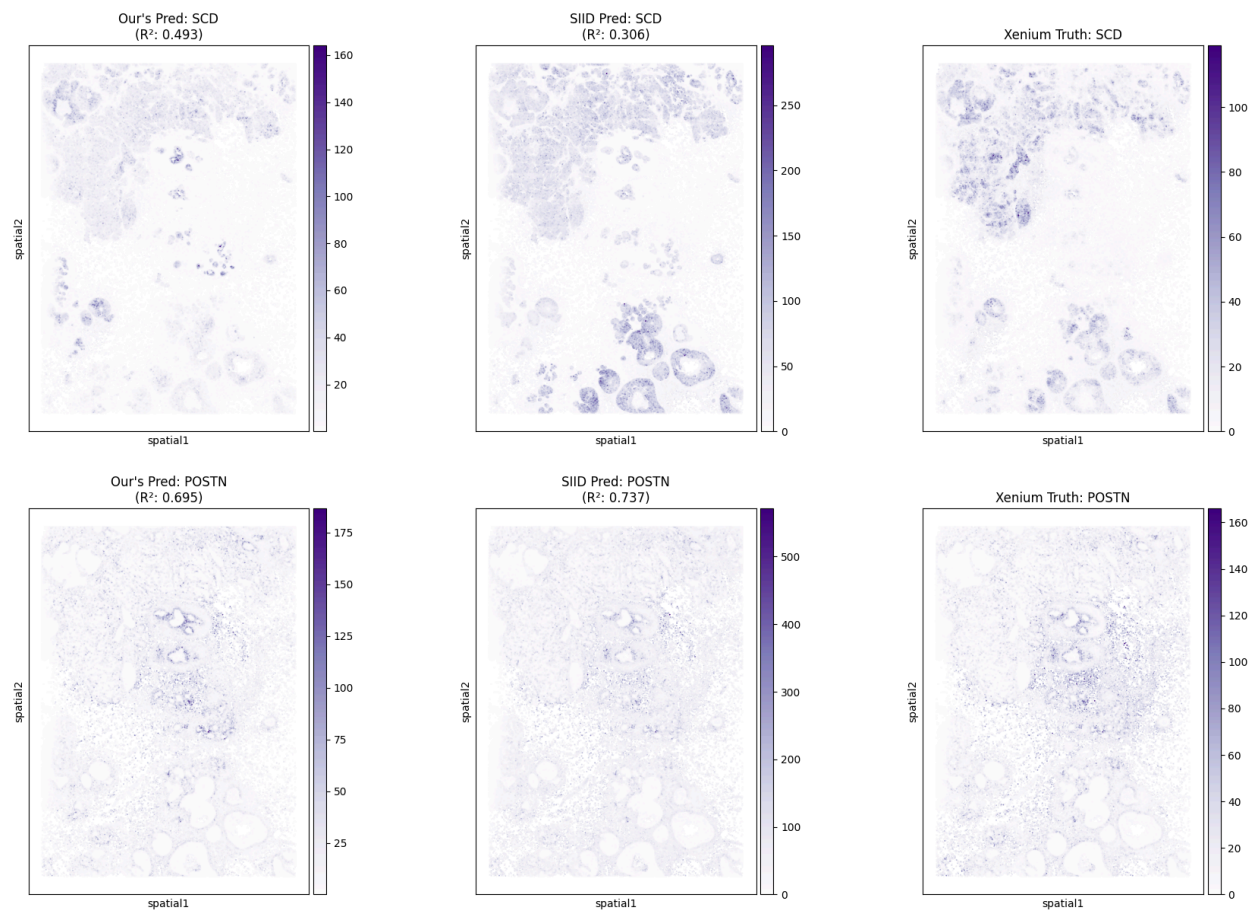


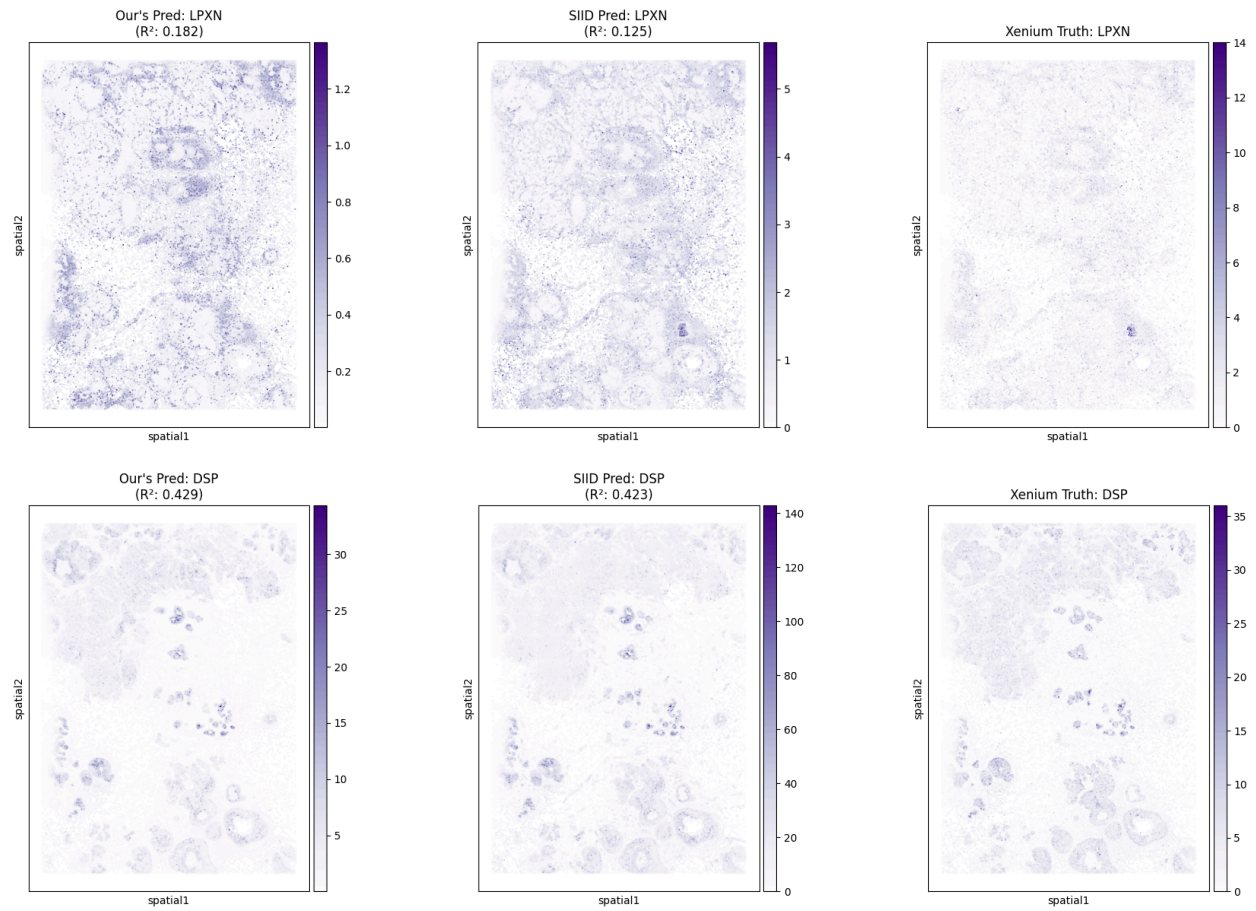
Results of our final model on the BRCA dataset :

Imputation:

Our model scores an average R^2 of **0.22** on the holdout genes

Comparison of holdout genes with truth and siid :





2. Deconvolution

Corresponding Xenium and Visium plots of different cell types predicted

