

Figure S1. Validation and selection of key lncRNAs in gliomas. (a) Expression profiles of three lncRNAs in normal samples as well as in cases of both lower-grade glioma (LGG) and glioblastoma (GBM). (b) ROC curves of three lncRNAs in gliomas. (c-h) Kaplan-Meier curves for patients with high and low expression of NDUFA6-DT, LINC02802, and LINC02978 in LGG and GBM in the TCGA dataset. (i-l) Kaplan-Meier curves for patients with high and low expression of NDUFA6-DT and LINC02802 in LGG and GBM in the CGGA dataset. ** $p < 0.01$, *** $p < 0.0001$.

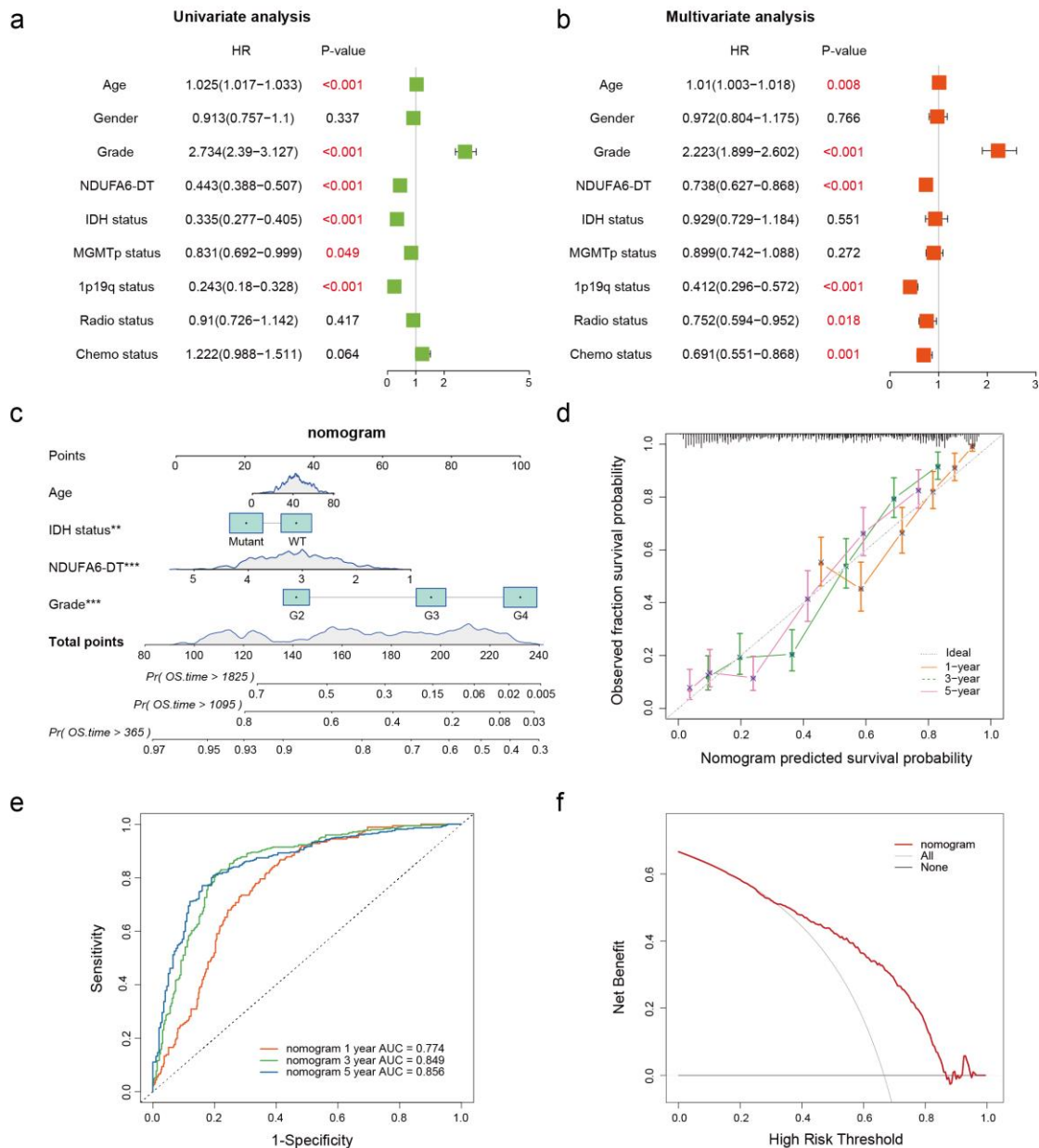


Figure S2. CGGA as an external validation dataset for constructing the nomogram. **(a-b)** Forest plots depicting univariate and multivariate Cox regression analyses of NDUFA6-DT with clinical characteristics in glioma. The red font indicates a variable with a value of $p < 0.05$. **(c)** A nomogram was constructed based on age, IDH mutation status, NDUFA6-DT expression, and disease grade. **(d)** Calibration curves for the nomogram were plotted at 1, 3, and 5 years. **(e)** ROC curves for the nomogram were generated at 1, 3, and 5 years. **(f)** The Decision curves for the nomogram. ** $p < 0.01$, *** $p < 0.001$.

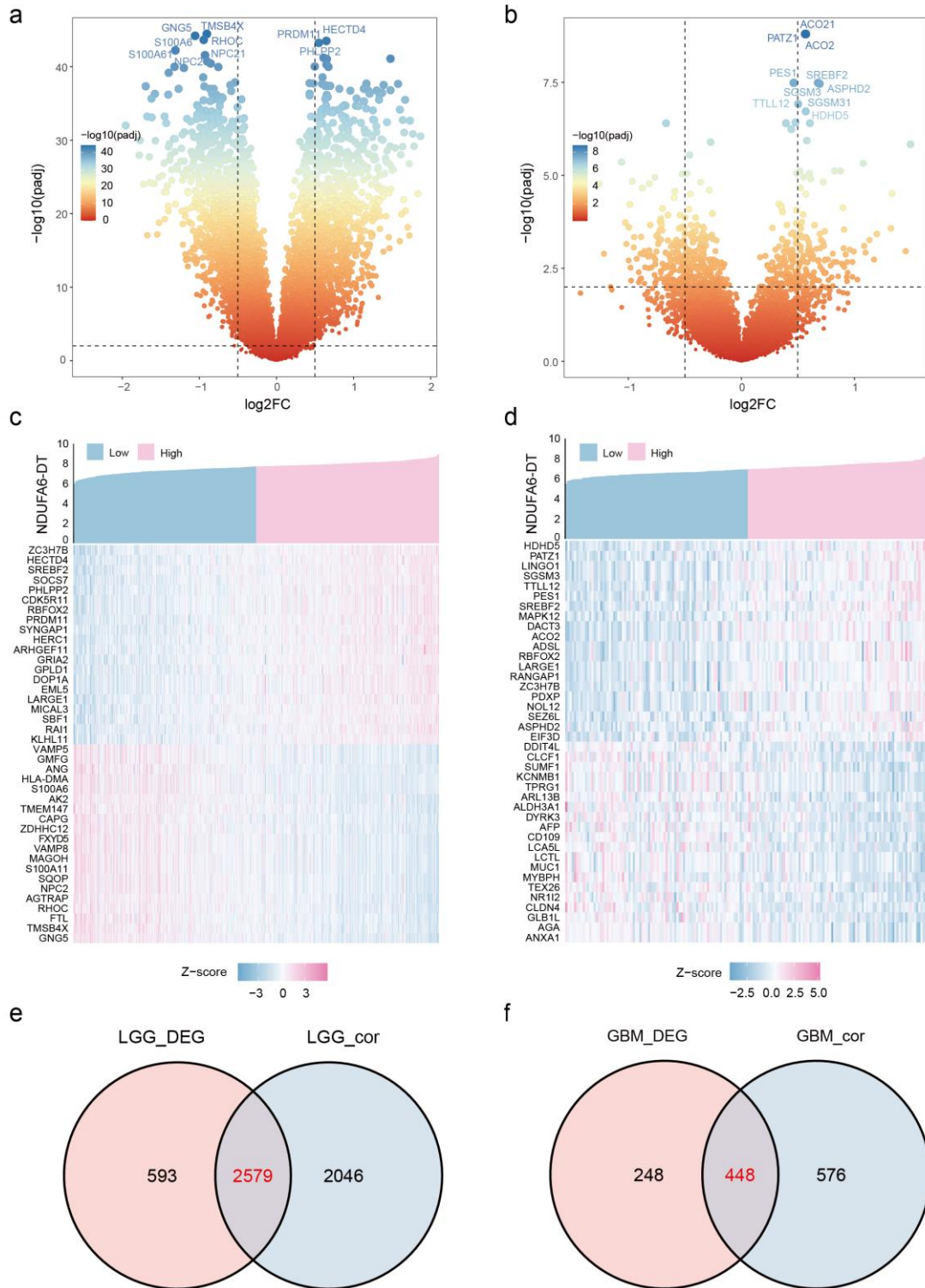
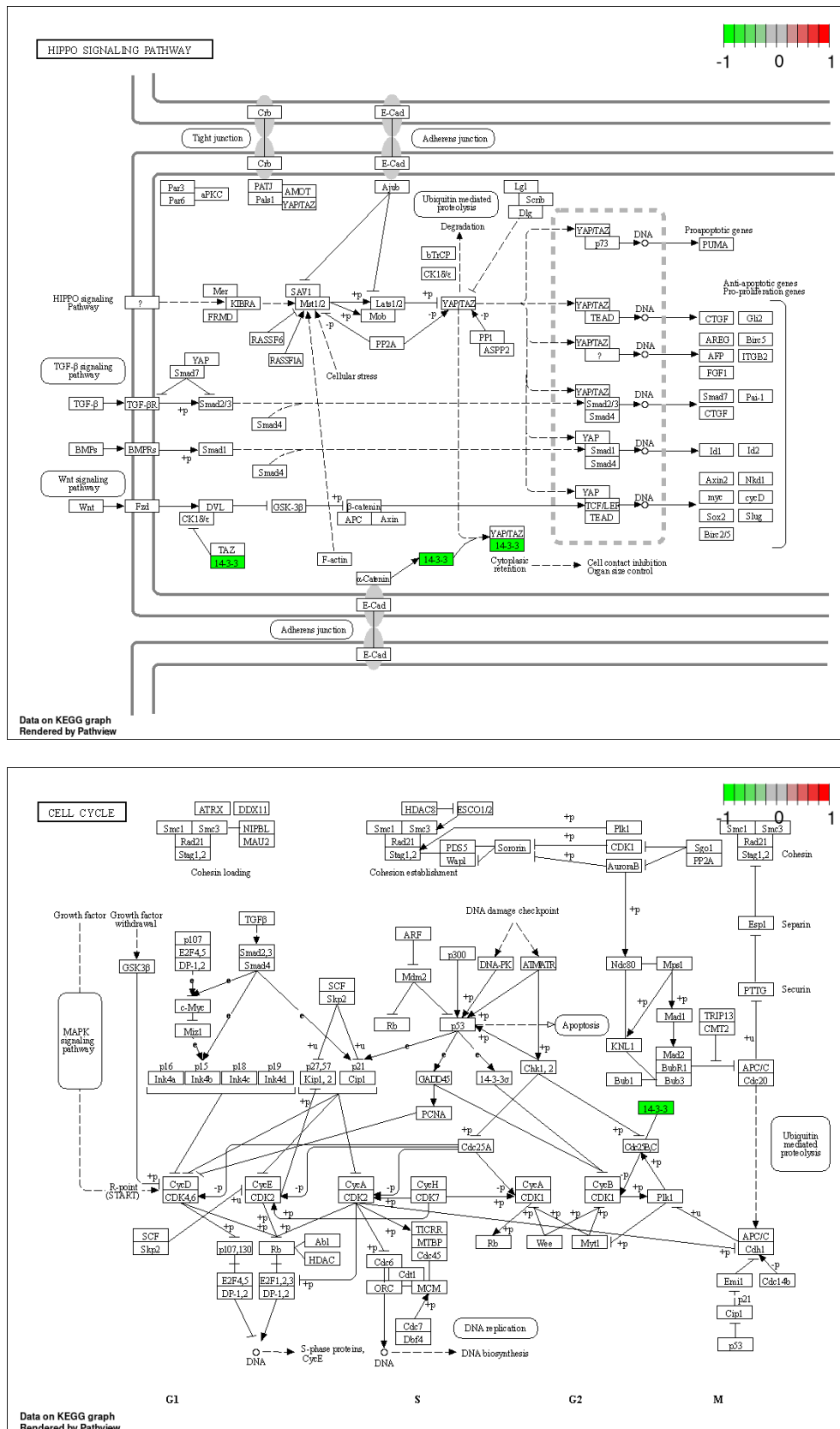


Figure S3. Co-expressed genes of NDUFA6-DT in gliomas. **(a-b)** Volcano plots depict differential expression analysis in high and low expression groups of NDUFA6-DT in LGG and GBM. **(c-d)** Heatmaps illustrate correlation analysis of NDUFA6-DT in LGG and GBM, with the top 20 genes positively correlated and the bottom 20 genes negatively correlated. **(e-f)** Venn diagrams show the intersection of differentially expressed and correlated genes as co-expressed genes with NDUFA6-DT in LGG and GBM.

The diagram illustrates the PI3K-AKT signaling pathway, showing the flow of information from various receptors to downstream effectors. Key components include:

- Upstream Activators:** RTK, GPCR, TLRs, BCR, JAK/STAT, Cytokine, Focal adhesion, Chemokine signaling.
- Core Pathway:** PI3K (Class I & II) → AKT → mTOR, GSK3, p21, p27, FOXO, BAD, CREB, IKK, MEK.
- Downstream Targets:** p4, p5, p7, p13, p15, p16, p18, p19, p20, p21, p27, p30, p31, p32, p33, p34, p35, p36, p37, p38, p39, p40, p41, p42, p43, p44, p45, p46, p47, p48, p49, p50, p51, p52, p53, p54, p55, p56, p57, p58, p59, p60, p61, p62, p63, p64, p65, p66, p67, p68, p69, p70, p71, p72, p73, p74, p75, p76, p77, p78, p79, p80, p81, p82, p83, p84, p85, p86, p87, p88, p89, p90, p91, p92, p93, p94, p95, p96, p97, p98, p99, p100.
- Cellular Processes:** Metabolism, Cell cycle, Cell survival, Apoptosis, NF-κB signaling, p53 signaling.

Data on KEGG graph
Rendered by Biohazard



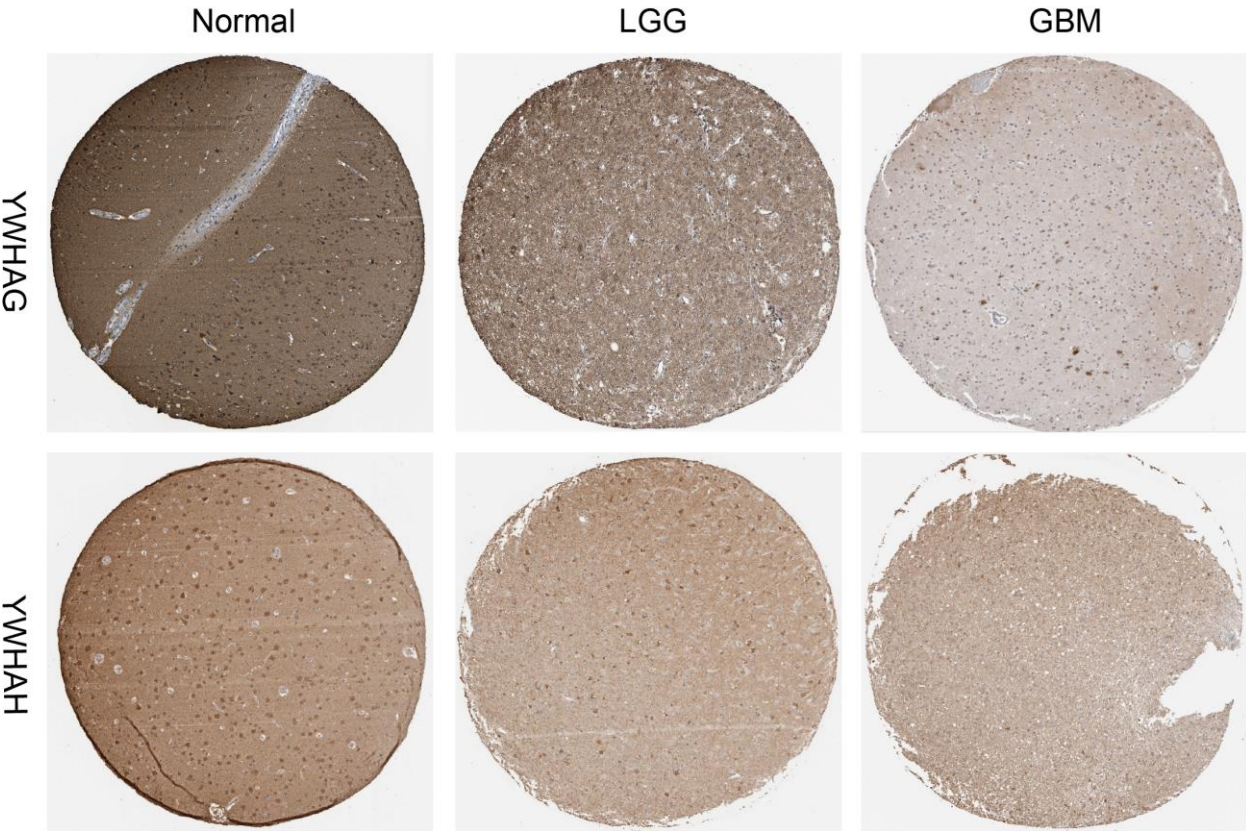


Figure S6. IHC staining plots of NDUFA6-DT-regulated downstream molecules YWHAG and YWHAH in normal brain, LGG and GBM from the HPA database.

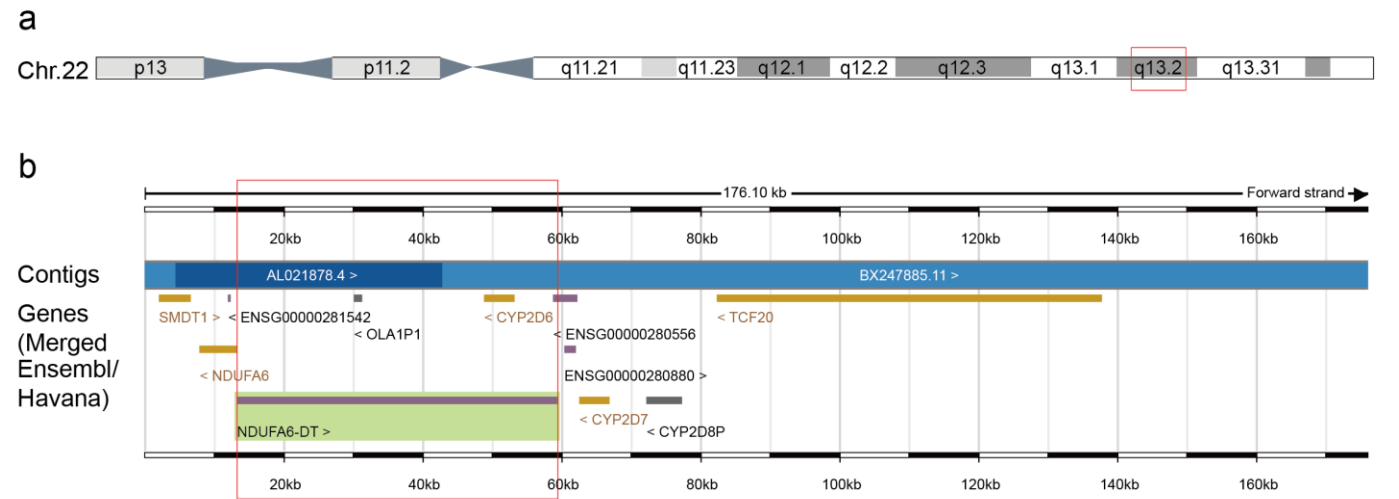


Figure S7. Sequence information of NDUFA6-DT. (a) Genomic location of NDUFA6-DT. (b) Length of NDUFA6-DT and nearby genes.