****

**Figure S1. Pairwise comparisons of survival prognosis between predicted and observed groups.** The median overall survival (mOS) times of curves is represented by a dotted red line. The mOS days of observed groups G1, G2, G3, G4, and G5 are 408, 266, 867, 330, and 357 days, respectively. In contrast, the mOS days predicted groups G1, G2, G3, and G4 are 388, 175, 505, and 424 days. Pairwise comparisons of survival curves between predicted and observed G1, G2, G3, G4, and G5 groups are shown as (a), (b), (c), (d), and (e) in sequence.

****

**Figure S2. Enrichment levels of immune cell subsets between G2 and G3 with RNASeq data.** X-axis indicates groups with different immune phenotypes, which represented in Figure 1. Y-axis indicates enrichment levels of immune cell subsets with normalized enrichment scores (NES). (a). CTL, aDC, Treg, and MDSC immune cell subsets enriched levels were evaluated with the 5, 51, 26, and 58 genes, respectively, in metagene lists and were the same as Figure 1. (b). Immune cell subsets enriched levels were evaluated with the modified gene sets such as 3, 50, 24, and 55 genes for CTL, aDC, Treg, and MDSC, respectively.



**Figure S3. Survival curves of GBM patients with highly/lowly enriched CTL subsets.** The enrichment levels of CTL subsets within TME were estimated with GSEA method. In Figure 1, enrichment levels of immune cell subsets from low to high are annotated with gradient colors from green to red. Obviously, G1 and G2 groups belong to low enrichment levels of CTL (CTL-low) and G3, G4, and G5 groups belong to high enrichment levels of CTL (CTL-high). The survival curves of CTL-low and CTL-high are annotated with red and green colors, respectively.