

Supplementary information

STHELAR, a multi-tissue dataset linking spatial transcriptomics and histology for cell type annotation

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1 Supplementary figure

1.1 Training and validation curves for CellViT fine-tuning on STHELAR

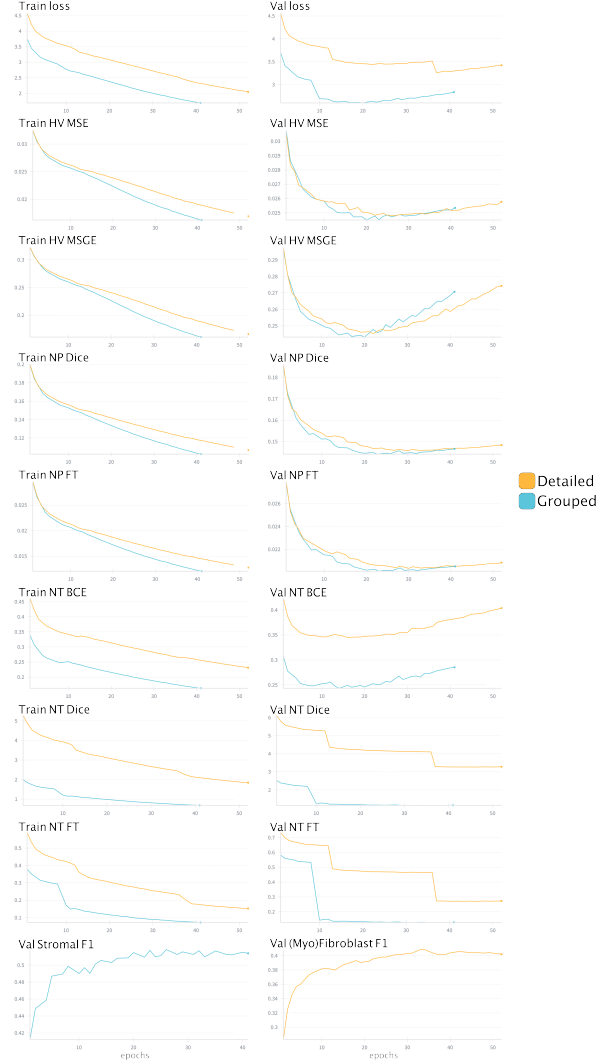


Figure S1: **Training and validation curves for CellViT fine-tuning on STHELAR.** The panels summarize the optimisation behaviour of the CellViT model fine-tuned on the STHELAR dataset for the two label configurations (detailed versus grouped). For each branch of the model, it shows the corresponding loss curves over training epochs, including both training and validation curves. Specifically, it reports: (i) HV-branch losses (mean squared error "HV MSE" and mean squared gradient error "HV MSGE"), (ii) NP-branch losses (Dice "NP Dice" and Focal Tversky "NP FT"), and (iii) NT-branch losses (binary cross-entropy "NT BCE", Dice "NT Dice", and multi-class Focal Tversky "NT FT"). In each panel, the curves for the fine-tuning with detailed cell-type labels are shown in yellow, and the curves for the fine-tuning with grouped labels are shown in blue. Two additional panels illustrate example validation F1 detection curves over epochs for (i) the **Stromal** class in the grouped-label configuration and (ii) the **(Myo)Fibroblast** class in the detailed-label configuration.