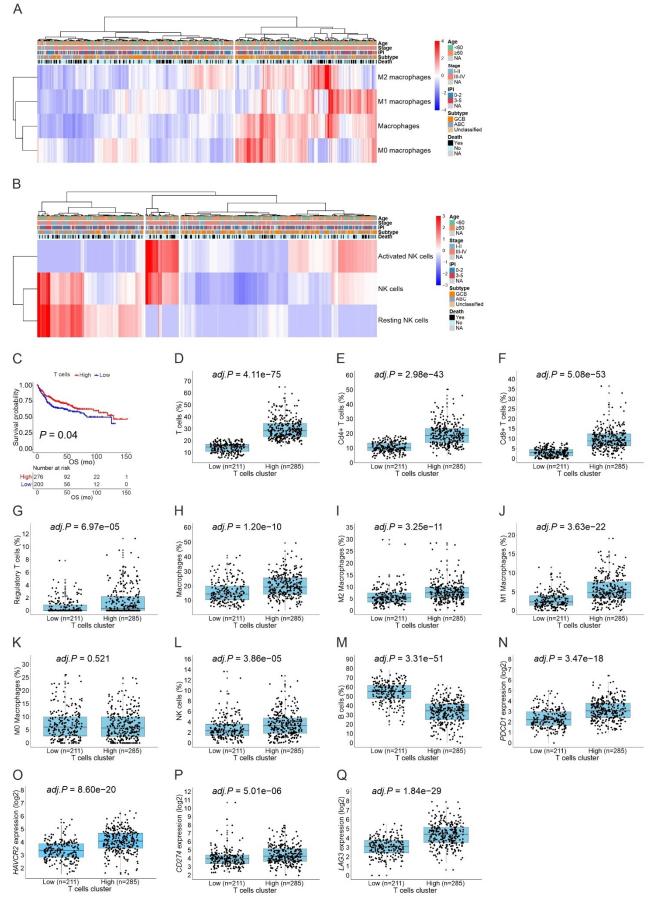
Supplementary Fig. S9: The clinical impact of macrophages, NK cells and T cells in the LME analyzed by CIBERSORT in the Reddy et al. validation cohort



Supplementary Fig. S9: The clinical impact of macrophages, NK cells and T cells in the LME analyzed by CIBERSORT in the Reddy et al. validation cohort. A-B) Unsupervised hierarchical clustering of samples based on the proportion of different macrophage (A) and NK cell subtypes (B). C) Kaplan-Meier (log-rank test) survival plot depicting OS in the groups with high and low proportion of T cells. D-M) Boxplots depicting the proportion of T cells (D), CD4+ T cells (E), CD8+ T cells (F), regulatory T cells (G), macrophages (H), M2 macrophages (I), M1 macrophages (J), M0 macrophages (K), NK cells (L), and B-cells (M) in the groups with high and low proportion of T cells. N-Q) The expression of PDCD1 (N), HAVCR2 (O), CD274 (P), and LAG3 (Q) genes in the groups with high and low proportion of T cells.