

Figure S1. Development of a risk scoring system with four CARD-associated genes. (A) Spearman correlation among the expressions of CARD-associated genes. (B) Distribution of groups based on the risk score. (C) Survival status of patients in different groups. (D) Heatmap of expression profiles of the four identified genes.

Figure S2. Proportion of tumors stratified by pathology or molecular subtypes between different risk groups. GBM, glioblastoma; LGG, lower-grade gliomas; CL, classical; ME, mesenchymal; NE, neural; PA, pilocytic astrocytoma. C1: wound healing; C2: IFN- γ dominant; C3: inflammatory; C4: lymphocyte depleted; C5: immunologically quiet; C6: TGF- β dominant.

Figure S3. CARD-associated risk score indicates distinct immune landscape in gliomas from CGGA cohort. (A) Heatmap showed ssGSEA score of each immune cell populations between high- and low-risk groups. (B) Comparisons of normalized score of cytotoxic activity (CYT), MHC and Batf3-DC gene sets, (C-D) expressions of cytokines and T-cell markers between high- and low-risk groups.

Figure S4. Fractions of infiltrating leukocyte in TCGA IDHwt gliomas estimated by using CIBERSORT algorithm.

(A) Overview of leukocyte infiltration. Samples were ranked by their CARS value. Immune cells were categorized into B cells, dendritic cells (DC), eosinophils, macrophages, mast cells, neutrophils, natural killer cells and T cells.

B cells include B.cells.naive, B.cells.memory and Plasma.cells.

DC include DC. resting and DC. activated.

Macrophages include Monocytes, Macrophages.M0, Macrophages.M1 and Macrophages.M2.

Mast cells include Mast.cells.resting and Mast.cells.activated.

NK include NK.cells.resting and NK.cells.activated.

T cells include T.cells.CD4.naive, T.cells.CD4.memory.resting, T.cells.CD4.memory.activated, T.cells.follicular.helper,, Tregs, T.cells.gamma.delta and T.cells.CD8.

(B) Macrophage M2 is the major type of macrophages infiltrating in gliomas and is significantly increased in high-risk group as compared with low-risk group.

Figure S5. Spearman correlations between CARS and ssGSEA score of oncogenic pathways in CGGA cohort.

Figure S6. Comparison of the mutation frequency of common mutated genes between high- and low-risk groups. Chi-squared test were used for comparison.

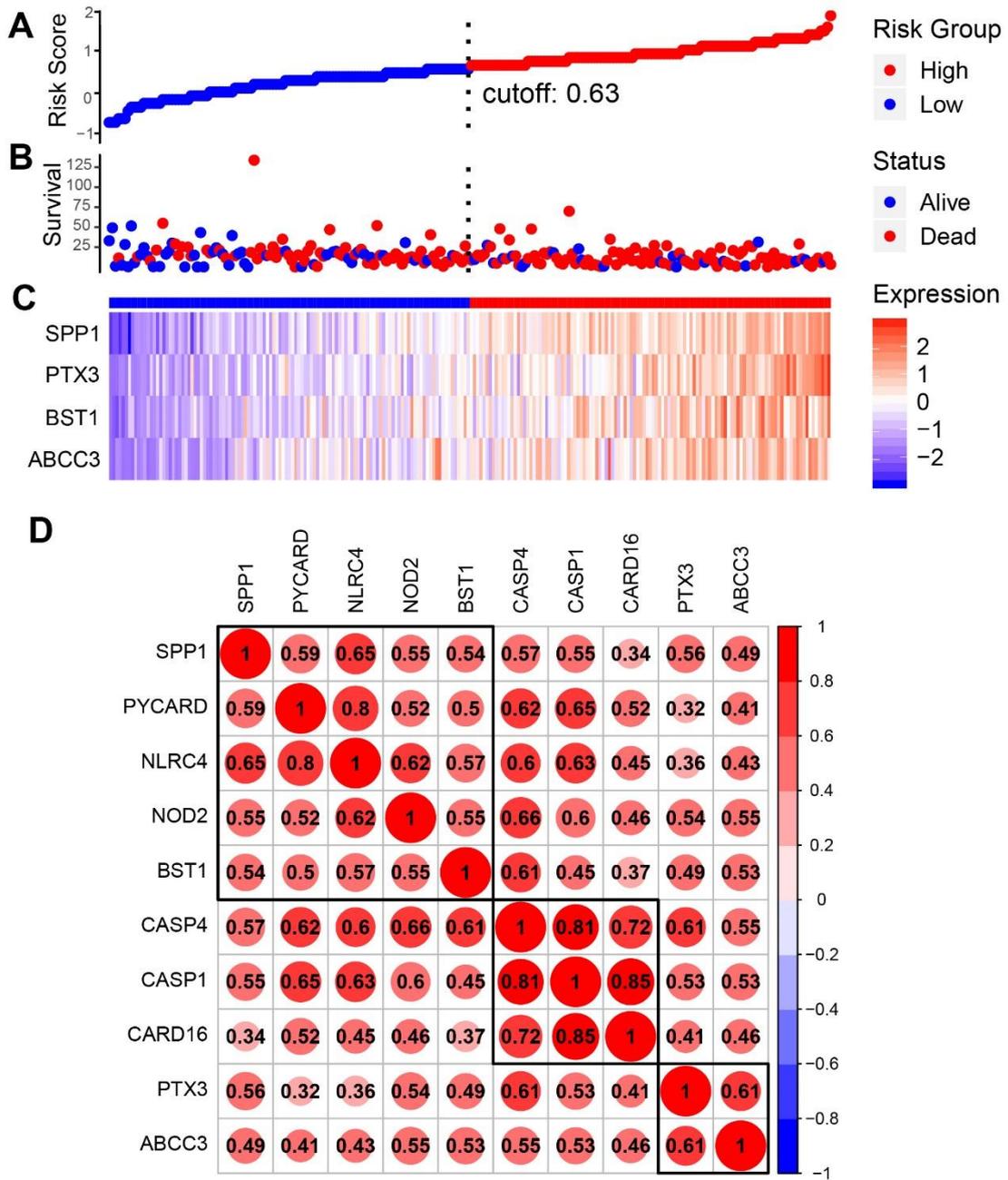


Figure S1

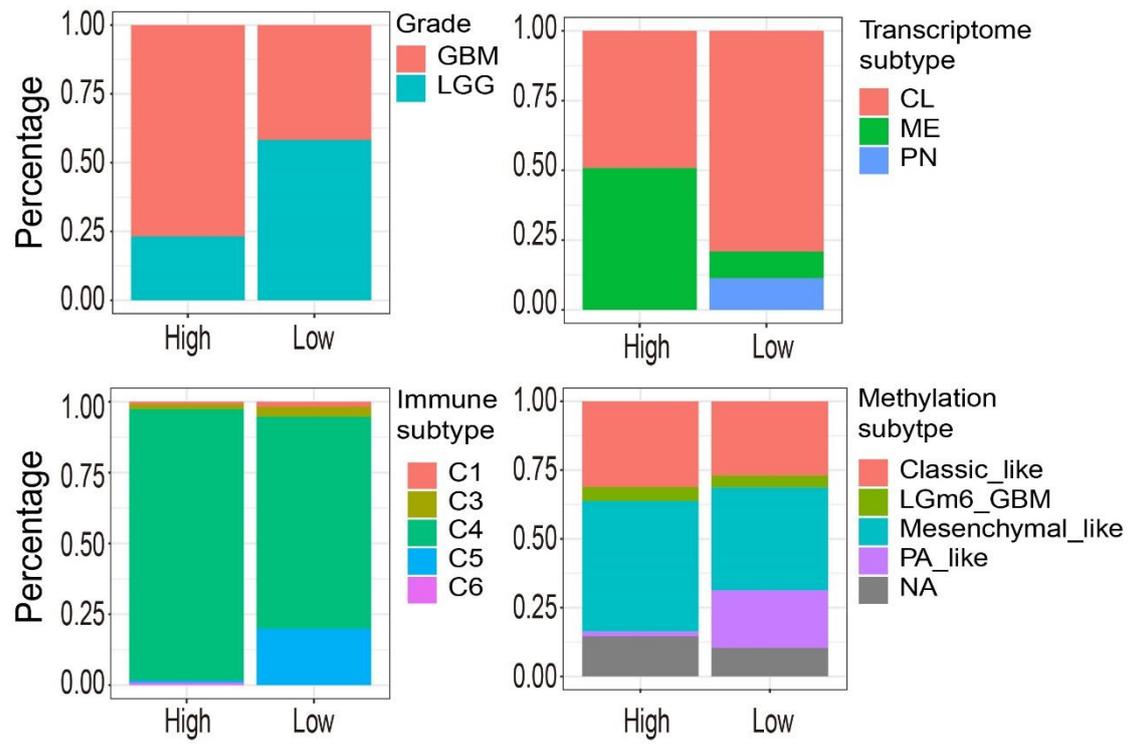


Figure S2

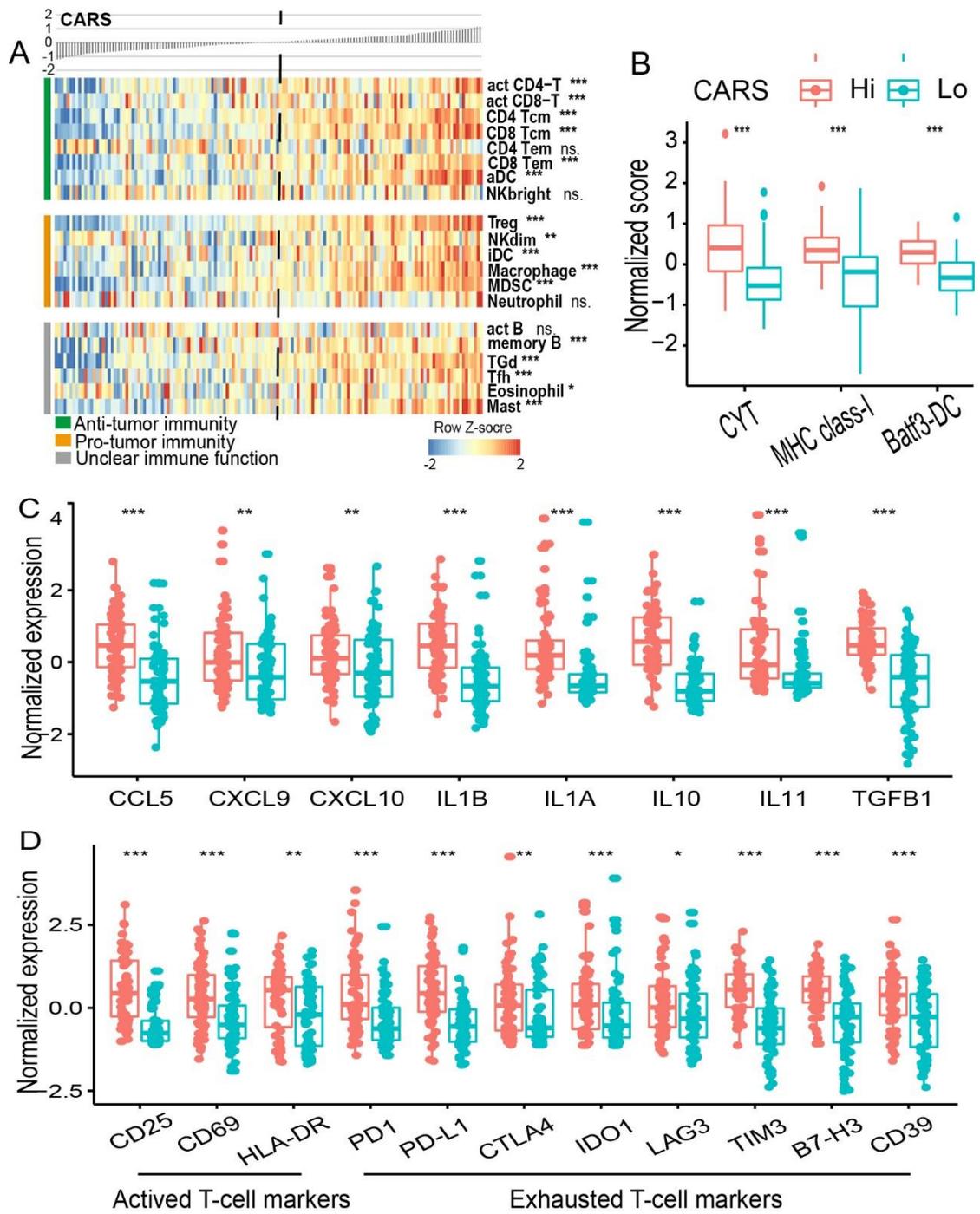


Figure S3

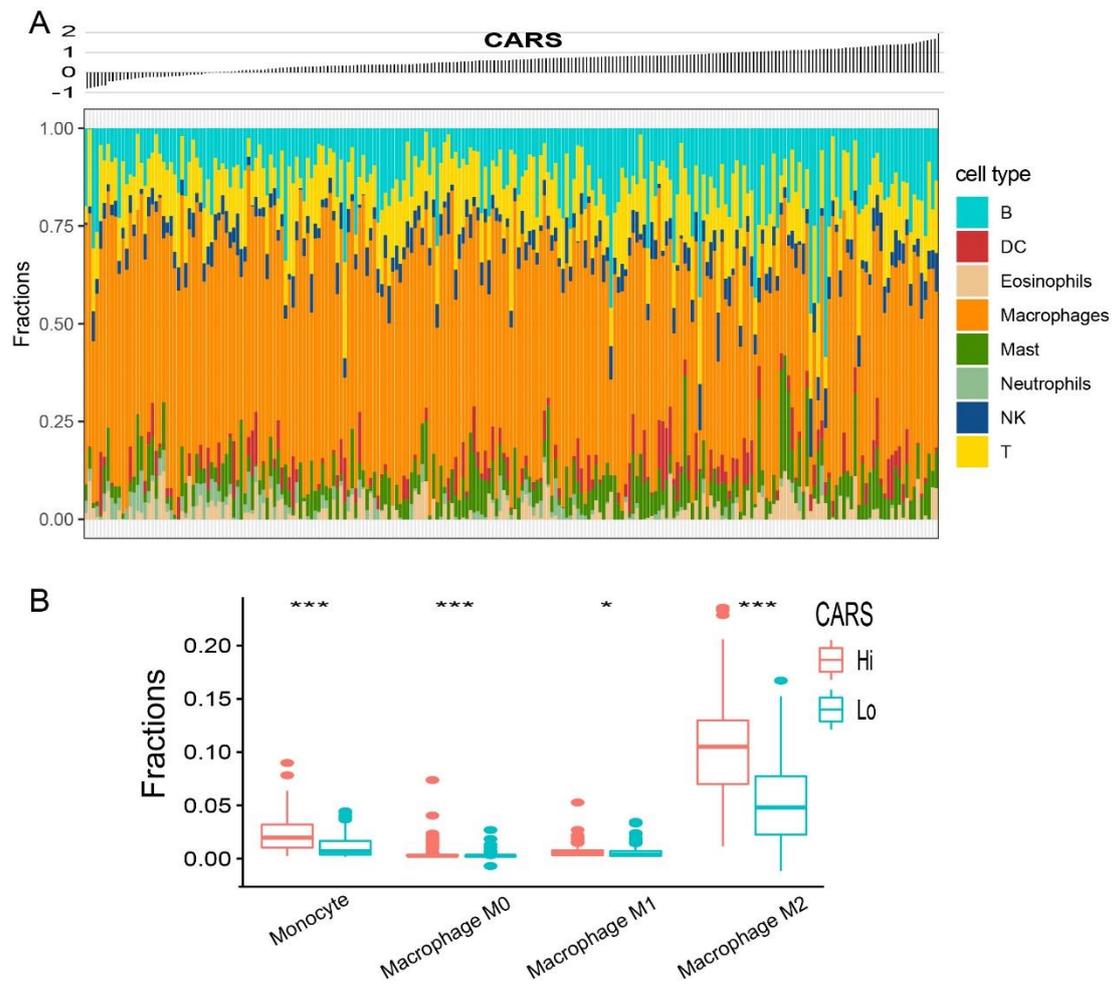


Figure S4

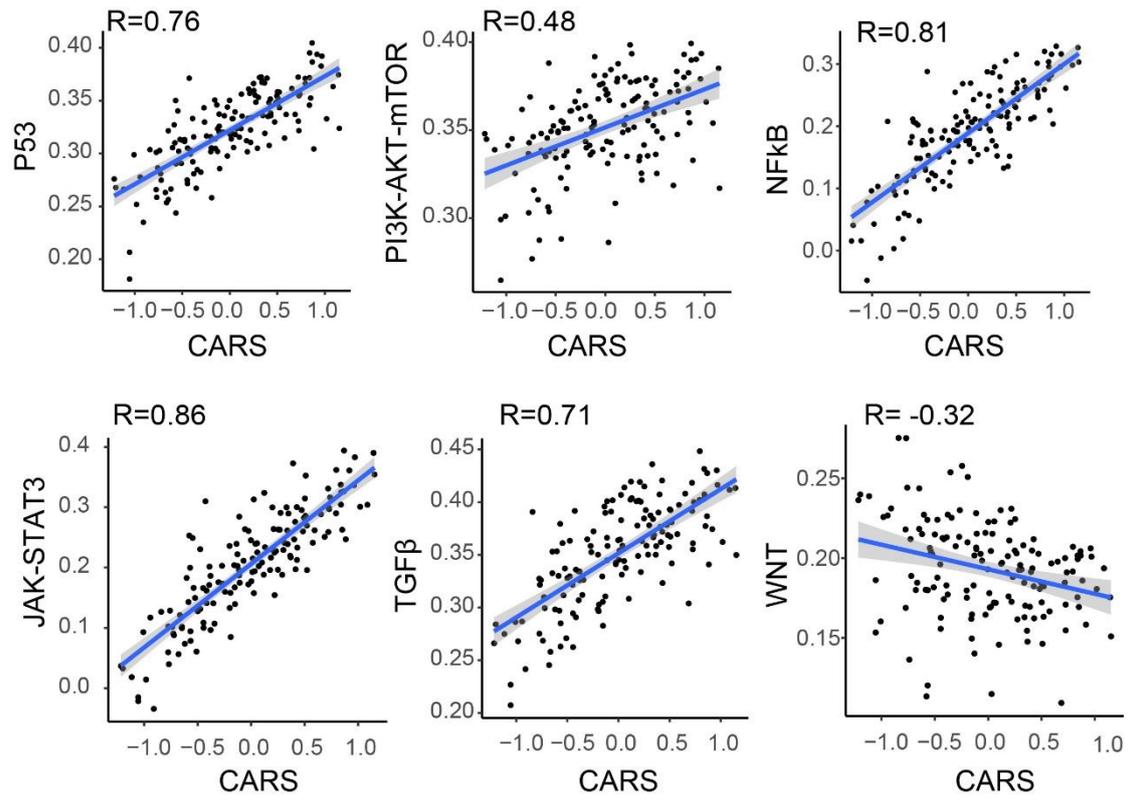


Figure S5

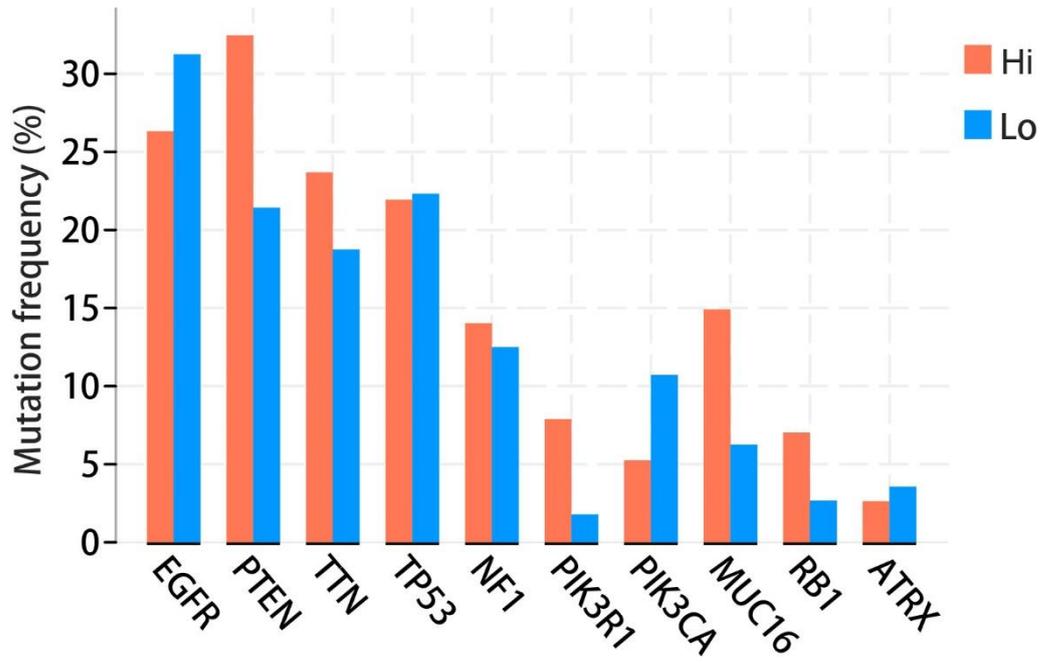


Figure S6