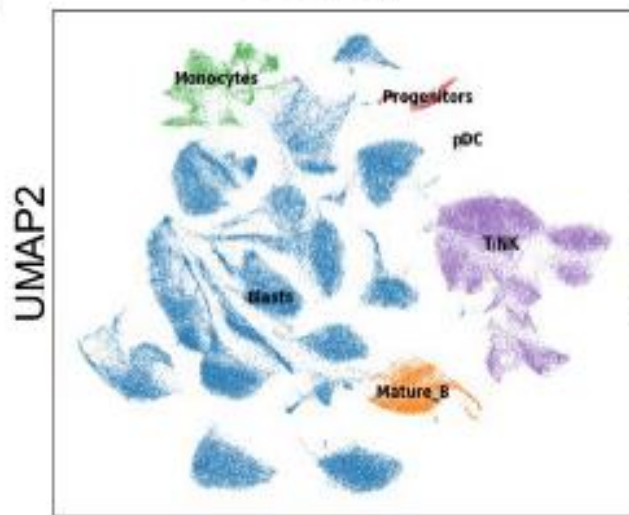


→ Ragomics
meta

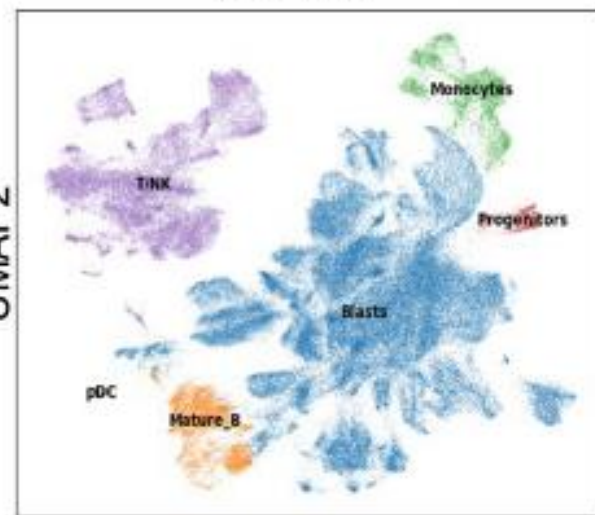
18 KMT2A-rALL infant
PBMCs

(G)

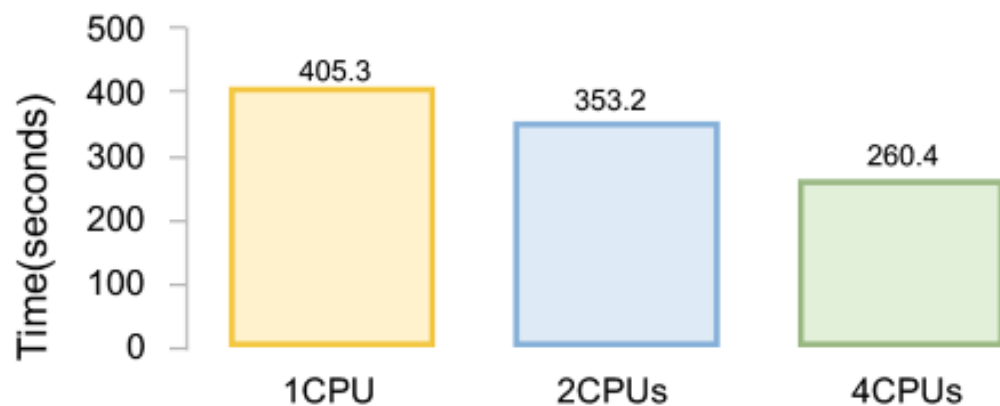
Scanpy



Seurat



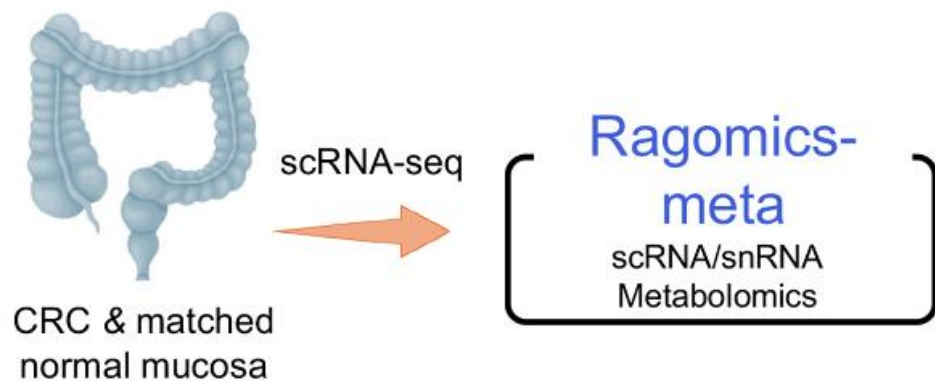
(H)



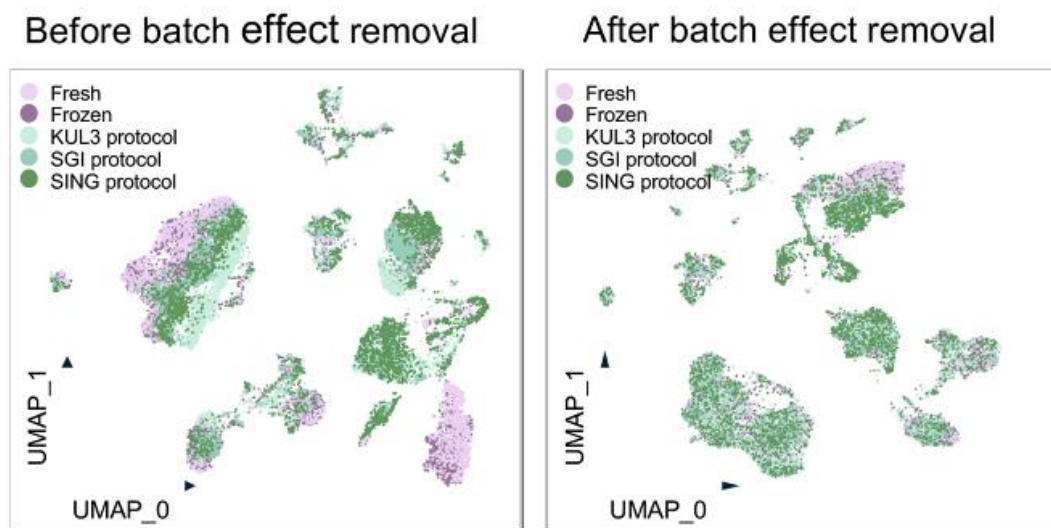


案例二：结直肠癌单细胞代谢分析

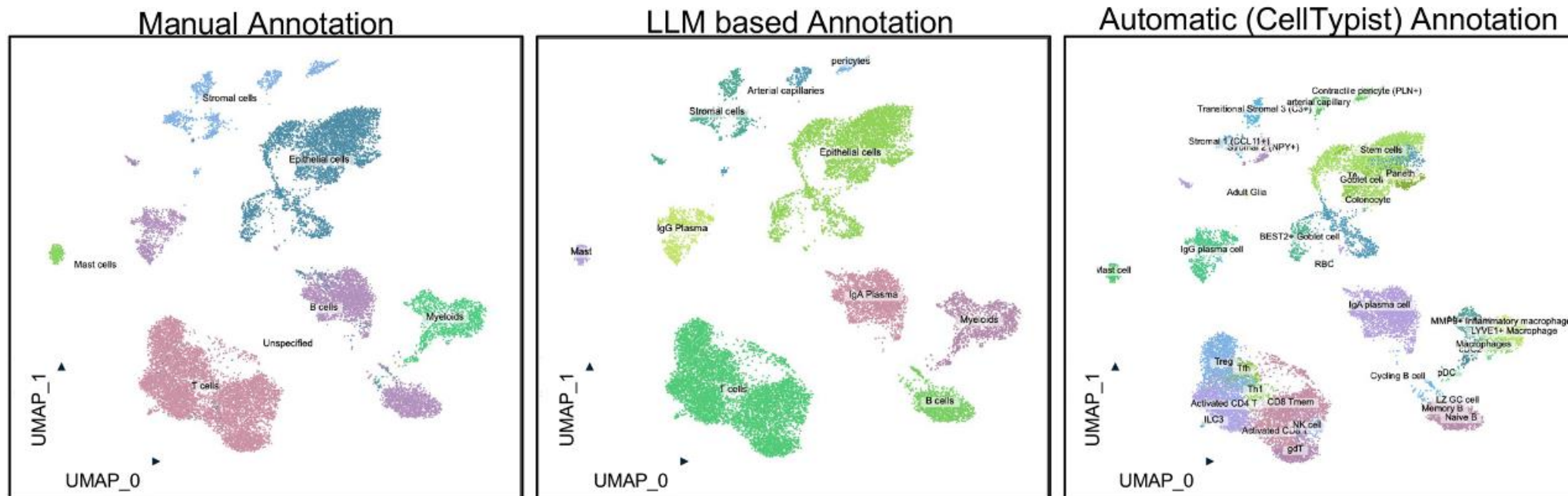
(A)



(B)



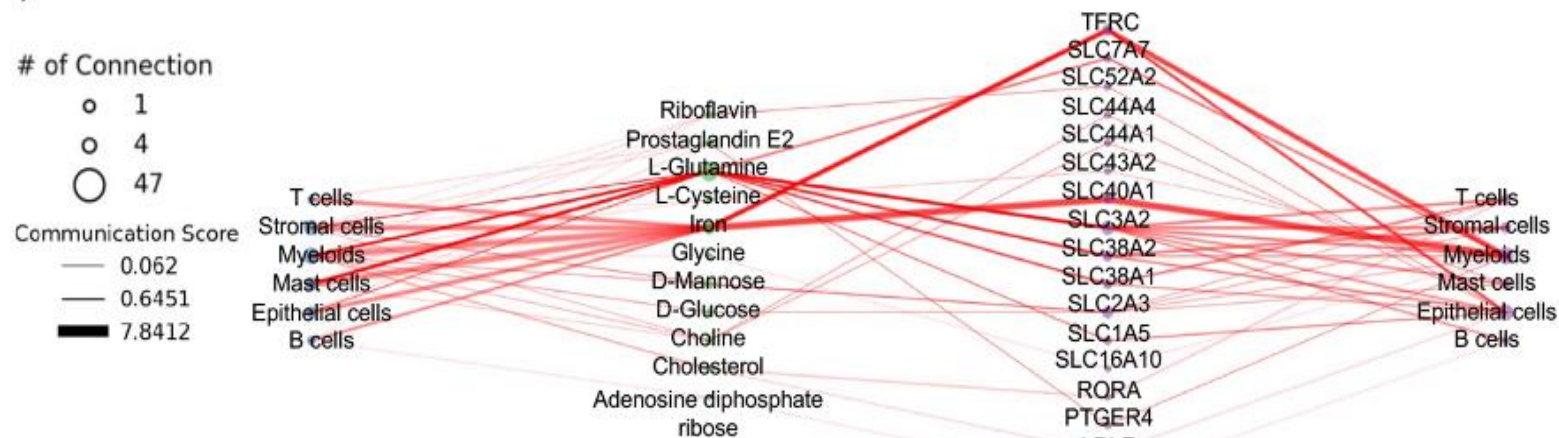
(C)



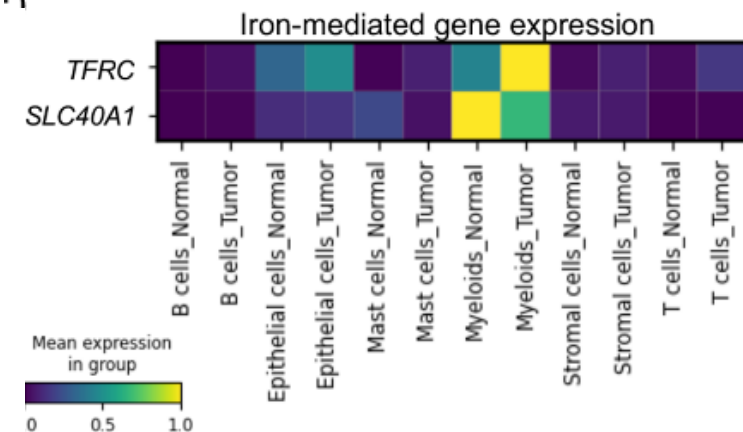


案例二：结肠癌铁代谢相关细胞通讯解析

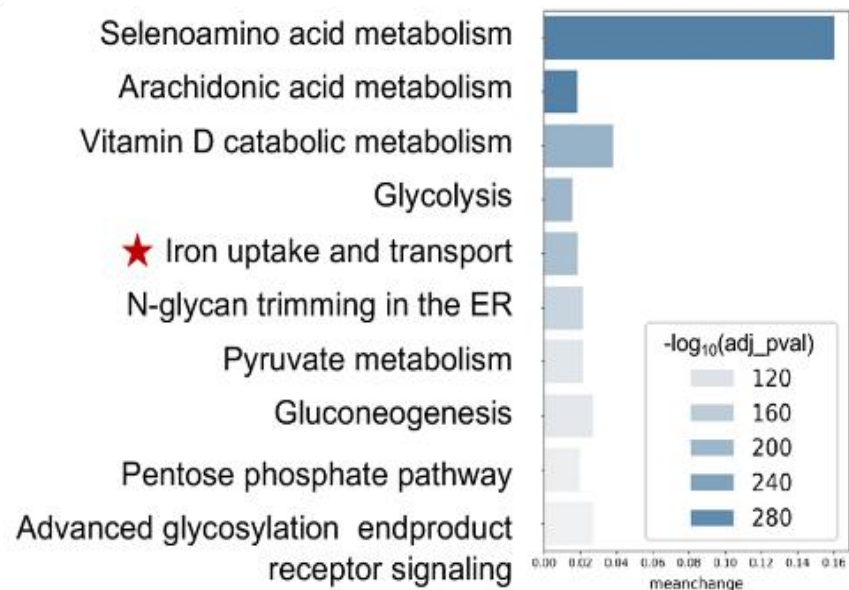
(D)



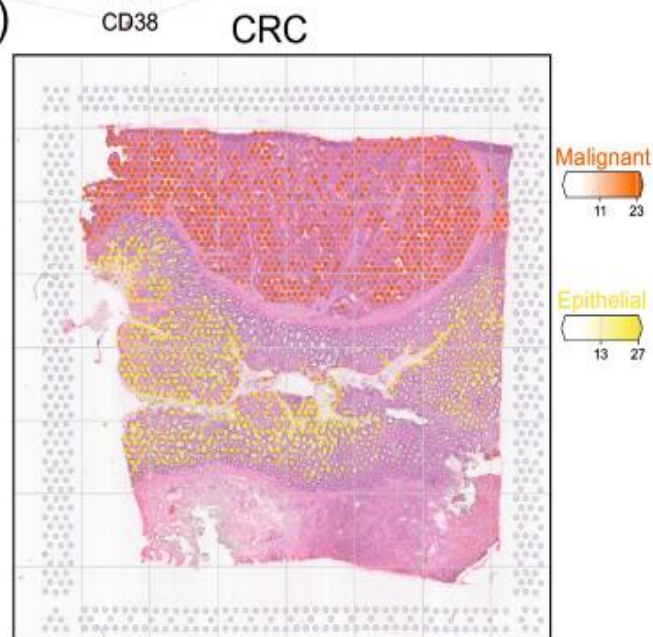
(E)



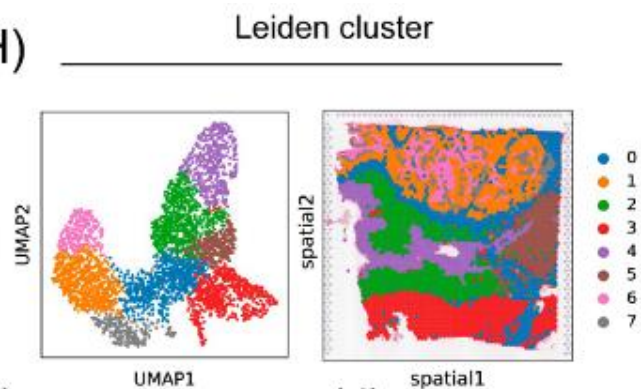
(F) CRC activated metabolic pathways in epithelium



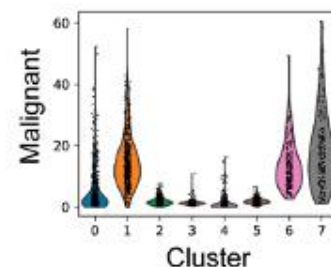
(G)



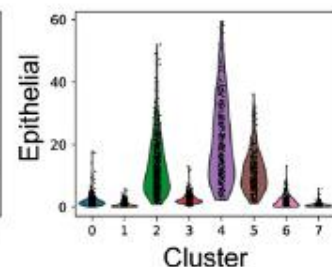
(H)



(I)



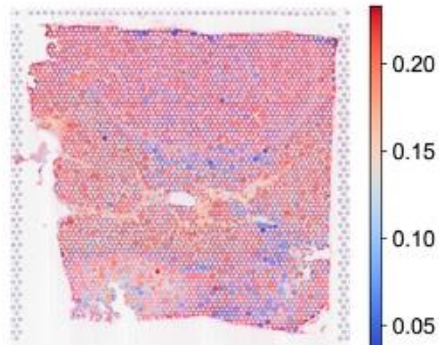
(J)



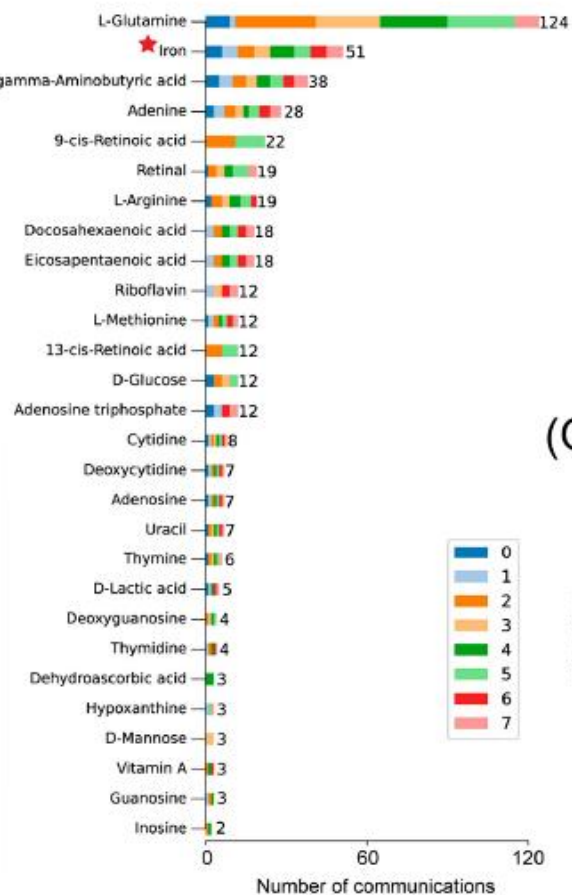


案例二：结肠癌空间代谢与表观调控整合分析

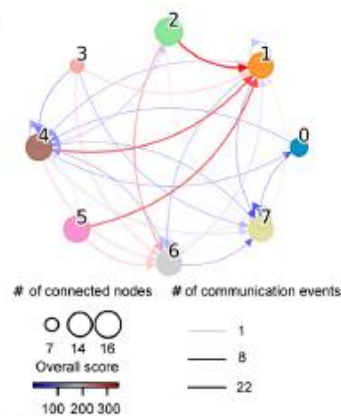
(K) Iron uptake and transport activity score



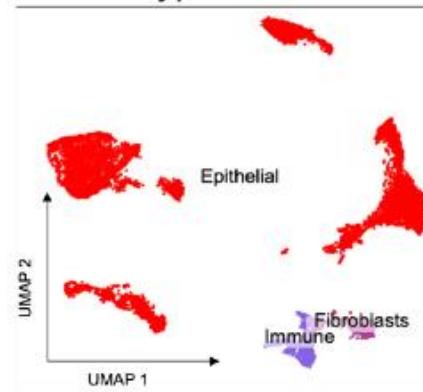
(M) Communication number of metabolite in sender



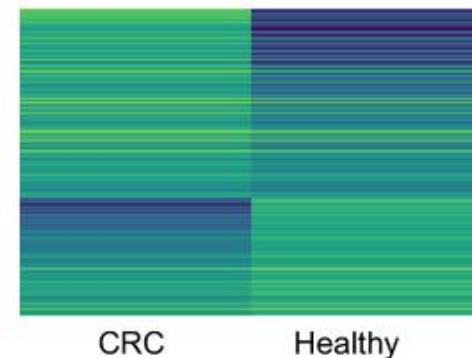
(N) Iron-mediated network



(P) Cell-type annotation



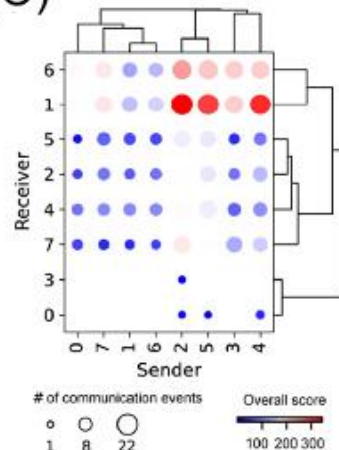
(Q) DARs in epithelial cells



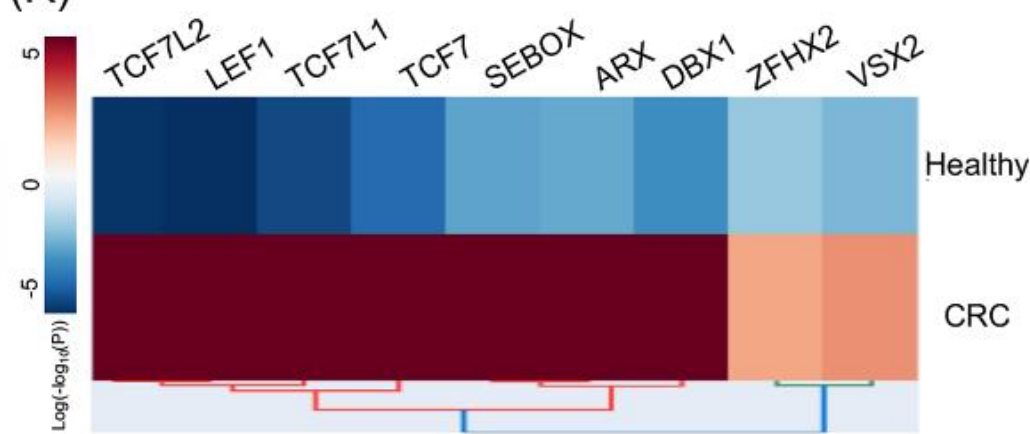
(L) Spatial cell-cell communication



(O)



(R)





总结

- ❑ 在这项研究中，我们介绍了一个开放式代谢中心化多组学分析 workflow Ragomics-Meta，支持 scRNA/snRNA-seq、scATAC-seq、空间转录组和空间代谢组等多模态数据分析；
- ❑ 整合 100 余个常用功能模块，包括 Scanpy、Seurat、SnapATAC2、Squidpy、COMMOT、MEBOCOST、scMetabolism、AUCcell 等主流工具，覆盖数据预处理、聚类注释、差异分析、代谢通路评分和可视化等关键步骤；
- ❑ 支持 AI 辅助分析与解释，可结合 ChatGPT、DeepSeek、Grok 等大语言模型辅助细胞类型注释、基因列表整理、通路结果解释和假设生成；
- ❑ 平台网址：<http://www.raganetwork.com>

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iMeta(宏)期刊由宏科学创办，对标**Cell**的生物/医学综合期刊，**SCIE**、**PubMed**收录，影响因子(IF)44.4，位列全球第47，中国第4，**分区表生物学1区Top**，外审平均21天，投稿至发表中位数87天(比同水平期刊快3倍)，欢迎高影响力的研究、方法和综述投稿，CNS外审稿件可带意见和回复转投。

iMetaOmics (宏组学)，定位IF>15对标**NC/SA**的生物/医学综合期刊，已被**ESCI**、**PubMed**等收录。

iMetaMed (宏医学)定位IF>15的医学综合期刊，欢迎投稿！



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