

# TCfinder (Tumor Cell finder) : 基于通路活性在单细胞转录组数据中鉴别肿瘤细胞

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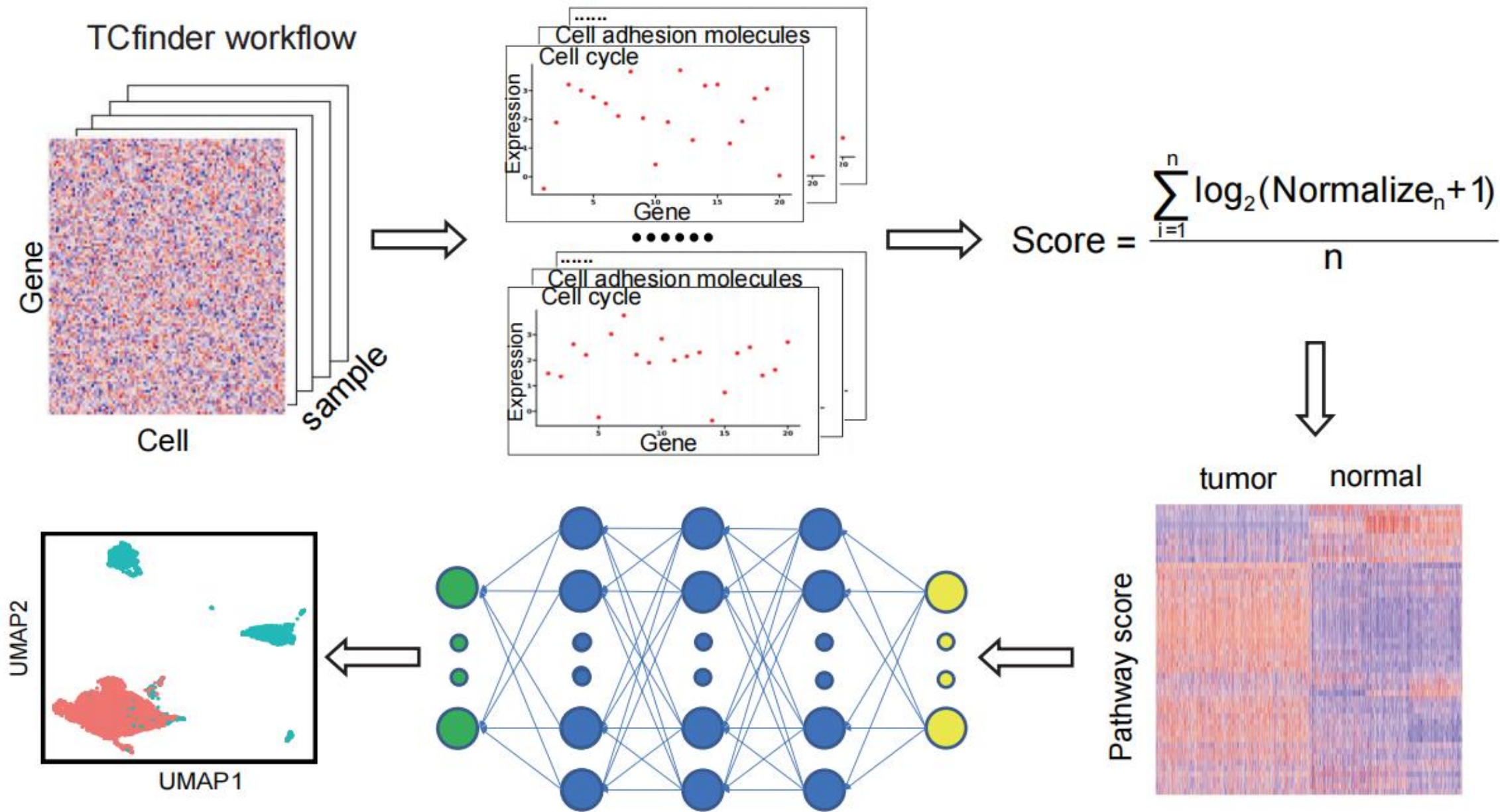
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Chenxu Wu, Wei Ning, Tao Wu, Jing Chen, Huizi Yao, Ziyu Tao, Xiangyu Zhao, Kaixuan Diao, Jinyu Wang, Weiliang Wang, Xinxing Li, Qianqian Song, Xue-Song Liu. 2024. TCfinder: Robust tumor cell discrimination in scRNA-seq based on gene pathway activity. *iMetaOmics* 1: e22. <https://doi.org/10.1002/imo2.22>



# 简介



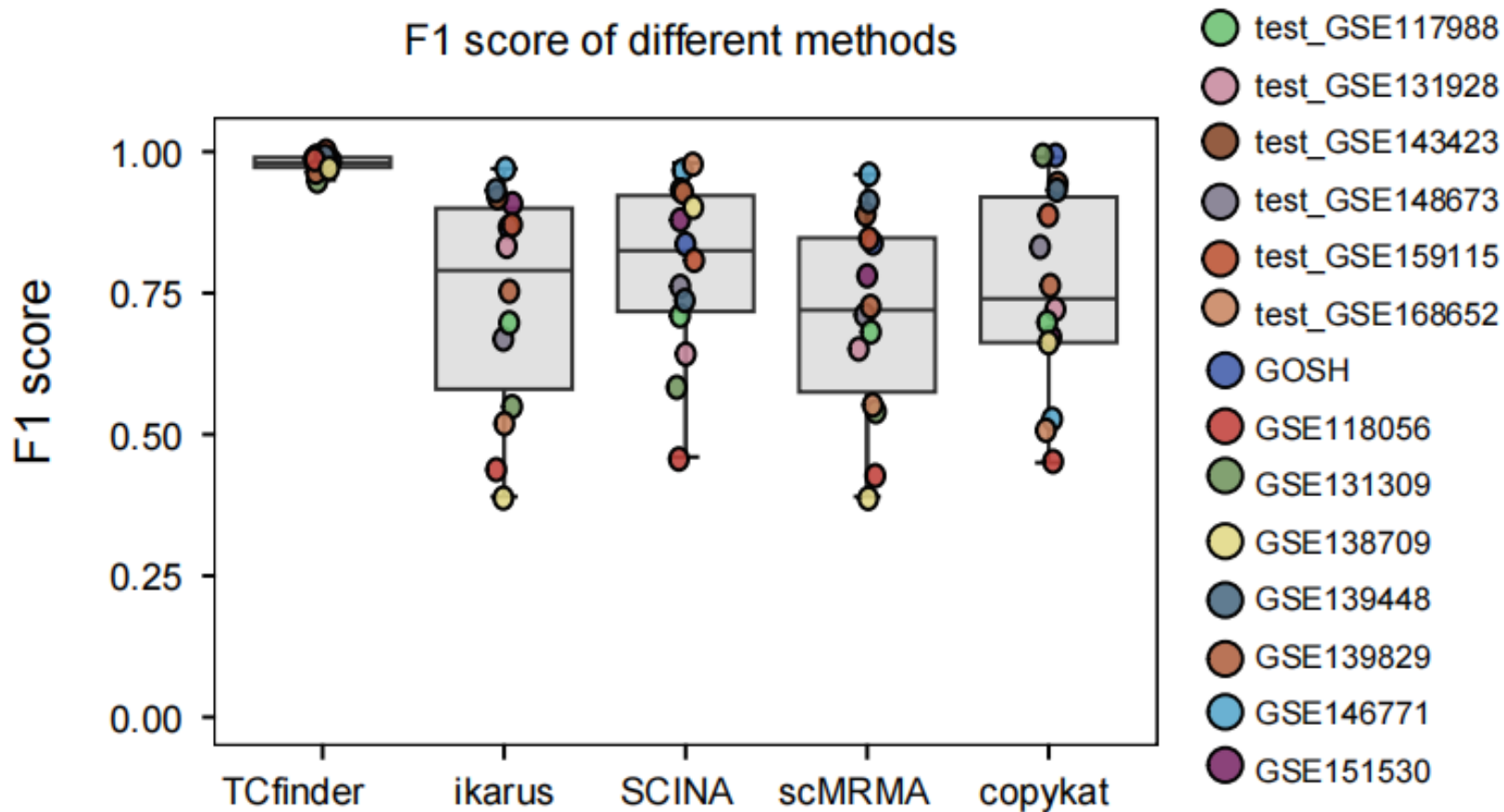


# 亮点

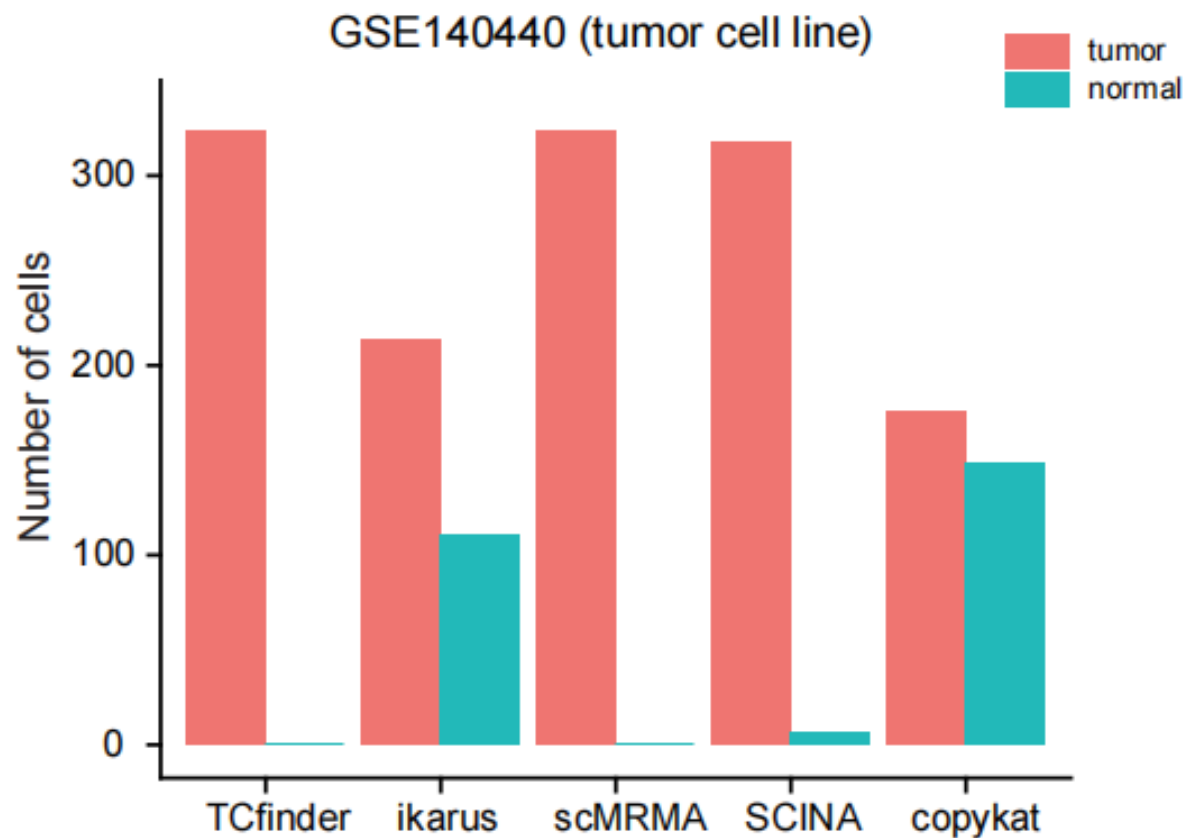
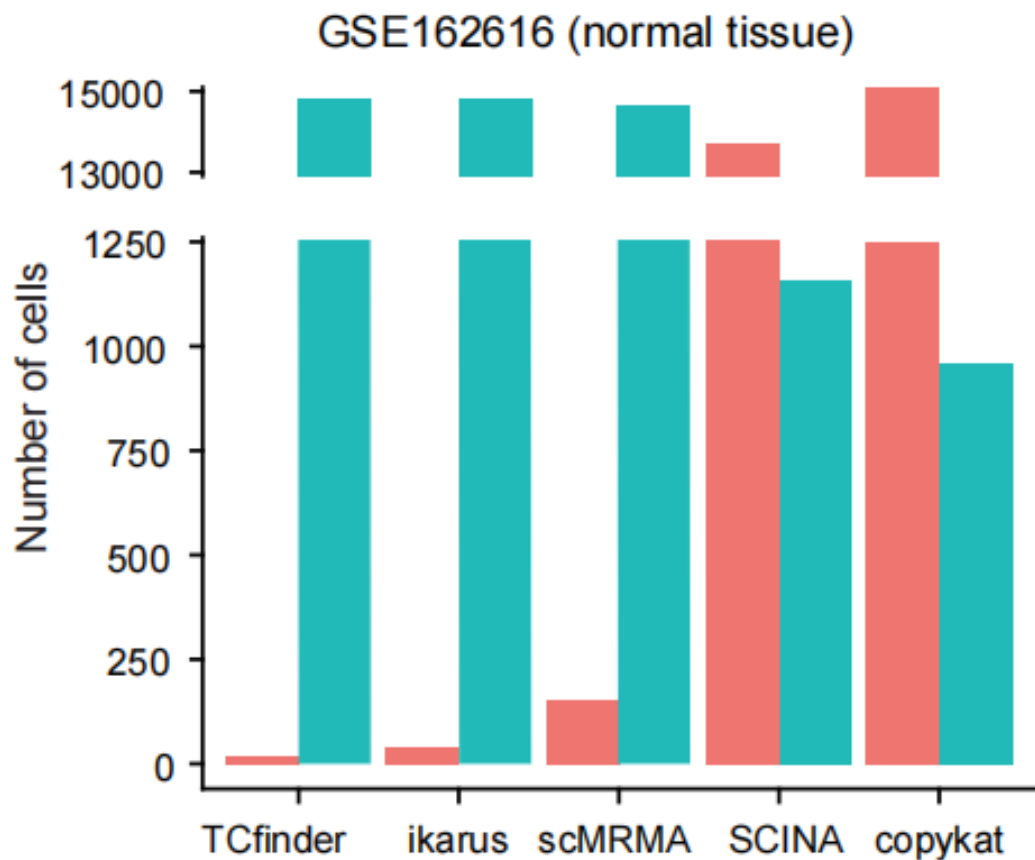
- 1、TCfinder使用通路评分来区分正常细胞和肿瘤细胞；
- 2、TCfinder的性能优于现有的肿瘤细胞识别工具；
- 3、TCfinder适用于多种单细胞建库方式和测序平台；
- 4、TCfinder性能稳定，在稀疏的数据中依然可以准确识别肿瘤细胞。



# 比较TCfinder与现有的注释方法



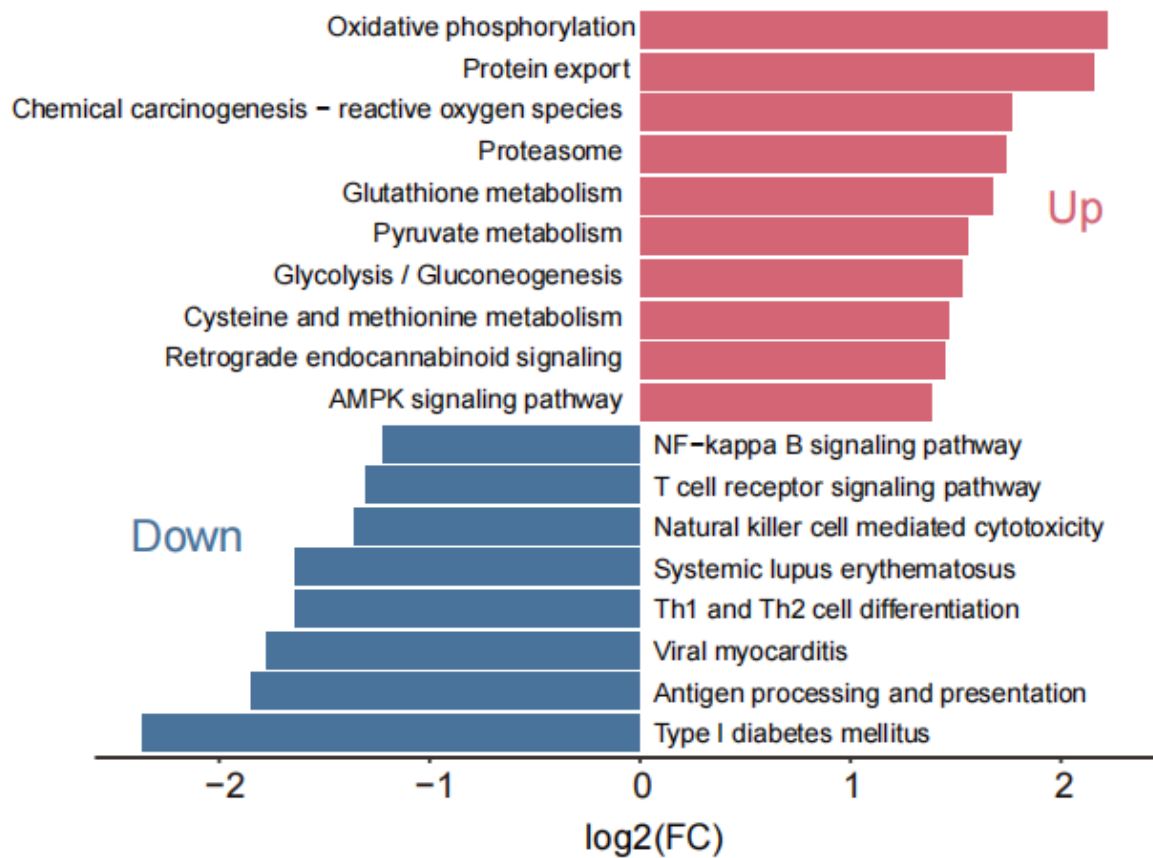
# 比较TCfinder与现有的注释方法



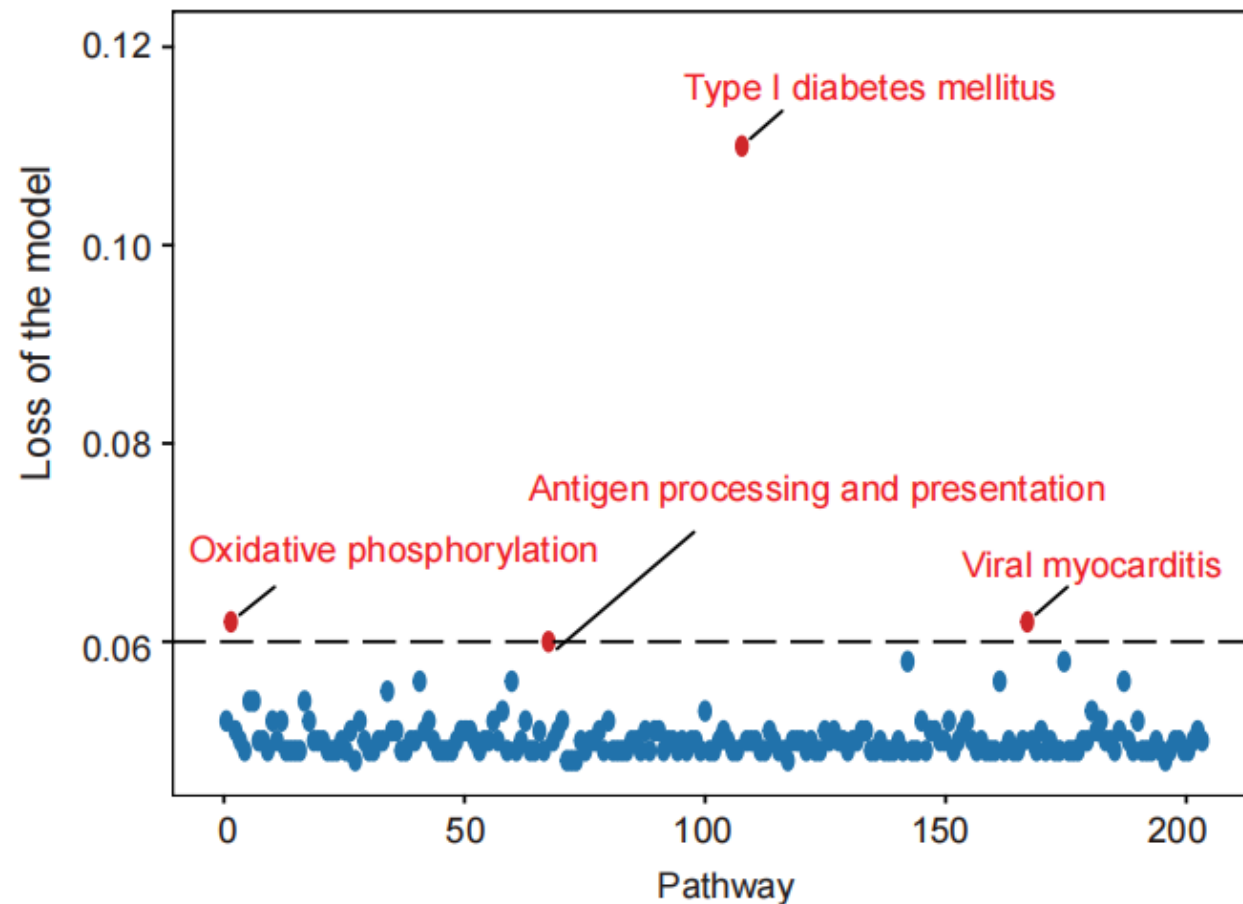


# 对识别肿瘤和正常细胞重要的通路

Differential analysis of pathway scores in tumor vs normal cells



Pathways important for predicting tumor vs normal cells





# TCfinder使用手册1

## Install

```
devtools::install_github("XSLiuLab/TCfinder")
```

TCfinder安装



TCfinder contains three functions, which respectively standardize the raw counts of single cells, score pathways, and predict tumor cells and normal cells.

## Data normalization

The input data needs to be a sparse matrix or data.frame data whose row name is gene name and column name is sample name.

If the single-cell sequencing method used is smart-seq2, method = "smart-seq2" is required, and needed to select genome = "hg19" or "hg38". For other single-cell sequencing methods, this parameter does not need to be filled in.

```
library(TCfinder)  
result1 <- data_normalized(expr_data = expr_data, method = "method", genome = "hg38")
```

数据标准化



<https://github.com/XSLiuLab/TCfinder>



# TCfinder使用手册2

## Pathway score

The path score is calculated using the built-in 213 pathways according to the formula in workflow.

The output of `data_normalized()` can be directly used as the input of `pathway_score()`. If the matrix is not normalized, "normalized = FALSE" is needed to set

```
result2 <- pathway_score(expr_data = result1, normalized = T)
```

计算评分



result2: pathway score

	hsa00010	hsa00190	...	hsa00270
AAACCTGCACATCCGG	0.3401667	0.9679245	...	0.2091803
AAACGGGGTTGAACTC	0.5657879	1.6702925	...	0.4492787
...	...	...	...	...
AAACGGGGTTGTCGCG	0.3202879	1.4834434	...	0.4590984



# TCfinder使用手册3

## Predict cell

The prediction process needs to call a python script, so the R package 'reticulate' is required. The input data is the pathway score result obtained by running the pathway\_score() function

```
install.packages("reticulate")
library(reticulate)
# Use the use_python() function to specify the version, here we use the python just created and configu
reticulate::use_python("XXX/XXX/XXX/anaconda3/envs/new_env/bin/python")
# View specified environment information
reticulate::py_config()
# Predict
predict_result <- predict_cell(path_score = result2)
```



识别肿瘤细胞

## predict\_result

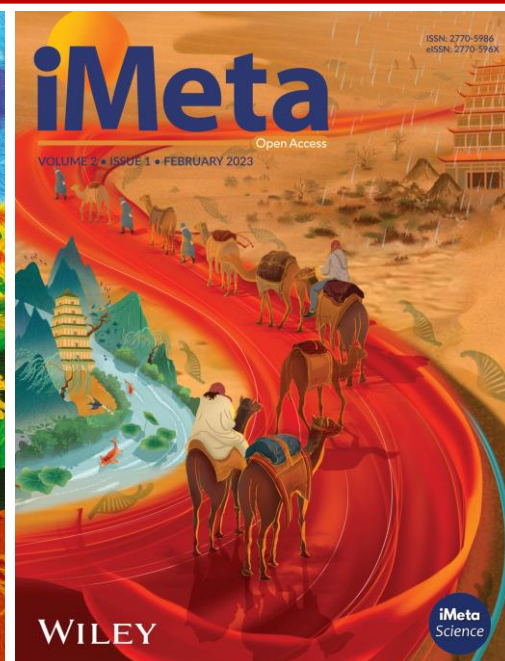
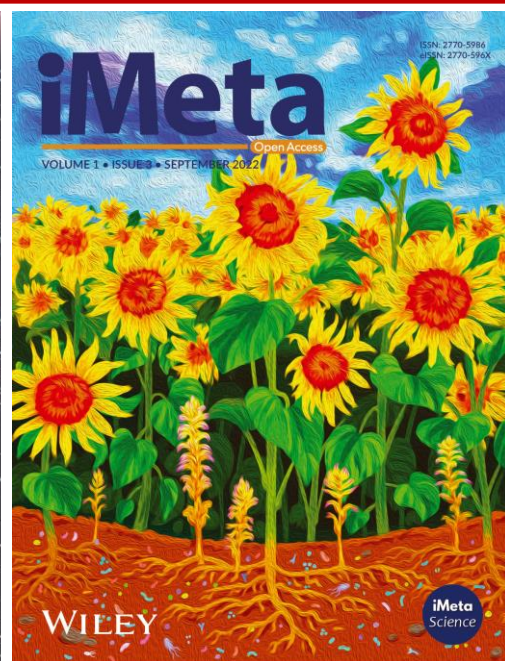
	value	cell_type	barcode
1	0.9996183	normal	AAACCTGCACATCCGG
2	0.9989167	normal	AAACGGGGTTGAACTC
3	0.0001887589	tumor	AAACGGGGTTGTCGCG
...	...	...	...



# 总结

- ❑ 在这项研究中，我们构建了一个在单细胞数据中专门识别肿瘤细胞的工具TCfinder;
- ❑ TCfinder的肿瘤细胞识别性能优于现有工具，而且在稀疏的单细胞数据中依然表现良好;
- ❑ 在对重要的通路研究中我们发现，肿瘤细胞表现出代谢过度活跃和免疫抑制的双重特征;
- ❑ R包网址：<https://github.com/XSLiuLab/TCfinder>

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