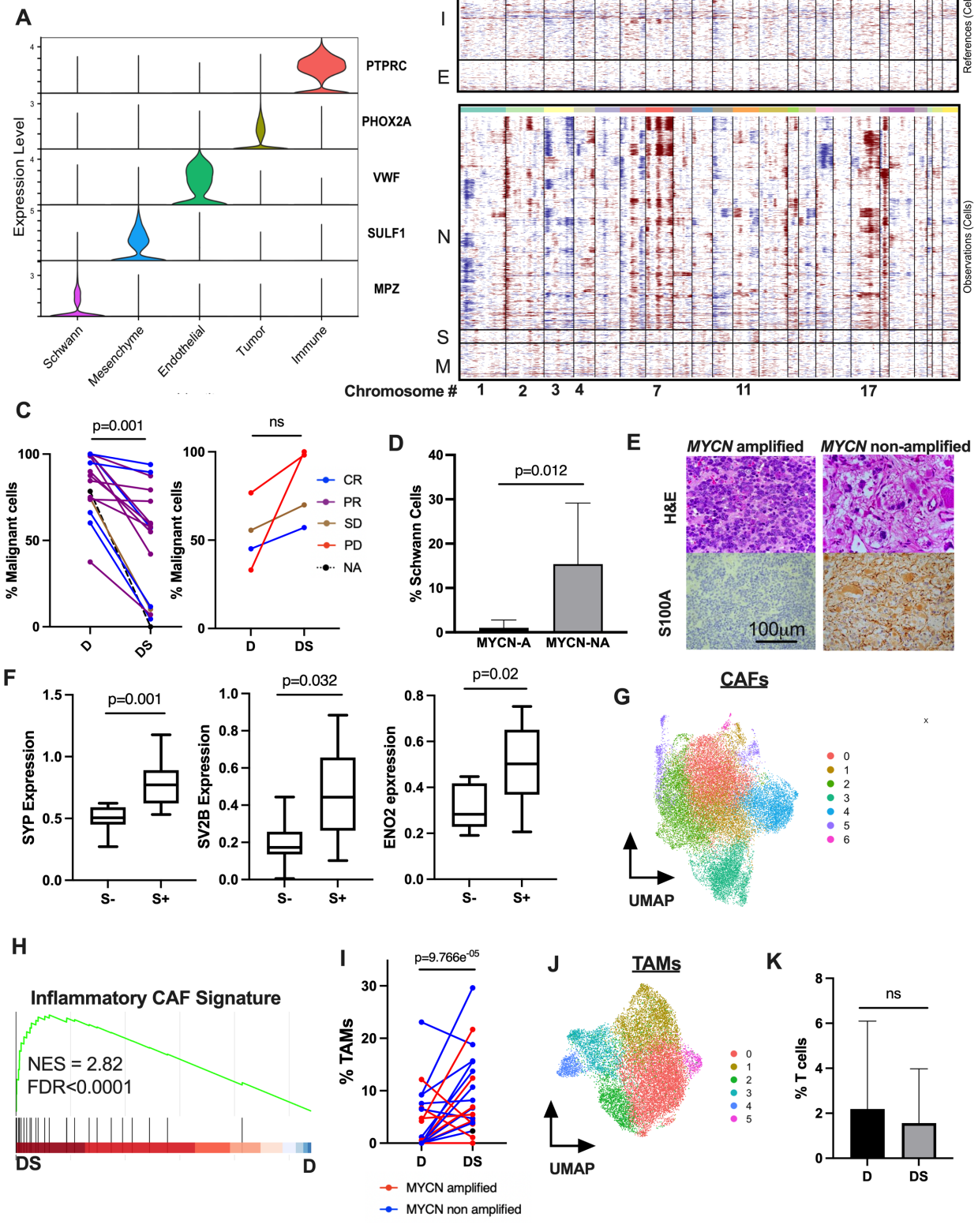
Supplementary Figure S1



Supplementary Figure S1. A. Violin plots showing marker genes for each cell type of Figure 1B UMAP. **B.** InferCNV heatmap for Figure 1B with immune cells (I) and endothelial cells (E) as reference cells and N – Neuroendocrine, S – Schwann, M – Mesenchymal as observations. Recurrently aberrated chromosomes are numbered -1 (1p loss), 2 (2p gain), 3 (3p loss), 4 (4p loss), 7 (7q gain), 11 (11q deletion) and 17 (17q gain). **C.** Malignant cells at diagnosis (D) and definitive surgery (DS) in tumors with decrease malignant (left) and increase in malignant component (right) at DS. Colors of lines represent response to induction therapy, CR- Complete Remission, PR- Partial Response, SD– Stable Disease, PD– Progressive Disease. **D.** Bar plot of Schwann cells fraction at time of definitive surgery in *MYCN* amplified and non-amplified tumors. **E.** H&E (upper) and immunohistochemistry staining of S100A, a Schwann cell marker (lower), in a definitive surgical sample from a *MYCN*-amplified tumor of CN8 (left) and in a definitive surgical sample from a MYC(N)-non-amplified tumor of CN3 (right)**. F.** Normalized expression of Synaptophysin (*SYP*), Synaptic Vesicle Protein II (*SV2B*) and Neuron Specific Enolase (*ENO2*) in persister cells from definitive surgery samples with and without Schwann cells. **G.** UMAP of CAFs grouped by Seurat clusters. **H.** GSEA analysis of differentially expressed genes between CAFs at definitive surgery and diagnosis shows enrichment for inflammatory CAF signature. NES- Normalized Enrichment Score. **H.** UMAP of TAMs grouped by Seurat clusters. **I.** Percent of TAMs at diagnosis (D) and definitive surgery (DS) in 20 tumor pairs. Lines are colored by *MYCN* amplification status – A- Amplified – red, NA- Non-amplified – blue. **J.** UMAP of TAMs. grouped by Seurat clusters **K.** T-cell percentage at diagnosis (D) and Definitive Surgery (DS). ns, not significant