



Quantifying cellular malignancy by tumor micro-environment measurement with multimodal fusion

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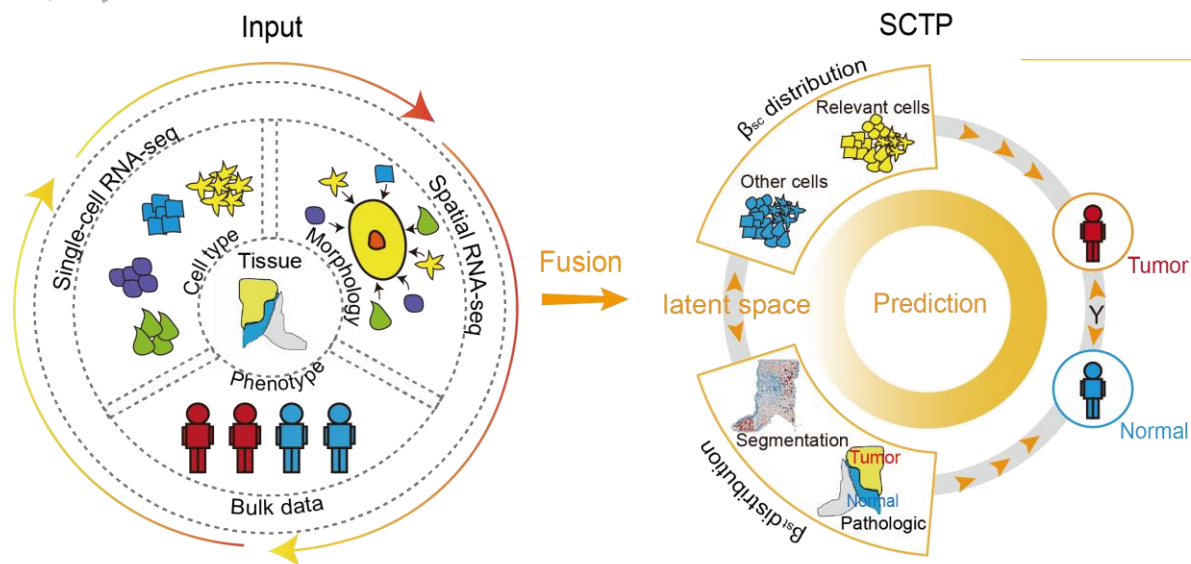
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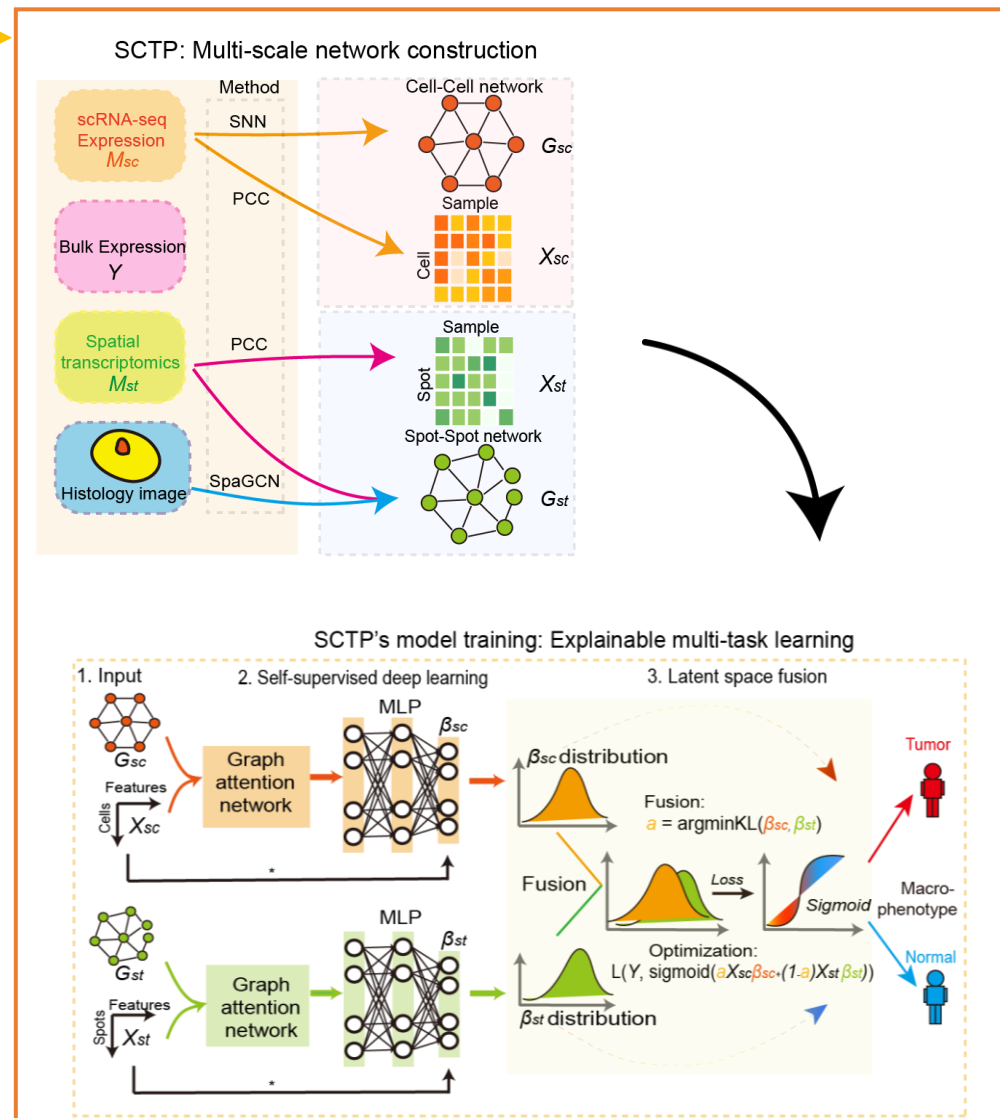
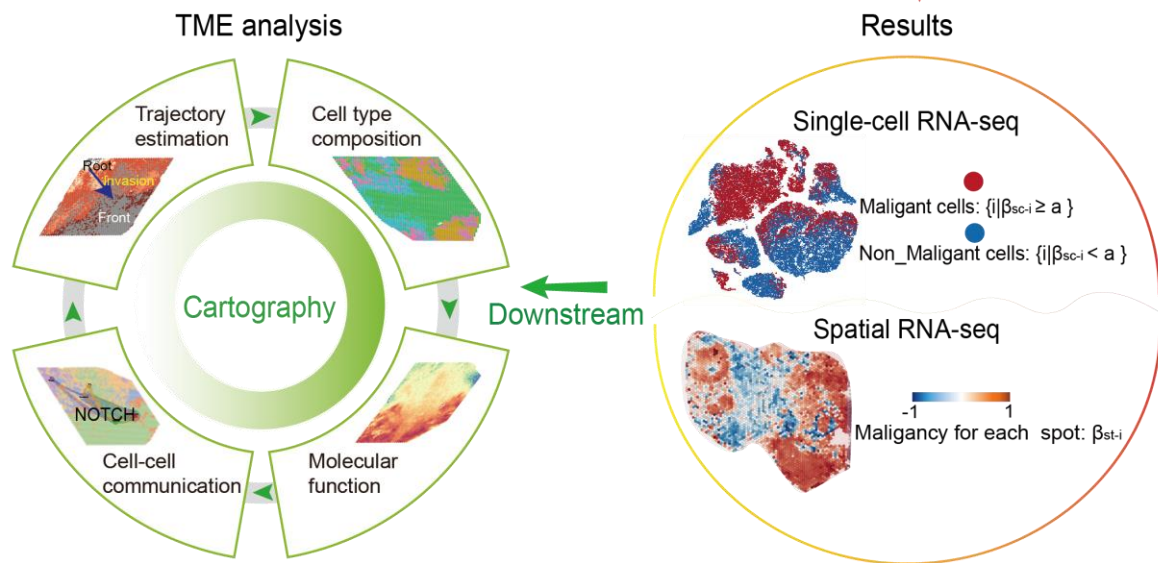


Introduction



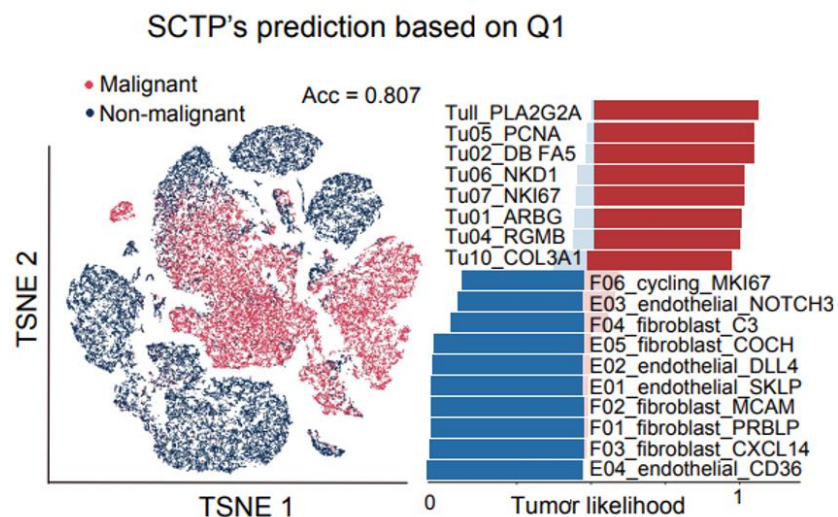
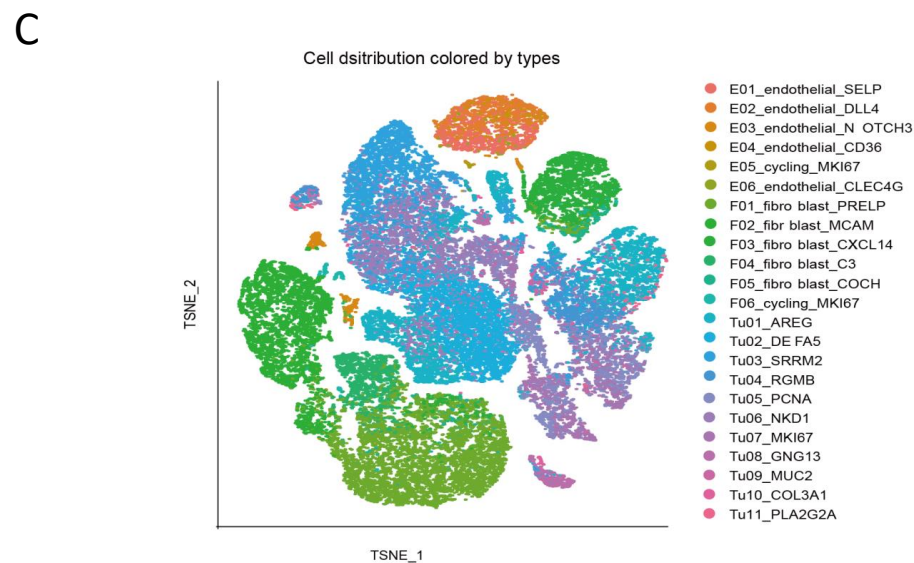
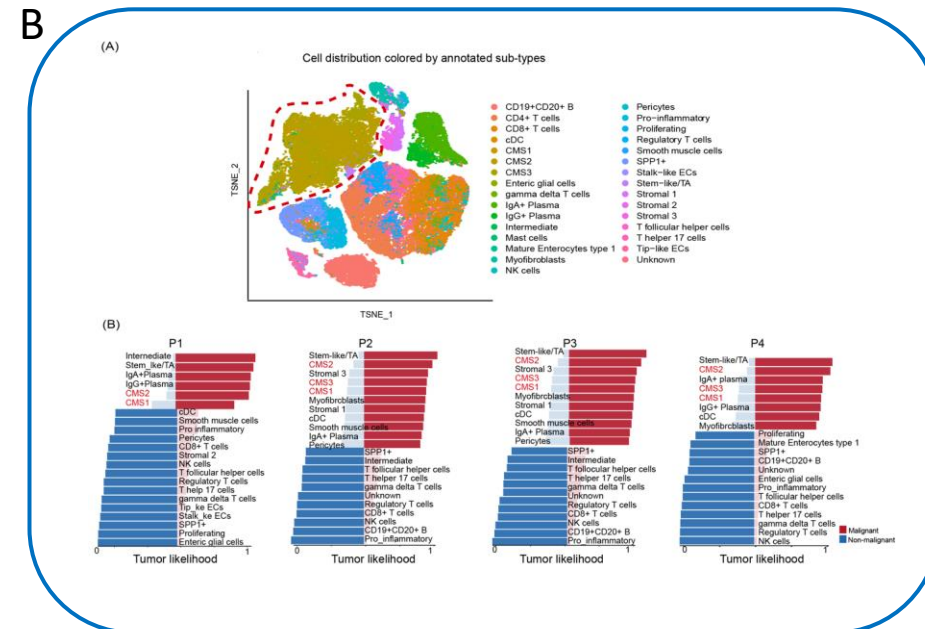
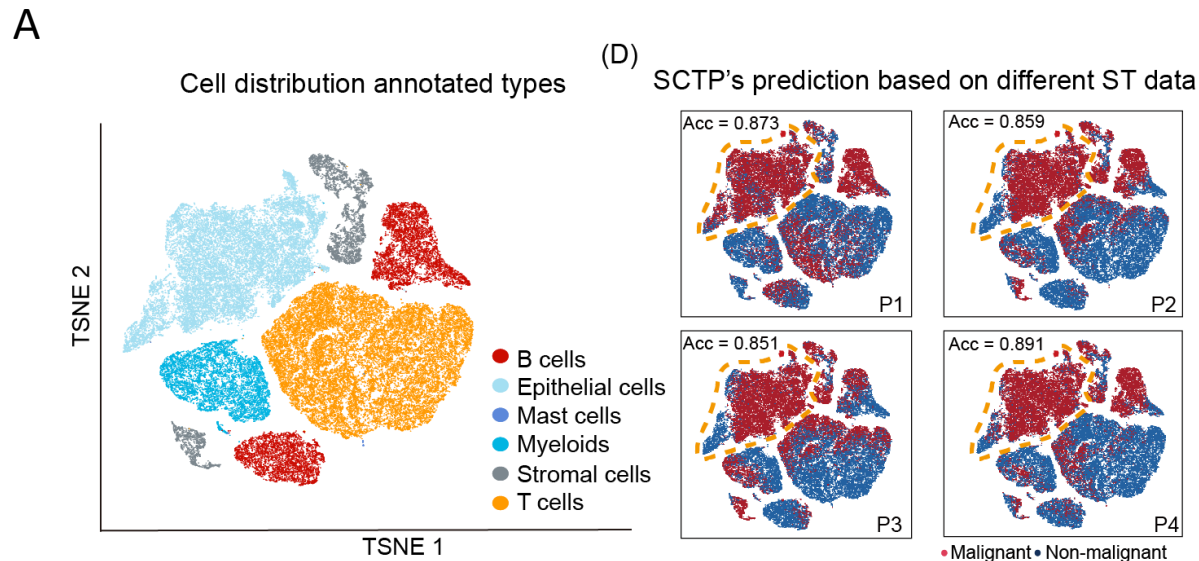
Quantifying malignancy

Results





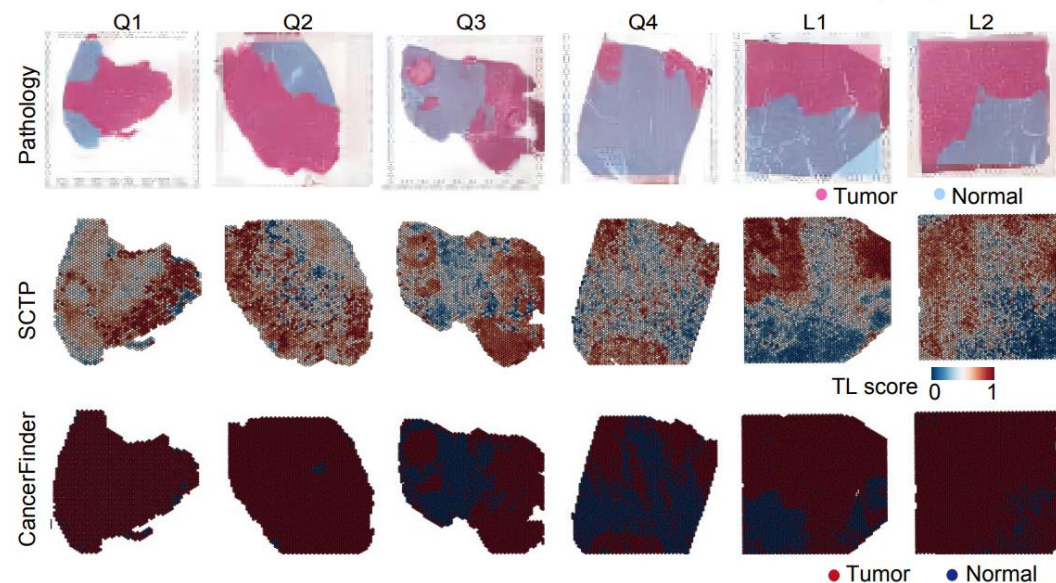
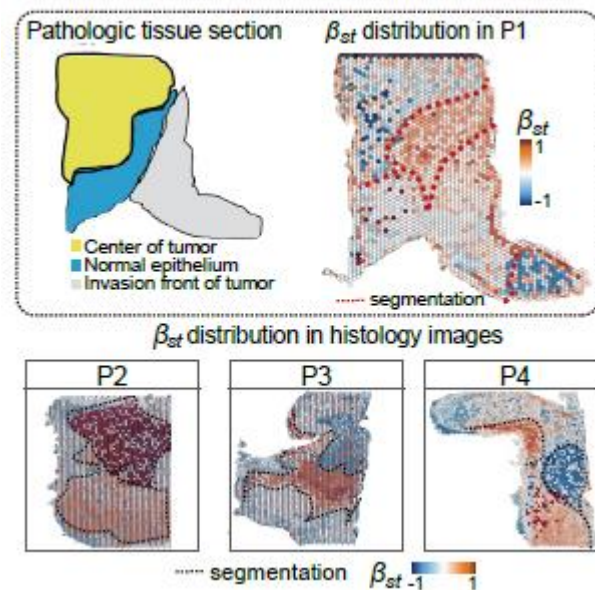
Validation & Accuracy (single cell RNAseq)



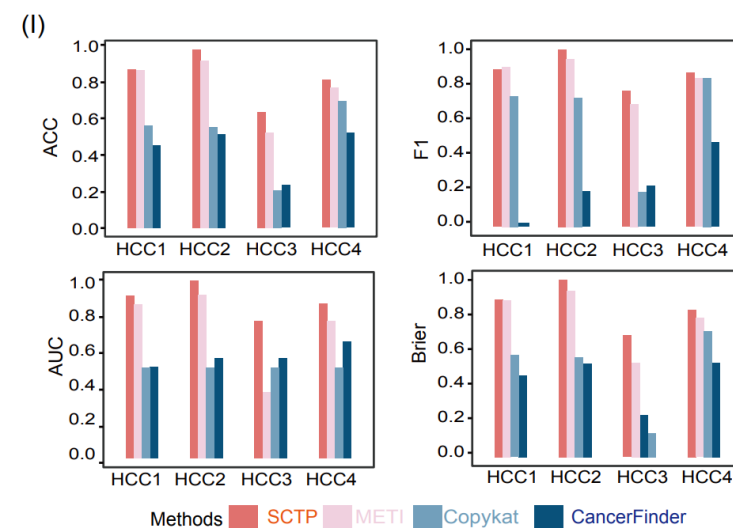
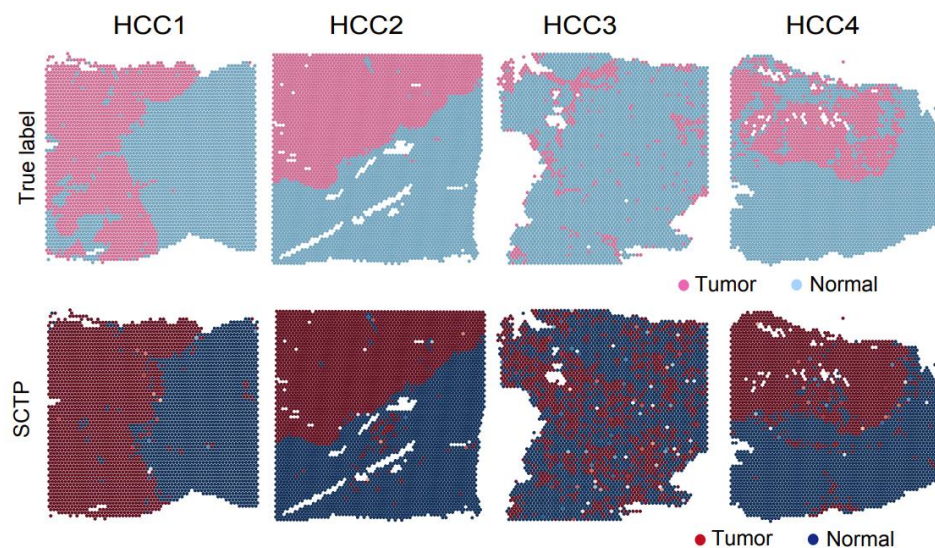


Validation & Accuracy (spatial transcriptomics)

SCTP-CRC



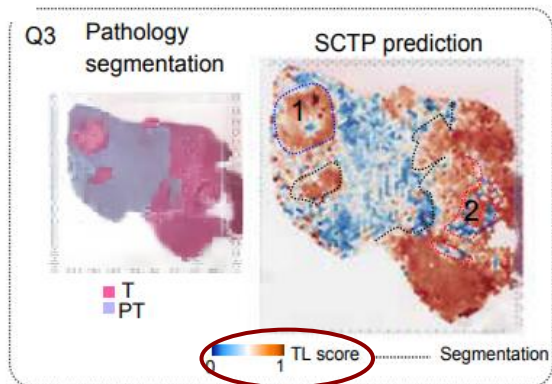
SCTP-HCC



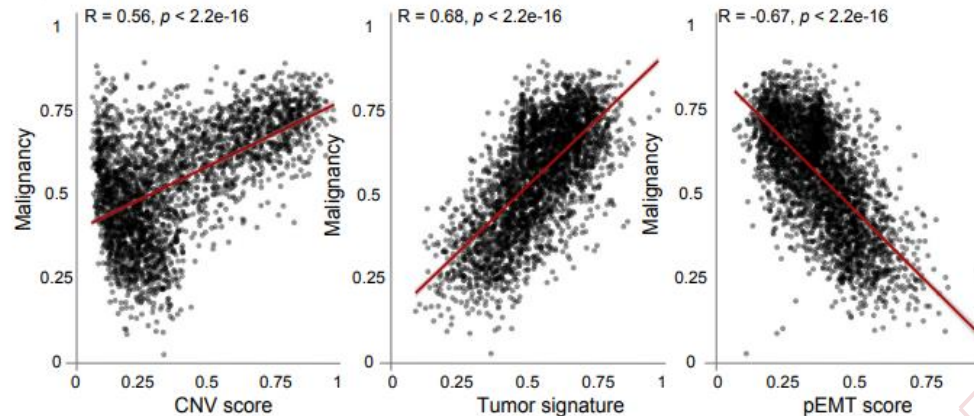


Biological Insights

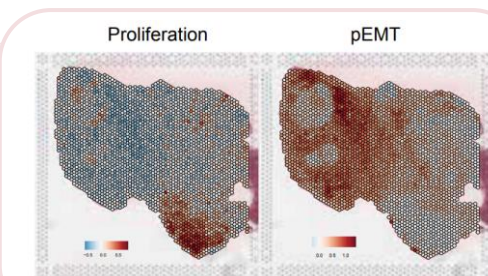
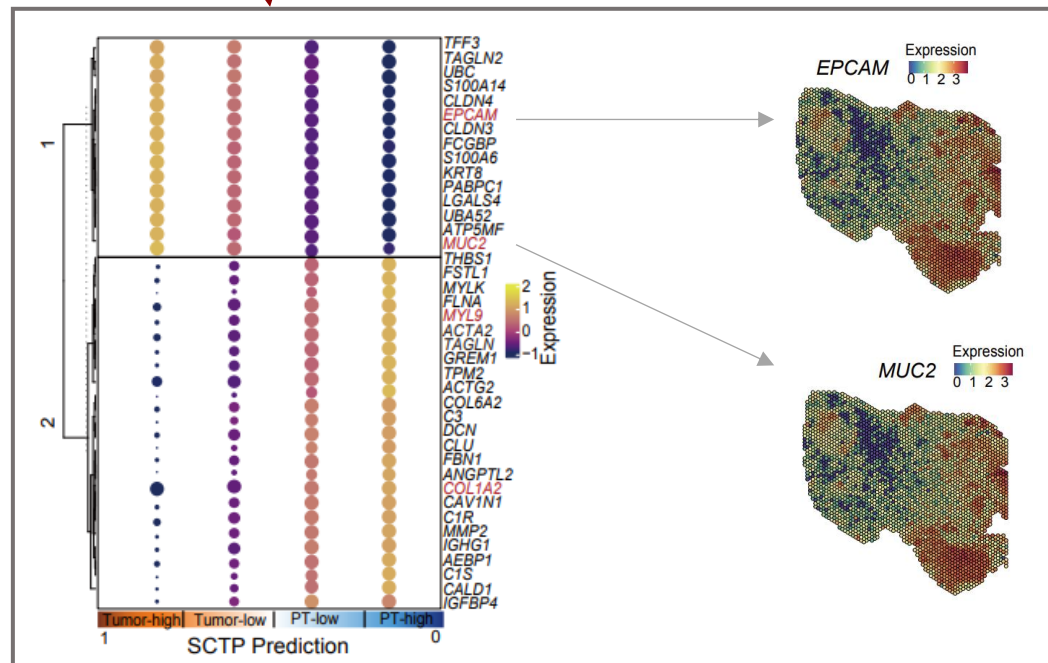
A



B



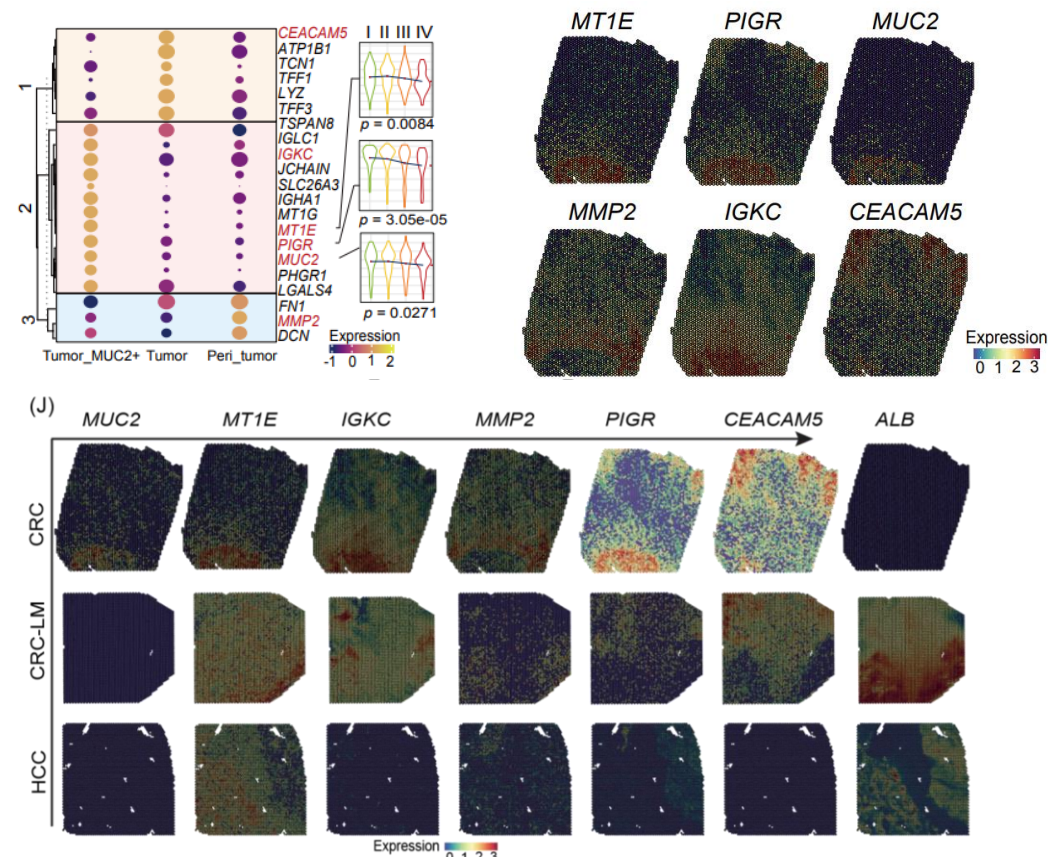
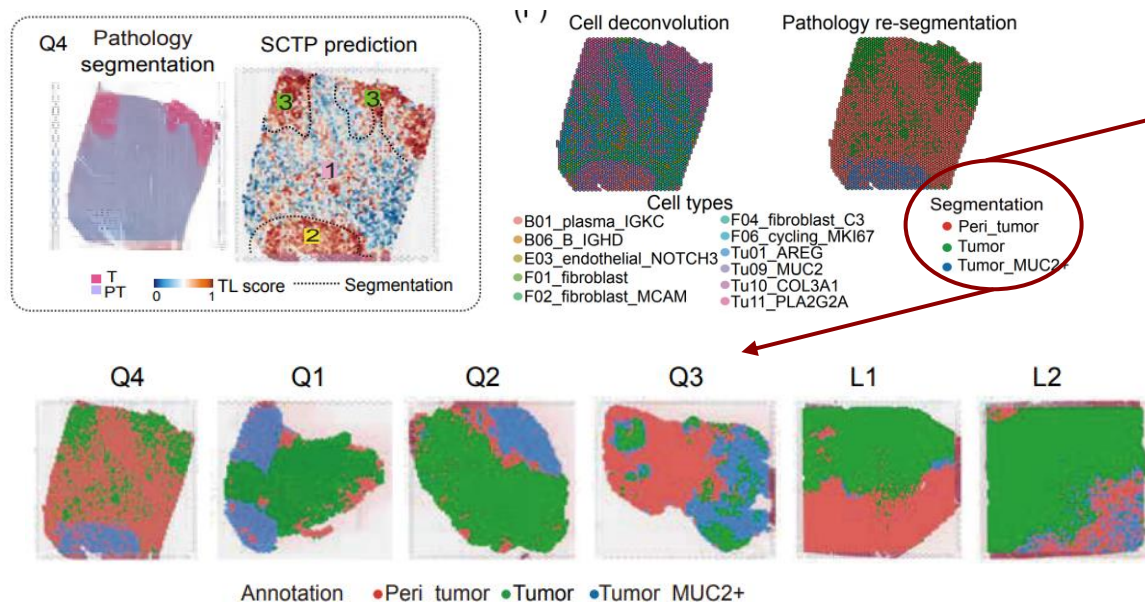
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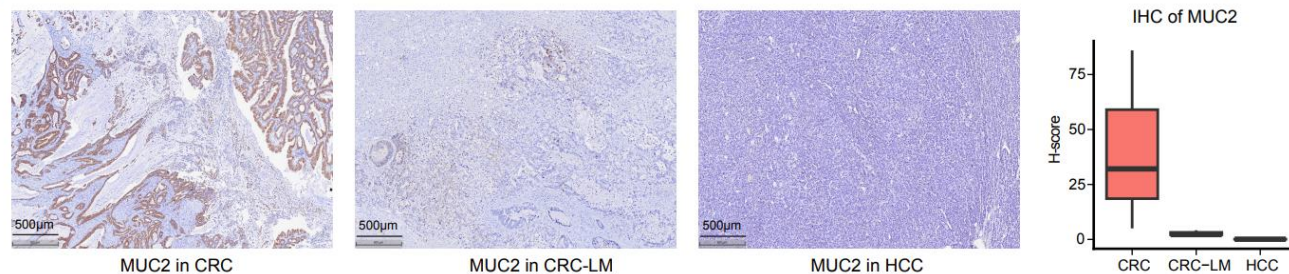


Early Malignant Subpopulation Discovery

Identification of Tumor MUC2+ subpopulation



Experimental validation





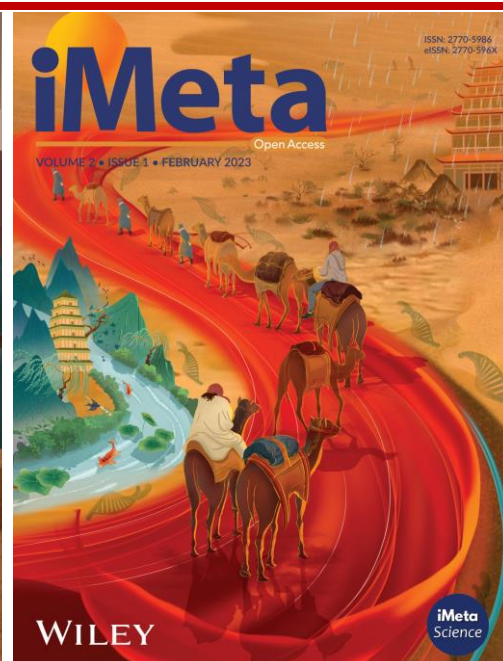
Summary

- ❑ SCTP provides a multimodal framework to quantify malignancy at high resolution.
- ❑ Achieves high classification accuracy across both single-cell and spatial transcriptomics datasets.
- ❑ Enables discovery of early malignant subpopulations with spatial validation
- ❑ Availability: <https://github.com/ztpub/SCTP>

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