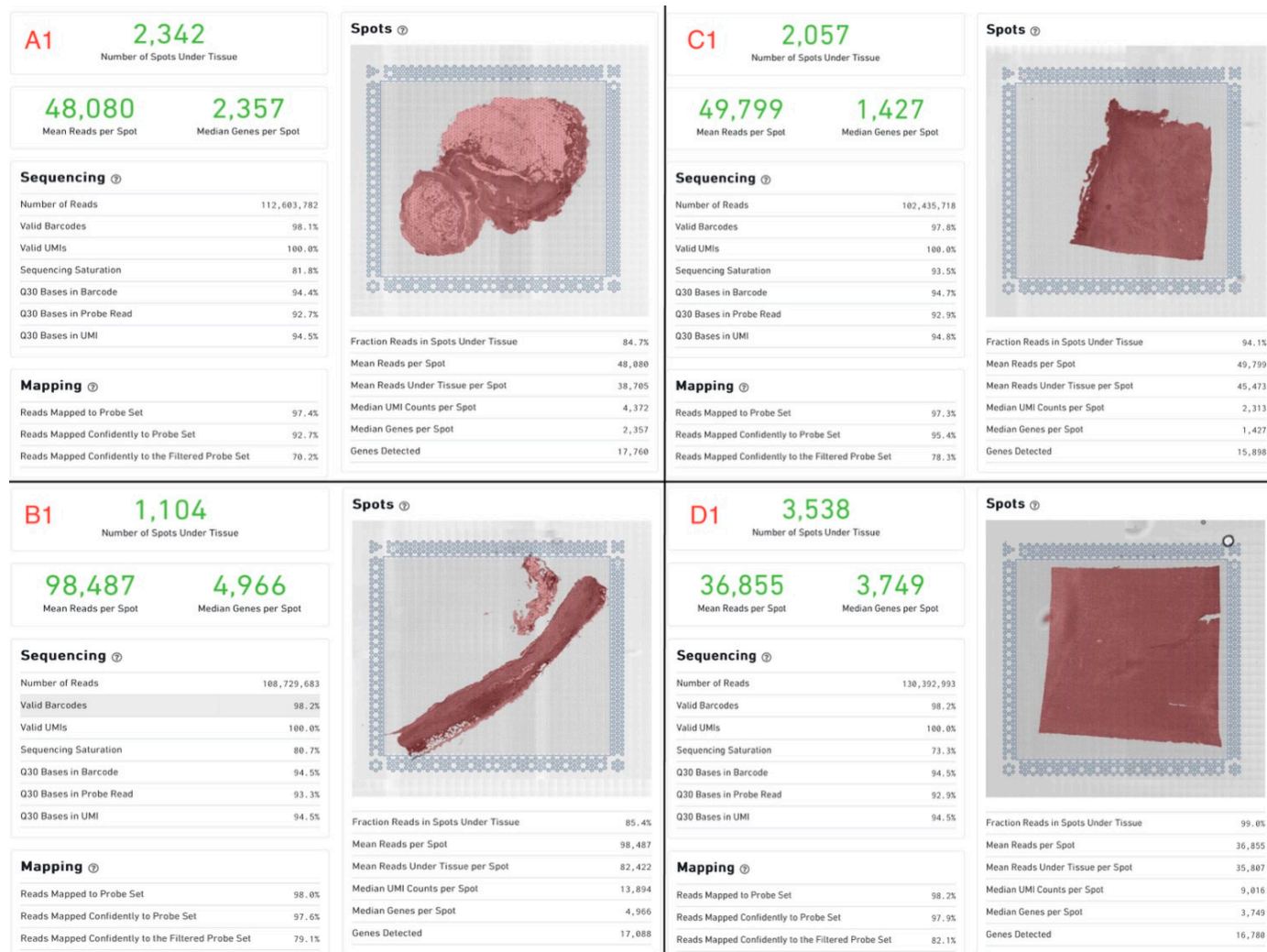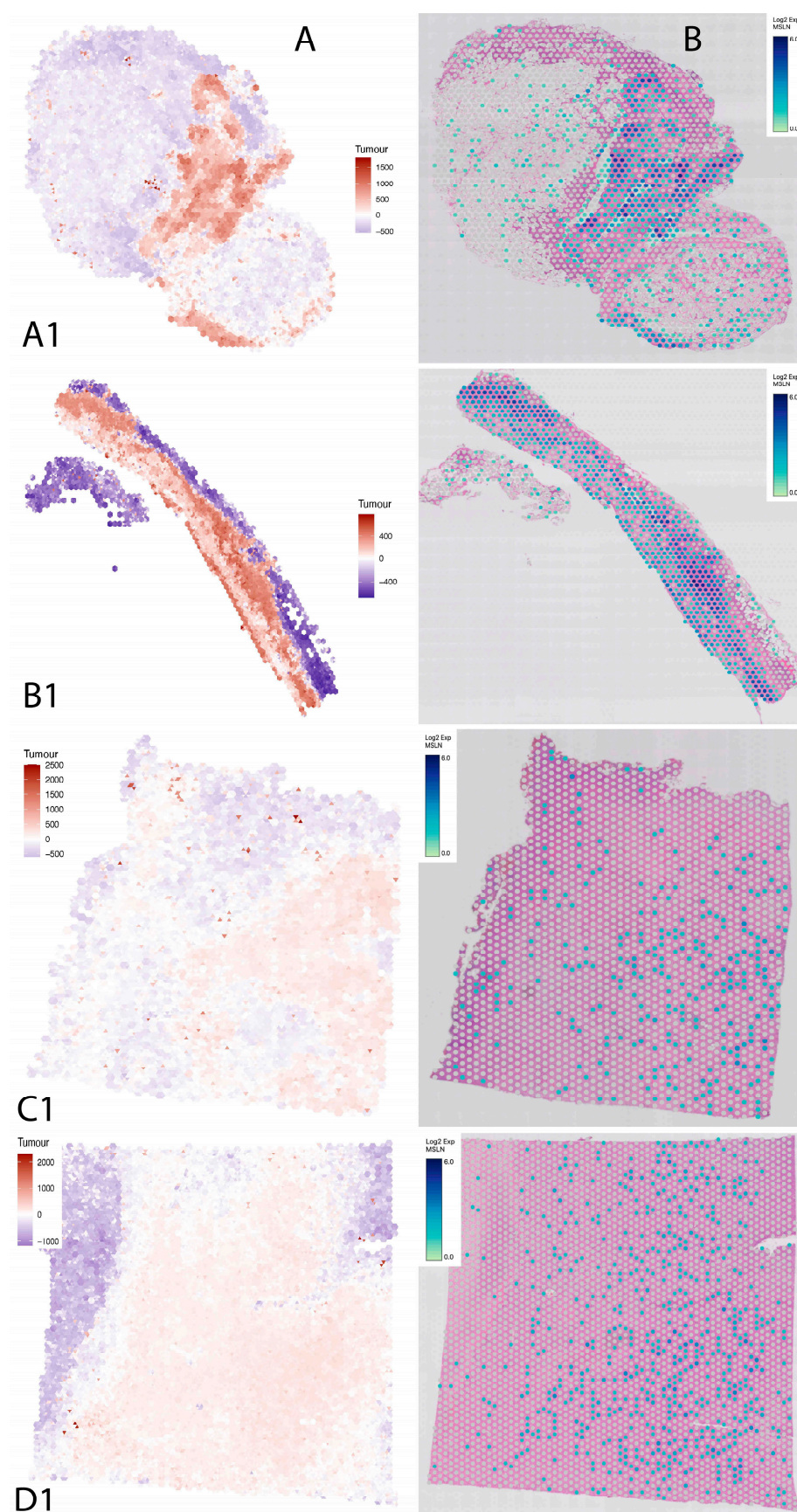# Supplementary materials

Figure S1. Technical Summary reports of spatially resolved transcriptomics datasets. Reports were obtained from Space Ranger software (10X Genomics) demonstrating sequencing efficiency and coverage. We detected a median of 6,694 Unique Molecular Identifier (UMI) counts per spot across all studied samples with a mean of 50,601 reads under tissue per spot.

Figure S2. Identification of malignant cells in examined tissues. A – Tumour cells identified witrh BayesSpace (a set of genes was used to precisley locate malignant cells). B – Tumour cells identified with Loupe browser using *MSLN* (mesothelin) gene as a specific MPM gene.