

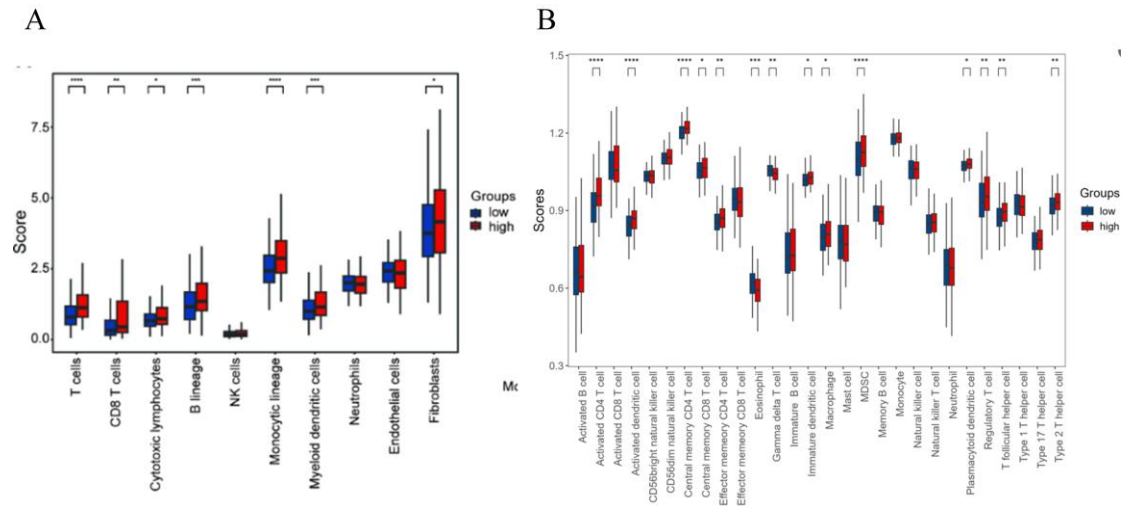


Fig. S1 Consistency verification of immune cell and subset abundance distribution across groups via multi-algorithm analysis. To improve the reliability of immune infiltration analysis, two algorithms were used to quantify immune cell abundance in this study: **(A)** (MCP algorithm) focuses on the abundance scores of immune/stromal cell types (e.g., T cells, NK cells); **(B)** (ssGSEA algorithm) further refines the analysis of immune subset abundance scores (e.g., activated B cells, effector memory CD8 T cells). In the figure, blue boxplots represent the "low" group, and red boxplots represent the "high" group; the box of the boxplot corresponds to the interquartile range (IQR), the middle line is the median, the whiskers extend to the extremes within $1.5 \times \text{IQR}$, and the scatter points are outliers (* $P < 0.05$, *** $P < 0.0001$).