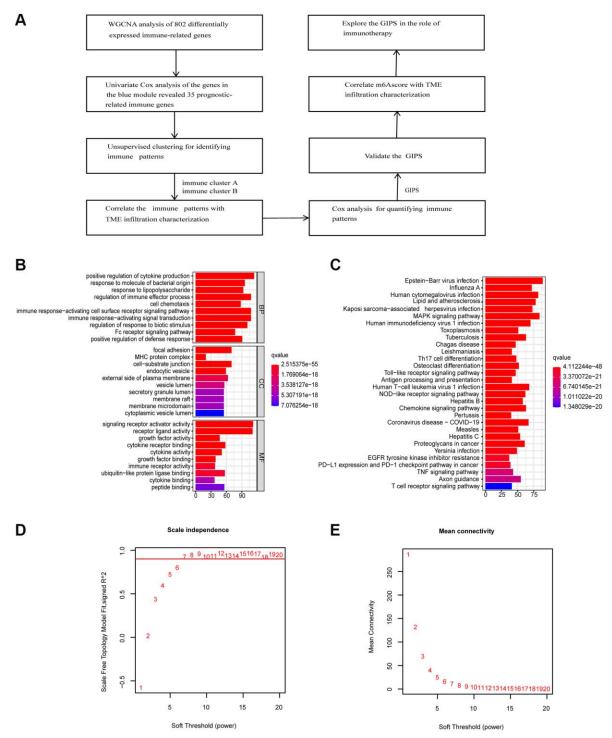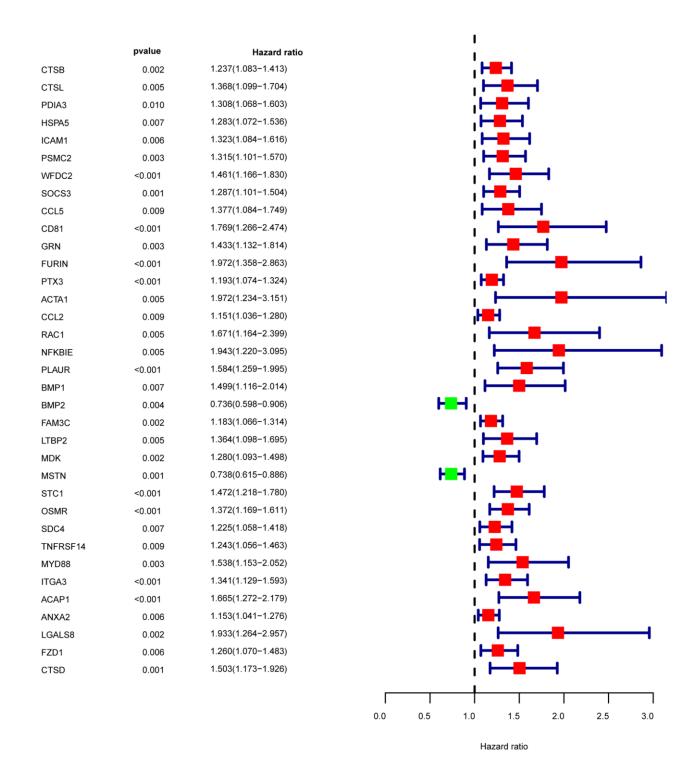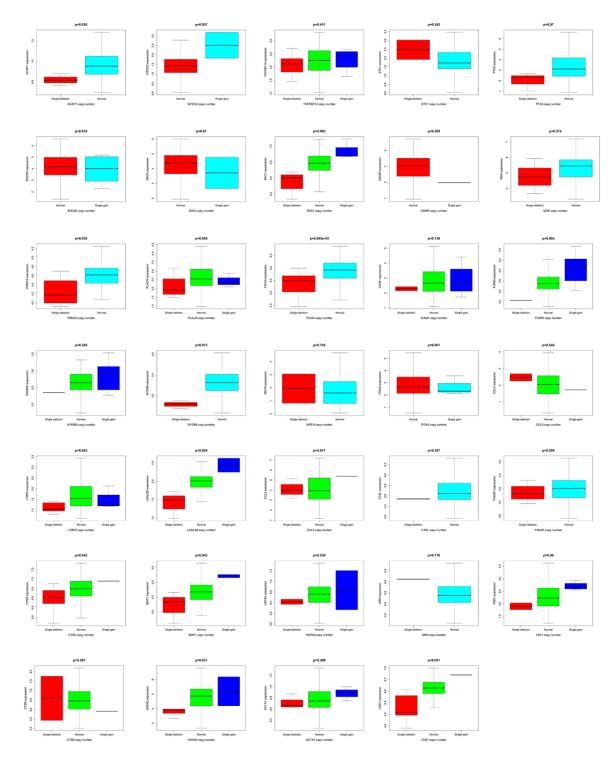Supplementary Figure 1. Differentially expressed immune-related genes in GBM. (**A**) This study's design overview. (**B**) GO enrichment analysis of the immune-related DEGs. (**C**) KEGG enrichment analysis of the immune-related DEGs. (**D**) The horizontal line denotes a threshold value of 0.9. (**E**) WGCNA's optimal soft threshold is 7.

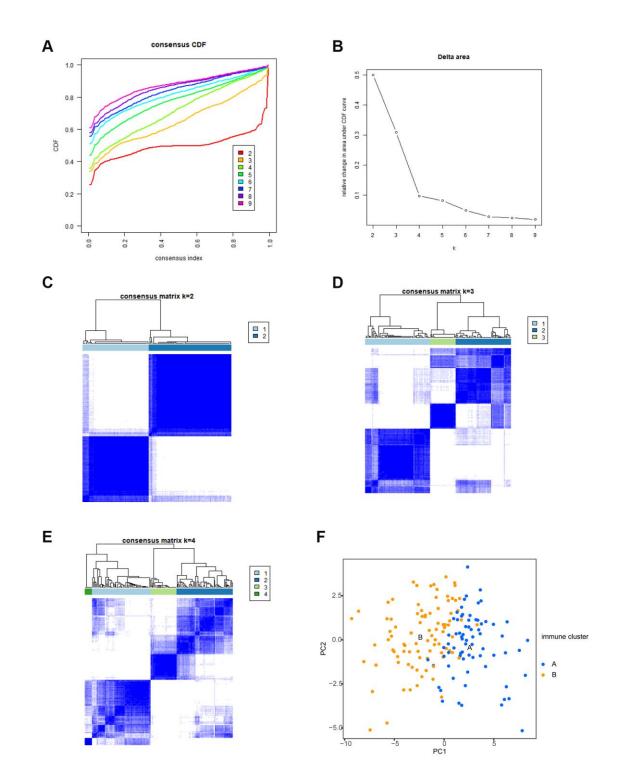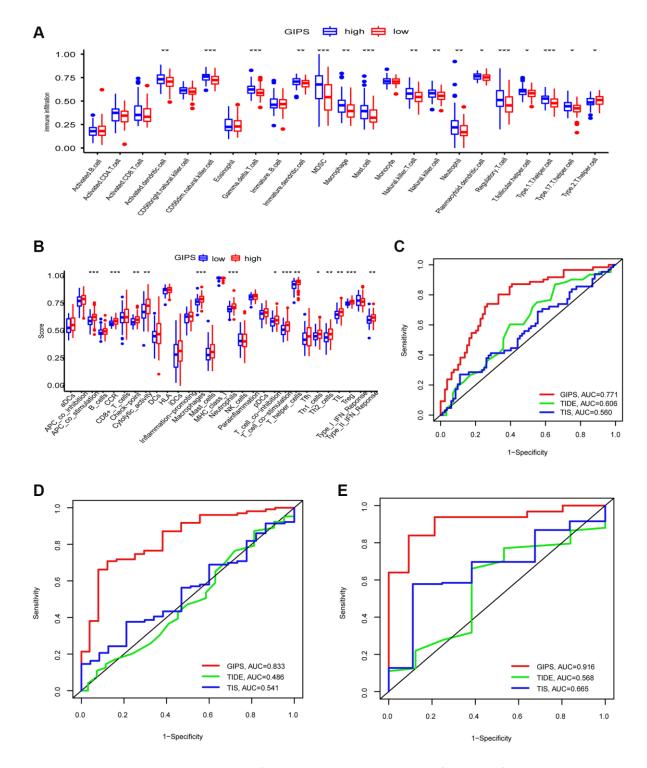|	pvalue	Hazard ratio
CTSB	0.002	1.237(1.083−1.413)
CTSL	0.005	1.368(1.099−1.704)
PDIA3	0.010	1.308(1.068−1.603)
HSPA5	0.007	1.283(1.072−1.536)
ICAM1	0.006	1.323(1.084−1.616)
PSMC2	0.003	1.315(1.101−1.570)
WFDC2	<0.001	1.461(1.166−1.830)
SOCS3	0.001	1.287(1.101−1.504)
CCL5	0.009	1.377(1.084−1.749)
CD81	<0.001	1.769(1.266−2.474)
GRN	0.003	1.433(1.132−1.814)
FURIN	<0.001	1.972(1.358−2.863)
PTX3	<0.001	1.193(1.074−1.324)
ACTA1	0.005	1.972(1.234−3.151)
CCL2	0.009	1.151(1.036−1.280)
RAC1	0.005	1.671(1.164−2.399)
NFKBIE	0.005	1.943(1.220−3.095)
PLAUR	<0.001	1.584(1.259−1.995)
BMP1	0.007	1.499(1.116−2.014)
BMP2	0.004	0.736(0.598−0.906)
FAM3C	0.002	1.183(1.066−1.314)
LTBP2	0.005	1.364(1.098−1.695)
MDK	0.002	1.280(1.093−1.498)
MSTN	0.001	0.738(0.615−0.886)
STC1	<0.001	1.472(1.218−1.780)
OSMR	<0.001	1.372(1.169−1.611)
SDC4	0.007	1.225(1.058−1.418)
TNFRSF14	0.009	1.243(1.056−1.463)
MYD88	0.003	1.538(1.153−2.052)
ITGA3	<0.001	1.341(1.129−1.593)
ACAP1	<0.001	1.665(1.272−2.179)
ANXA2	0.006	1.153(1.041−1.276)
LGALS8	0.002	1.933(1.264−2.957)
FZD1	0.006	1.260(1.070−1.483)
CTSD	0.001	1.503(1.173−1.926)

Supplementary Figure 2. Univariate Cox analysis of the genes in the blue module. Forest plot of 35 immune-related prognostic genes.

Supplementary Figure 3. The correlation between expression level and copy number of the 35 prognostic-related immune genes.

Supplementary Figure 4. Unsupervised clustering analysis in GBM meta cohort. (**A** and **B**) The empirical cumulative distribution function (CDF) plots show the consensus distributions for k (1–9). (**C**–**E**) Consensus matrix of TCGA-GBM dataset (k = 2–4). (**F**) Principal component analysis of expression profiles in the two immune clusters.

Supplementary Figure 5. The immune cells infiltration and immune-related function of distinct GIPS subgroup. (**A**) Differential analysis of immune cell abundance between two GIPS subgroups. (**B**) Differential of immune function between the two GIPS subgroups. (**C**–**E**) ROC analysis of GIPS, TIS, and TIDE on OS at 1-, 2-, and 3-year.