Supplementary Information

Supplement to: Causer A., Tan X., Lu X. *et al. Deep spatial-omics analysis of Head & Neck carcinomas provides alternative therapeutic targets and rationale for treatment failure*

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1. Supplementary Table 1

Supplementary table 1. **Spatial proteomics: PhenoCycler antibody panel.**

2. Supplementary Table 2

Supplementary table 2. **Spatial proteomics: cell type annotation based on surface protein expression.**

Supplementary Figure 1. **Flow-diagram representing the implemented workflow. A.** Displays the different samples being analyzed within the study. Two comparisons are performed: 1) between healthy and tumor samples of MAR21 sample. 2) between MAR21 and SEP21 tumor samples. Both comparisons undergo analysis through the same pipeline which includes: **B.** Data quality control and normalization, **C.** Batch correction between samples, **D.** Unsupervised clustering to identify spots of similar transcriptomic profiles. **E.** Differential gene expression analysis, **F.** Gene ontology term enrichment analysis, and **G.** Cell cycle state analysis. **H.** In addition to spatial transcriptomics, spatial proteomics was performed on the MAR21 tumor sample. Integration of spatial transcriptomics and proteomics was performed to inform **I.** Spot cell composition. The overall analysis was used to identify and analyze the tumor regions within the samples. **J.** Ligand-receptor (L-R) interaction analysis was then performed to identify the most active L-R pairs which are druggable targets. **K.** An additional patient was analyzed in combination to assess if the L-R pairs are patient-specific. **L.** L-R pair activity was further assessed through pathway analysis of differentially expressed genes. **M.** The collective findings were then used to determine the top druggable targets specific to the patient.

SEP21

Supplementary Figure 2. **High-resolution H&E images of MAR21 and SEP21 samples. A.** Displays the high-resolution H&E image of both the healthy and tumor MAR21 sample. **B.** The high-resolution H&E image of SEP21 tumor samples. C. The highlighted box represents the tissue region which pathologists identified as high-grade dysplasia after re-analysis of the original H&E image. The raw images have been made publicly accessible at https://doi.org/10.48610/698bb9e.

Supplementary Figure 3. **UMAP representation of unbiased Visium clustering of MAR21 and healthy paired samples**. UMAP of clusters highlights distinction and separation between populations. **A.** Cluster annotations were generated by comparing differentially overexpressed genes with a reference database (JENSENs Tissues; EnrichR). **B.** Sample type UMAP displays batch correction between healthy (blue) and MAR21 OPSCC (red) samples.

6. Supplementary Figure 4

Supplementary Figure 4. **Distinct transcriptional profiles of inner core and leading-edge clusters.** DEGs between newly defined Visium clusters 4 (dark green) and 5 (light green). Significant DEGs with Wilcoxon test p-value < 0.001 and fold-change >1 are colored based on cluster.

Supplementary Figure 5. **Spatial transcriptomics (Phenocycler)-informed cell identification (***SPiCi***) and established transcription-based deconvolution methods. A.** Displays spot cell annotation of tumor sample using each algorithm. Spots are represented as pie graphs denoting the proportions of each cell type identified within each spot capture region. Enlarged regions encapsulate the outer proliferating ring of the tumor and the immune cell infiltrated core. **B.** Overall percentages of different cell types identified by each approach (across all spots combined).

Supplementary Figure 6. **Integrated Spatial-Omic characterization of tumor immune cell microenvironments. A.** Visium spot cell identification of MAR21 OPSCC using *SPiCi*. Spots are presented as pie-charts representing the relative proportions of cell types located within each spot. **B.** Quantification of cell-types found within each Visium cluster.

Supplementary Figure 7. **Comparison of deconvolution methods and** *SPiCi* **results with pathologist annotation. A.** Confusion matrices were calculated to evaluate the performance of each method at detecting tumor and lymphocyte cells compared to the ground truth pathological annotation. The cell type label for each spot is determined by the cell type with the highest proportion (i.e., classification probability) for that spot, calculated by each method. The inferred spot labels were then compared with the ground truth pathological annotations. Accuracy rates were calculated based on results generated from each confusion matrix. **B.** Bar graphs indicate the proportion of various cell types predicted by each method with respect to each cell type identified by pathological annotation.

Supplementary Figure 8. Localization of proliferating tumor cells. A. PhenoCycler fluorescence images displaying PanCK+ (Purple) and Ki67+ (Orange) cells across the MAR21 OPSCC sample. **B.** Tumor region of interest presents with leading edge of active proliferating cells and inactive tumor core.

Supplementary Figure 9. **Differential analysis of transcriptional profiles of tumor clusters within MAR21 OPSCC.** DEGs of the combined tumor clusters relative to all other clusters. Significantly upregulated and down-regulated genes are highlighted in red and blue respectively (Wilcoxon test pvalue < 0.001 and an absolute fold- change > 1). The top 10 over- and under-expressed genes are annotated.

MAR21

Supplementary Figure 10. **PD-L1 and PD-1 protein staining. A.** PHENOCYCLER fluorescence images displaying PanCK+ (green) and PD-L1 (red, *left*) or PD-1 (red, *right*) cells across the MAR21 and SEP21 OPSCC samples.

13. Supplementary Figure 11

Supplementary Figure 11. **Visium data integration and batch correction of tumor tissues.** Spatial transcriptomic data generated from MAR21 and SEP21 tumors was integrated (*left)* and batch effect corrected (*right*) using the Seurat anchor integration pipeline.

Supplementary Figure 12. **Tumor transcriptional profile recapitulated in recurrent SEP21 OPSCC.** Relative expression of poor prognosis markers (red), oncogenes (orange) and drug resistance genes (green), previously identified from the combined tumor cluster within MAR21, across each newly defined cluster generated through comparing OPSCC samples. The top 9 genes of each category were displayed. Colors gradient represents average normalized expression values across all spots in each cluster, which were z-transformed by genes (rows of the heatmap).

Supplementary Figure 13. **Initial Pathologist annotation of SEP21 OPSCC sample.** Colored spots identify different morphological tissue structure identified from the H&E image by a clinical pathologist.

16. Supplementary Figure 14

Supplementary Figure 14. **Differential expression analysis of tumor clusters 4 and 7 in the MAR21- SEP21 OPSCC integrated dataset.** DEGs of the tumor clusters CL4 (A) and CL7 (B) from MAR21 and SEP21 samples. Significantly up-regulated and down-regulated genes are highlighted in red and blue respectively (Wilcoxon test p-value < 0.001 and an absolute fold-change > 1). The top over- and underexpressed genes based on fold change and P-values are annotated.

Supplementary Figure 15. **Ligand-receptor interaction analysis in MAR21 and SEP21 tissues. A.** Ranking of top 60 Ligand/Receptor (L/R) expressed by the MAR21 (*top*) and recurrent SEP21 (bottom). Rank was based on the number of spots with significant interactions of each L/R pair across each sample. **B.** Spatial expression of top L/R pairs expressed by MAR21(*left*) and SEP21(*right*). In all feature plots, the relative gene expression per spot is indicated by the coloured scale bars.

Supplementary Figure 16. **Transcriptional comparison between MAR21 and recurrent SEP21 and ligand-receptor interaction analysis for therapeutic target selection.** Spider-plot represents the top 5 most active L-R pairs found across tumor tissue based on the number of spots with significant interactions using the L-R pairs. Red line, healthy tissue; dark blue, SEP21; light blue, MAR21.

Supplementary Figure 17. **Top druggable targets differ between additional OPSCC patients. A.** Spatial representation of Visium clusters identified as tumor leading edge (dark green) and inner core (light green) within an additional OPSCC patient. **B.** Cell cycle phase of each spot based on relative expression of specific cell phase genes. **C.** Spatial expression of genes targeted by Nivolumab and Pembrolizumab targeted *PD-1/PD-L1* pathway. **D.** Spatial visualization of gene expression of genes targeted by previously identified clinical therapies. **E.** Spatial localization of gene expression levels for select experimental drug therapies. In all feature plots, the relative gene expression per spot is indicated by the coloured scale bars.

Supplementary table 3. **Gene classification based on function reported in the literature in the cancer setting.**

Supplementary table 4. **Identified clinical and preclinical targets.**

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