TBCancer: A database for exploring characteristics and functions of tissue-biased genes in cancer

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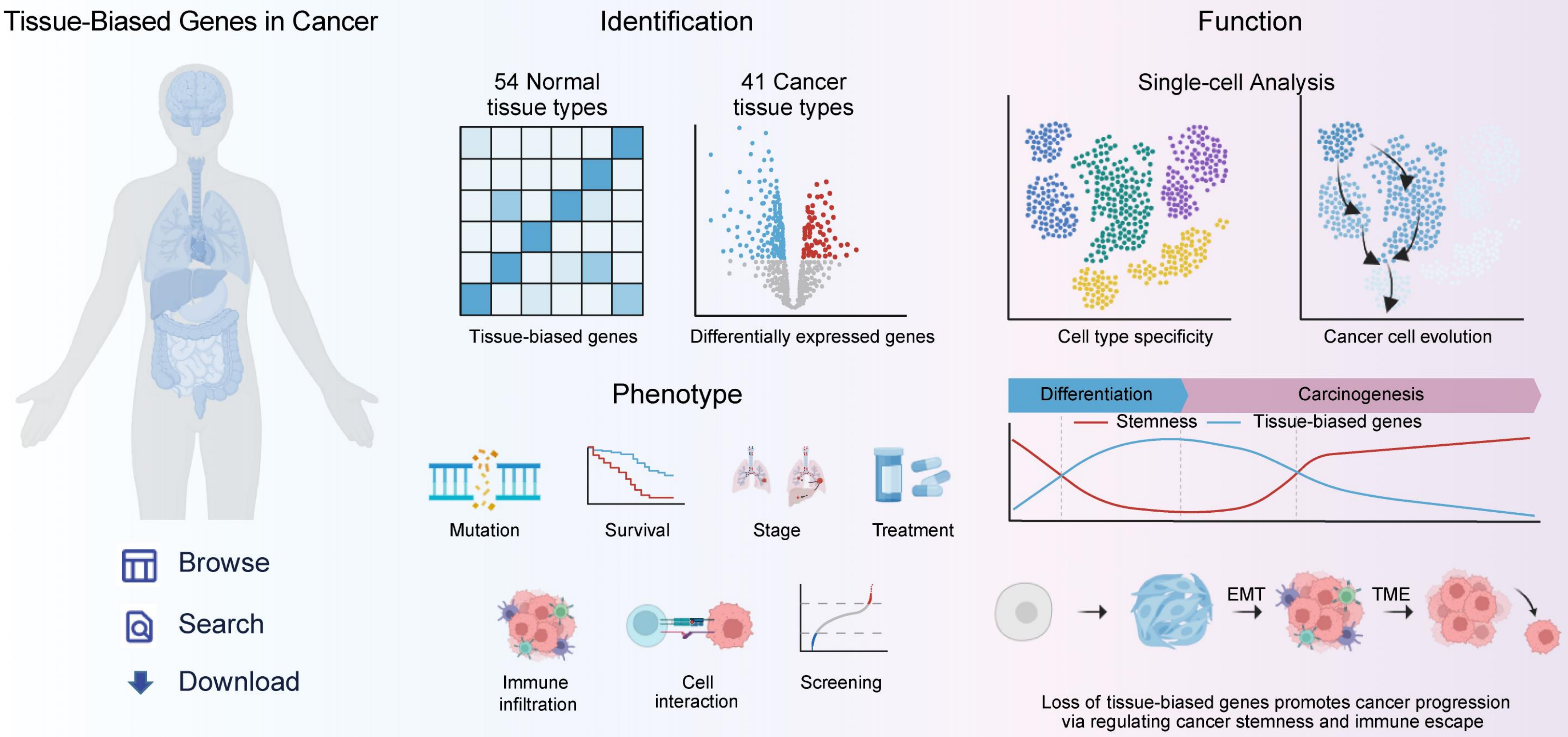
Introduction



Tissue-Biased Genes in Cancer

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Identification

54 Normal tissue types

Tissue-biased genes

41 Cancer tissue types

Differentially expressed genes

Phenotype

Mutation

Survival

Stage

Treatment

Immune infiltration

Cell interaction

Screening

Function

Single-cell Analysis

Cell type specificity

Cancer cell evolution

Loss of tissue-biased genes promotes cancer progression via regulating cancer stemness and immune escape

Highlights

- First, through pan-cancer multi-omics analysis at the bulk level, we revealed common molecular features of TBGs in cancer, including inactivation, mutations, and methylation alterations.
- Second, using single-cell transcriptomic data from multiple cancer types, we uncovered how TBG inactivation promotes tumorigenesis by enhancing cancer stemness and immune evasion during tumor evolution.
- Building upon these findings and by integrating diverse omics data including clinical outcomes, treatment responses, and gene editing/screening results, we established TBCancer as a comprehensive analytical database for TBGs in cancer.

http://tsbcancer.canceromics.org

Pan-cancer multi-omics analysis

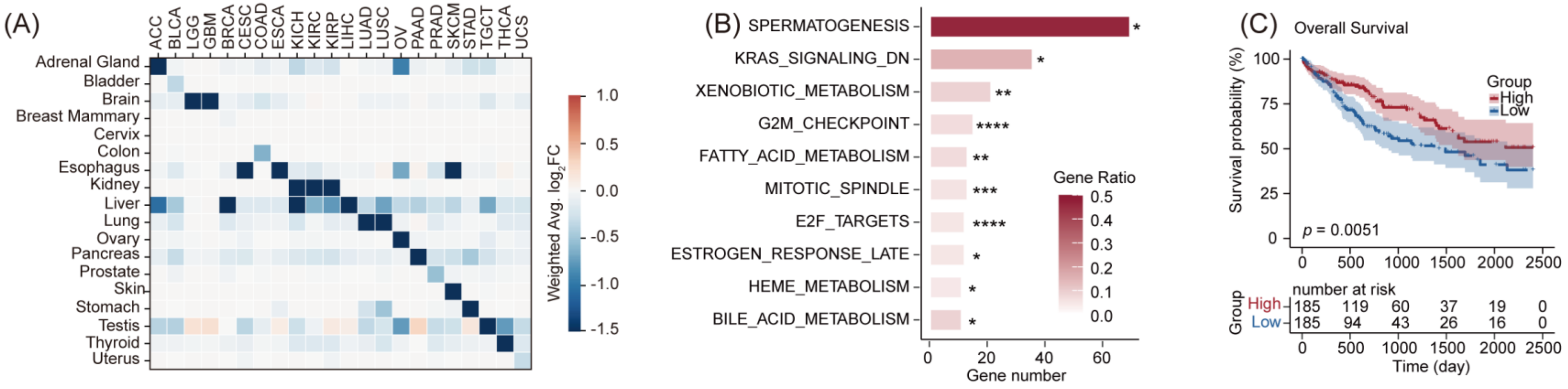

Figure 1. The characteristics and functions of tissue-biased genes in cancer.

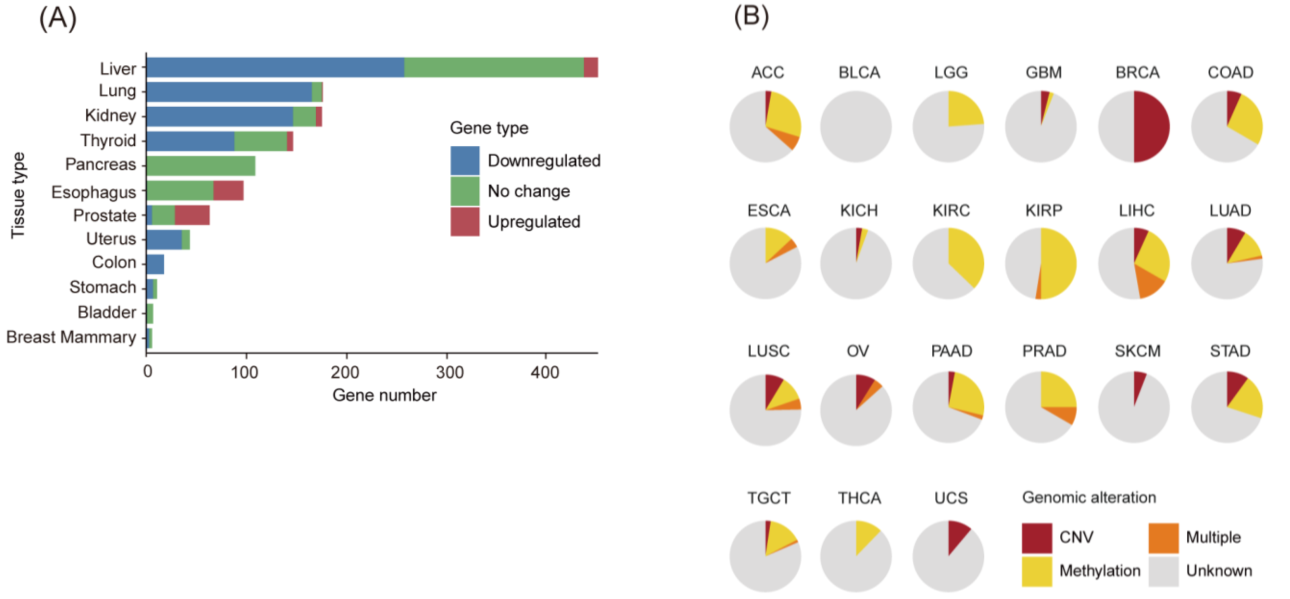

Figure S1. Pan-cancer profiles of tissue-biased genes in tumors.

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Single-cell analysis

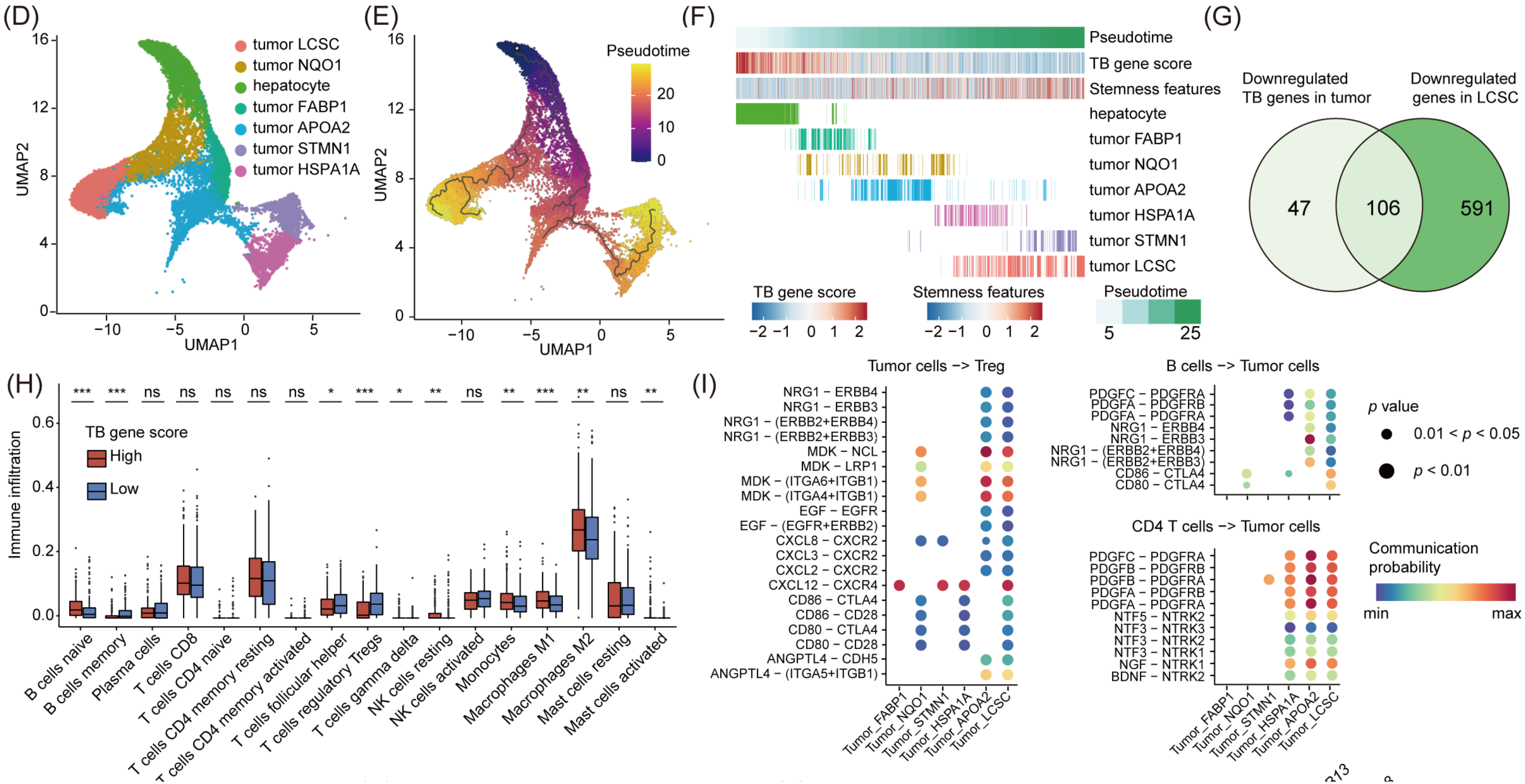

Figure 1. The characteristics and functions of tissue-biased genes in cancer.

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Experimental validation

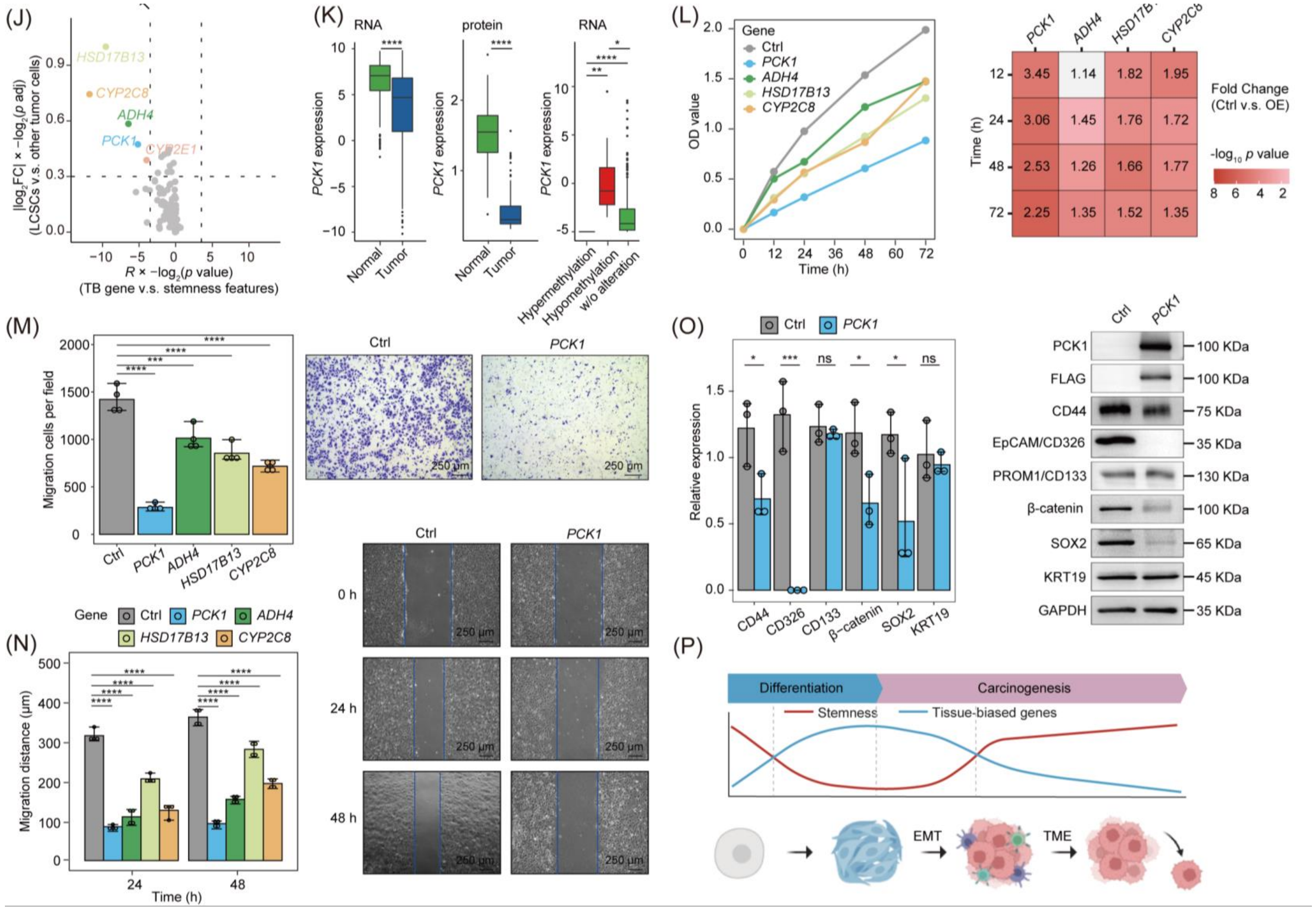

Figure 1. The characteristics and functions of tissue-biased genes in cancer.

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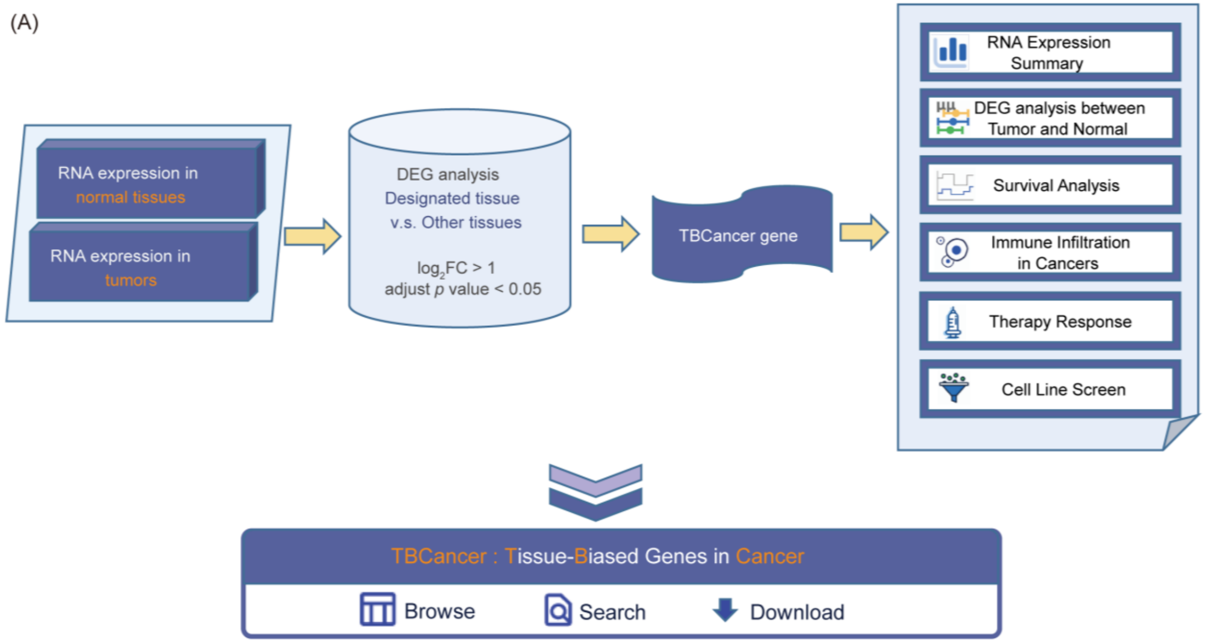
Overview of TBCancer



(A)

RNA expression in normal tissues

RNA expression in tumors

DEG analysis
Designated tissue v.s. Other tissues

$\log_2 FC > 1$
adjust p value < 0.05

TBCancer gene

- RNA Expression Summary
- DEG analysis between Tumor and Normal
- Survival Analysis
- Immune Infiltration in Cancers
- Therapy Response
- Cell Line Screen

TBCancer : Tissue-Biased Genes in Cancer

Browse Search Download

(B)

Browse

Select a type of gene

Tissue-biased gene

◎ TBGs in male samples ◎ TBGs in female samples ◎ TBGs in all samples

Histogram of gene numbers

Browse Results

Chromosome: ☐ Tissue/Cancer Type: ☐

Gene Type: ☐ Gene Symbol: ☐

Filter: ◎ Survival Related ◎ Chemotherapy Response ◎ Immunotherapy Response ◎ Immune Infiltration ◎ Differentially Expressed (Tumor v.s. Normal)

TBCancer ID	Gene Symbol	Analysis ID	Chr	Tissue Type	Gene Type	...
TB00001	A1BG	ANA0001	19	Liver	Protein coding	...
TB00002	AFP	ANA0002	4	Liver	Protein coding	...

Analysis Page

Analysis Information

Analysis ID: GTEX_NT_21
Dataset ID: GTEX_Liver
Dataset Source: GTEX
Dataset Title: Liver tissue from GTEX
PMID: -
Tissue Type: Liver tissue

Analysis Results

TBCancer ID	Gene Symbol	Chr	Liver	Bladder	Brain	Breast	...
TB00001	A1BG	19	1115.566	6.516	18.546	6.546	...
TB00002	A1CF	1	23.409	0.014	0.034	0.026	...
TB00003	ABCB11	2	7.3917	0.274	0.019	0.014	...

Detail Page

Gene Information

Gene Symbol: A1BG
Genomic Location: chr19:58345183-58353492 (-)
Gene Type: Protein coding
Official Name: Alpha-1-B glycoprotein
Also Known as: A1B, ABG, GAB...
Related ID: NCBI ID:1 ...

Analysis Details

Analysis ID: GTEX_NT_21
Dataset ID: GTEX_Liver
Dataset Source: GTEX
Dataset Title: Liver tissue from GTEX
Gene Symbol: A1BG
Tissue Type: Liver tissue

Tissue_A v.s. Tissue_B	Expression (A)	Expression (B)	$\log_2$FC (A v.s. B)	*p*	*p* adj
Liver v.s. Brain	1115.566	6.516	12.27	0	0

Expression Summary

DEG analysis

Gene Symbol	Gene Type	Tumor	$\log_2$FC	*p*	*p* adj
A1BG	Protein coding	6.516	12.27	0	0

Survival analysis

Cancer Type	Data source	HR	*p*	*p* adj
Liver v.s. Brain	1115.5	6.516	0	0

Immune Infiltration

	ACC	BLCA	BRCA	CESC	...
T cell	0.318	0.421	-0.24	0.01	0
B cell	0.562	0.312	-0.32	0.03	0

Cell Line Screen

Cancer Type	Source	Cell Line	Screen Type	Z	*p*
GBM	sanger	ACH-001	Negative	0.08	0.4
HNSC	sanger	ACH-002	Negative	0.30	0.3
PAAD	sanger	ACH-003	Negative	0.46	0.1
HNSC	sanger	ACH-004	Negative	0.03	0.3
HNSC	sanger	ACH-005	Negative	0.13	0.5

Therapy Response

Dataset ID	Cancer Type	Drug	Data source	$\log_2$FC	*p*	*p* adj	HR	*p*	*p* adj
A1BG	LIHC	Csplatin	TCGA_LIHC	-0.14	0.63	0.98	0.285	0.72	0.89

- Expression summary
- Differential gene expression analysis
- Survival analysis
- Immune infiltration
- Therapy sensitivity
- CRISPR screening

Figure 2. Overall design and construction of TBCancer.

http://tsbcancer.canceromics.org

Summary

- In summary, our systematic multi-omics study elucidated fundamental mechanisms whereby TBG inactivation promotes tumorigenesis through enhanced stemness and immune evasion during cancer progression.

- The resulting TBCancer database integrates comprehensive omics data on TBGs, including clinical outcomes, treatment responses, and gene editing/screening results, providing users with an intuitive visualization interface, efficient analytical tools, and streamlined exploration workflows.

- Website: http://tsbcancer.canceromics.org

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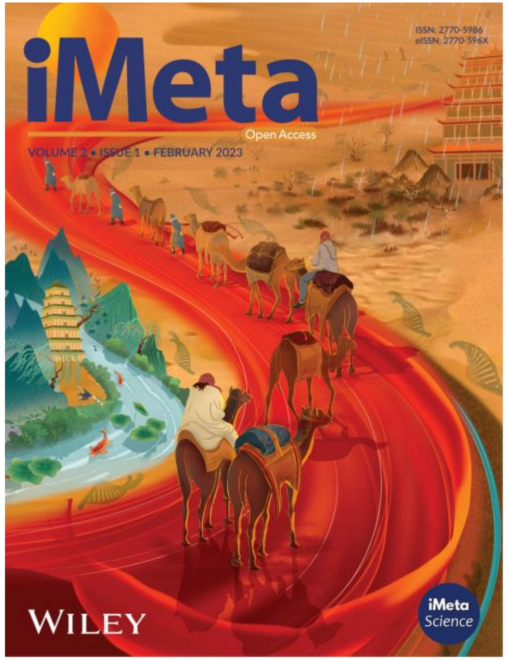

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