



# TCfinder: Robust tumor cell discrimination in scRNA-seq based on gene pathway activity.

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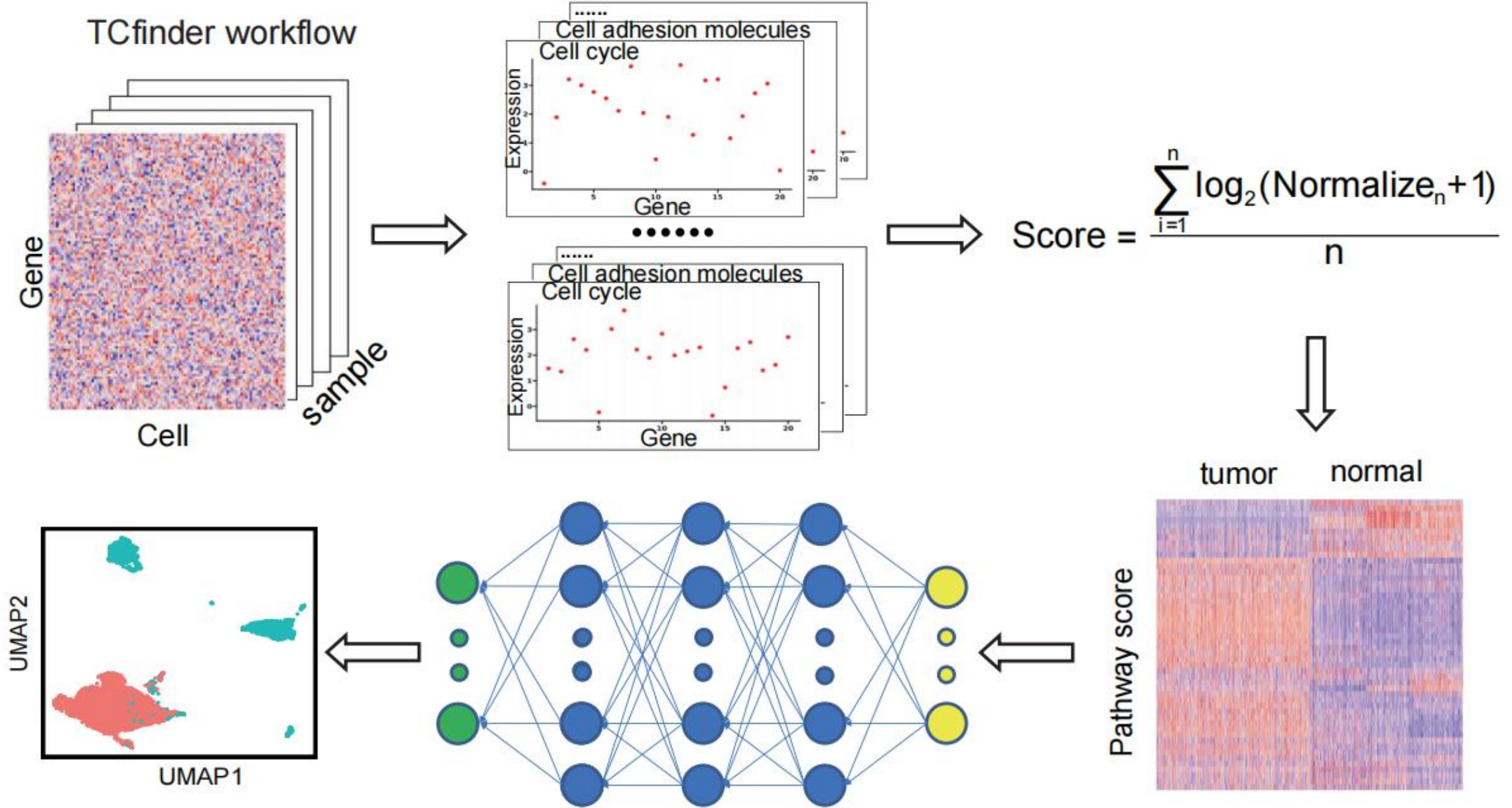
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# Introduction



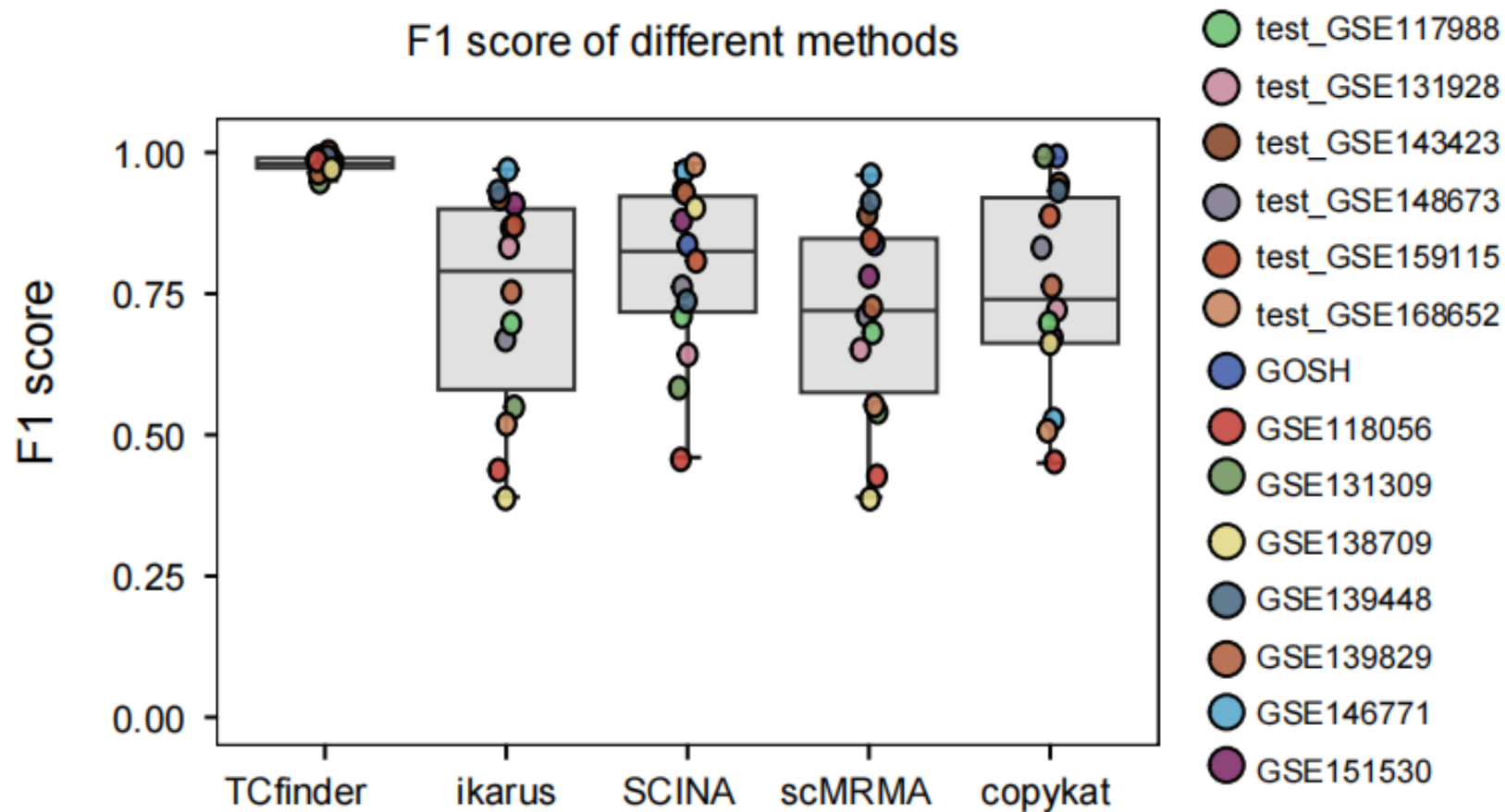


# Highlights

1. TCfinder uses pathway scores to differentiate between normal and tumor cells;
2. TCfinder outperforms existing tumor cell identification tools;
3. TCfinder performs well in multiple single-cell sequencing platforms;
4. TCfinder has stable performance and works well under extreme conditions.

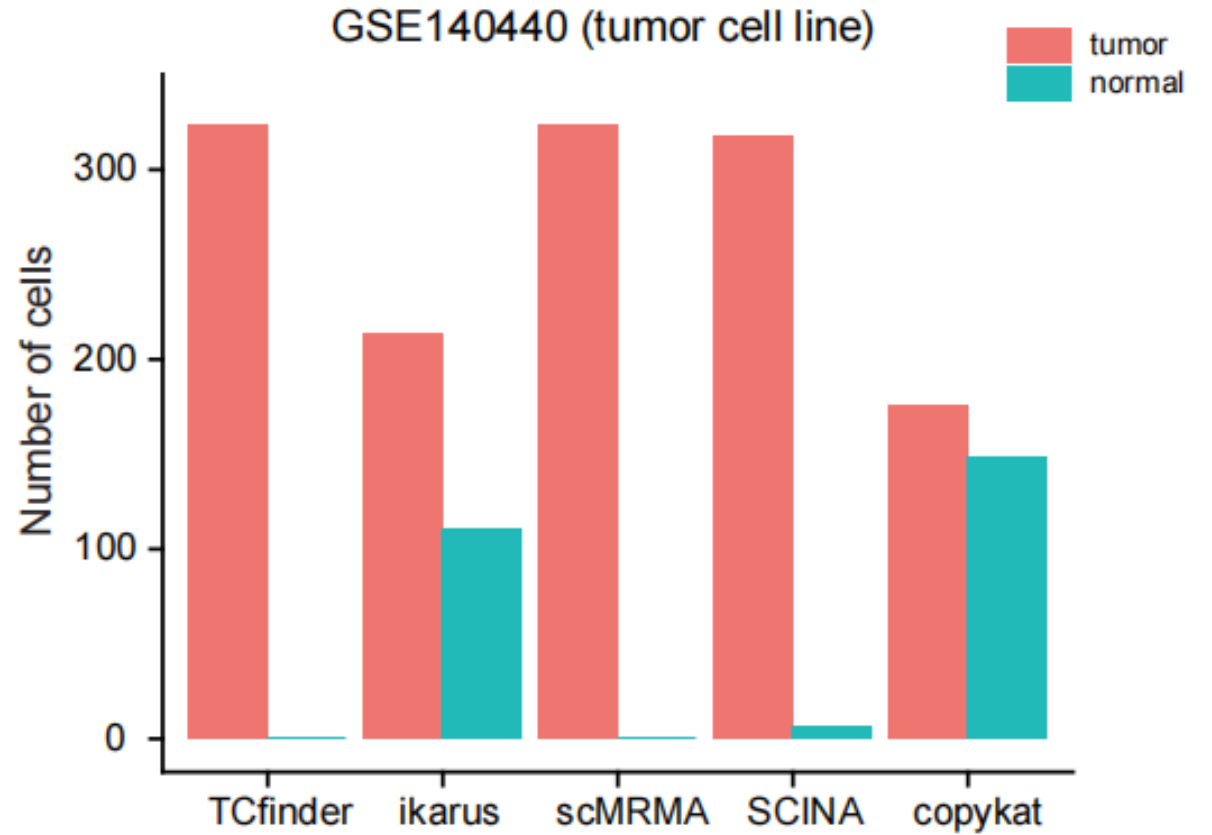
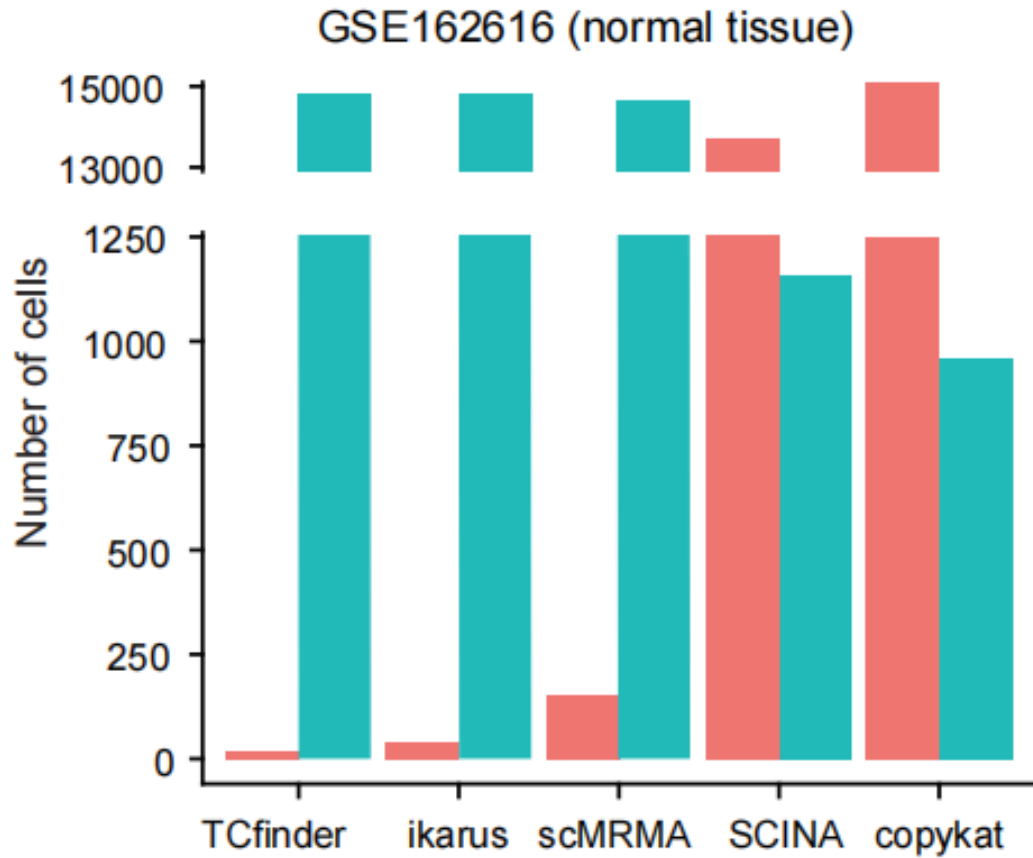


# Comparison of TCfinder with other tools





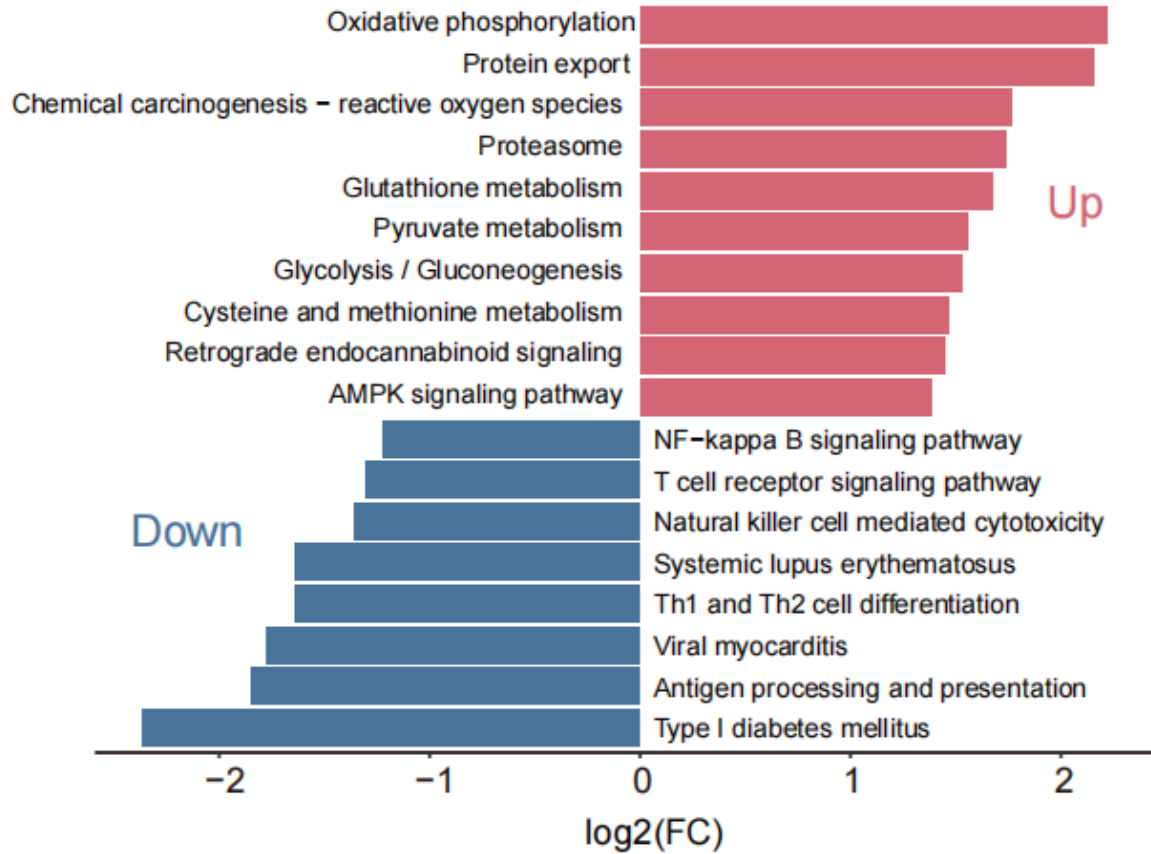
# Comparison of TCfinder with other tools



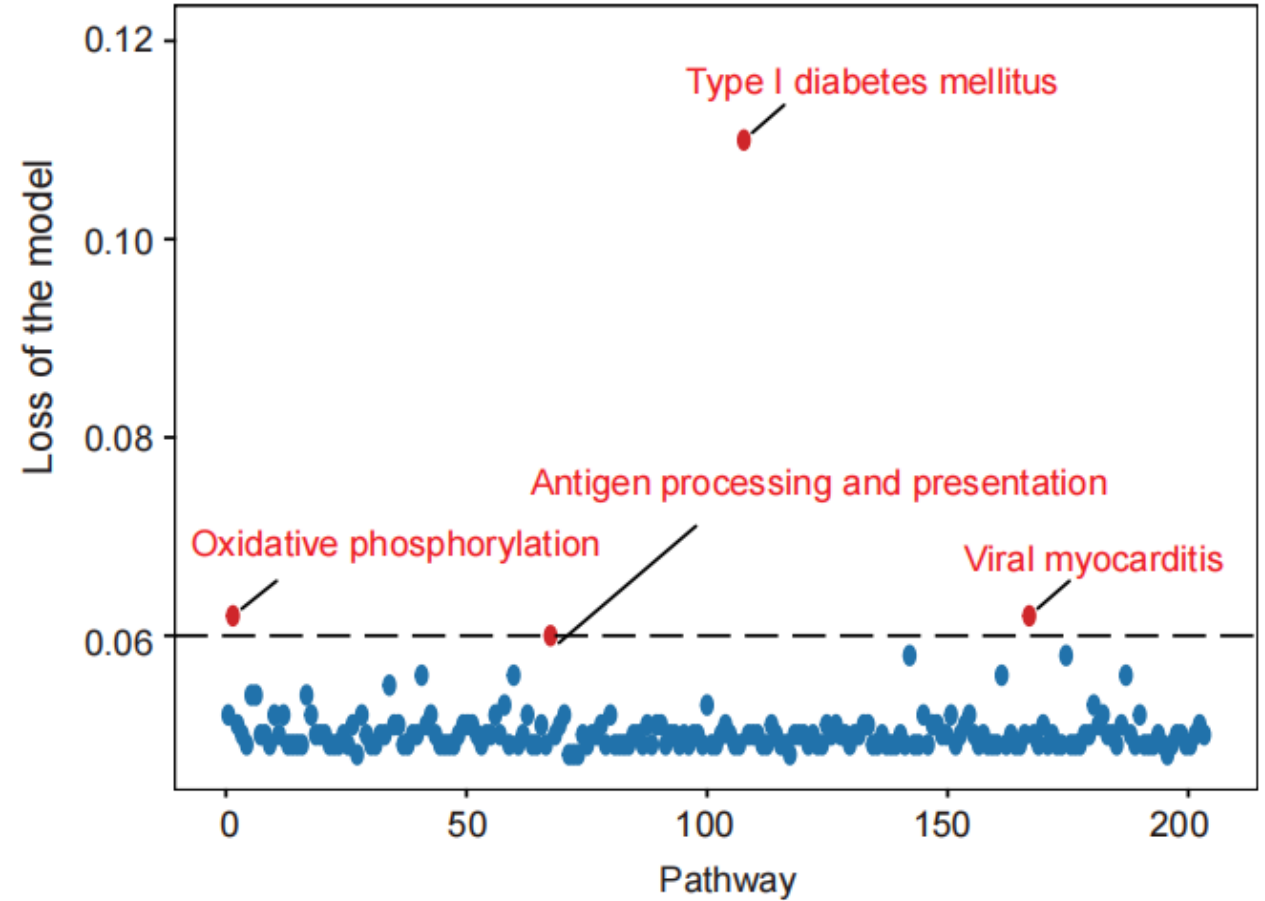


# Pathways important for tumor cells

Differential analysis of pathway scores in tumor vs normal cells



Pathways important for predicting tumor vs normal cells





# TCfinder User Guide 1

## Install

**TCfinder install**

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



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")
```

**data normalize**



# TCfinder User Guide 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)
```

**pathway score**



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

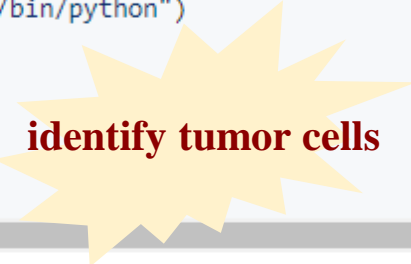


# TCfinder User Guide 3

## 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)
```



## predict\_result

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



# Summary

- ❑ In this study, we developed a tool called TCfinder, which is specifically designed to identify tumor cells in single-cell data;
- ❑ TCfinder outperforms existing tumor cell identification tools and performs well even in sparse single-cell data;
- ❑ In the study of key pathways, we found that tumor cells exhibit dual characteristics of metabolic hyperactivity and immune suppression;
- ❑ R package link: <https://github.com/XSLiuLab/TCfinder>

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