Cite this as: Kang XU, Xiyun JIN, Ya LUO, Haozhe ZOU, Dezhong LV, Liping WANG, Limei FU, Yangyang CAI, Tingting SHAO, Yongsheng LI, Juan XU. Spatial transcriptome analysis of long non-coding RNAs reveals tissue specificity and functional roles in cancer[J]. Journal of Zhejiang University Science B, 2023, 24(1): 15-31. http://doi.org/10.1631/jzus.B2200206

Spatial transcriptome analysis of long non-coding RNAs reveals tissue specificity and functional roles in cancer

Key words: Spatial expression; Transcriptome; Long non-coding RNAs; Cancer; Biomarkers

Research Summary

This study mainly focused on the tissue specificity and functional roles of lncRNAs across normal and cancer tissue in the following aspects:



GTEx



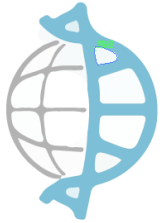
HPA



HBM2.0



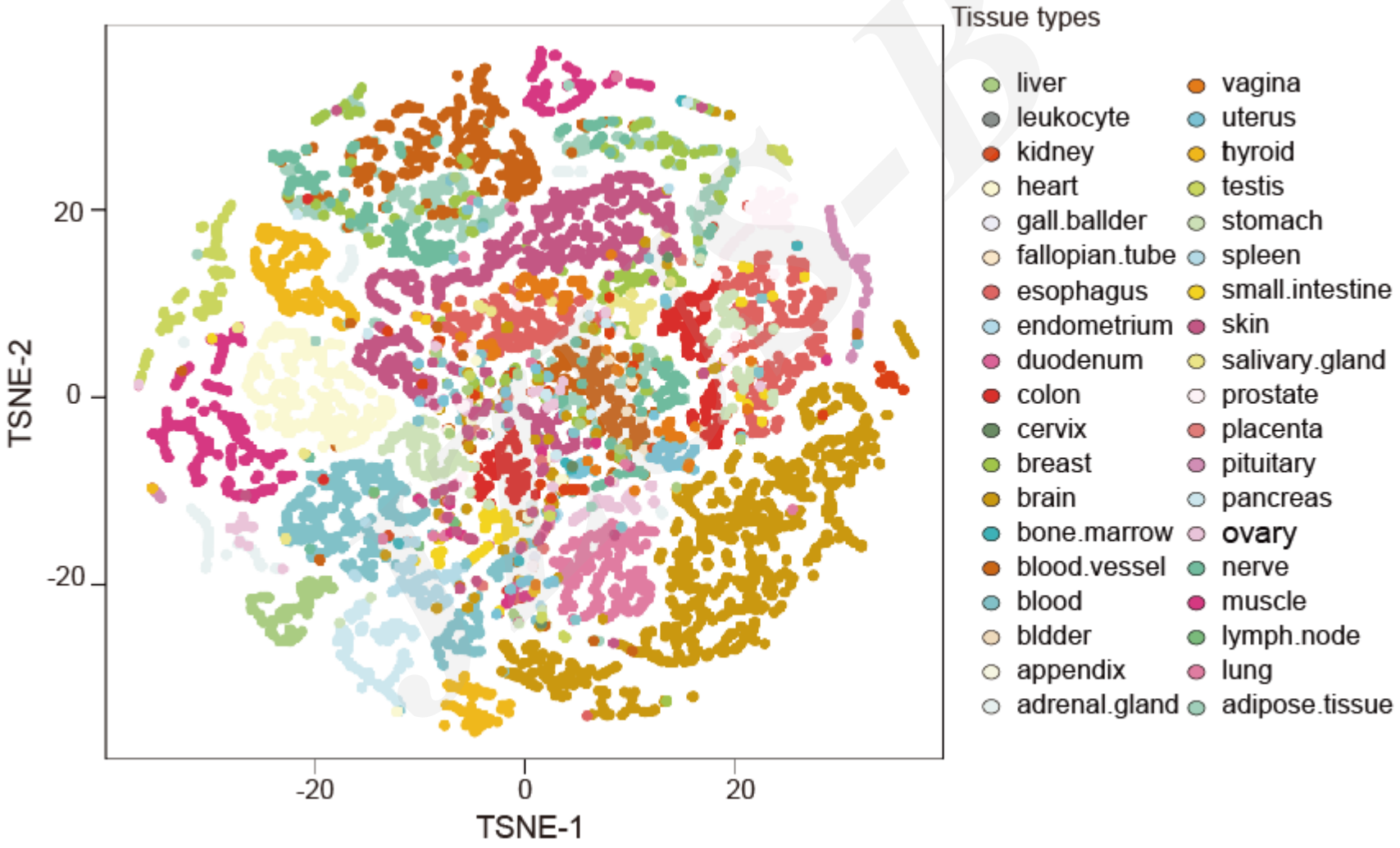
FANTOM5



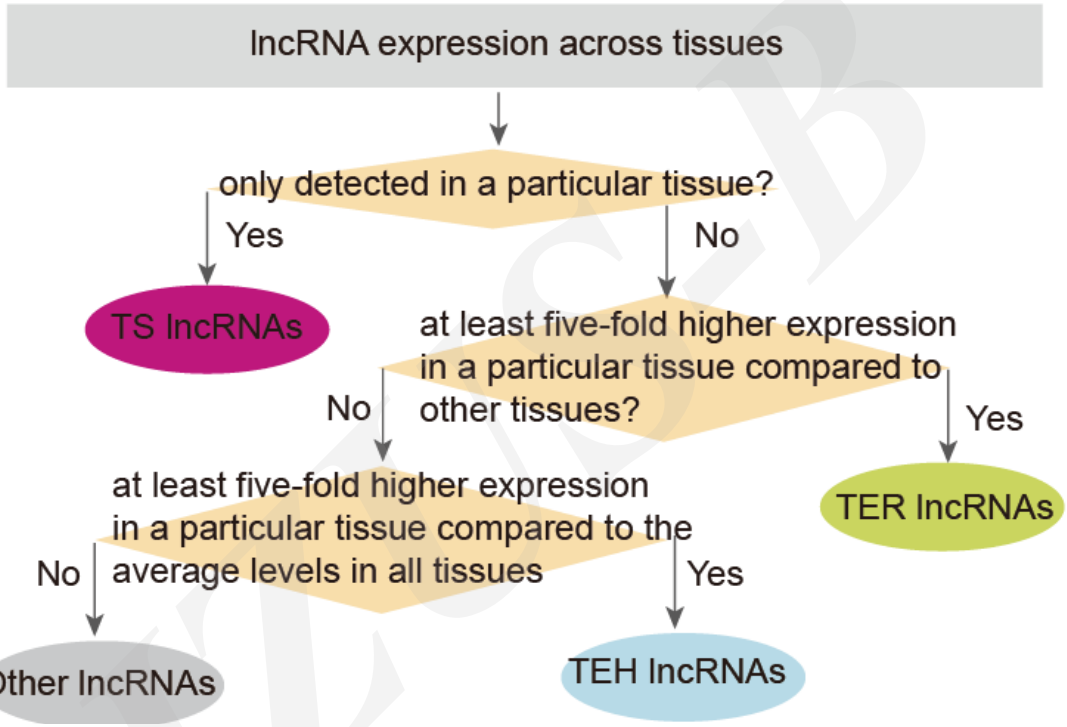
TCGA

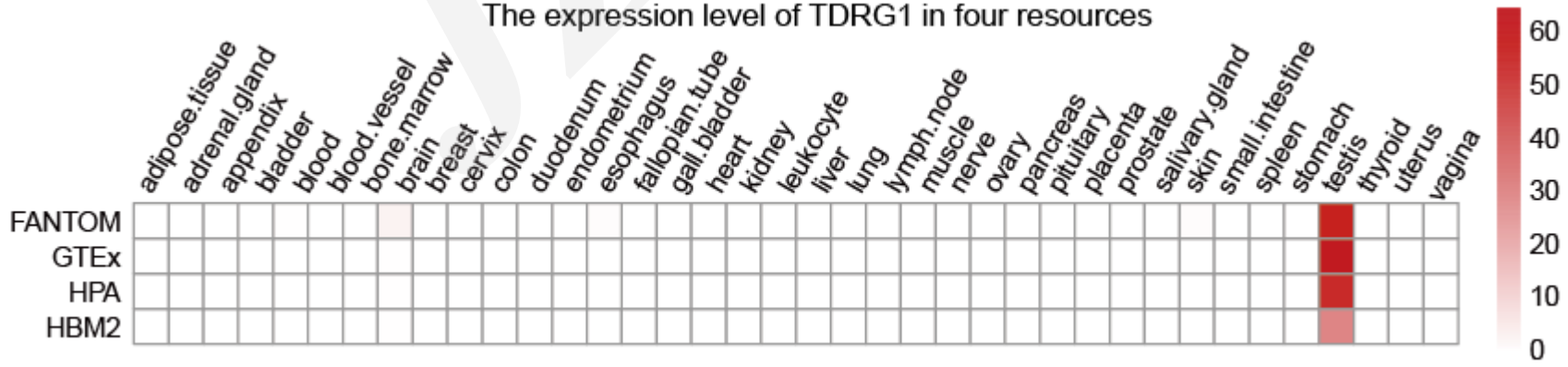
- **The lncRNA transcriptomes exhibited high consistency**
- **Identifing Tissue-elevated (TE) lncRNAs**
- **Robust TE lncRNAs distinguish tissues**
- **TE lncRNAs can serve as biomarkers**

The lncRNA transcriptomes exhibited high consistency

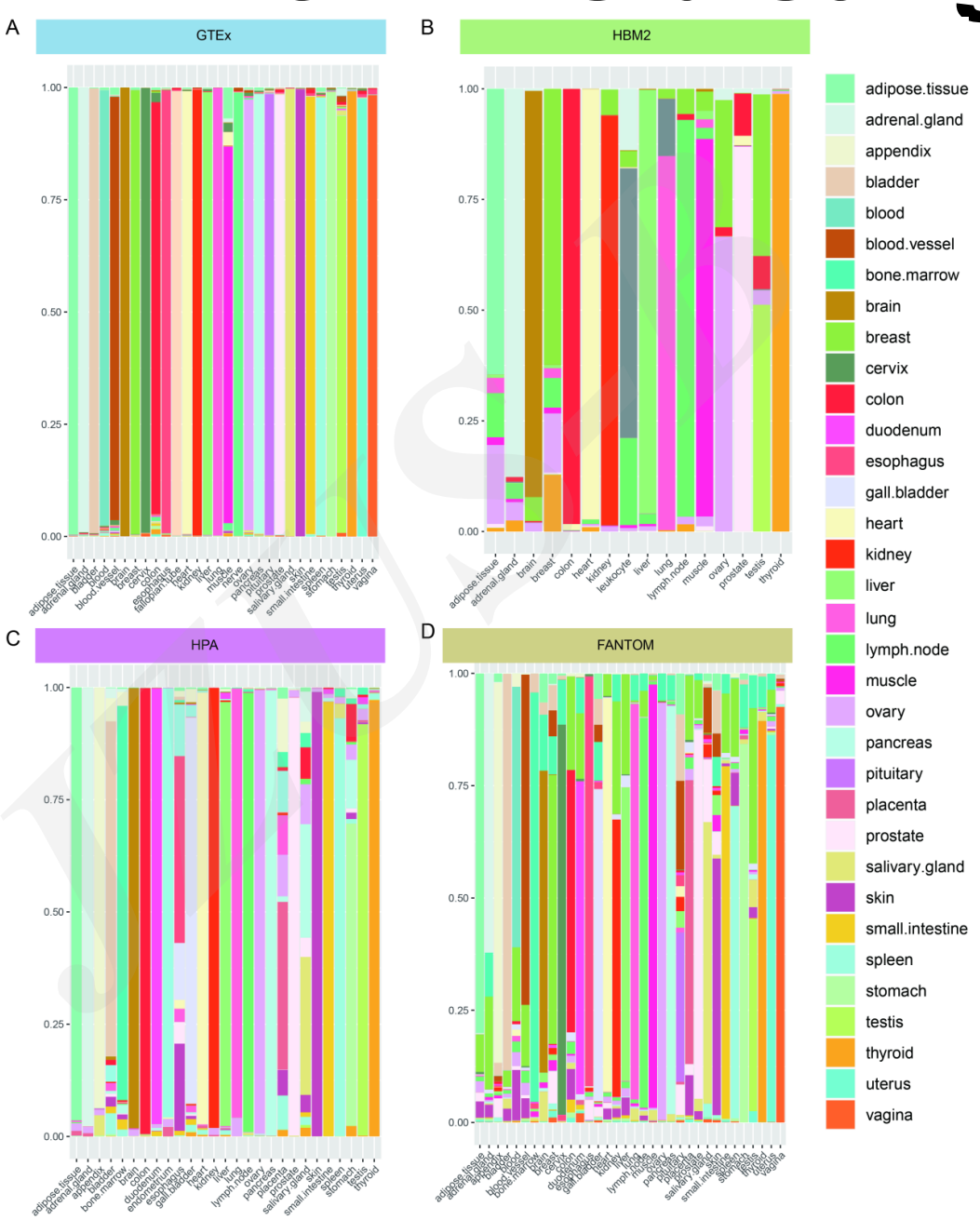


Identifing Tissue-elevated (TE) lncRNAs

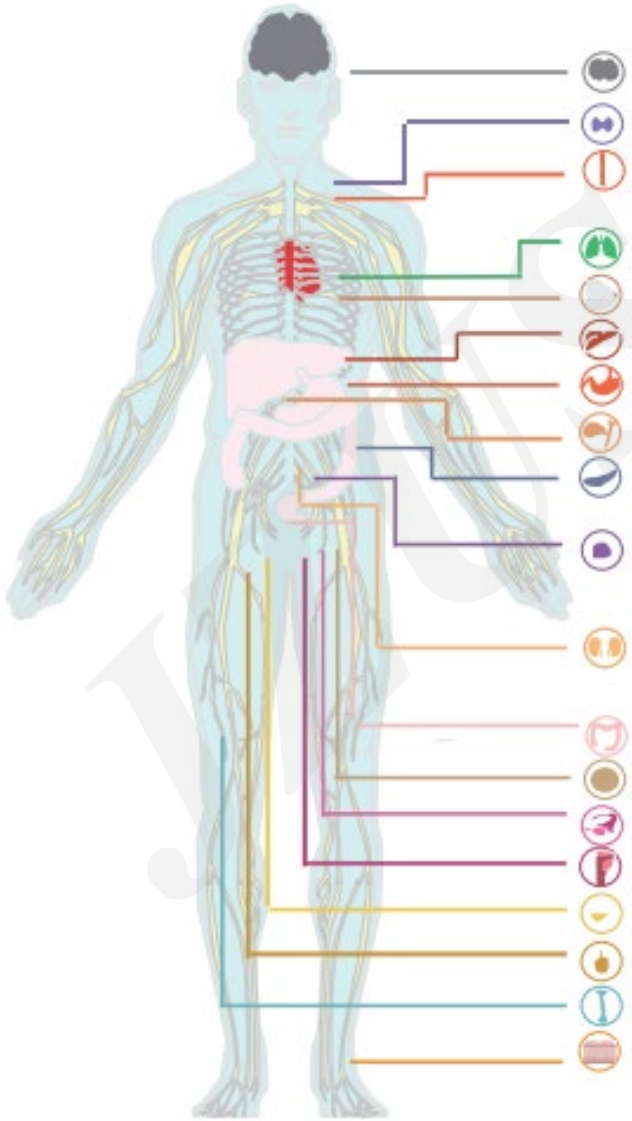




Robust TE lncRNAs distinguish tissues



TE lncRNAs can serve as biomarkers



TE	lncRNA	Protected	Risk	Down	Up
GBM	181	11	5	0	0
LGG	328	178	21	0	0
THCA	73	4	0	11	5
ESCA	12	0	0	0	1
LUAD	33	16	0	11	4
LUSC	7	0	1	0	2
BRCA	10	2	0	3	0
LIHC	199	52	2	46	10
STAD	7	0	0	1	2
CHOL	8	0	0	1	5
PAAD	11	0	1	0	0
ACC	53	9	7	0	0
PCPG	19	1	1	0	0
KICH	77	10	0	15	26
KIRC	79	45	1	15	25
KIRP	95	30	0	13	27
COAD	25	2	0	7	3
BLCA	17	5	0	0	5
OV	7	0	0	0	0
UCEC	2	0	0	0	0
PRAD	102	6	1	6	42
TGCT	271	0	1	0	0
LAML	23	7	1	0	0
SKCM	9	0	3	0	0