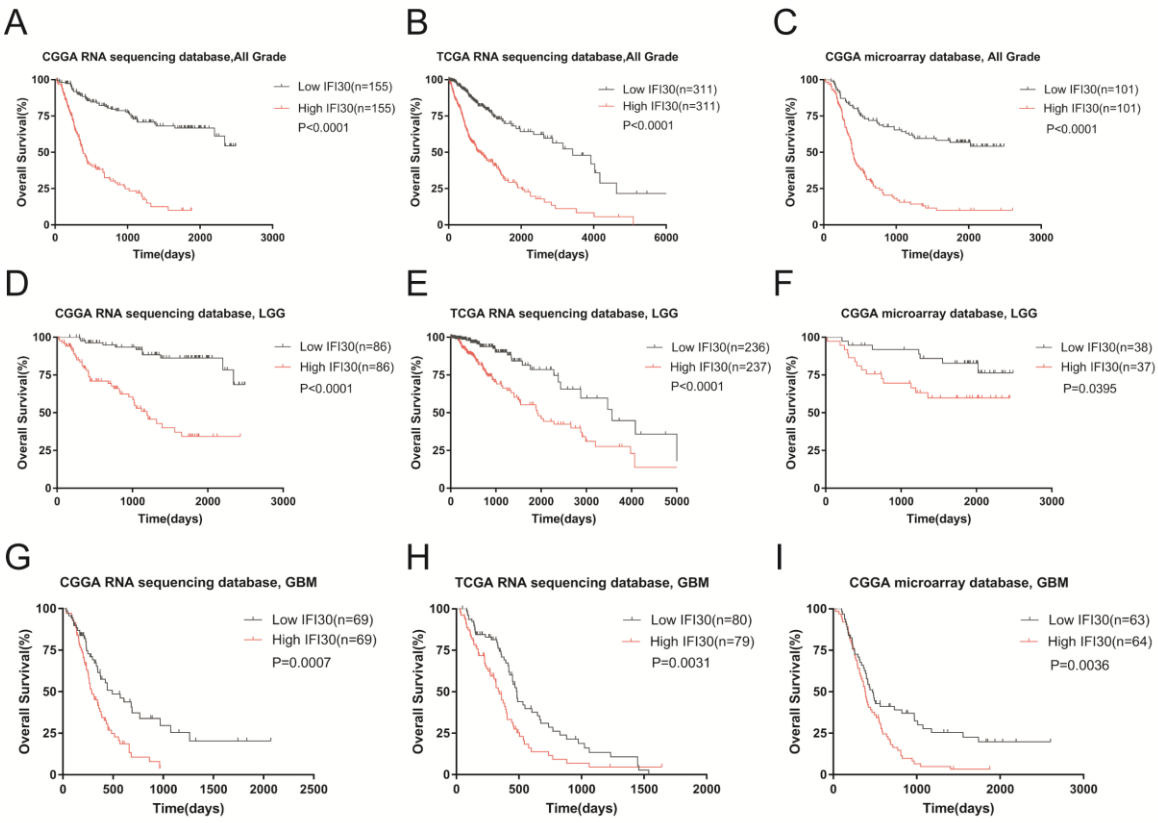
# Supplementary figures

## Supplementary figure 1

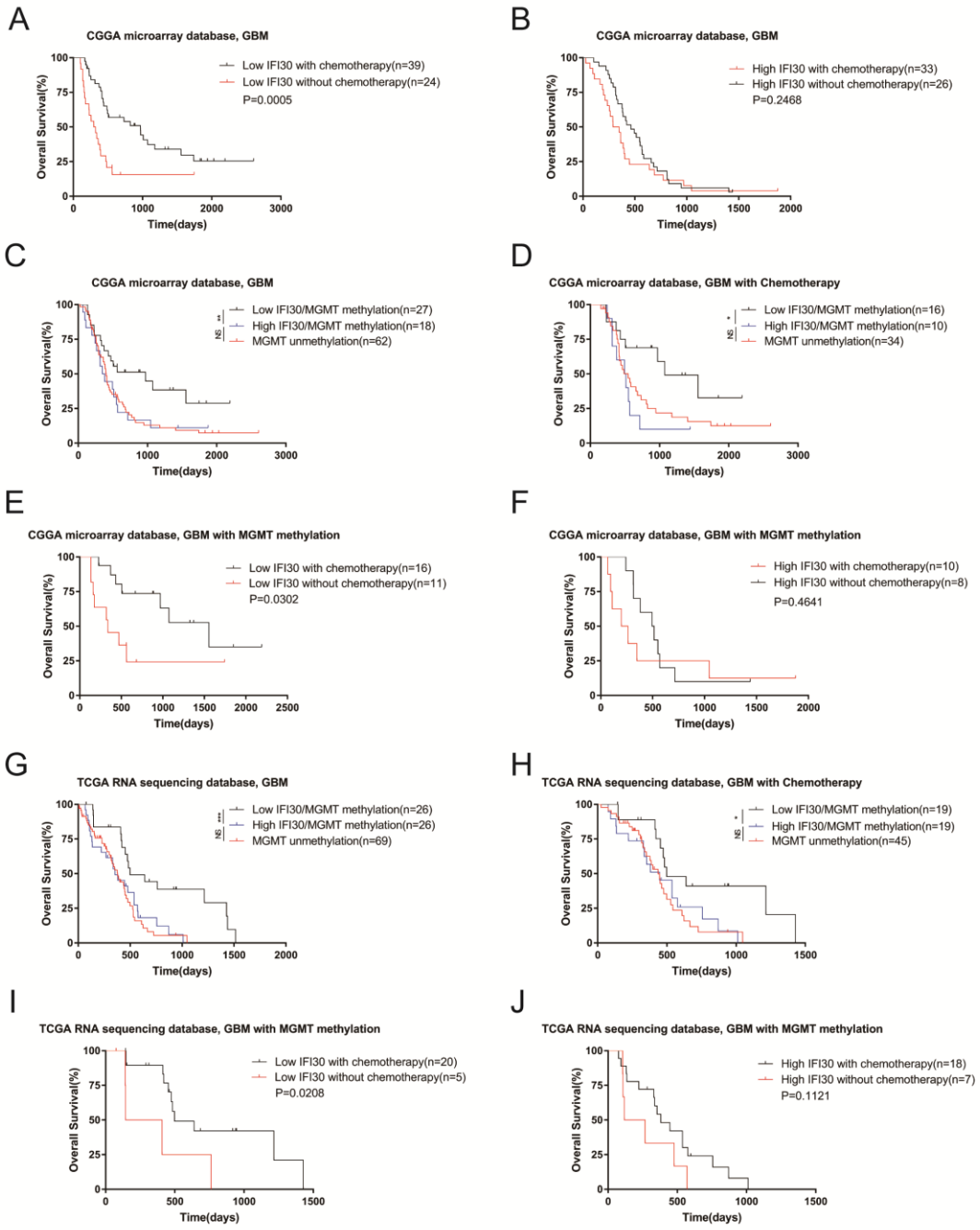



**Supplementary figure 1.** High IFI30 expression was a predictor of poor OS in glioma.

(A-C) Glioma patients with high IFI30 level had shorter OS than low-IFI30 patients in three database. (D-F) High IFI30 group occupied a significantly decreased survival in LGG patients. (G-I) GBM patents with low IFI30 expression benefited a longer survival than high IFI30 group.

**Abbreviations:** OS, overall survival; CGGA, Chinese Glioma Genome Atlas; TCGA, The Cancer Genome Atlas; LGG, lower grade glioma; GBM, glioblastoma.

**Supplementary figure 2**



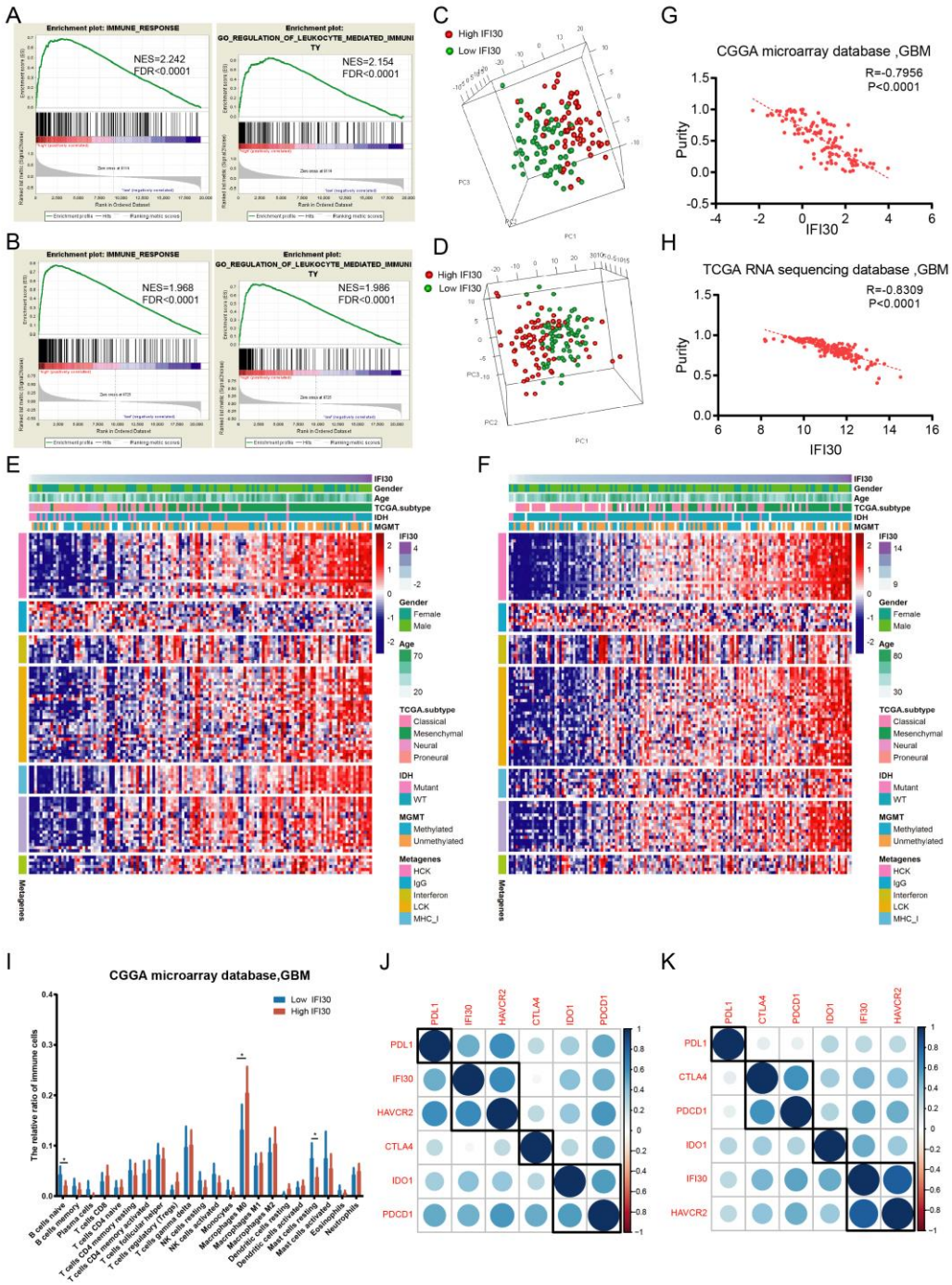

**Supplementary figure 2.** IFI30 decreased chemotherapy sensitivity in GBM in CGGA microarray and TCGA RNA-seq cohorts.

(A-B) GBM patients with low IFI30 level benefited from chemotherapy while high group did not survive longer even under chemotherapy in the two validated cohorts.

(C-D, G-H) For all GBM patients or who received chemotherapy, only the MGMT promoter methylated patients with a low IFI30 level had a survival advantage over the methylated-high IFI30 and unmethylated ones; MGMT promoter methylated patients with high IFI30 level exhibited similar survival time to that of unmethylated patients in the two cohorts. (E, I) Under MGMT promoter methylated, chemotherapy group performed an elevated survival compared to untreated group in low IFI30 patients in these two database. (F, J) In these two cohorts, for high IFI30 expression patients with MGMT promoter methylated, chemotherapy showed no prognostic significance.

**Abbreviations:** CGGA, Chinese Glioma Genome Atlas; TCGA, The Cancer Genome Atlas; GBM, glioblastoma.

**Supplementary figure 3**



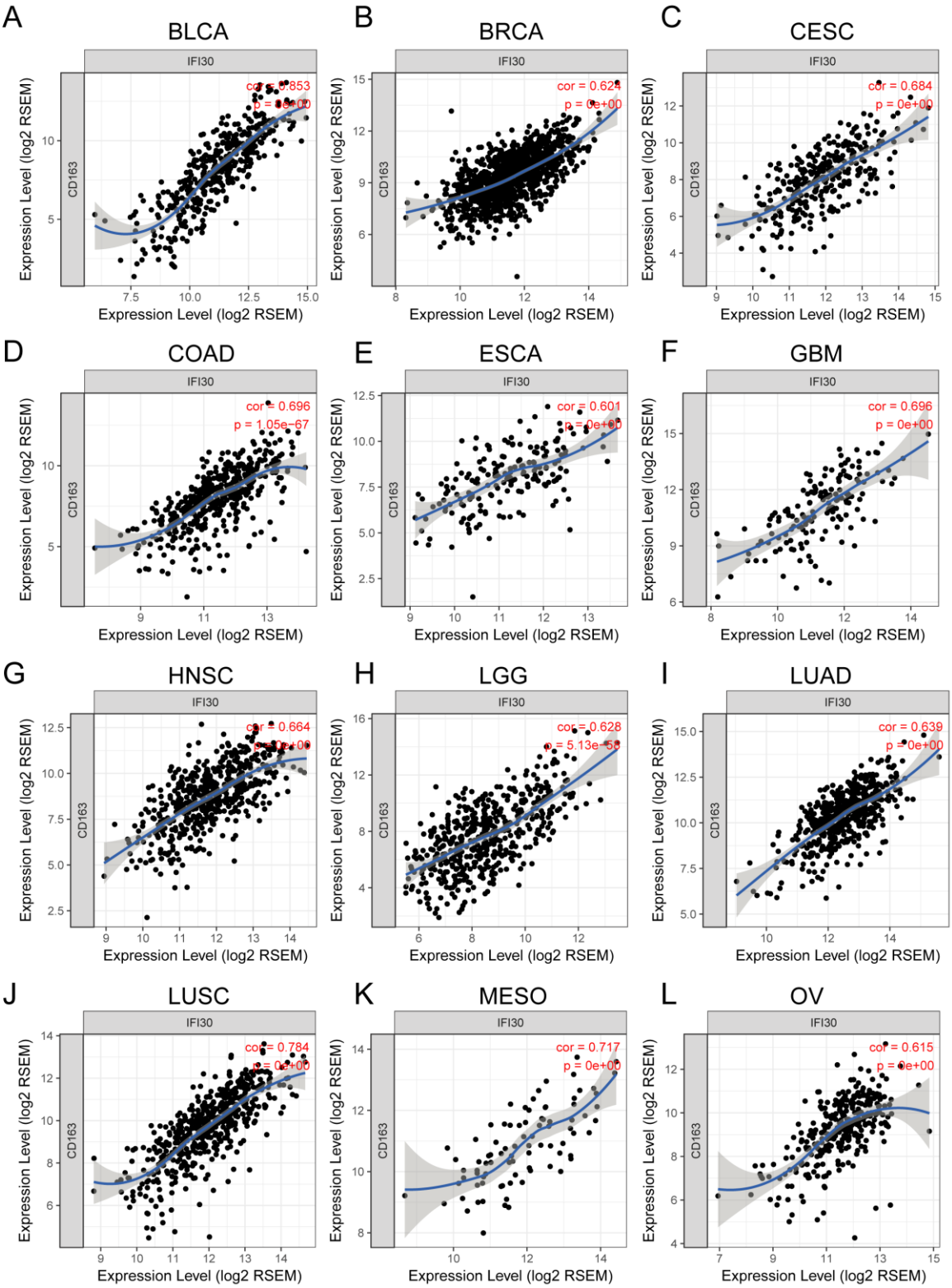

**Supplementary figure 3.** IFI30 associated with enhanced immune response and the microenvironment.

(A-B) Increased immune response enriched in high IFI30 group in CGGA microarray

and TCGA RNA-seq cohorts. (C-D) PCA analysis showed that high and low IFI30 groups conferred different immune status in two validated cohorts. (E-F) Inflammation and immunity clusters of metagenes enriched in high IFI30 group in two cohorts. (G-H) Relationship between IFI30 and purity in two cohorts. (I) In CGGA microarray database, GBM patients with high IFI30 level recruited more M0 cells and less B naive and resting mast cells. (J-K) IFI30 correlated with immunosuppressive checkpoints in two validated cohorts. (* means $P<0.05$)

**Abbreviations:** CGGA, Chinese Glioma Genome Atlas; TCGA, The Cancer Genome Atlas; GBM, glioblastoma; PCA, principle component analysis; GSEA, gene set enrichment analysis.

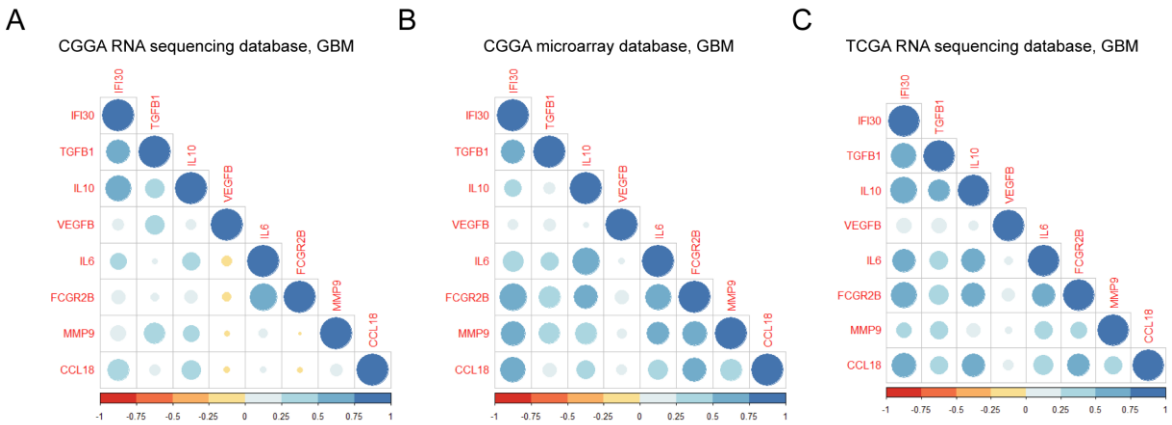
**Supplementary figure 4**




**Supplementary figure 4.** Correlation between M2 marker CD163 and IFI30 in pan-cancer (A-L).

**Abbreviations:** TCGA, The Cancer Genome Atlas; BLCA, Bladder Urothelial Carcinoma; BRCA, Breast invasive carcinoma; CESC, Cervical squamous cell carcinoma and endocervical adenocarcinoma; COAD, Colon adenocarcinoma; ESCA, Esophageal carcinoma; GBM, Glioblastoma multiforme; HNSC, Head and Neck squamous cell carcinoma; LGG, Lower Grade Glioma; LUAD, Lung adenocarcinoma; LUSC, Lung squamous cell carcinoma; MESO, Mesothelioma; OV, Ovarian serous cystadenocarcinoma.

**Supplementary figure 5**




**Supplementary figure 5.** Correlation between IFI30 and classical anti-inflammatory cytokines and chemokines (A-C).

## Supplementary tables

Table S1 The list of 20 classical interferon- γ stimulated genes.

| |
|---|
| ISG15 |
| ISG20L2 |
| ISG20 |
| IFI27L2 |
| IFI27L1 |
| IFI27 |
| IFI30 |
| IFI35 |
| IFI44 |
| IFI44L |
| IFI6 |
| IFIT1 |
| IFIT2 |
| IFIT3 |
| IFIT5 |
| IFITM1 |
| IFITM2 |
| IFITM3 |
| IFITM4P |

IFITM5

Table S2: Cox Regression Analysis of TCGA RNA sequencing database, GBM.

**Abbreviations:** TCGA, The Cancer Genome Atlas; GBM, glioblastoma; HR, hazard ratio.

| Variable | Univariate Regression | | Multivariate Regression | |
|---|---|---|---|---|
| | HR | P value | HR | P value |
| Age (young≤60 VS old>60) | 0.6827 | 0.04 | 1.0944 | 0.72963 |
| Gender (Male VS Female) | 0.8624 | 0.448 | | |
| KPS (Low≤70 VS Low>70） | 1.4711 | 0.117 | | |
| IDH1 status (Wild VS Mutant) | 5.1697 | 0.00153 | 3.4528 | 0.09532 |
| MGMT promoter status (Unmethylated VS Methylated) | 1.7563 | 0.0137 | 1.9310 | 0.01208 |
| Radiotherapy (Treated VS Untreated) | 0.1657 | 3.65e-12 | 0.1519 | 0.00409 |
| Chemotherapy (Treated VS Untreated) | 0.2506 | 7.17e-09 | 0.8713 | 0.81586 |
| IFI30 | 1.4815 | 0.042 | 1.8839 | 0.01499 |

| (High VS Low) | | | | |
|---|---|---|---|---|

Table S3: Cox Regression Analysis of CGGA microarray database, GBM

**Abbreviations:** CGGA, Chinese Glioma Genome Atlas; GBM, glioblastoma; HR, hazard ratio.

| Variable | Univariate Regression | | Multivariate Regression | |
|---|---|---|---|---|
| | HR | P value | HR | P value |
| Age (young≤60 VS old>60) | 0.7669 | 0.344 | | |
| Gender (Male VS Female) | 1.1730 | 0.43 | | |
| KPS (Low≤70 VS Low>70） | 2.0025 | 0.000469 | 2.1792 | 0.000246 |
| IDH1 status (Wild VS Mutant) | 1.5780 | 0.0985 | | |
| MGMT promoter status (Unmethylated VS Methylated) | 1.4919 | 0.0744 | | |
| Radiotherapy (Treated VS Untreated) | 0.3821 | 0.000195 | 0.4158 | 0.001584 |
| Chemotherapy (Treated VS Untreated) | 0.4706 | 0.000207 | 0.4158 | 0.004059 |
| IFI30 | 1.7403 | 0.0057 | 1.7047 | 0.011781 |

(High VS Low)

Table S4 Clinical and molecular information of GBM patients included in the study

**Abbreviations:** CGGA, Chinese Glioma Genome Atlas; TCGA, The Cancer Genome Atlas; GBM, glioblastoma;

| Cohort | CGGA-RNAseq (n=325) | TCGA-RNAseq (n=669) | CGGA microarray (n=306) |
|---|---|---|---|
| Database | CGGA | TCGA | CGGA |
| Age(years) | 43(8-81) | 60(14-89) | 43(13-70) |
| Gender | | | |
| Male | 203 | 394 | 180 |
| Female | 122 | 288 | 121 |
| Unavailable | 0 | 1 | 5 |
| Survival(days) | 396.59±341.86 | 415.57±381.56 | |
| TCGA Subtype (GBM) | | | |
| Classical | 48 | 39 | 16 |
| Neural | 12 | 26 | 12 |
| Proneural | 33 | 29 | 21 |
| Mesenchymal | 51 | 48 | 79 |
| Unavailable | 0 | 11 | 0 |
| IDH1 status (GBM) | | | |

| | | | |
|---|---|---|---|
| Wild type | 108 | 135 | 106 |
| Mutant | 36 | 8 | 22 |
| Unavailable | 0 | 10 | 0 |
| MGMT promoter status (GBM) | | | |
| Unmethylated | 71 | 70 | 45 |
| Methylated | 61 | 52 | 63 |
| Unavailable | 12 | 31 | 20 |
| Chemotherapy (GBM) | | | |
| Treated | 84 | 107 | 72 |
| Untreated | 44 | 45 | 50 |
| Unavailable | 16 | 1 | 6 |
| Radiotherapy | | | |
| Treated | 81 | 123 | 98 |
| Untreated | 47 | 29 | 22 |
| Unavailable | 16 | 1 | 8 |
| Overall survival,months | | | |
| Median | 37.37 | 48.6 | 27.47 |
| Survival status | | | |
| Alive | 168 | 422 | 132 |
| Dead | 142 | 206 | 165 |
| Unavailable | 15 | 55 | 9 |