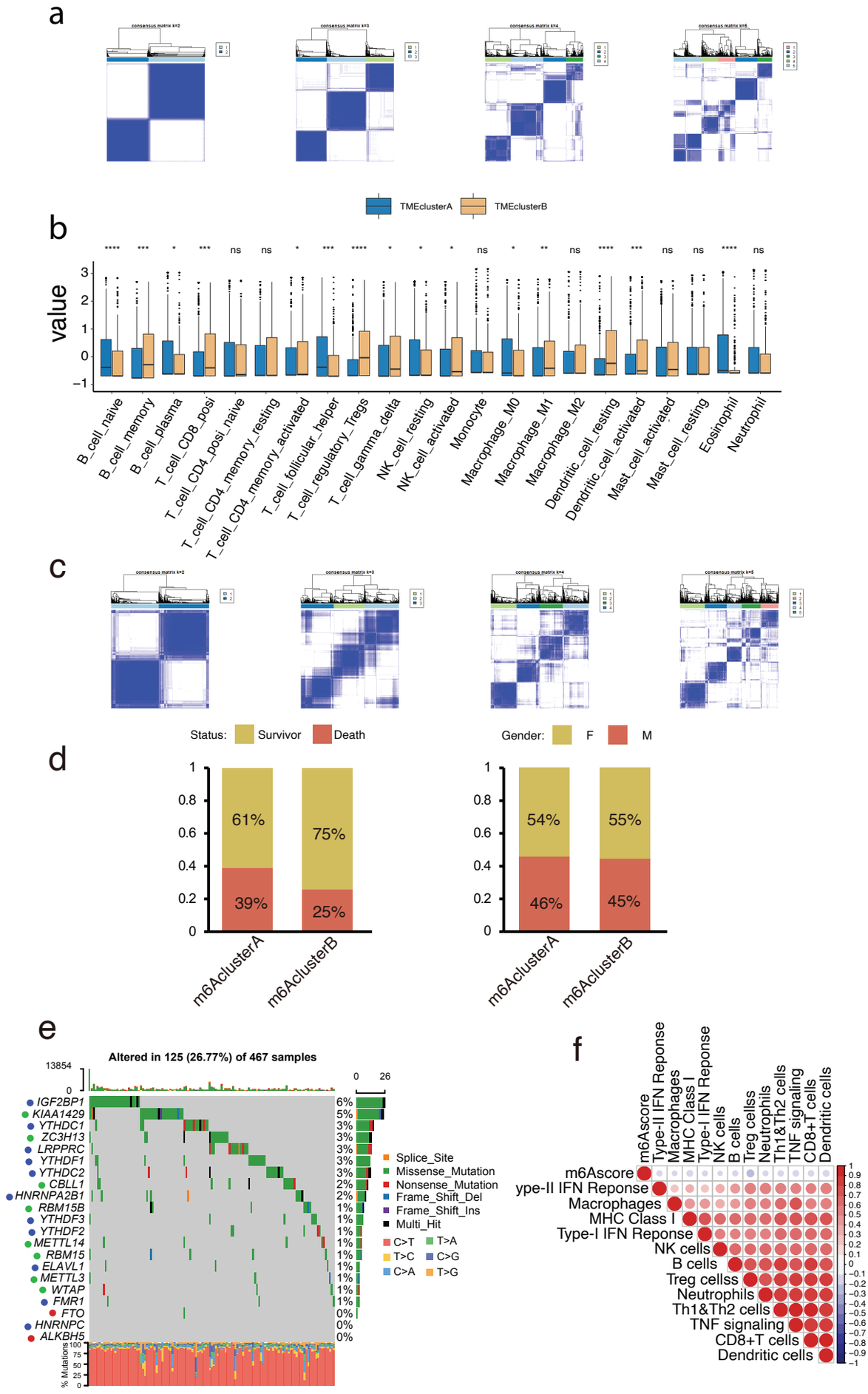

Figure S1: Consensus matrices of Leeds melanoma cohort
(a) Consensus matrices based on tumor microenvironment infiltrating immune cells of Leeds melanoma cohort that include all samples for each k (k = 2–5). Shown is the clustering stability by using 1000 event iterations of hierarchical clustering. **(b)** The fraction of immune cells of LMC patients in TMEclusterA and B. The upper and lower ends of the vertical line represent the maximum and minimum values. The three horizontal lines of the boxplot represent the first quartile, median, and third quartile. Outliers are expressed in scattered dots. The Kruskal–Wallis test was used to calculate the statistical difference (*p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001). "NS" indicates no significant difference. **(c)** Consensus matrices based on m6A modification patterns of Leeds melanoma cohort that include all samples for each k (k = 2–5). Shown is the clustering stability by using 1000 event iterations of hierarchical clustering. **(d)** The clinicopathological parameters in m6A clusterB were associated with better survival status in the Leeds melanoma cohort. Gender is allocated evenly. **(e)** Waterfall plot of tumor somatic mutation established by 21 m6A genes in the TCGA-SKCM cohort. Each column represents individual patients. The upper barplot shows TMB. The number on the right indicates the mutation frequency in each gene. The right barplot shows the proportion of each variant type. (f) Correlation of m6Ascore and infiltrating immune cells and immune response by Spearman correlation analysis in LMC shows that m6Ascore is negatively correlated with active immune singling.