

Figure S1

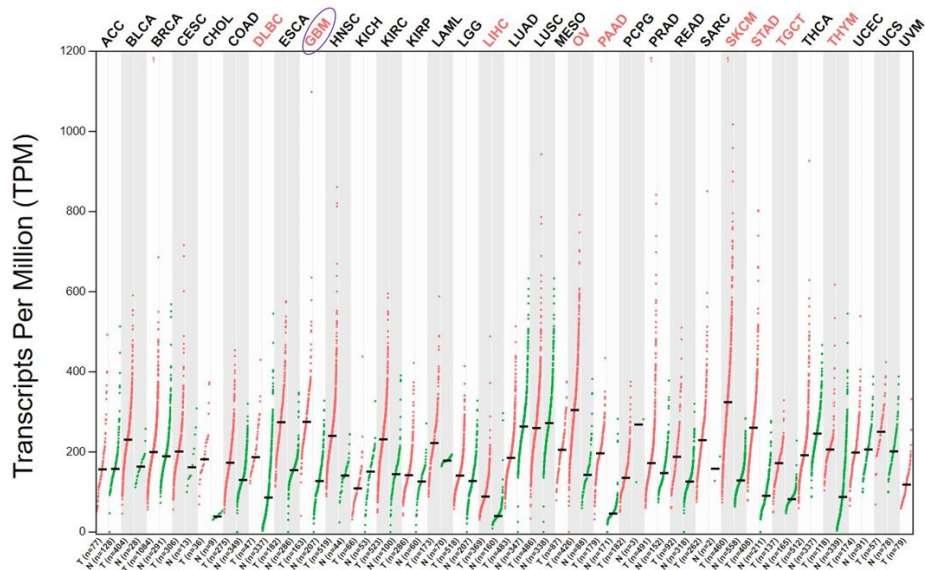


Figure S1. FKBP1A mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S2

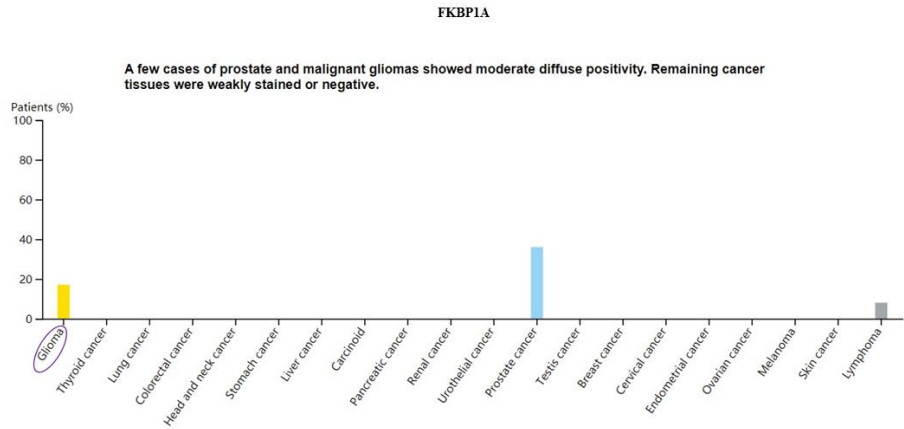


Figure S2. FKBP1A protein expression in malignant tumors (HPA database).

Figure S3

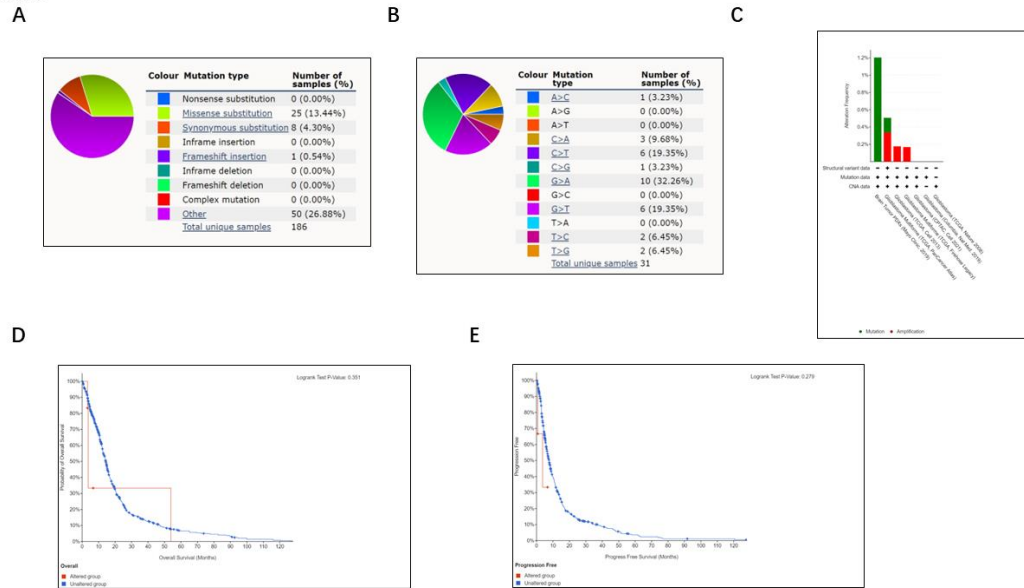


Figure S3. FKBP1A genes expression and mutation analysis in GBM (COSMIC and cBioPortal). (A, B) Pie-chart showed the percentage of the mutation type of FKBP1A in GBM according to COSMIC database. (C) Oncoprint in cBioPortal represented the proportion and distribution of samples with alterations in FKBP1A gene. (D) Kaplan-Meier plots comparing OS in cases with/without FKBP1A gene alterations. (E) Kaplan-Meier plots comparing DFS in cases with/without FKBP1A gene alterations.

Figure S4

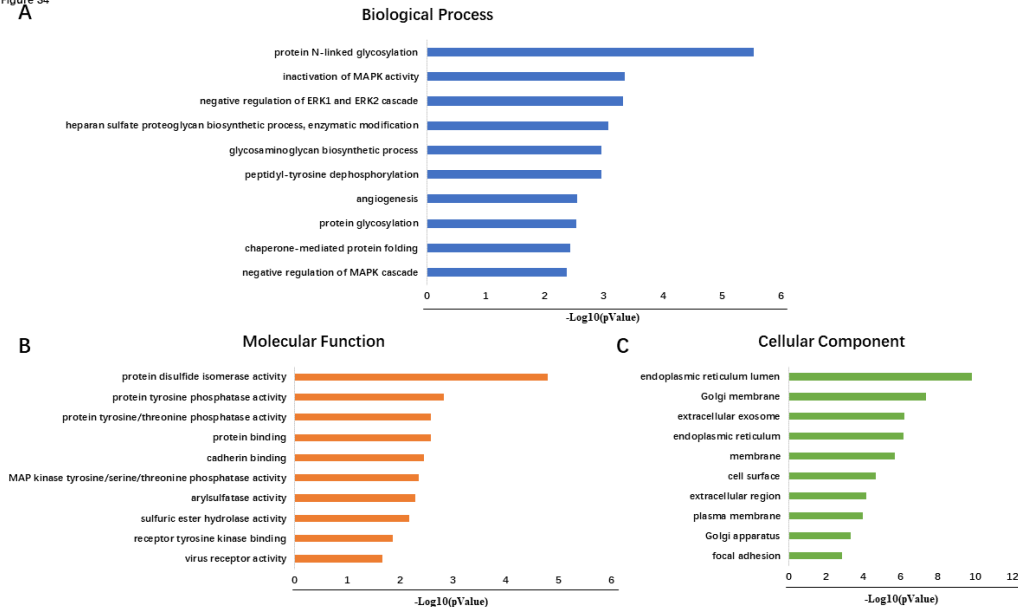


Figure S4. Diagrams of top 10 significant pathways of GO enrichment analysis. (A) Graph of the 10 most significant pathways of BP category. (B) Top 10 significant terms in the MF category. (C) Ten most valuable annotations of the CC category.

Figure S5

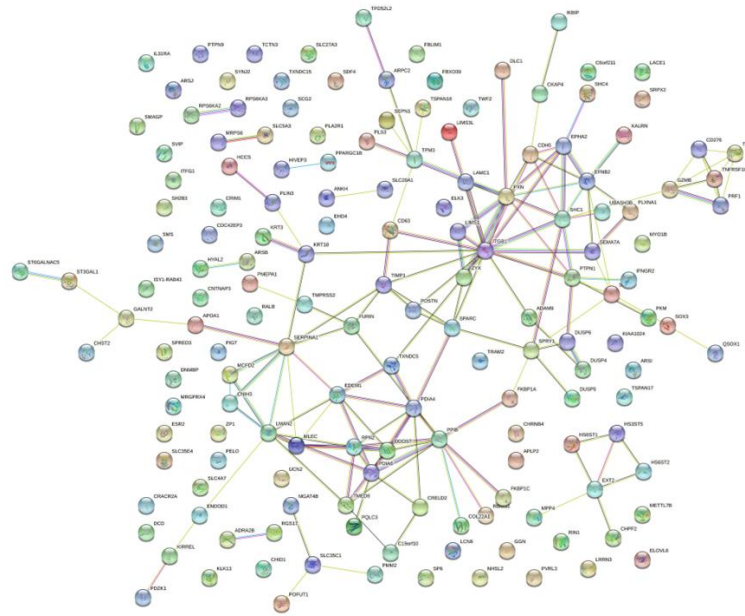


Figure S5. Interactions between different pairs of FKBP1A co-expressed genes. Nodes represent various symbols of genes; edges represent protein-protein associations.

Figure S6

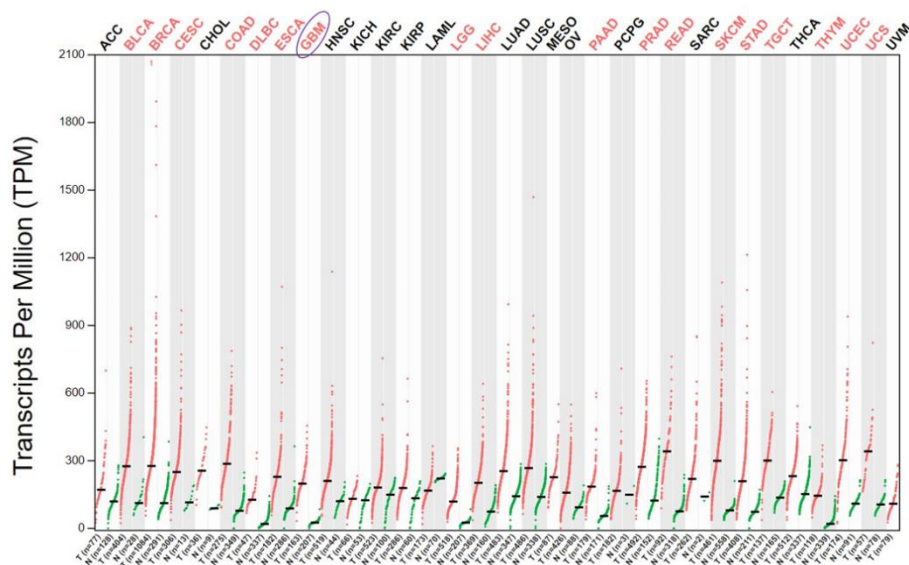


Figure S6. RPN2 mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S7

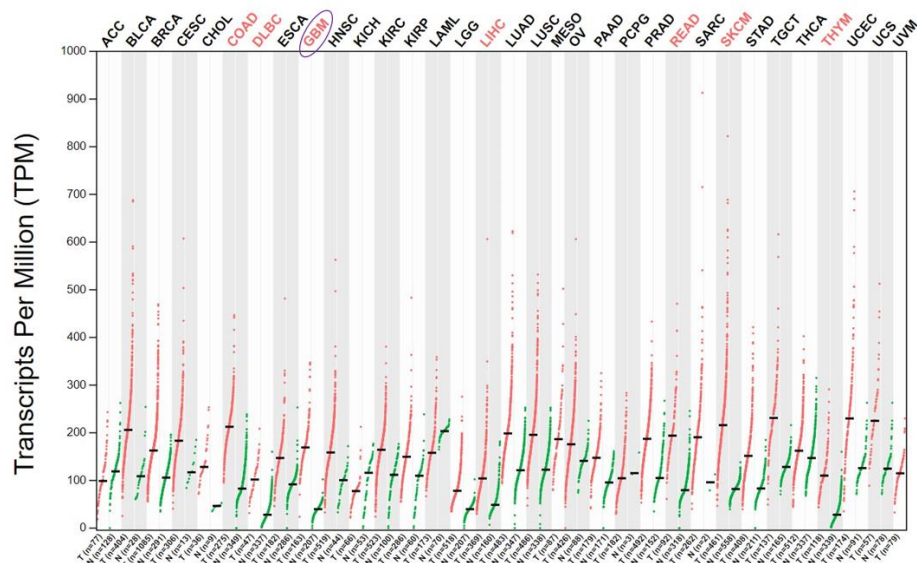


Figure S7. DOST mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S8

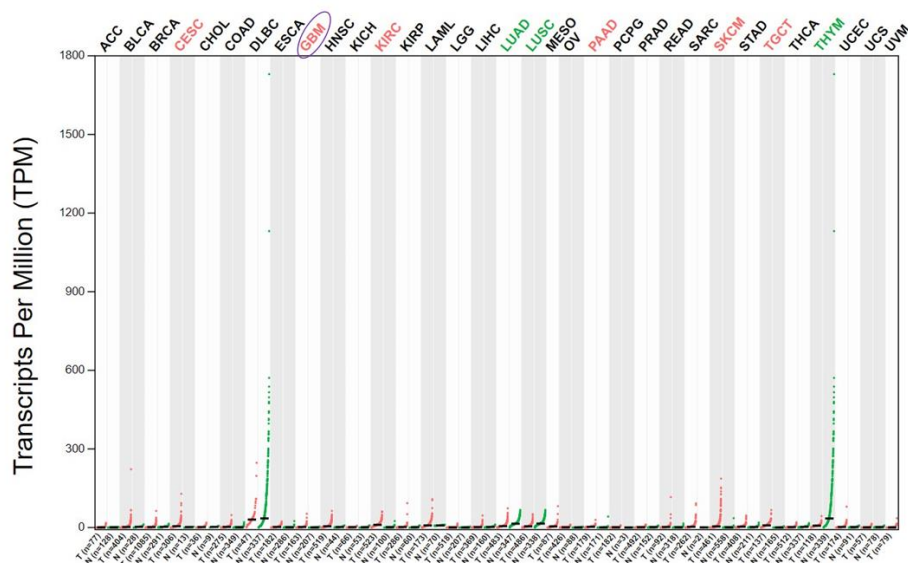


Figure S8. PRF1 mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S9

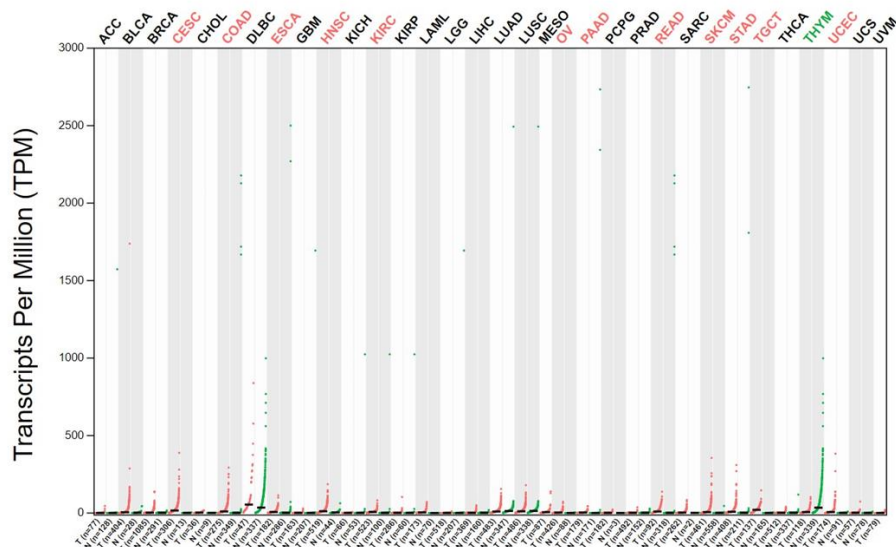


Figure S9. GZMB mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S10

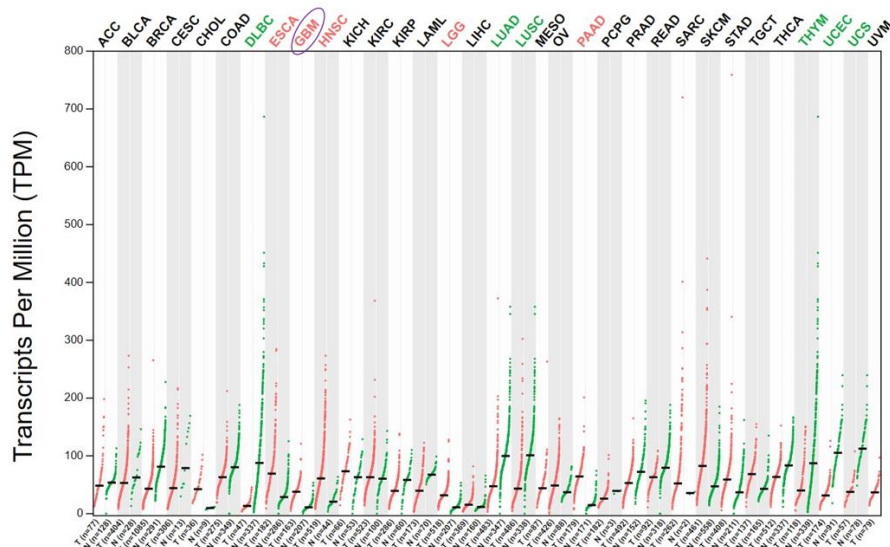


Figure S10. PXN mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S11

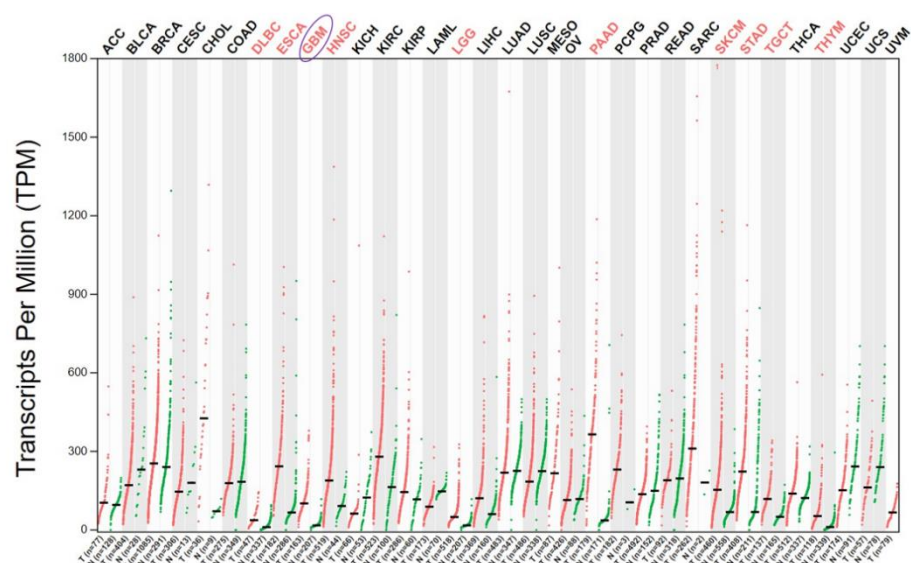
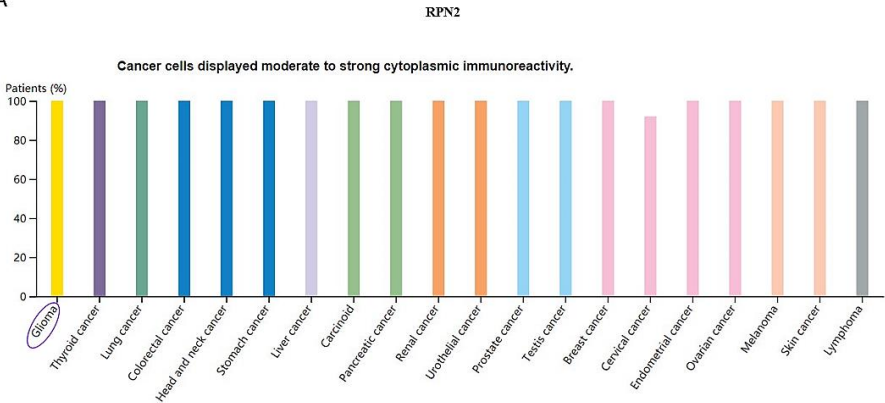


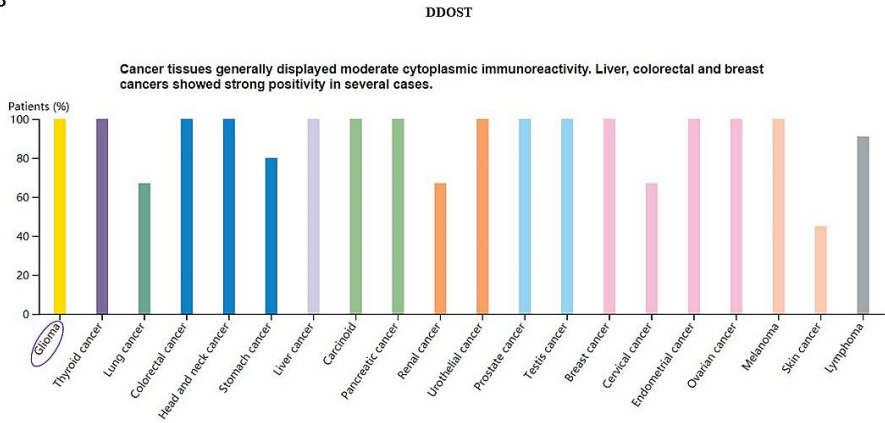
Figure S11. ITGB1 mRNA expression in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S12

A



B



C

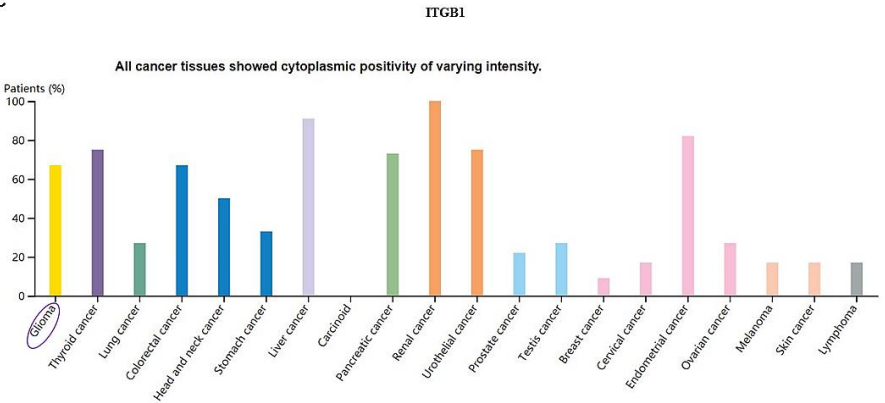


Figure S12. Protein expression of (A) RPN2, (B) DDOST and (C) ITGB1 in malignant tumors (HPA database).

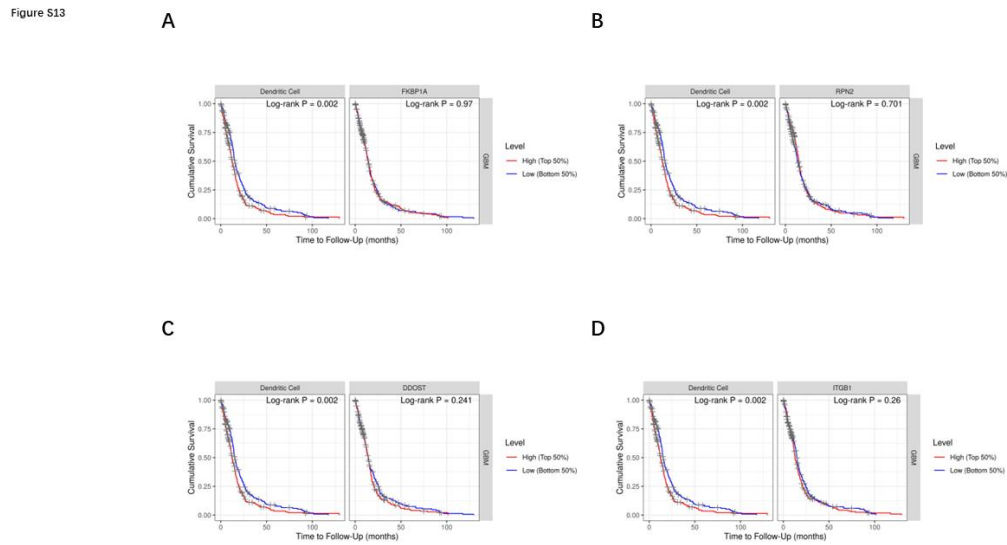


Figure S13. Overall survival stratified by a combined analysis of immune infiltration level and (A) FKBP1A, (B) RPN2, (C) DDOST and (D) ITGB1 expression in TIMER2.0.

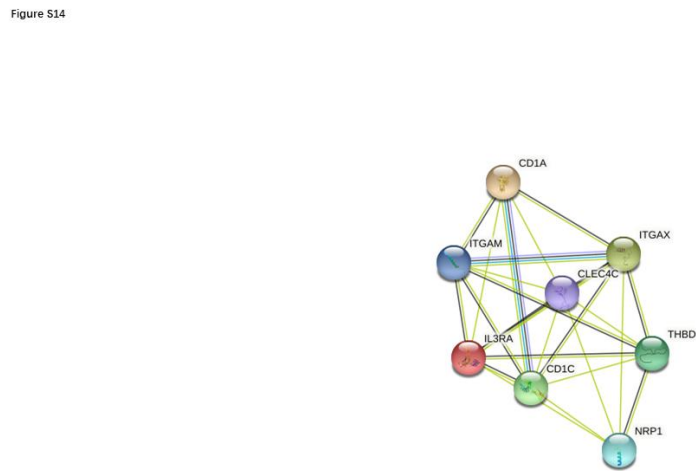


Figure S14. Interactions between different pairs of DC cell related markers. Nodes represent various symbols of genes; edges represent protein-protein associations.

Figure S15

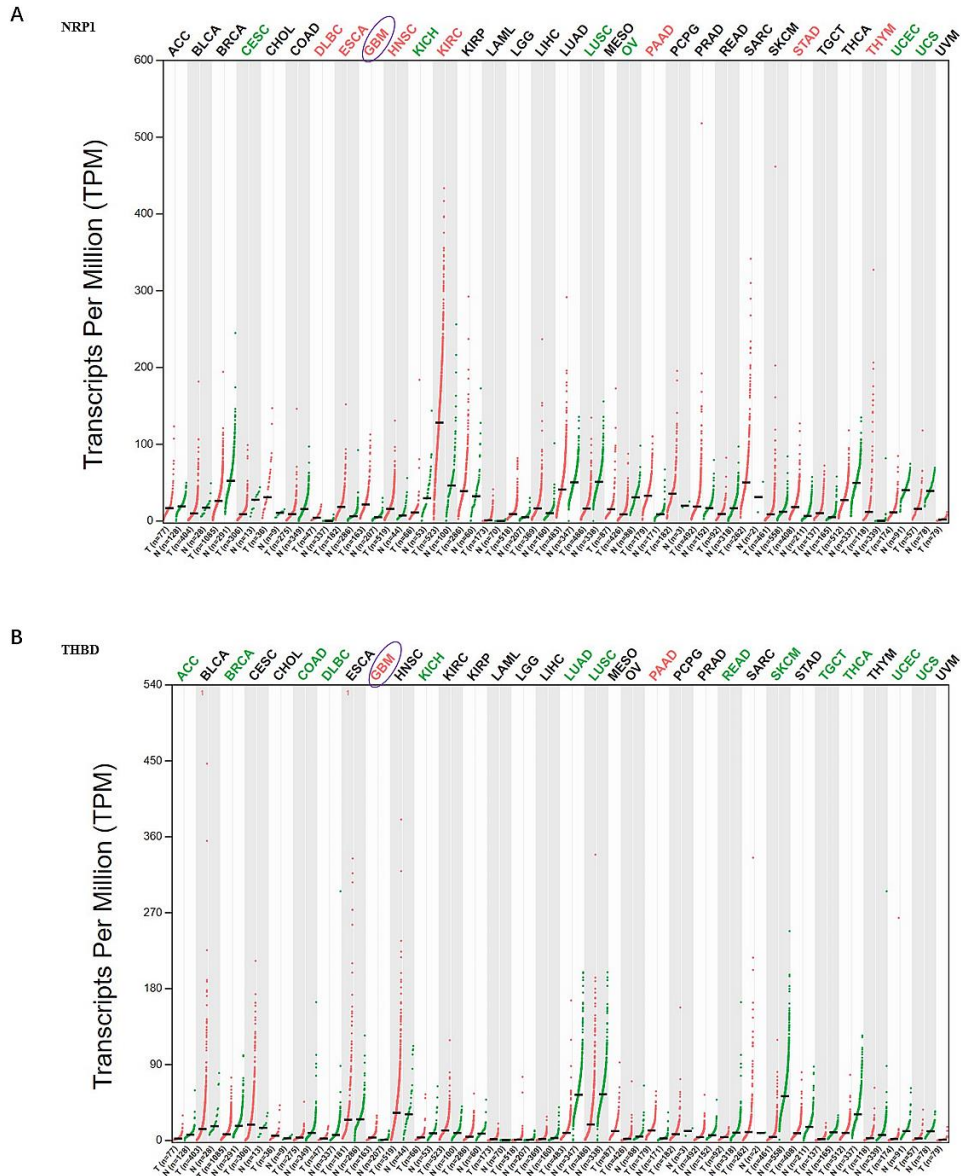


Figure S15. MRNA expression of (A) NRP1, (B) THBD in malignant tumors (GEPIA2 database). The gene expression profile across all tumor samples and paired normal tissues, each dots represent expression of samples, T represents tumor group, N represents normal group.

Figure S16

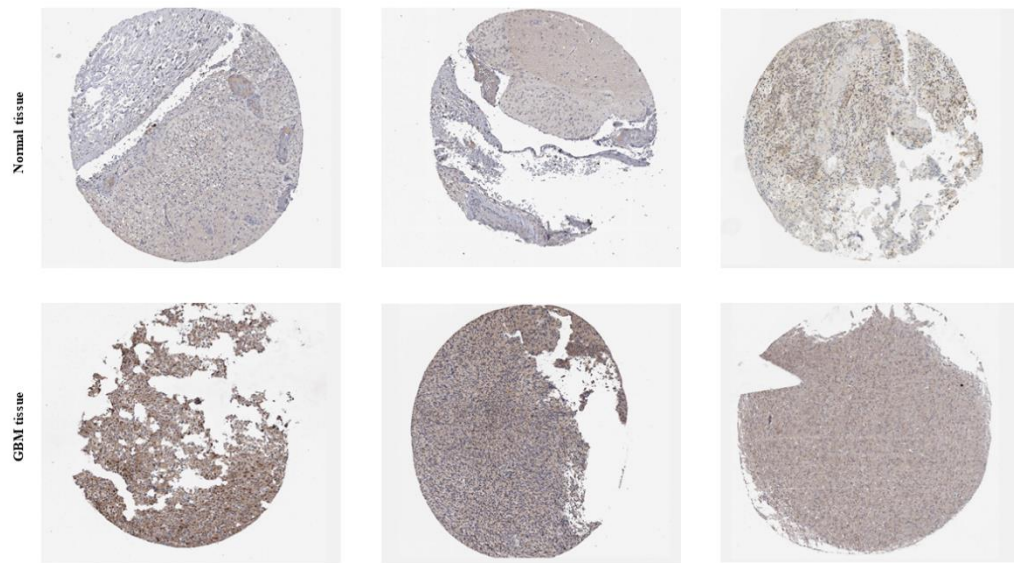


Figure S16. Immunohistochemical staining of NRP1 protein in GBM (HPA database). Representative images of immunohistochemical staining of NRP1 expression in GBM samples and matched adjacent normal tissues.

Figure S17

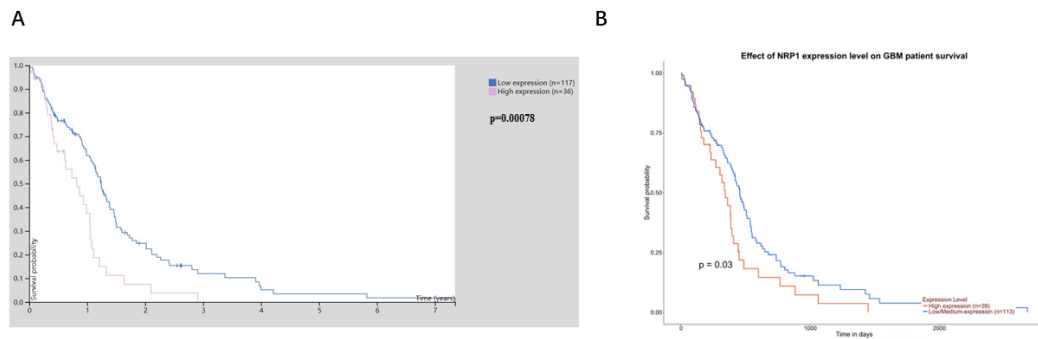


Figure S17. Relationship of NRP1 with the prognostic merit in GBM using (A) HPA database, (B) UALCAN database.

Figure S18

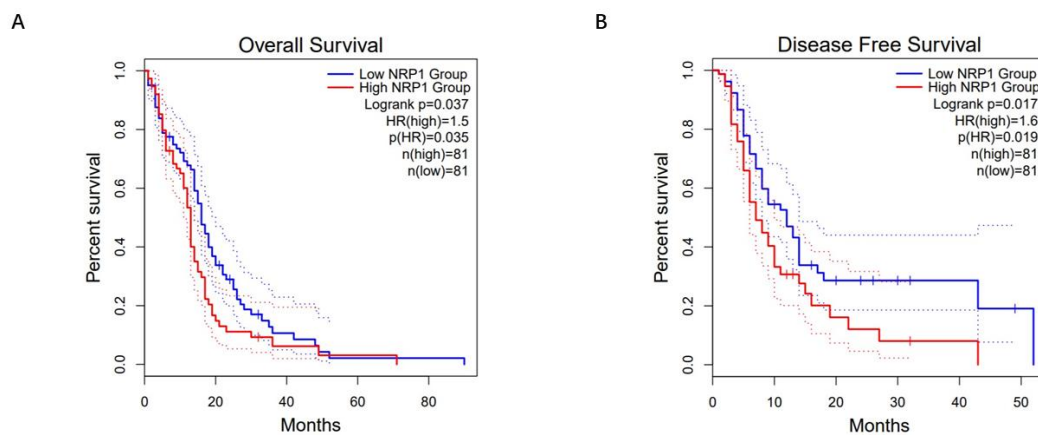


Figure S18. Relationship of NRP1 with the prognostic merit using GEPIA2 database. Kaplan–Meier plots showed (A) overall survival and (B) disease free survival.

Figure S19

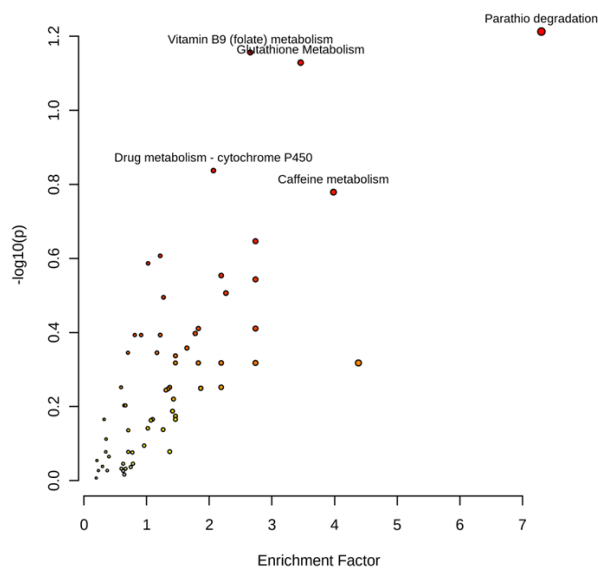


Figure S19. Relationship of FKBP1A and metabolic pathways in DC cells of glioblastoma patients using MetaboAnalyst database.

Figure S20

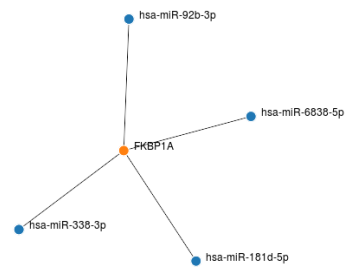


Figure S20. FKBP1A mRNA-miRNA regulatory axis using miRWalk database.