



Key findings of the study. **a** UMAP of macrophages in the TLS-positive samples showed five MAMs subpopulations. **b** Heatmap showing 15 most differentially expressed markers for each MAM subpopulation. **c** Summary of the markers and characteristics for the five phenotypes identified. **d** Distribution of M1 and M2 markers’s expression inside and outside TLS areas. P- values indicate whether there is significant change in expression of those markers between different regions. Mean values are also visualized as a red dot. (*) means the p-values are smaller than 0,05. P-values smaller than 0.005 and 0.001 are indicated by (**) and (***), respectively. **e** Comparision of four M1 and 4 M2 markers across TLS spatial spots. Color indicates whether M1 or M2 expression are significantly higher, while size represents the level of significance. **f** Up- and downregulated gene lists of TLS-associated TAMs and their corresponding frequency across the samples. **g** Volcano plot of differential expression analysis between TLS regions and non-TLS regions of one sample. The threshold for p-values is 0,05. Overexpressed genes have log2 foldchange larger than 0.4, while underexpressed genes have log2 foldchange smaller than -0.4.