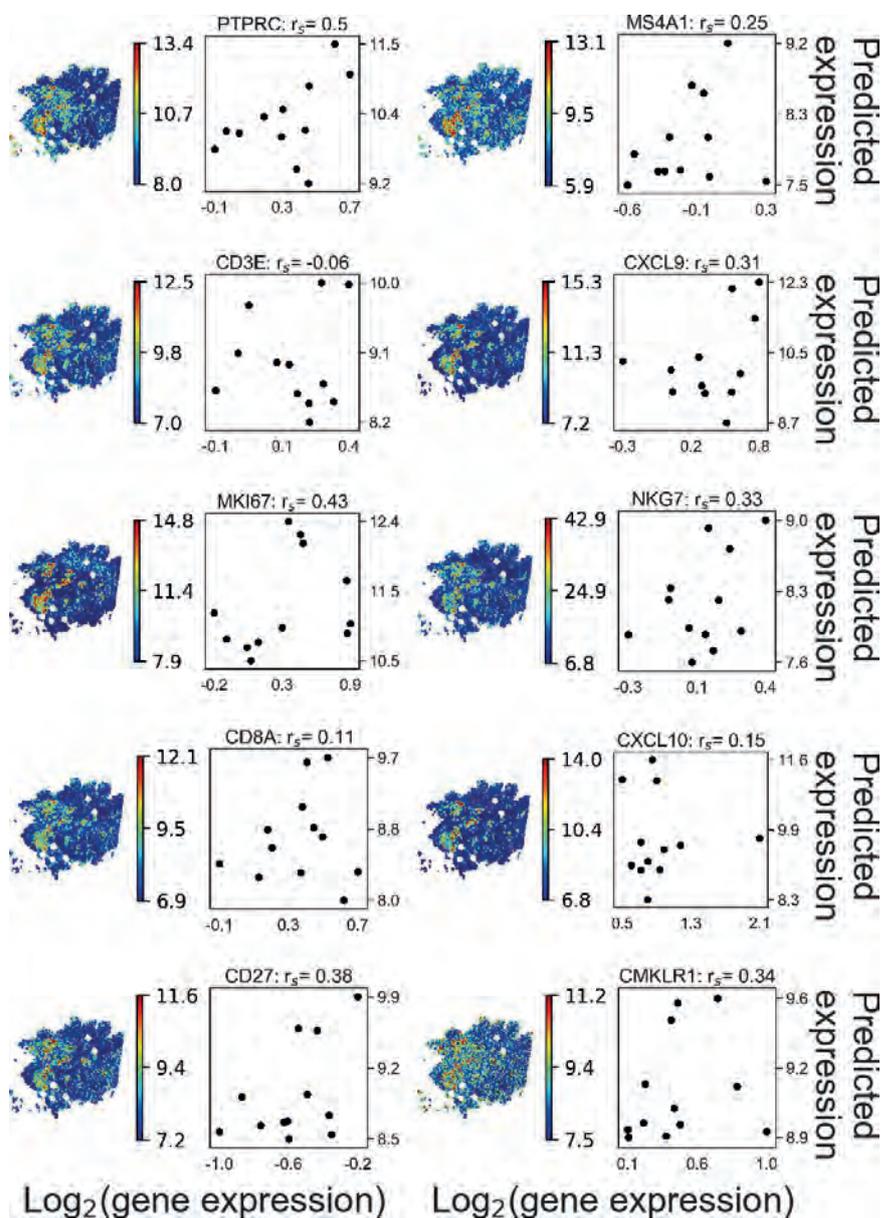
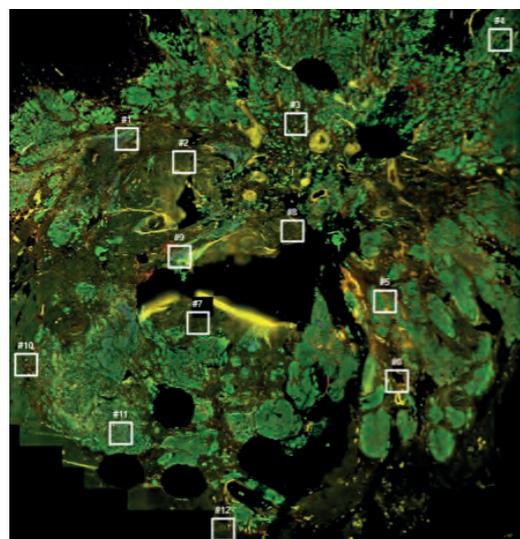
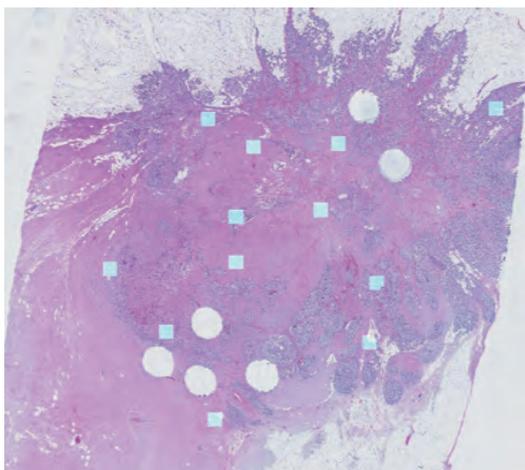
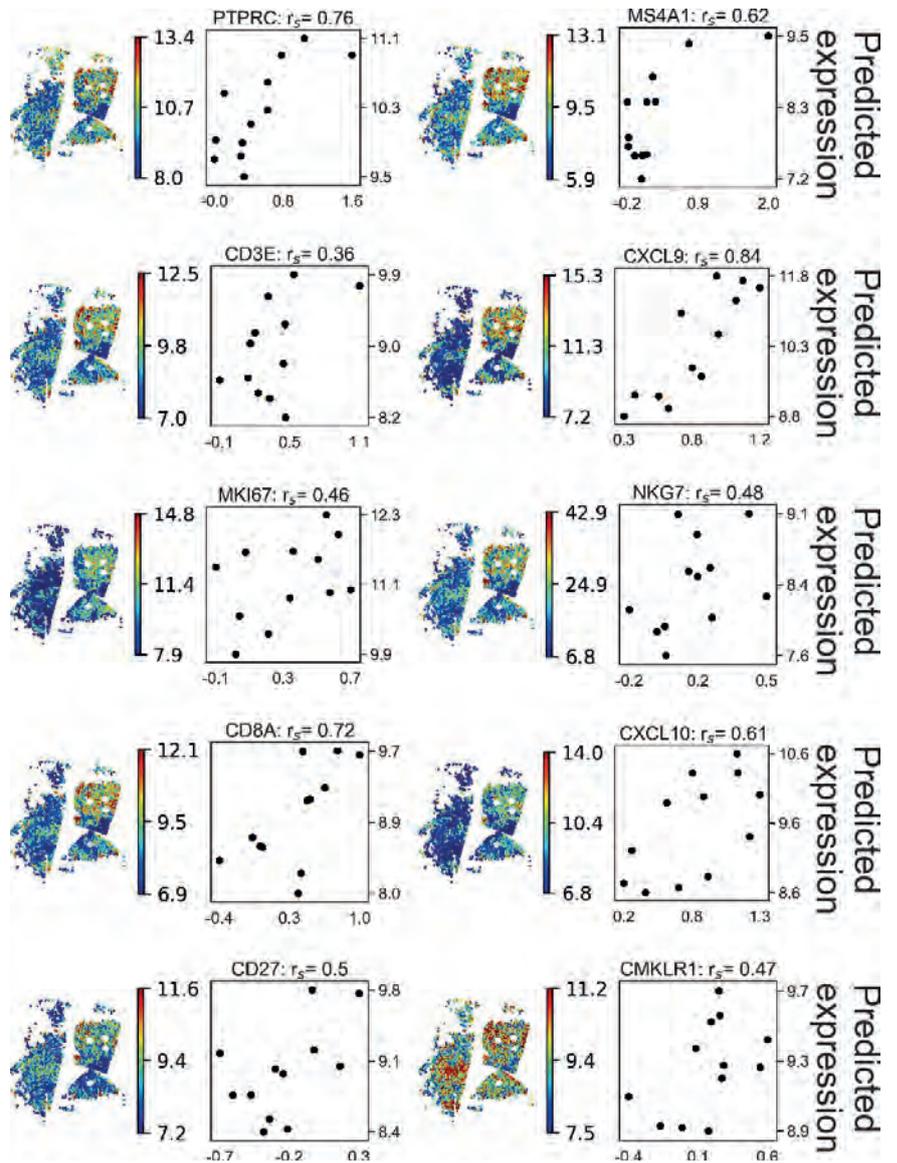
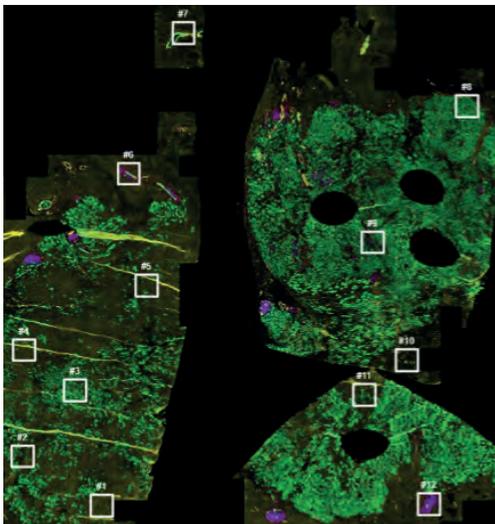
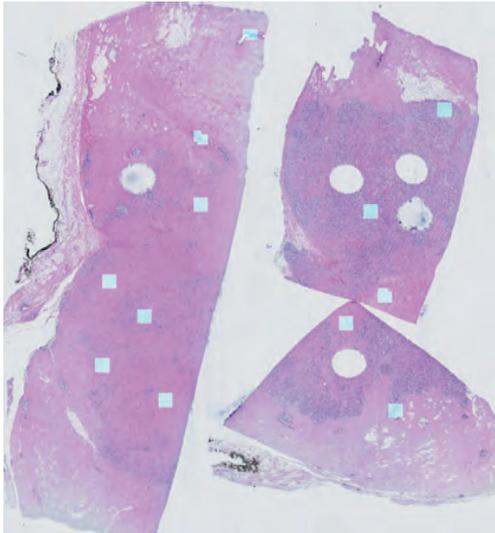


Tumour 2



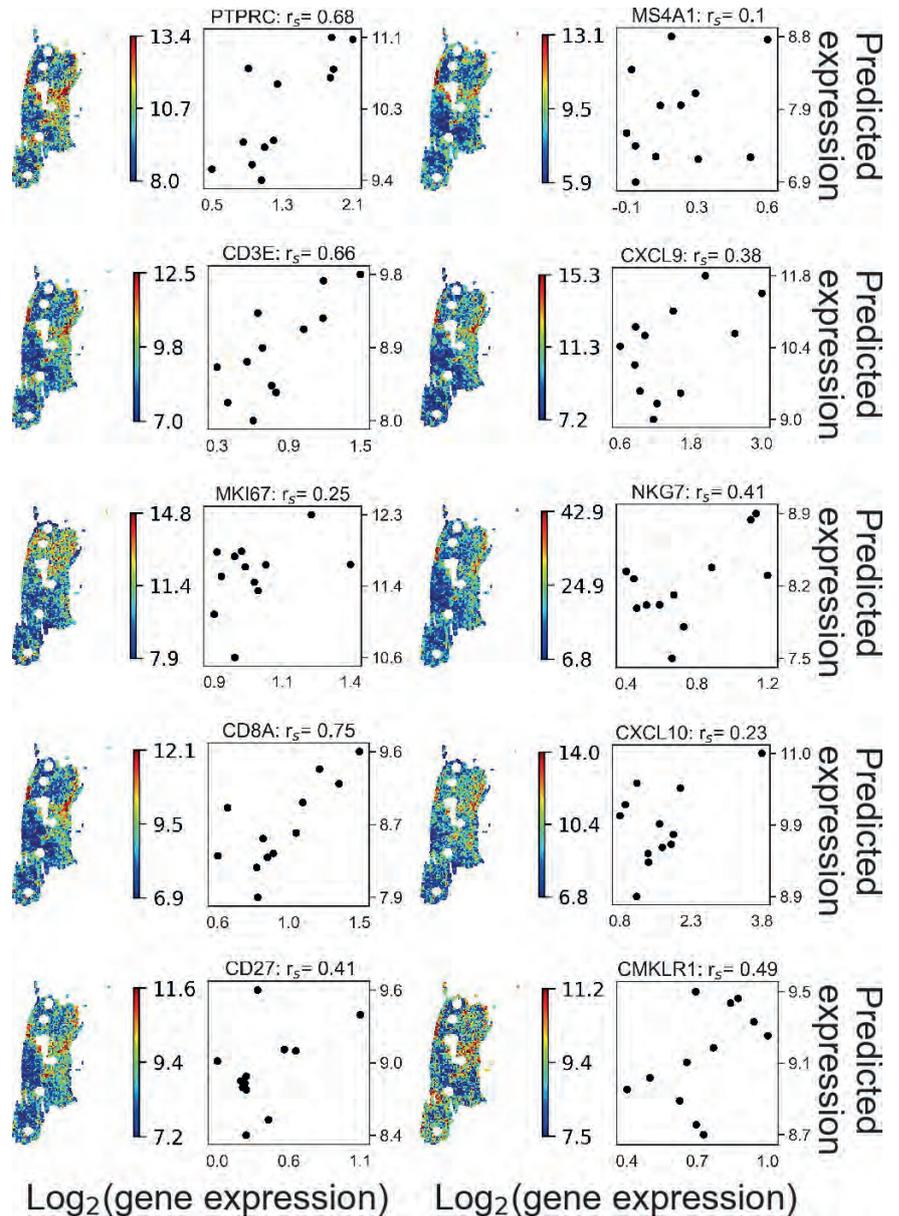
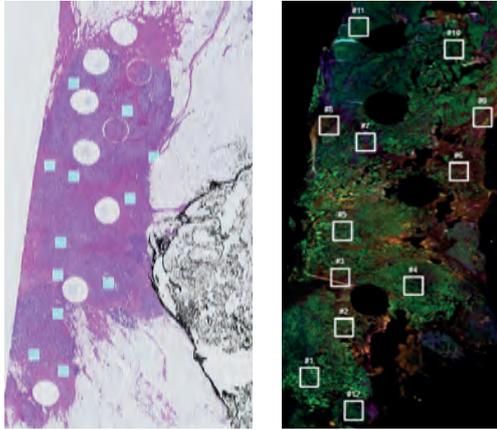
Supplementary Figure 5 (1/22). ST analysis results for Tumour 2. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescently stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 3



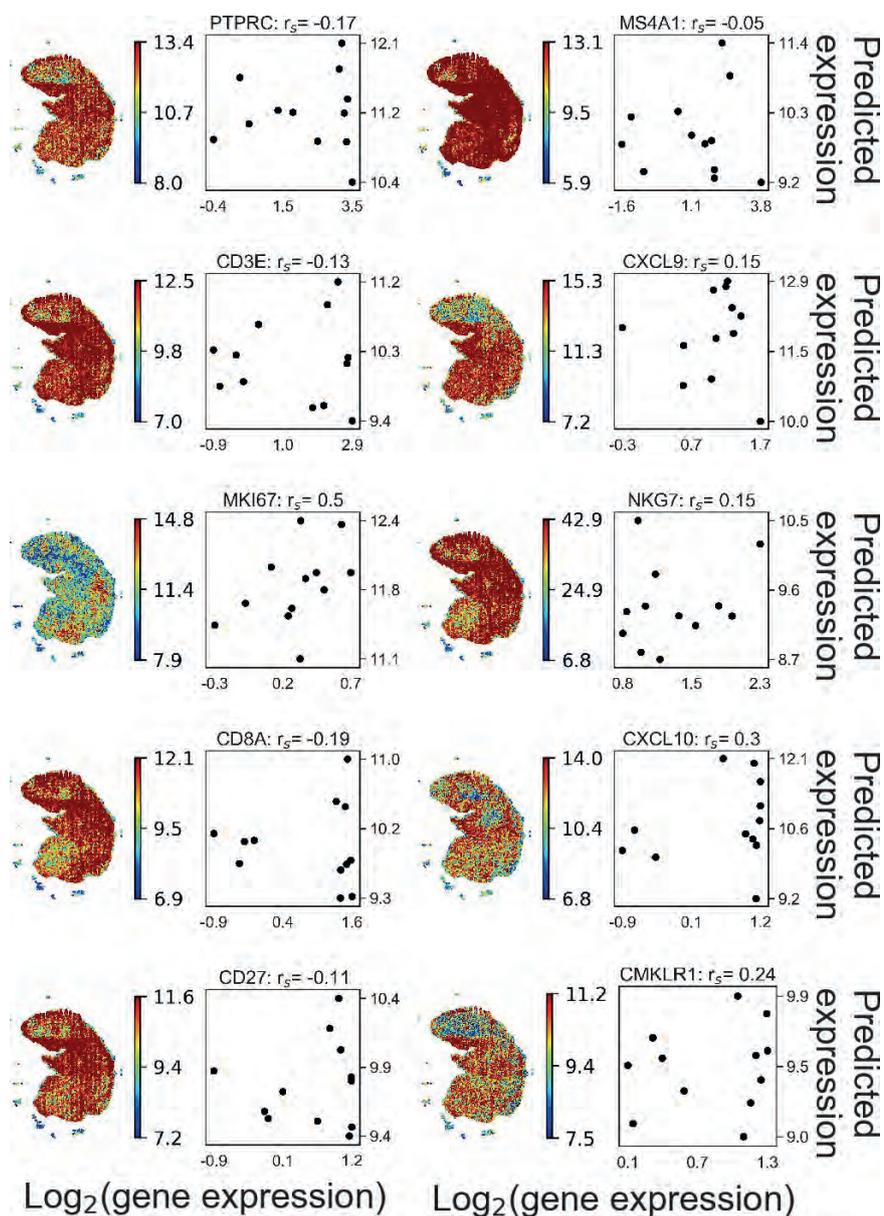
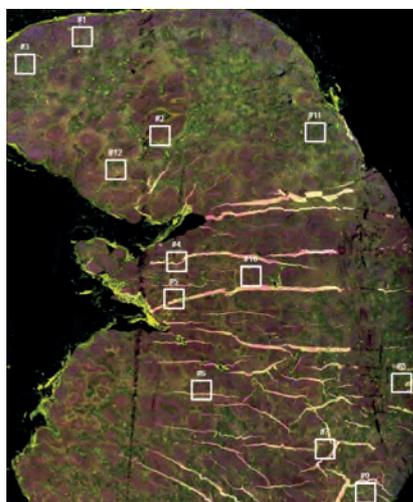
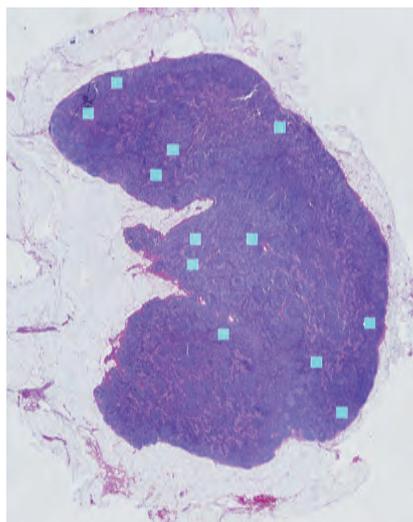
Supplementary Figure 5 (2/22). ST analysis results for Tumour 3. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 4



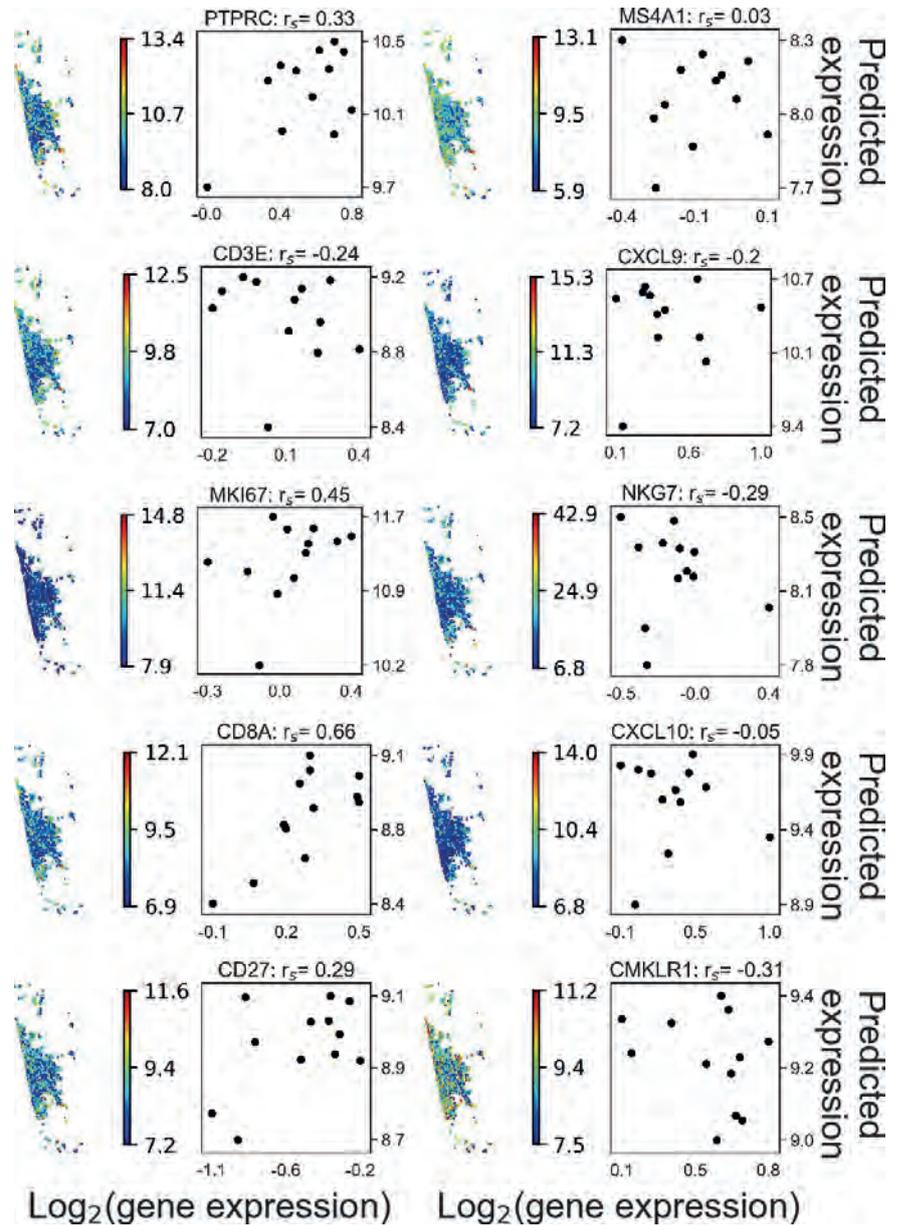
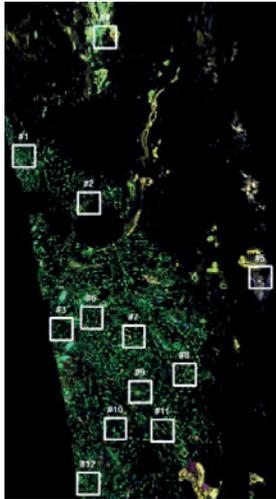
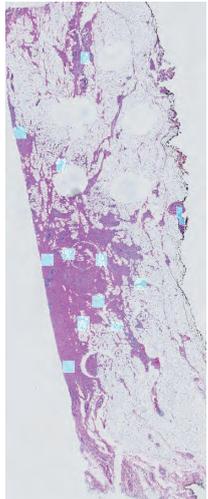
Supplementary Figure 5 (3/22). ST analysis results for Tumour 4. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 5



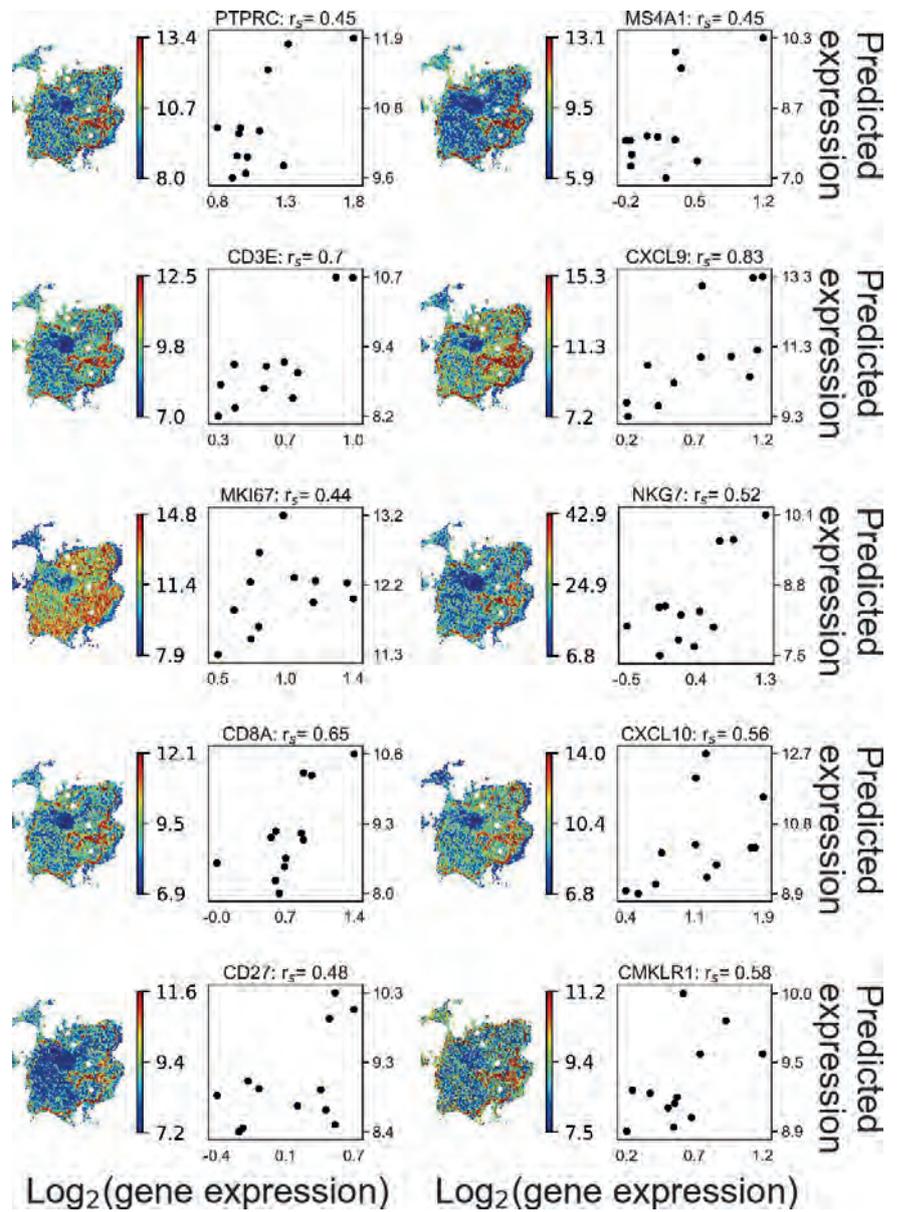
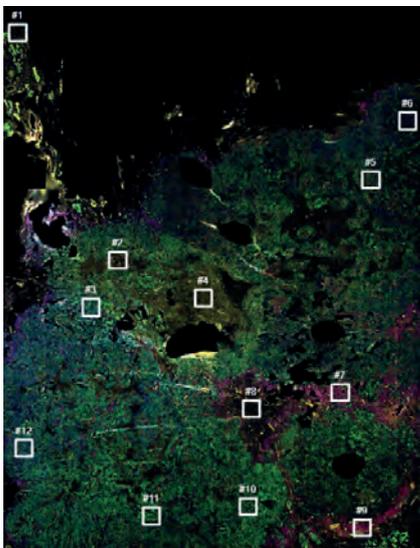
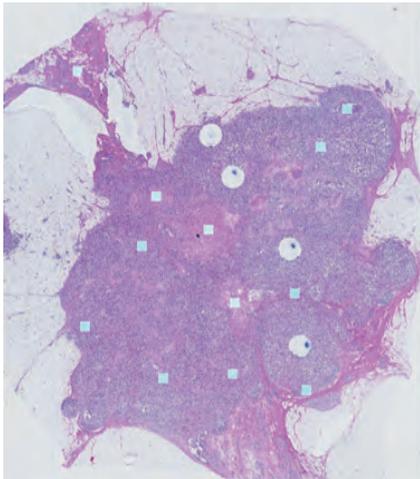
Supplementary Figure 5 (4/22). ST analysis results for Tumour 5. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman s correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 6



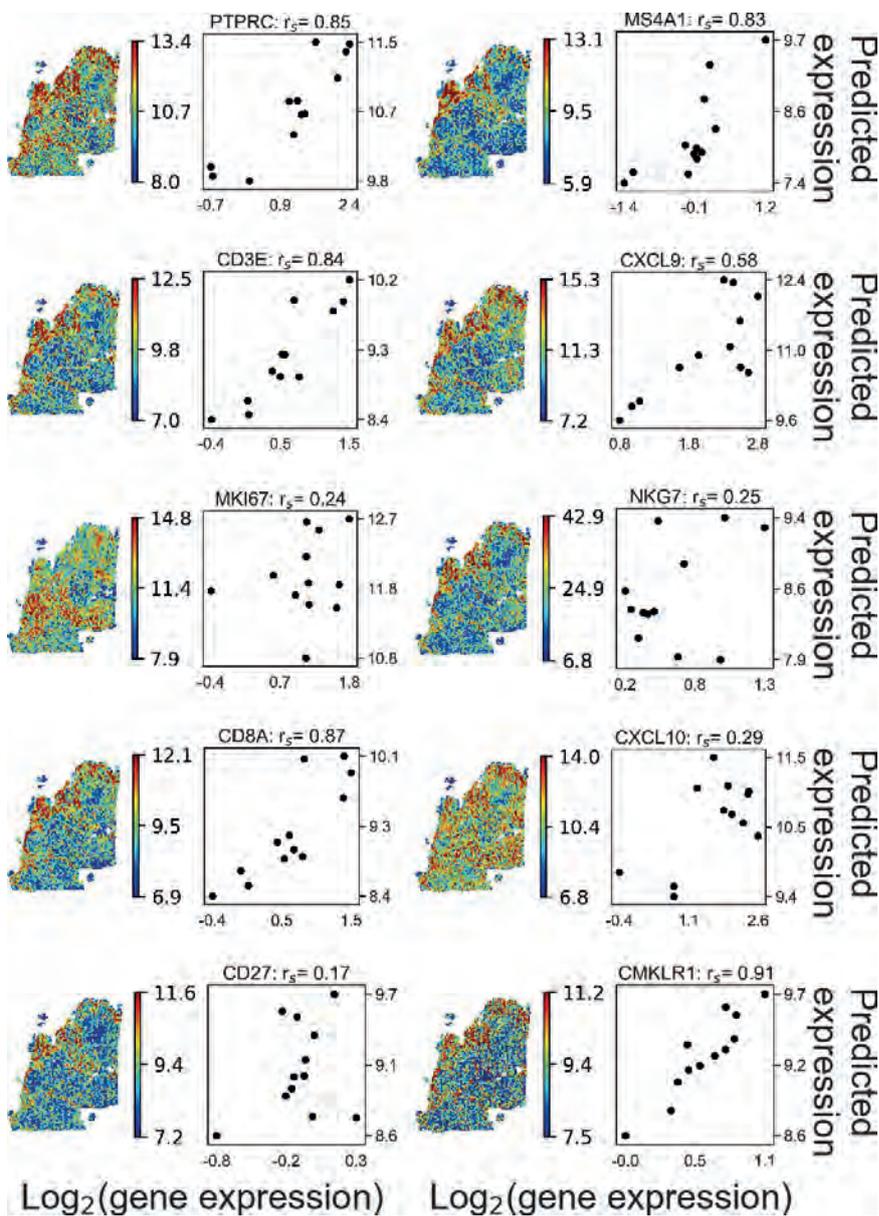
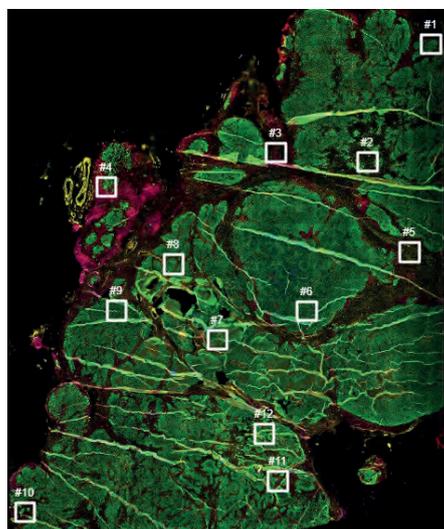
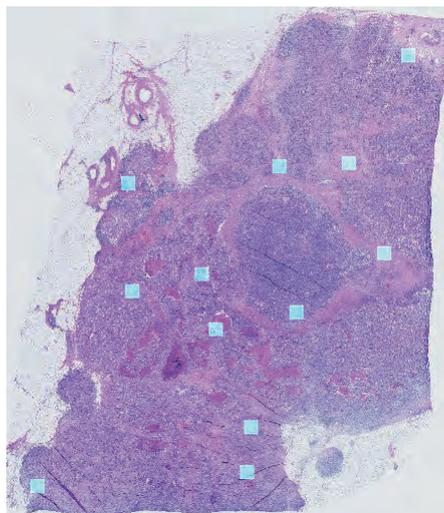
Supplementary Figure 5 (5/22). ST analysis results for Tumour 6. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 8



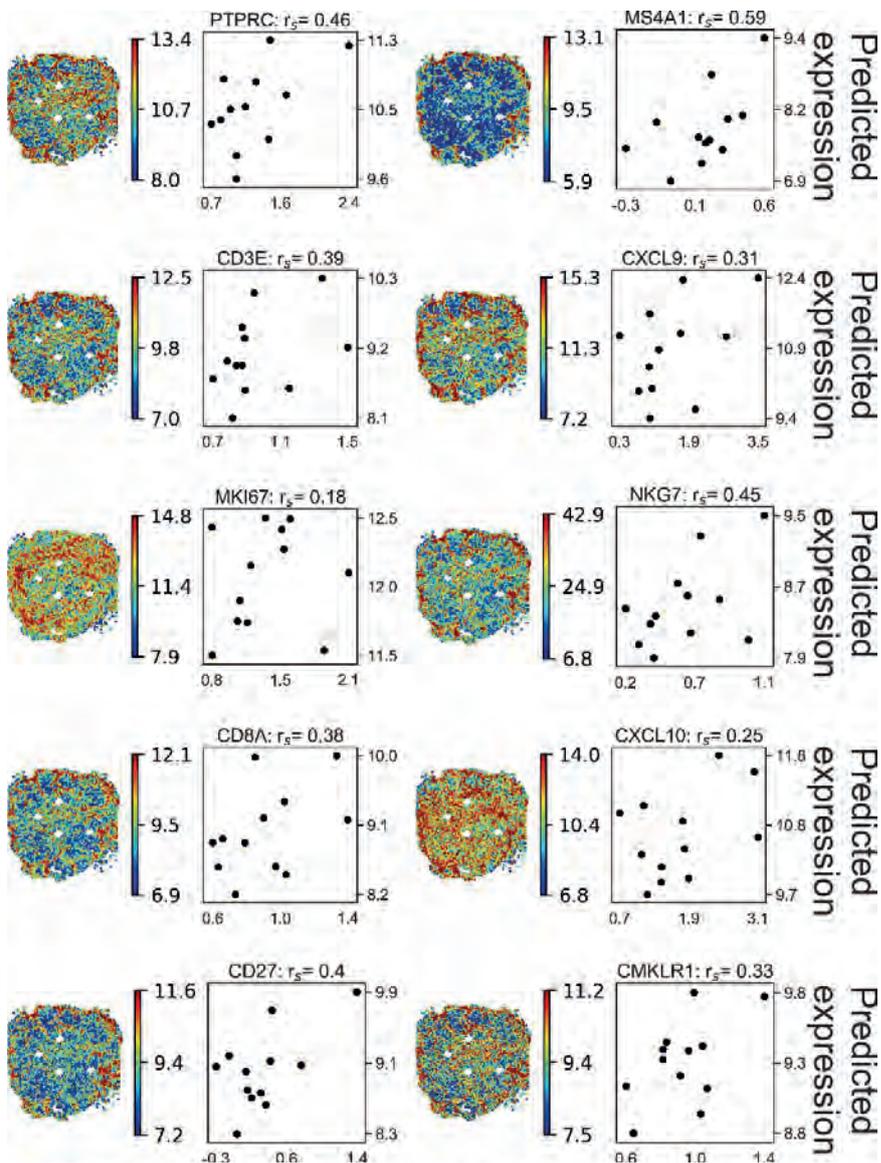
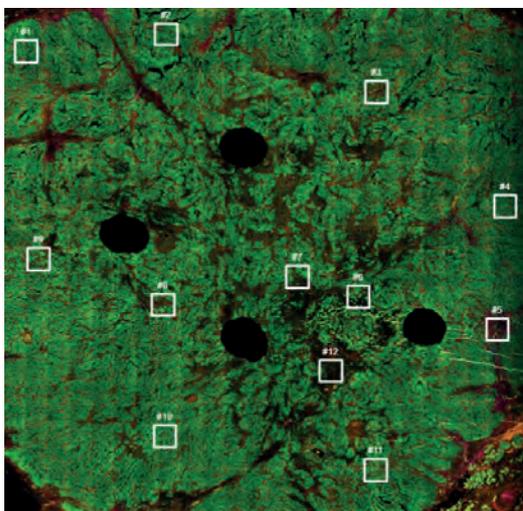
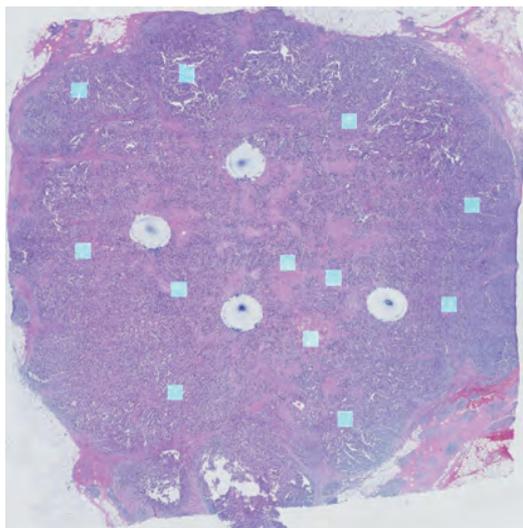
Supplementary Figure 5 (/22). ST analysis results for Tumour 8. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 9



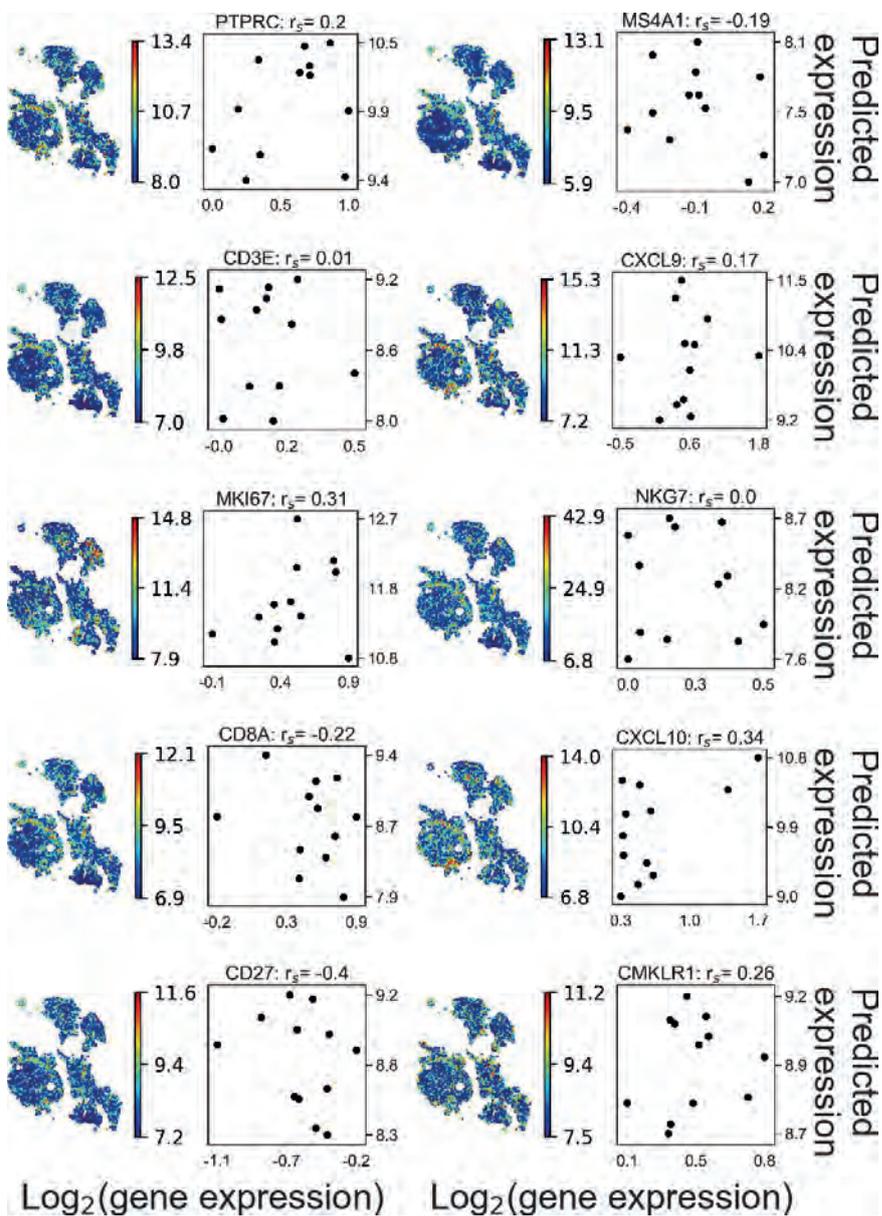
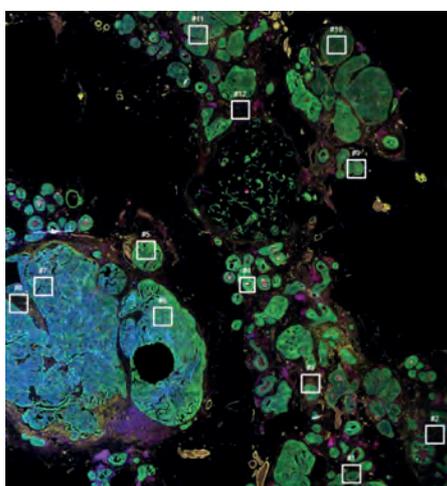
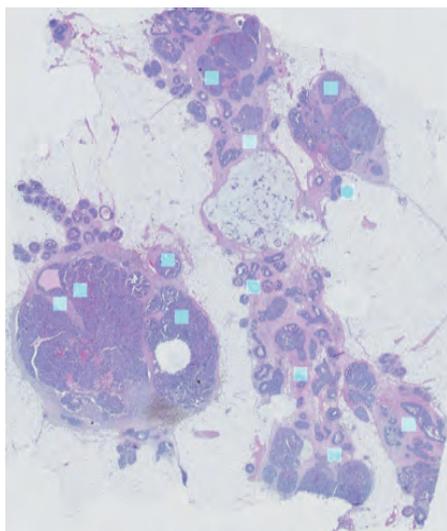
Supplementary Figure 5 (7/22). ST analysis results for Tumour 9. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman r_s correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 10



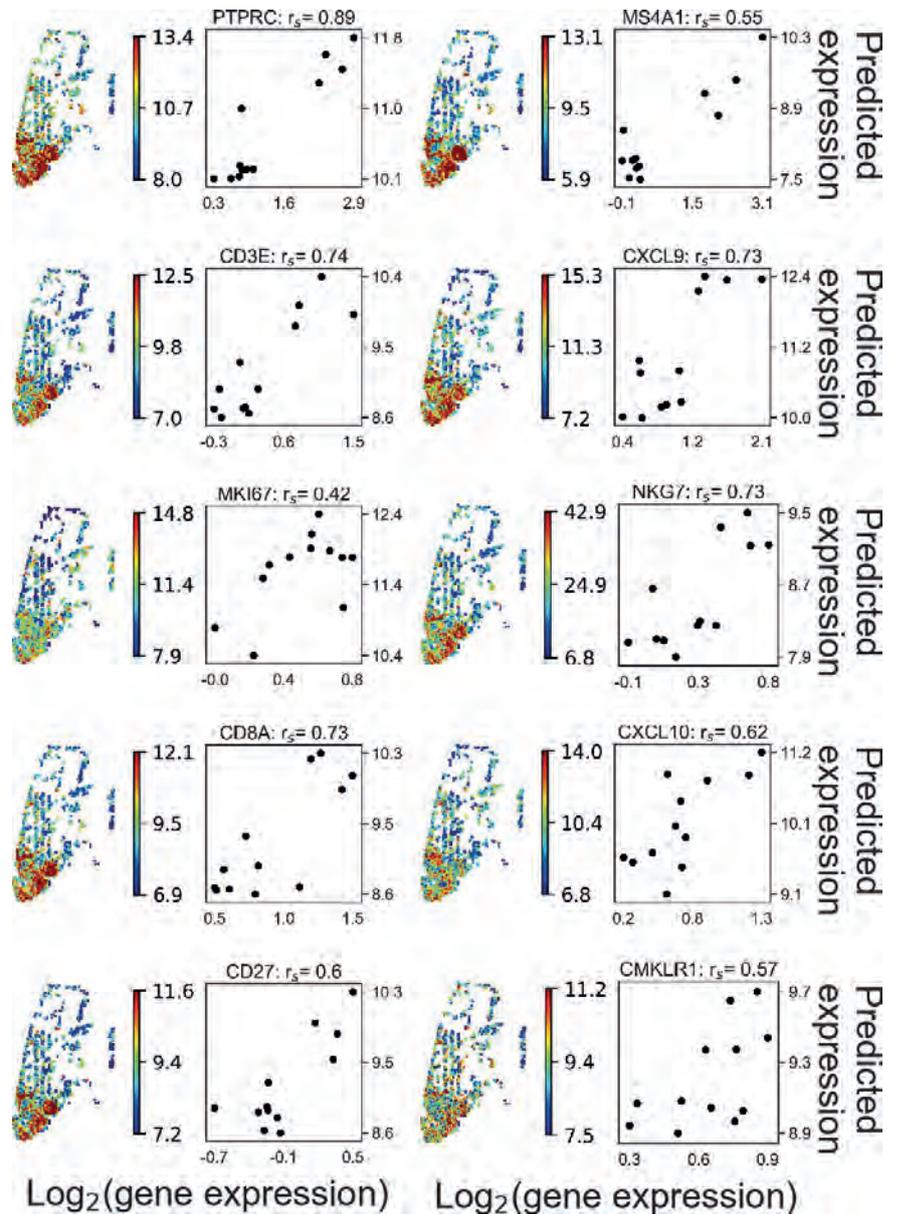
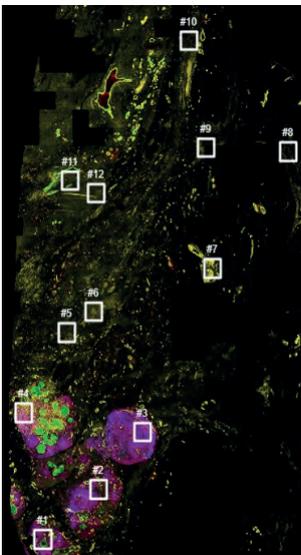
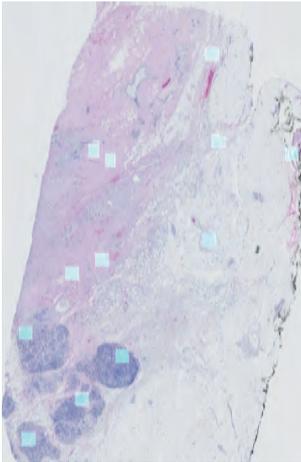
Supplementary Figure 5 (8/22). ST analysis results for Tumour 10. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 11



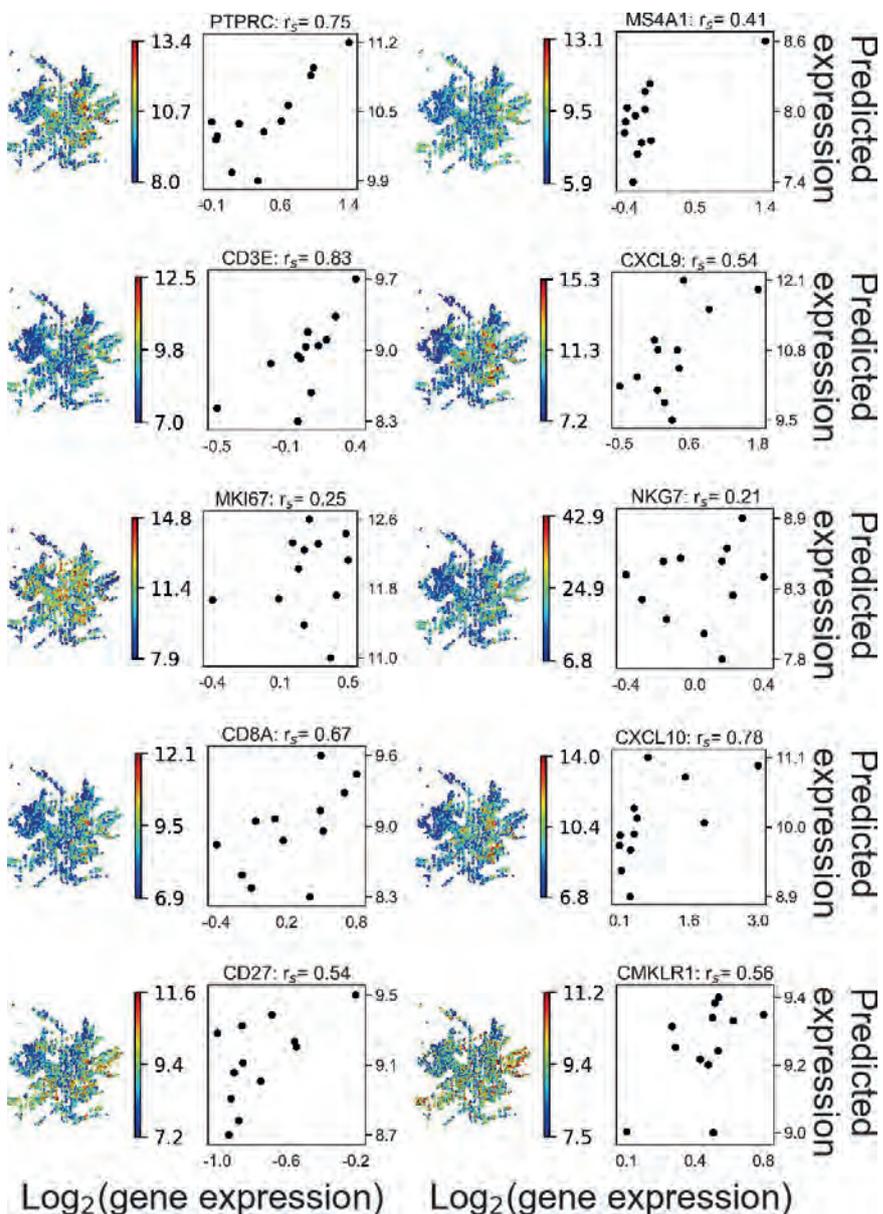
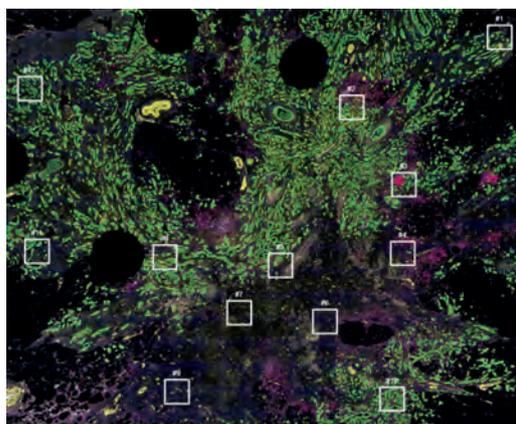
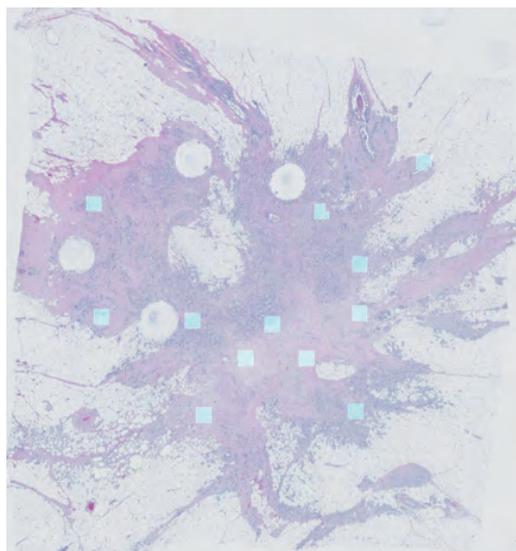
Supplementary Figure 5 (9/22). ST analysis results for Tumour 11. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 12



Supplementary Figure 5 (10/22). ST analysis results for Tumour 12. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescently stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.

Tumour 13



Supplementary Figure 5 (11/22). ST analysis results for Tumour 13. Left. 12 ROIs from the HE stained WSI were selected and manually registered in the corresponding fluorescent stained slide. Right. Demonstration of results from 10 top performing genes. For each gene, the heatmap shows the spatial predictions and the scatter plot shows the association between ST measured gene expression and EMO-spatial predictions per slide. The association was evaluated by Spearman correlation and the Spearman's correlation coefficient (r_s) is indicated on top of each scatter plot.