

Fig. S4

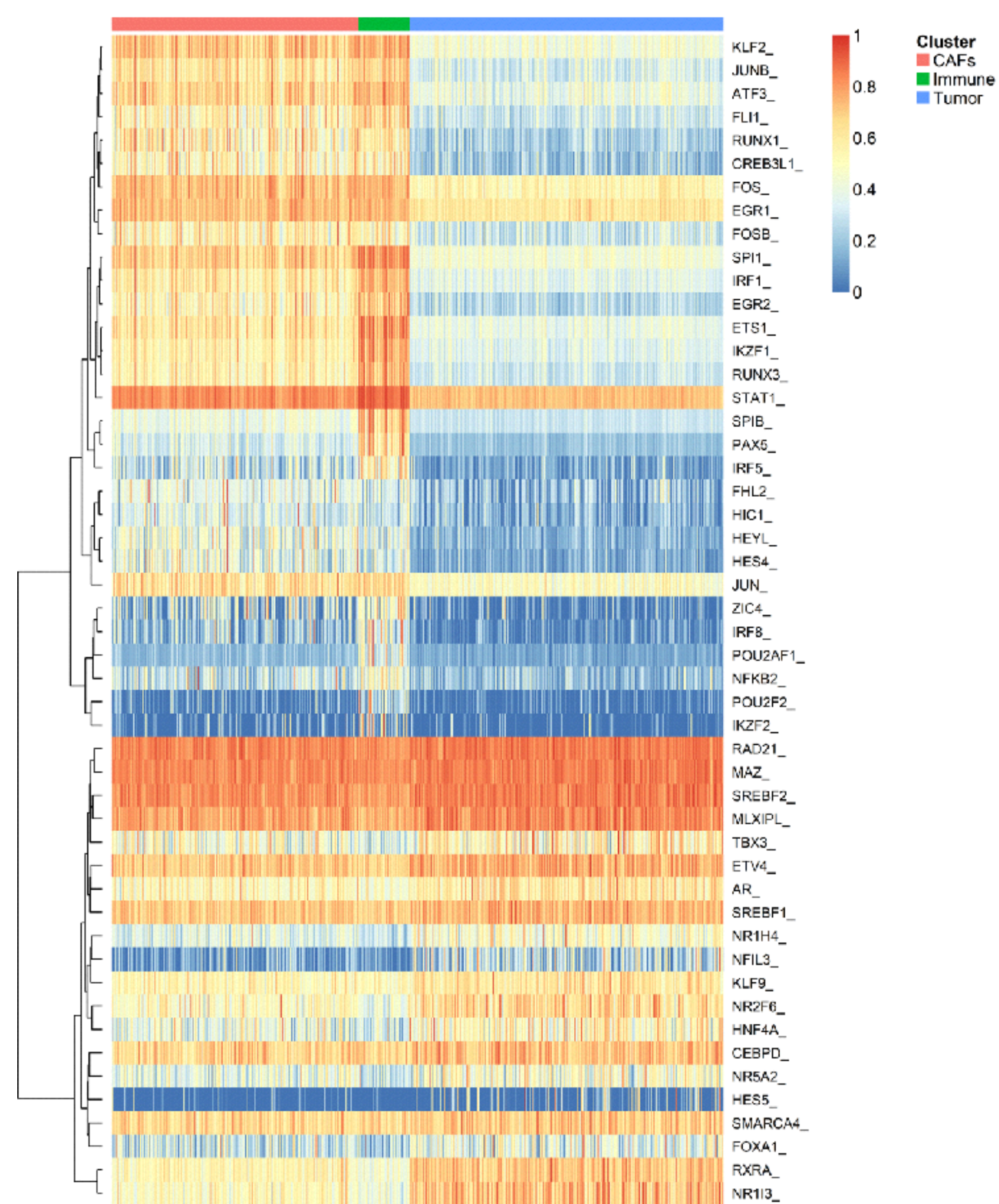


Fig. S4 - Heatmap of transcription factor network scores from patient HCC3-R as a representation of the DOMINO networks obtained from the interaction analysis. Each column represents a single spot from the spatial transcriptomics data and the rows represent the transcription factor networks. Spots are grouped by spatial clusters (cell types).