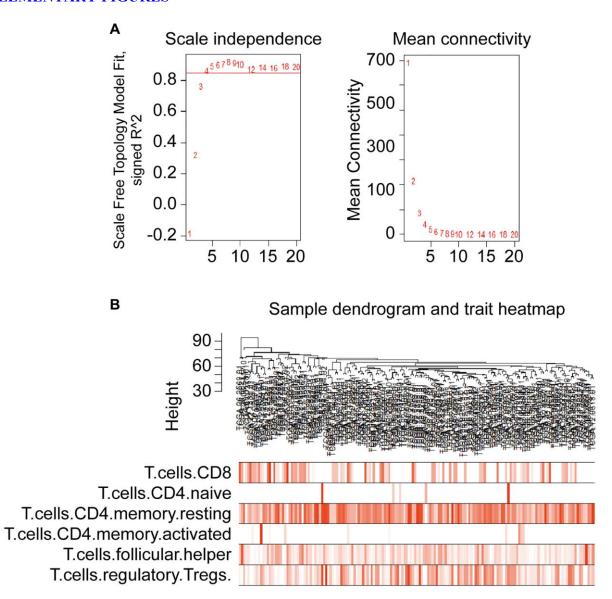
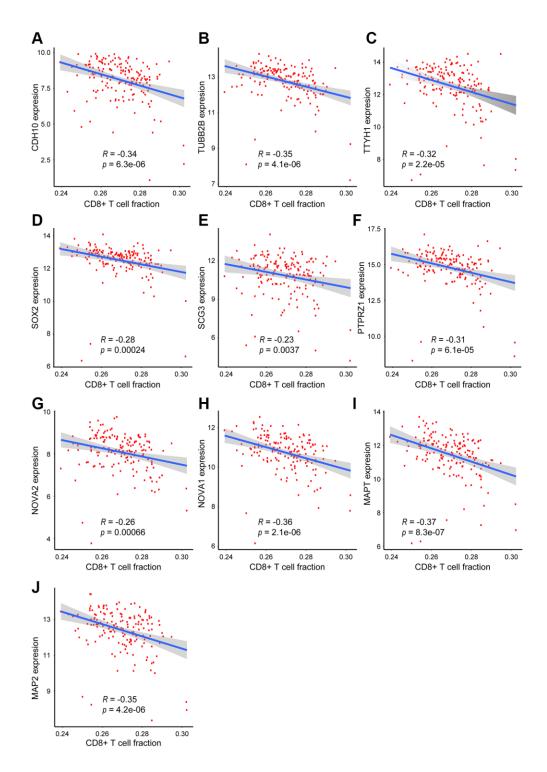
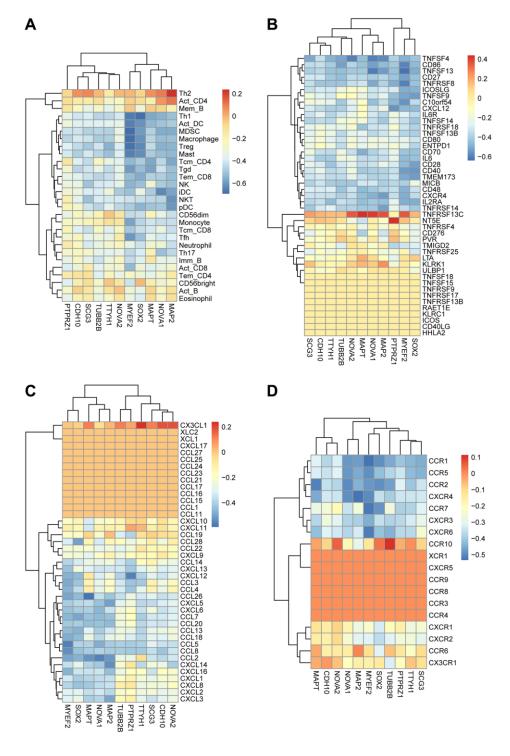
SUPPLEMENTARY FIGURES



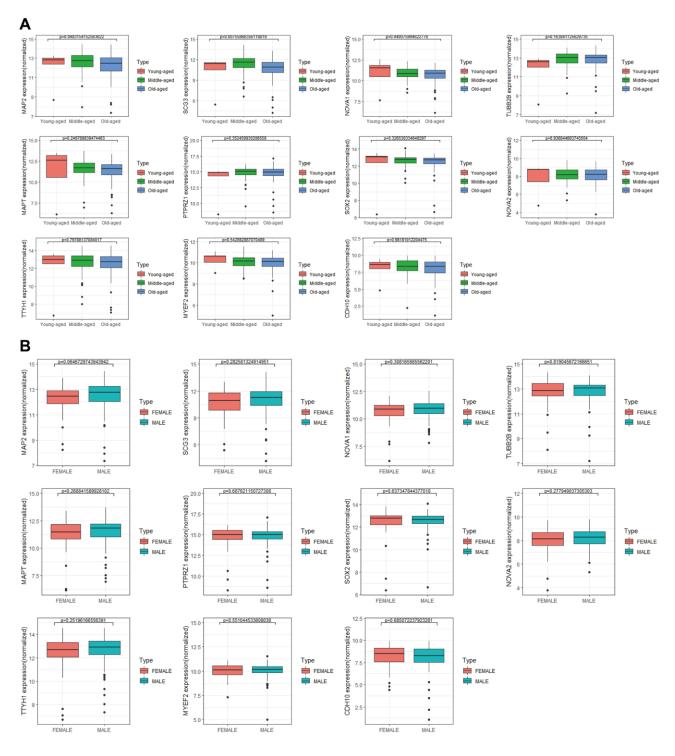
Supplementary Figure 1. Soft-thresholding power analysis and Hierarchical clustering tree of WGCNA analysis. (A) Soft-thresholding power analysis including scale-free index and the mean connectivity. (B) Hierarchical clustering tree of the 164 TCGA IDH wild-type GBM samples (Value of T cell gamma delta was 0 among all samples).



Supplementary Figure 2. (A–J) Scatter plot of the correlation between hub genes expression and CD8+ T cell infiltration level in TIMER database.



Supplementary Figure 3. Heatmaps of spearman correlations between hub genes expression and TIICs and expression of immune factors in TISIDB database. (A) TIICs. (B) Immune-stimulatory factors. (C) Chemokines. (D) Receptors.



Supplementary Figure 4. Determination of hub genes and clinical characteristics in TCGA database. (A) Box plots of hub gene expression in different ages. (B) Box plots of hub gene expression in different genders.