

Supplementary methods

1. This T cell-inflamed score model is shown as follows: T cell-inflamed score = $0.008346 \times \text{EXP}_{\text{CCL5}} + 0.072293 \times \text{EXP}_{\text{CD27}} + 0.042853 \times \text{EXP}_{\text{CD274}} - 0.0239 \times \text{EXP}_{\text{CD276}} + 0.031021 \times \text{EXP}_{\text{CD8A}} + 0.151253 \times \text{EXP}_{\text{CMKLR1}} + 0.074135 \times \text{EXP}_{\text{CXCL9}} + 0.004313 \times \text{EXP}_{\text{CXCR6}} + 0.020091 \times \text{EXP}_{\text{HLA-DQA1}} + 0.058806 \times \text{EXP}_{\text{HLA-DRB1}} + 0.07175 \times \text{EXP}_{\text{HLA-E}} + 0.060679 \times \text{EXP}_{\text{IDO1}} + 0.123895 \times \text{EXP}_{\text{LAG3}} + 0.075524 \times \text{EXP}_{\text{NKG7}} + 0.003734 \times \text{EXP}_{\text{PDCD1LG2}} + 0.032999 \times \text{EXP}_{\text{PSMB10}} + 0.250229 \times \text{EXP}_{\text{STAT1}} + 0.084767 \times \text{EXP}_{\text{TIGIT}}$.
2. Cancer-Immunity Cycle: the status of anti-cancer immunity across seven-step Cancer-Immunity Cycle included: Step 1, release of cancer cell antigens; Step 2, cancer antigen presentation; Step 3, priming and activation; Step 4, trafficking of immune cells to tumors; Step 5, infiltration of immune cells into tumors; Step 6, recognition of cancer cells by T cells; Step 7, killing of cancer cell.

Supplementary Figures

Figure S1

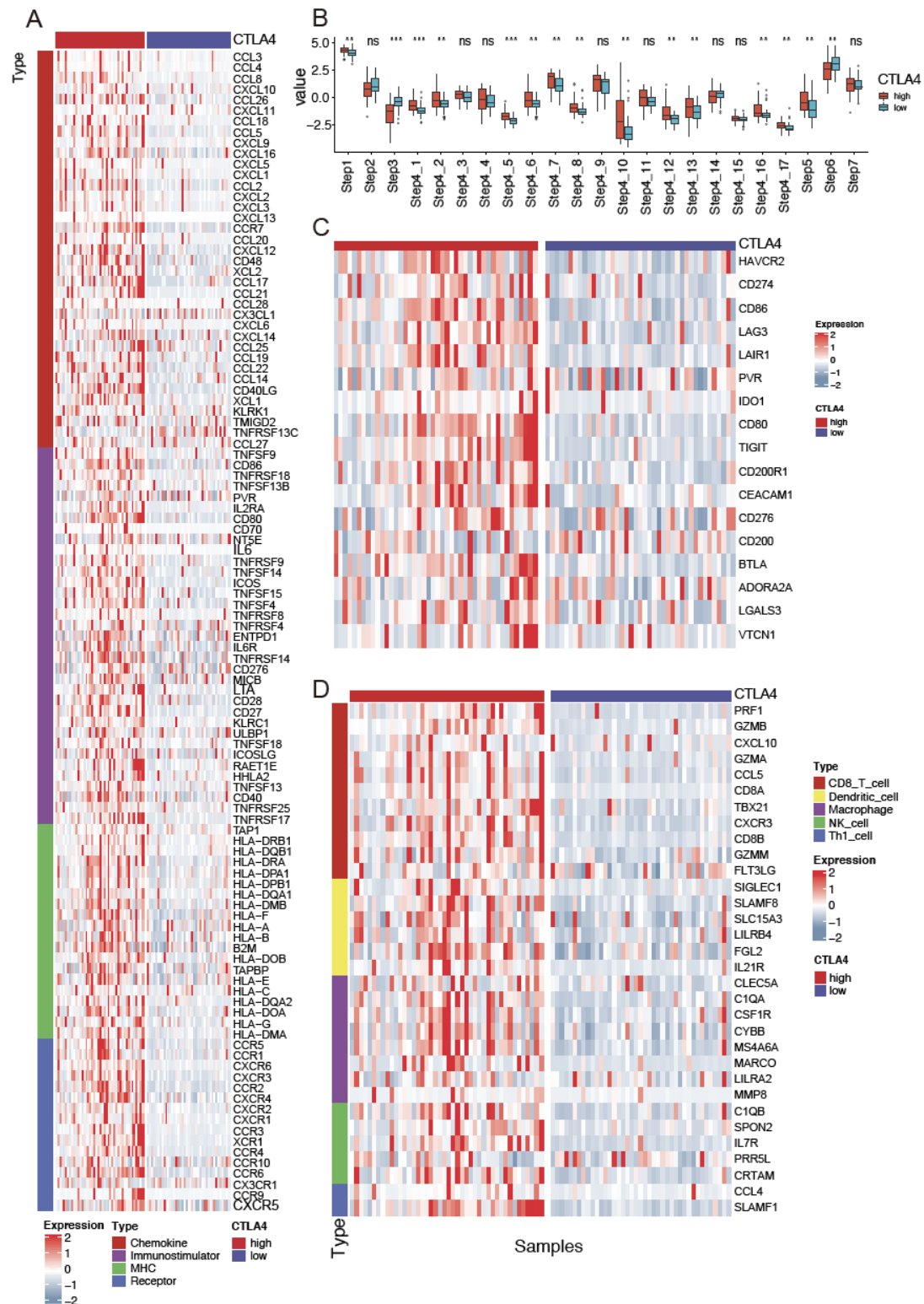


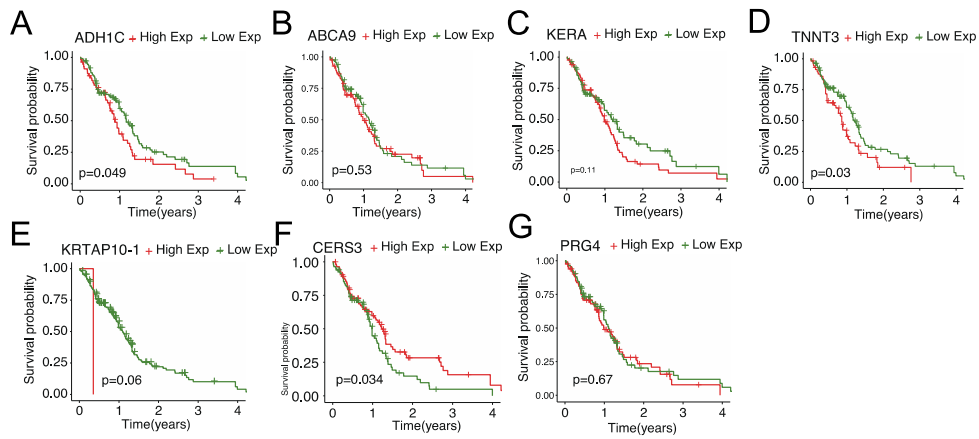
Figure S1: CTLA4 shapes a non-inflamed TME in CGGA GBM cohort. (A)

Differences in the expression of 108 immunomodulators (chemokines,

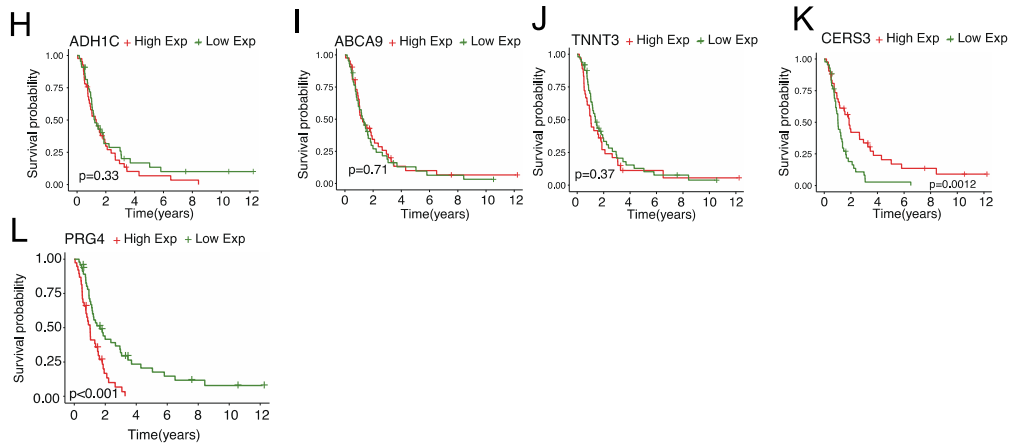
receptors, MHC, and immunostimulators) between high- and low-CTLA4 groups in GBM. (B) Differences in the various steps of the cancer immunity cycle between high- and low-CTLA4 groups. Step1: release of cancer cell antigens; Step 2: cancer antigen presentation; Step 3: priming and activation; Step 4_1- Step 4_17: B cell, Basophil CD4+ T cell, CD8+ T cell, Dendritic cell, Eosinophil, Macrophage, MDSC, Monocyte, Neutrophil, NK cell, T cell, Th1 cell, Th17 cell, Th2 cell, Th22 cell, Treg cell recruiting, respectively; Step 5: infiltration of immune cells into tumors; Step 6: recognition of cancer cells by T cells; Step 7: killing of cancer cells. (C) Differences in the expression of 17 inhibitory immune checkpoints between high- and low-CTLA4 groups. (D) Differences in the effector genes of the above tumor-associated immune cells between high- and low-CTLA4 groups. **P < 0.01, ***P < 0.001, ns non-significant. MDSC = myeloid derived suppress cell.

Figure S2

TCGA Cohort



CGGA Cohort



REMBRANDT Cohort

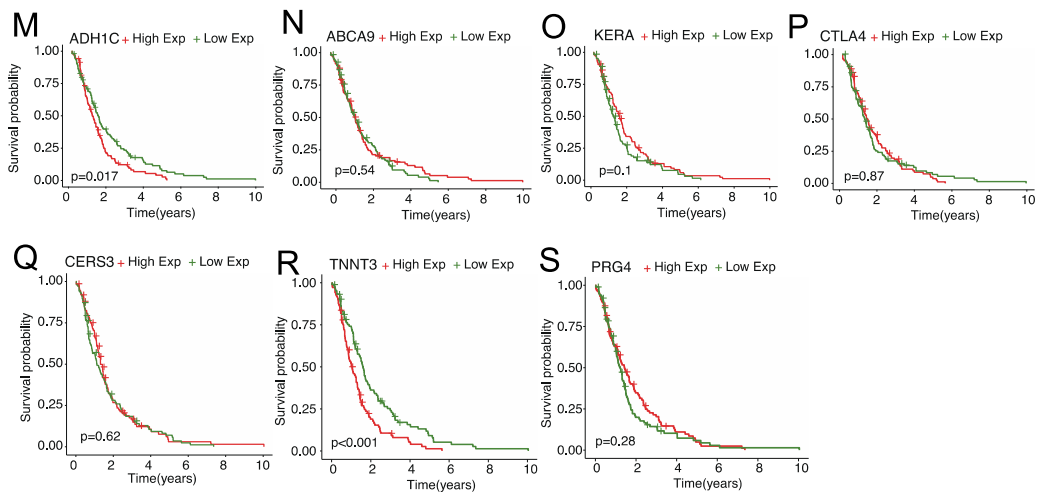


Figure S2: (A-S) Kaplan–Meier survival analysis of hub genes calculated by MEGENA algorithm in three GBM cohorts.

Figure S3

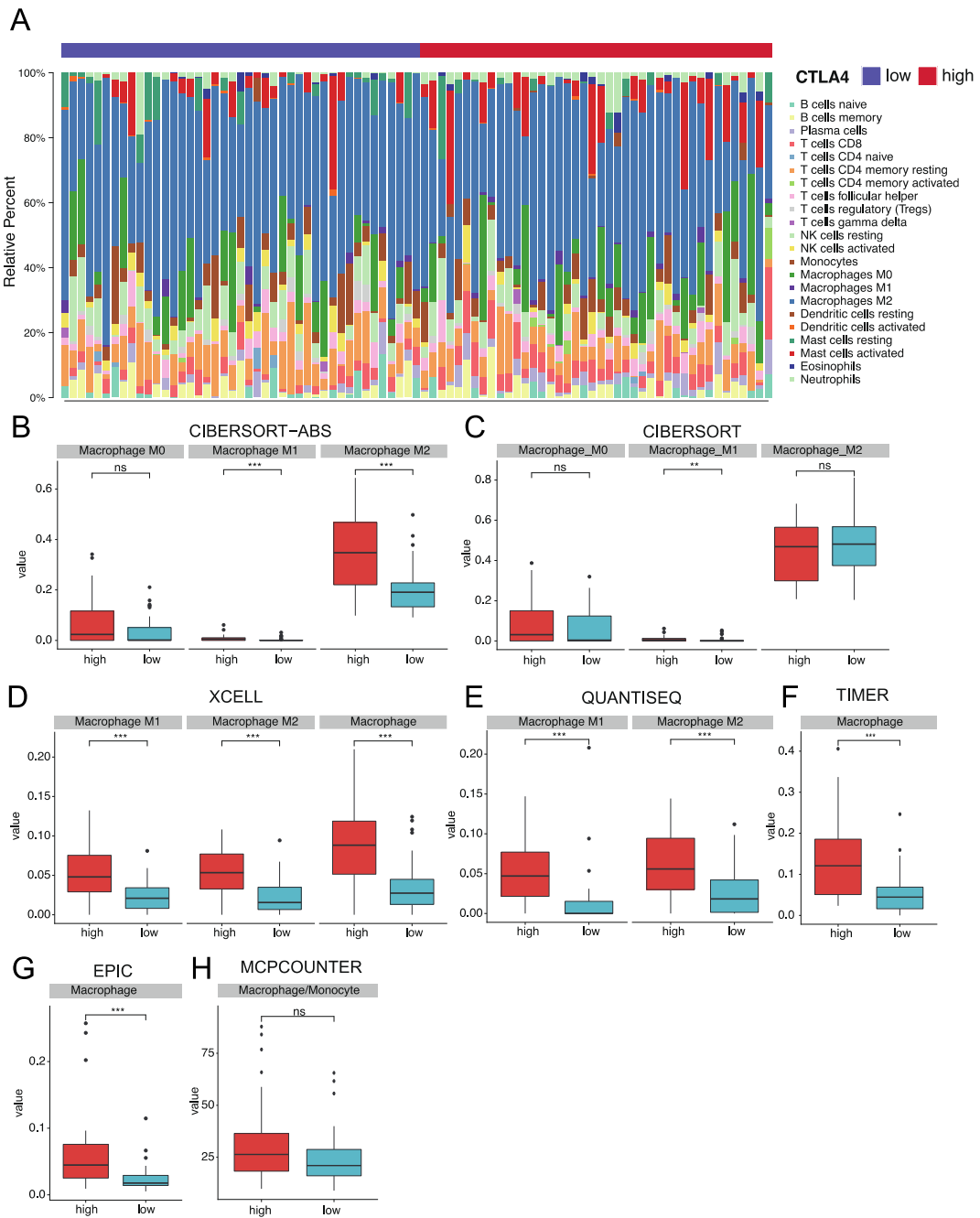


Figure S3: Immune landscape between high- and low-CTLA4 groups in CGGA GBM cohort. (A) Relative proportion of TIICs based on CIBERSORT algorithm in CGGA GBM cohort. (B-H) The association between CTLA4 and macrophage using seven independent algorithms. ** $P < 0.01$, *** $P < 0.001$, ns non-significant.

Figure S4

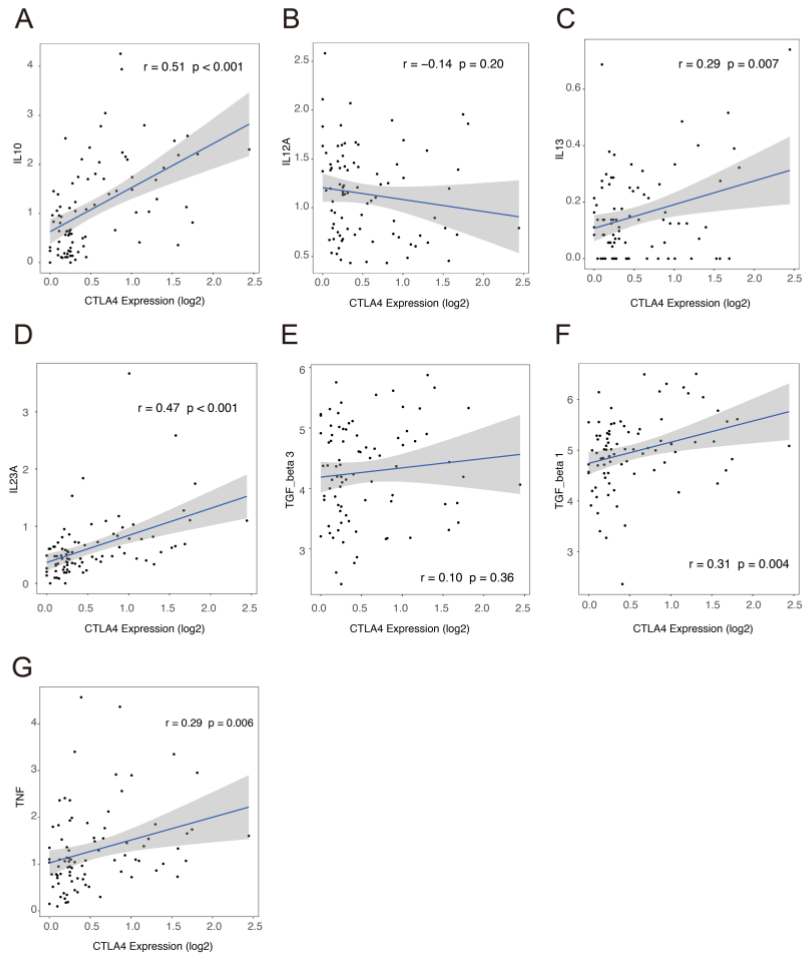


Figure S4: (A-G) Correlation between CTLA4 and classical chemokines and surface markers of macrophage in CGGA GBM cohort.