

Supplementary Materials

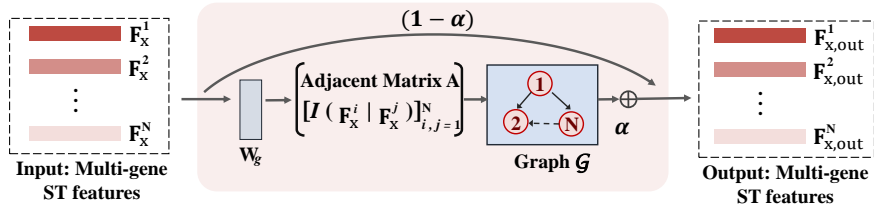


Fig. 1. Pipelines of CIGC-Graph network.

Table 1. Implementation details of our proposed method.

Number of genes N for ST maps	25
Number of cell-level patches M per histology image	256
Features channels d_t of F_{tissue}	128
Features channels d_c of F_{cell}^s	128
Intermediate channels d in cross-attention modelling	128
Region size a in cross-modal adaptive modulation	32
Number of features C for the input nodes of CPLC-Graph	676
Graph balancing weight α	0.2
Exponential decay rate β_1 and β_2 for AdamW optimization	0.9 and 0.999
Epsilon ϵ for AdamW optimization	1×10^{-8}
Weight decay for AdamW optimization	1×10^{-5}

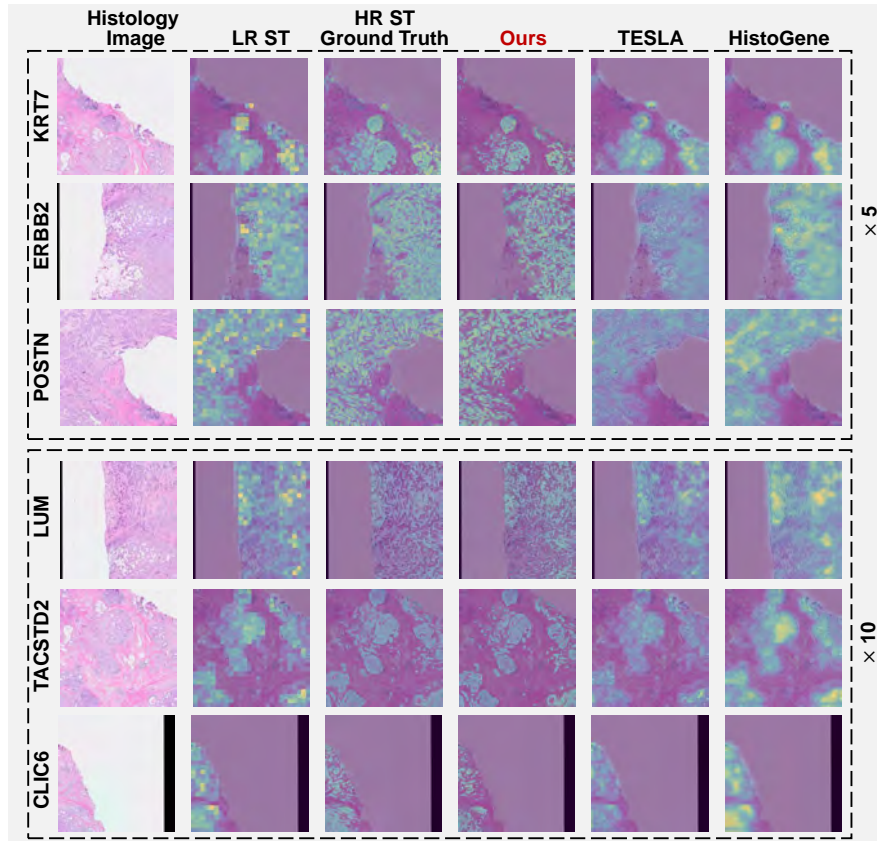


Fig. 2. Additional visual comparisons at 5 \times and 10 \times scales on the Xenium dataset. The ST maps are overlaid on the paired histology image for better visualisation. Note that KRT7, ERBB2, POSTN, LUM, TACSTD2 and CLIC6 denote different genes.