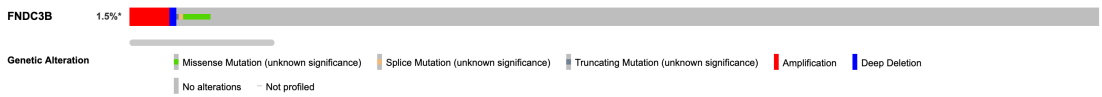
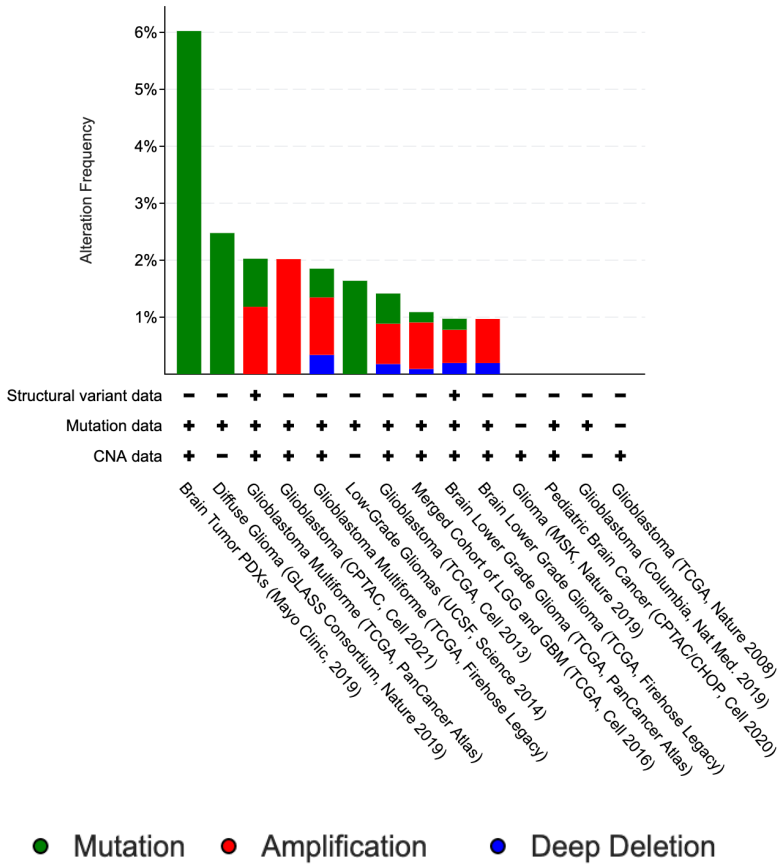
Supplementary Figure 1. Genetic alterations of FNDC3B in glioma patients. (A) OncoPrint visual summary of variations on FNDC3B; (B) Summary of genetic alterations for FNDC3B in 14 glioma datasets.

(A)

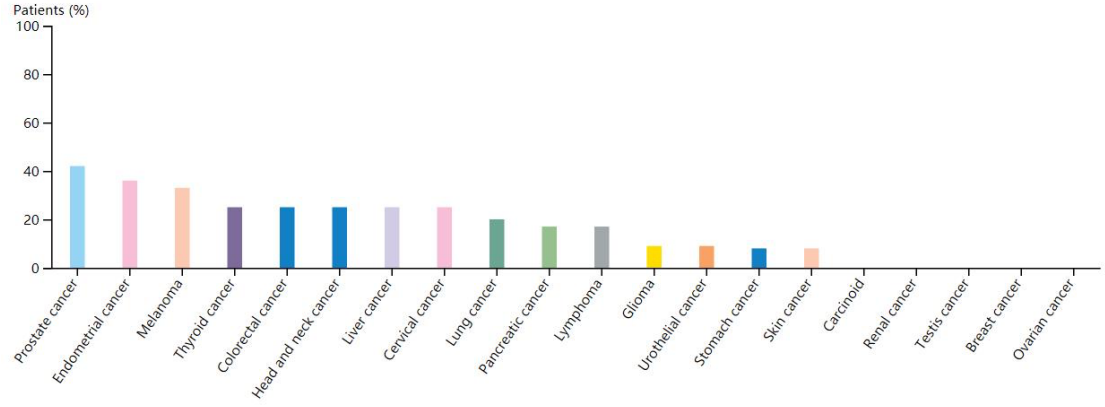



(B)



Supplementary Figure 2. FNDC3B expression profiles in human tissues and cancer cell lines. (A) The protein expression profiles of FNDC3B in human cancer tissues. (B) FNDC3B expression profiles in normal human tissues. (C) The expression of FNDC3B in glioma cell lines analyzed by Cancer Cell Line Encyclopedia (CCLE).

(A)

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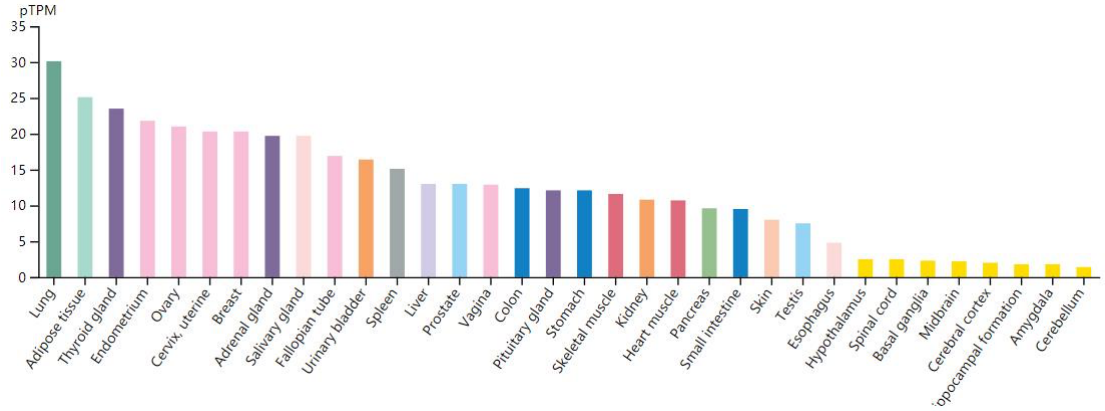


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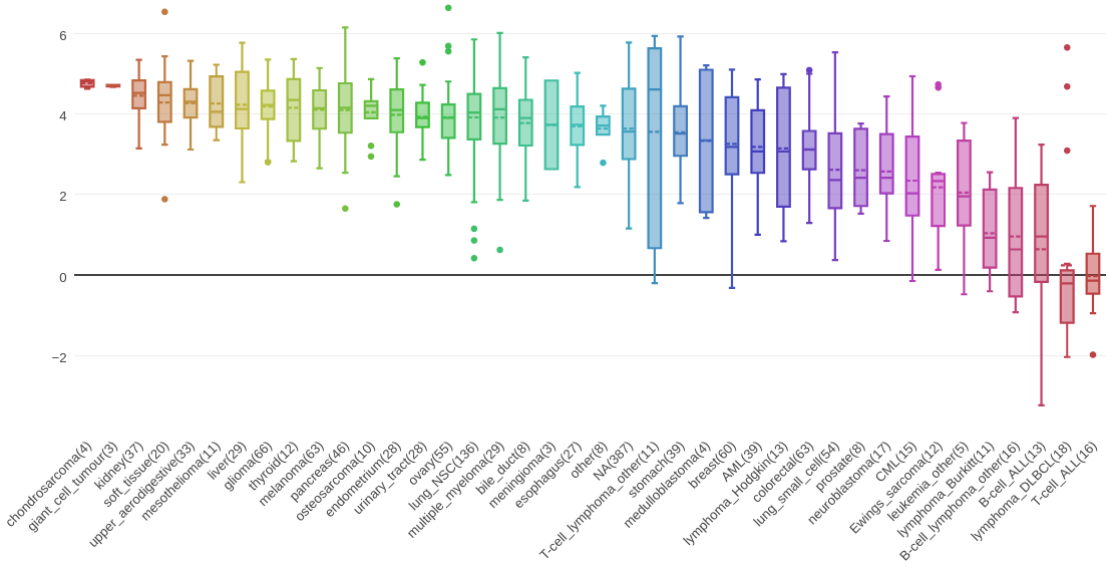
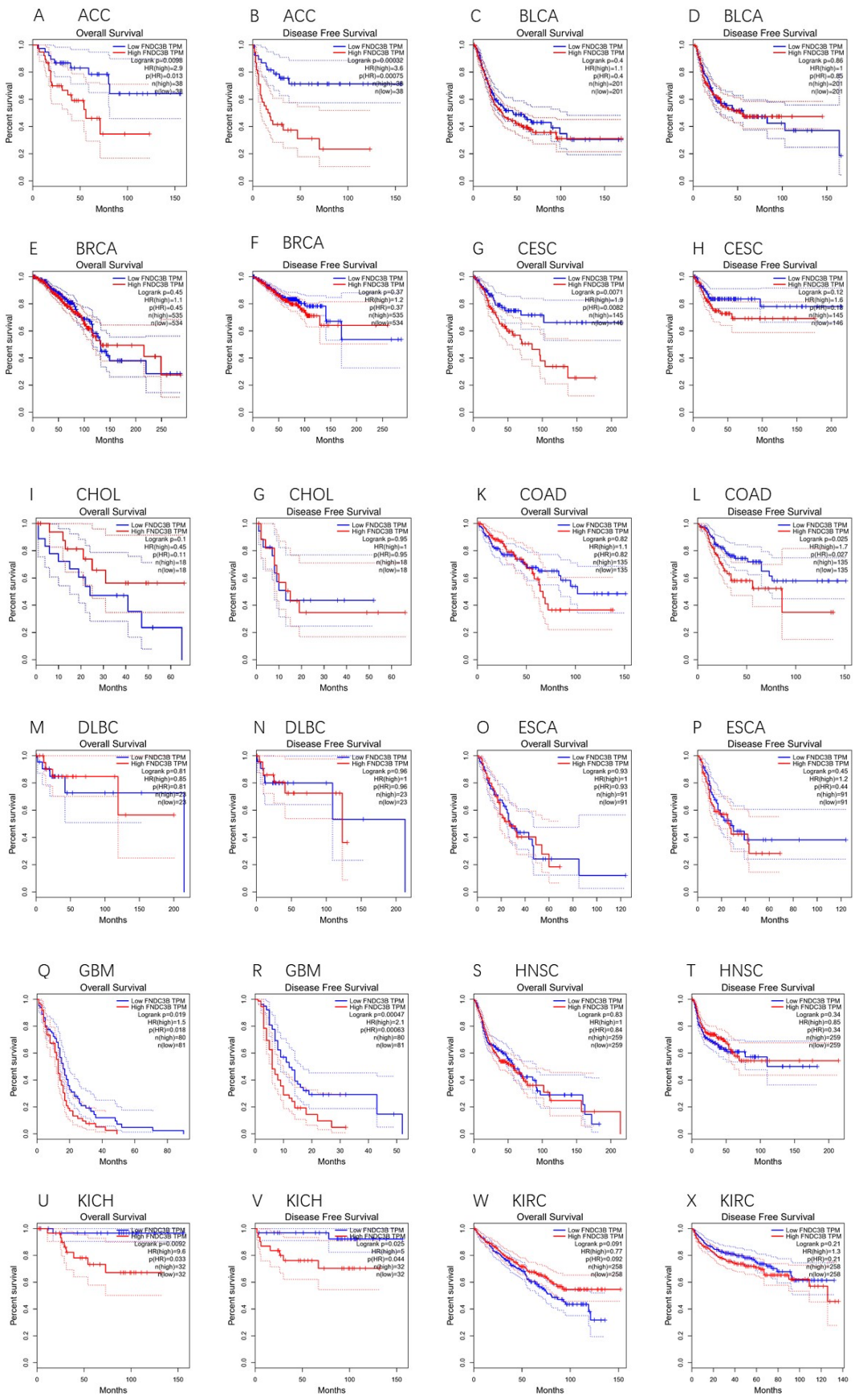
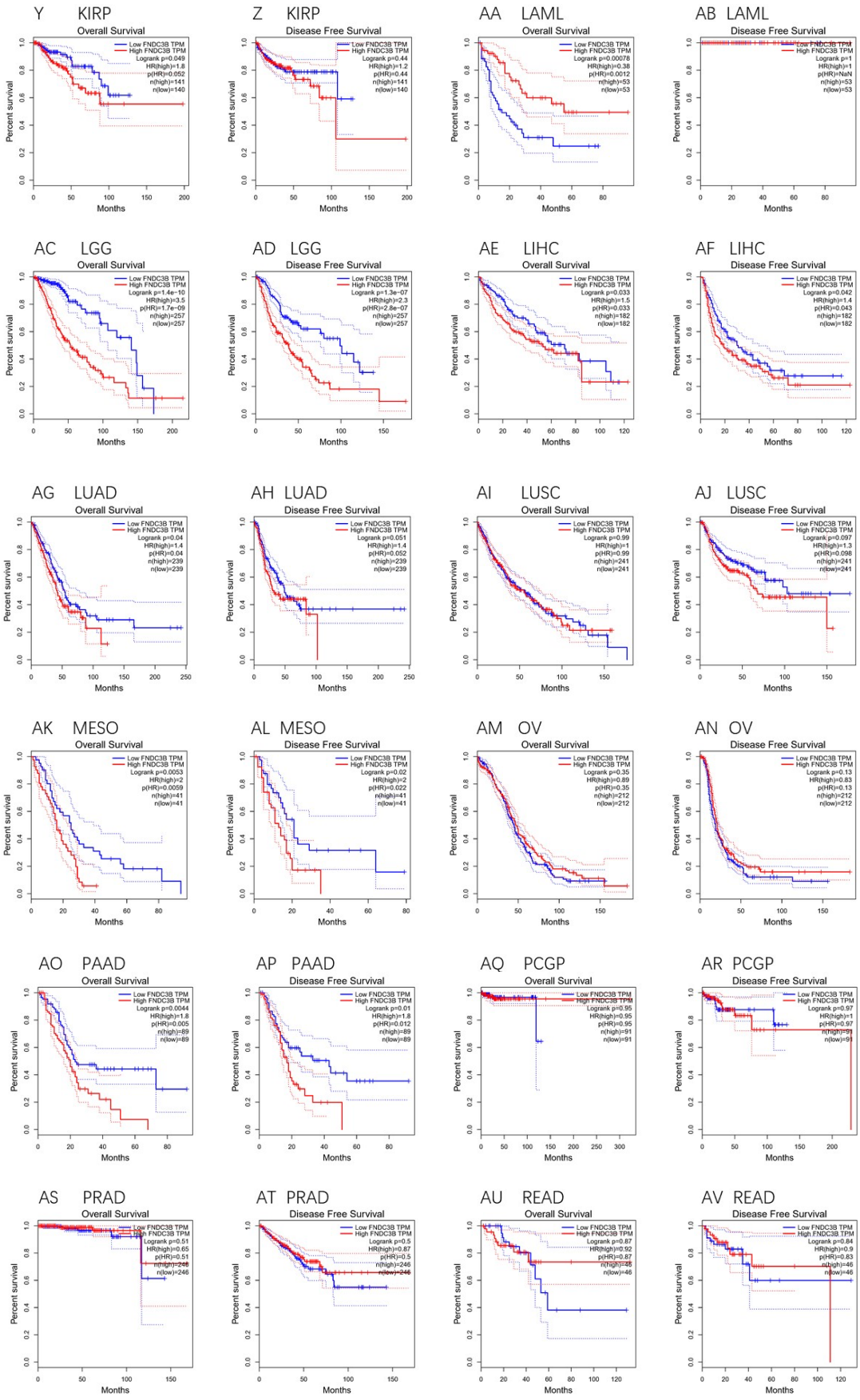


Supplementary Figure 3. Correlation of FNDC3B expression with prognostic values in diverse types of cancer. Overall survival and disease free curves comparing the high and low expression of FNDC3B in (A-B) Adrenocortical carcinoma (ACC), (C-D) Bladder Urothelial Carcinoma (BLCA), (E-F) Breast invasive carcinoma (BRCA), (G-H) Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), (I-J) Cholangio carcinoma (CHOL), (K-L) Colon adenocarcinoma (COAD), (M-N) Lymphoid Neoplasm Diffuse Large B-cell Lymphoma (DLBC), (O-P) Esophageal carcinoma (ESCA), (QR) Glioblastoma multiforme (GBM), (S-T) Head and Neck squamous cell carcinoma (HNSC), (U-V) Kidney Chromophobe (KICH), (W-X) Kidney renal clear cell carcinoma (KIRC), (Y-Z) Kidney renal papillary cell carcinoma (KIRP), (AA-AB) Acute Myeloid Leukemia (LAML), (AC-AD) Brain Lower Grade Glioma (LGG), (AE-AF) Liver hepatocellular carcinoma (LIHC), (AG-AH) Lung adenocarcinoma (LUAD), (AI-AJ) Lung squamous cell carcinoma (LUSC), (AK-AL) Mesothelioma (MESO), (AM-AN) Ovarian serous cystadenocarcinoma (OV), (AO-AP) Pancreatic adenocarcinoma (PAAD), (AQ-AR) Pheochromocytoma and Paraganglioma (PCPG), (AS-AT) Prostate adenocarcinoma (PRAD), (AU-AV) Rectum adenocarcinoma (READ), (AW-AX) Sarcoma (SARC), (AY-AZ) Skin Cutaneous Melanoma (SKCM), (BA-BB) Stomach adenocarcinoma (STAD), (BC-BD) Testicular Germ Cell Tumors (TGCT), (BE-BF) Thyroid carcinoma (THCA), (BG-BH) Thymoma (THYM), (BI-BJ) Uterine Corpus Endometrial Carcinoma (UCEC), (BK-BL) Uterine Carcinosarcoma (UCS), (BM-BN) Uveal Melanoma (UVM).


A ACC
Overall Survival
B ACC
Disease Free Survival
C BLCA
Overall Survival
D BLCA
Disease Free Survival
E BRCA
Overall Survival
F BRCA
Disease Free Survival
G CESC
Overall Survival
H CESC
Disease Free Survival
I CHOL
Overall Survival
G CHOL
Disease Free Survival
K COAD
Overall Survival
L COAD
Disease Free Survival
M DLBC
Overall Survival
N DLBC
Disease Free Survival
O ESCA
Overall Survival
P ESCA
Disease Free Survival
Q GBM
Overall Survival
R GBM
Disease Free Survival
S HNSC
Overall Survival
T HNSC
Disease Free Survival
U KICH
Overall Survival
V KICH
Disease Free Survival
W KIRC
Overall Survival
X KIRC
Disease Free Survival
Percent survival
Months
Low FNDC3B TPM
High FNDC3B TPM


Y KIRP
Overall Survival
Z KIRP
Disease Free Survival
AA LAML
Overall Survival
AB LAML
Disease Free Survival
AC LGG
Overall Survival
AD LGG
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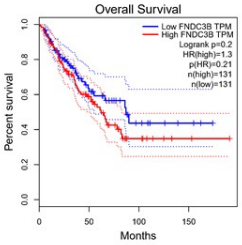
AE LIHC
Overall Survival
AF LIHC
Disease Free Survival
AG LUAD
Overall Survival
AH LUAD
Disease Free Survival
AI LUSC
Overall Survival
AJ LUSC
Disease Free Survival
AK MESO
Overall Survival
AL MESO
Disease Free Survival
AM OV
Overall Survival
AN OV
Disease Free Survival
AO PAAD
Overall Survival
AP PAAD
Disease Free Survival
AQ PCGP
Overall Survival
AR PCGP
Disease Free Survival
AS PRAD
Overall Survival
AT PRAD
Disease Free Survival
AU READ
Overall Survival
AV READ
Disease Free Survival
Percent survival
Months
Low FNDC3B TPM
High FNDC3B TPM

AW SARC

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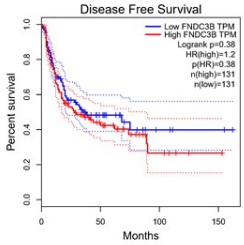


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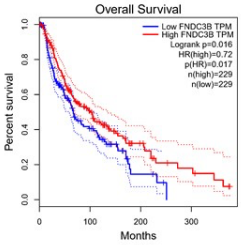


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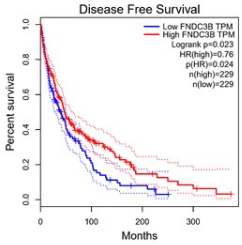


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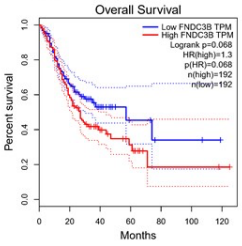


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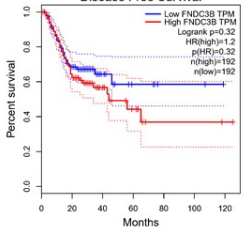


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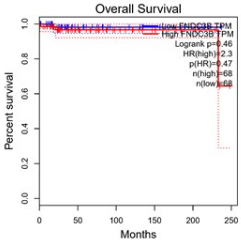


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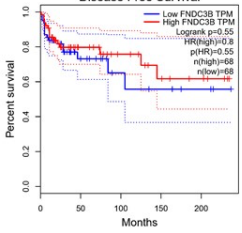
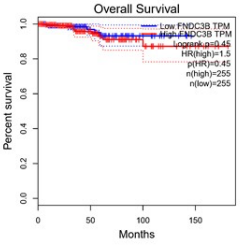



BE THCA

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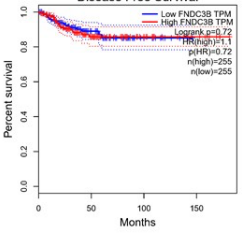
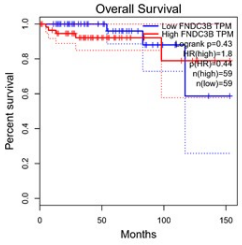



BG THYM

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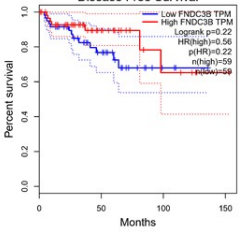


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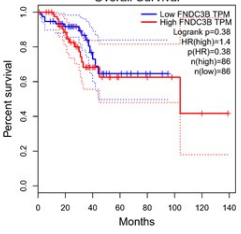


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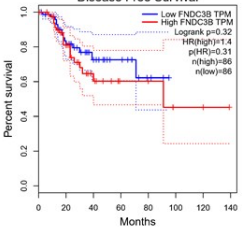


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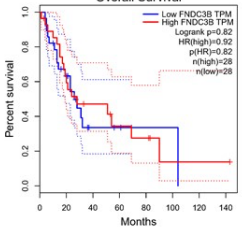


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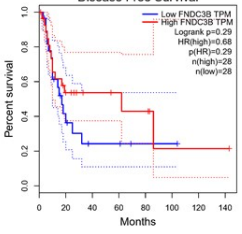


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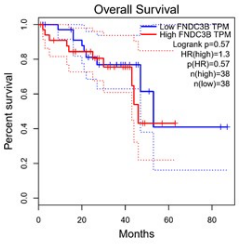


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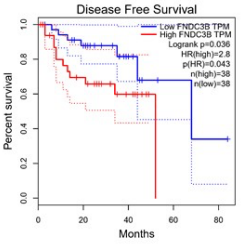
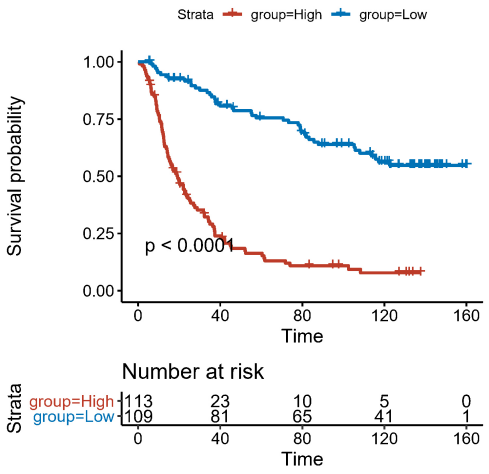


Supplementary Figure 4. Kaplan-Meier analysis of overall survival (OS) based on high vs low expression of FNDC3B in pan-glioma patients in the CGGA data sets. (A) mRNAseq_325 data set; (B) mRNAseq_693 data set; (C) mRNA_array_301 data set. The red curve represents patients with high expression of FNDC3B, and the blue curve represents patients with low expression of FNDC3B.

(A)

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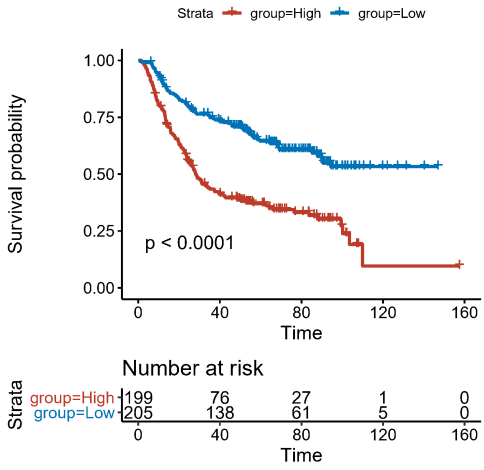


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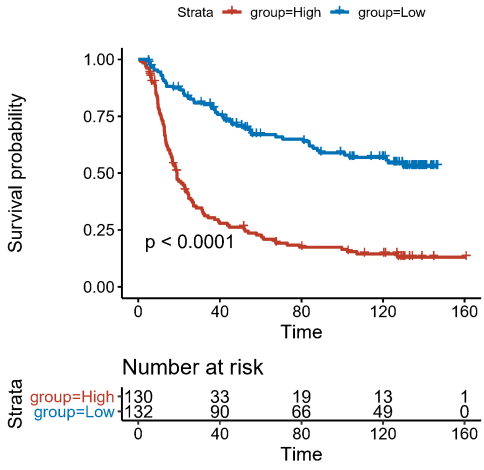
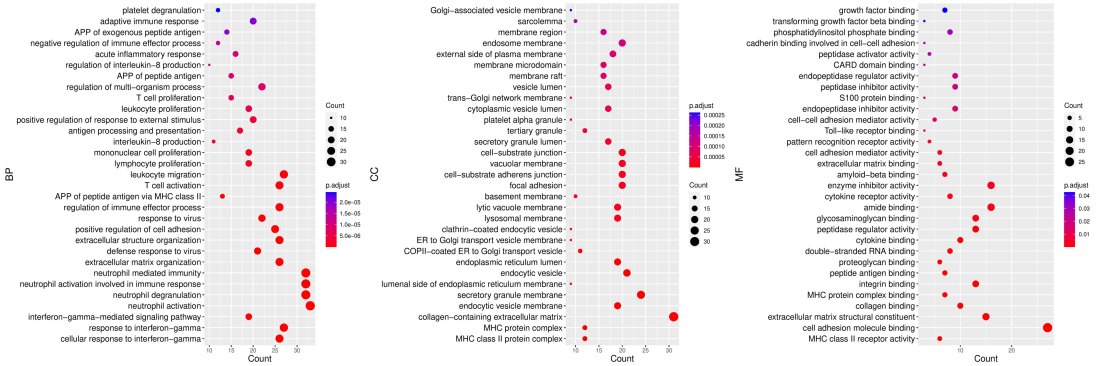
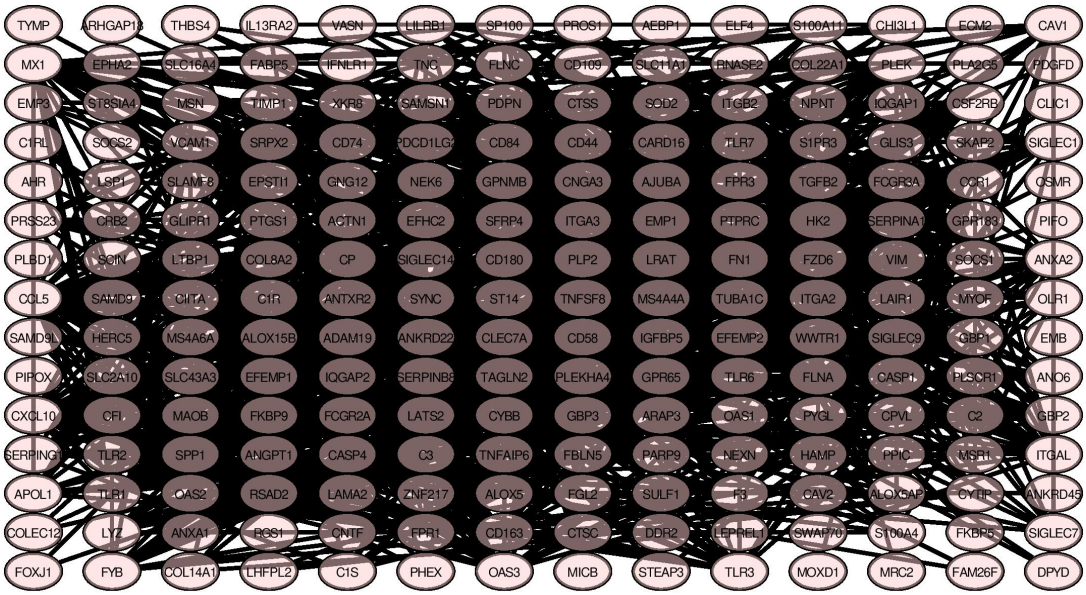


Supplementary Figure 5. Gene ontology (GO) functional annotation and hub gene analysis for the turquoise module. The top GO terms in the enrichment analysis.



Supplementary Figure 6. 210 genes remained in the PPI network construction for the turquoise module. A total of 210 nodes and 1,061 edges were mapped for the turquoise module genes in the PPI network.



Supplementary Figure 7. High expression of the hub genes predicts shorter overall survival (OS) of low-grade glioma (LGG) patients. Kaplan-Meier curves showed that LGG patients with high expression of TLR2 (A), TLR7 (B), PTPRC (C), CCR1 (D), CCL5 (E), TLR1 (F), FN1 (G), VCAM1 (H), CXCL10 (I), and TLR6 (J) had reduced OS.