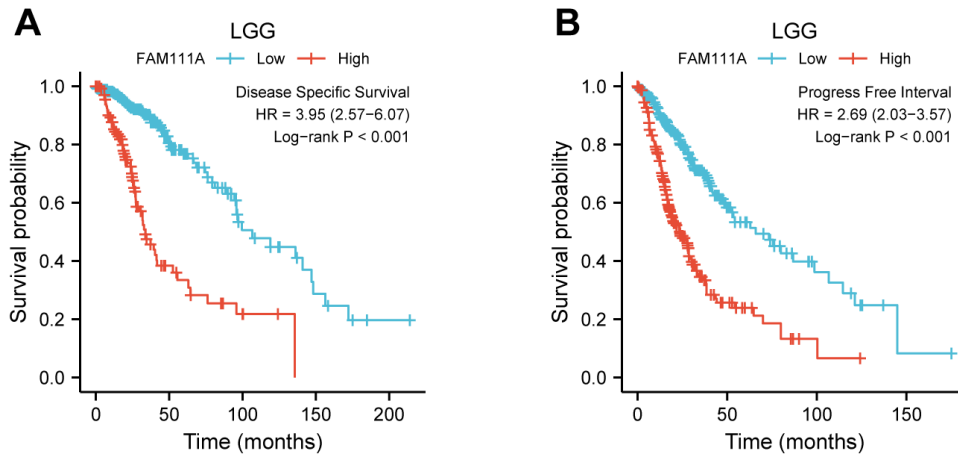
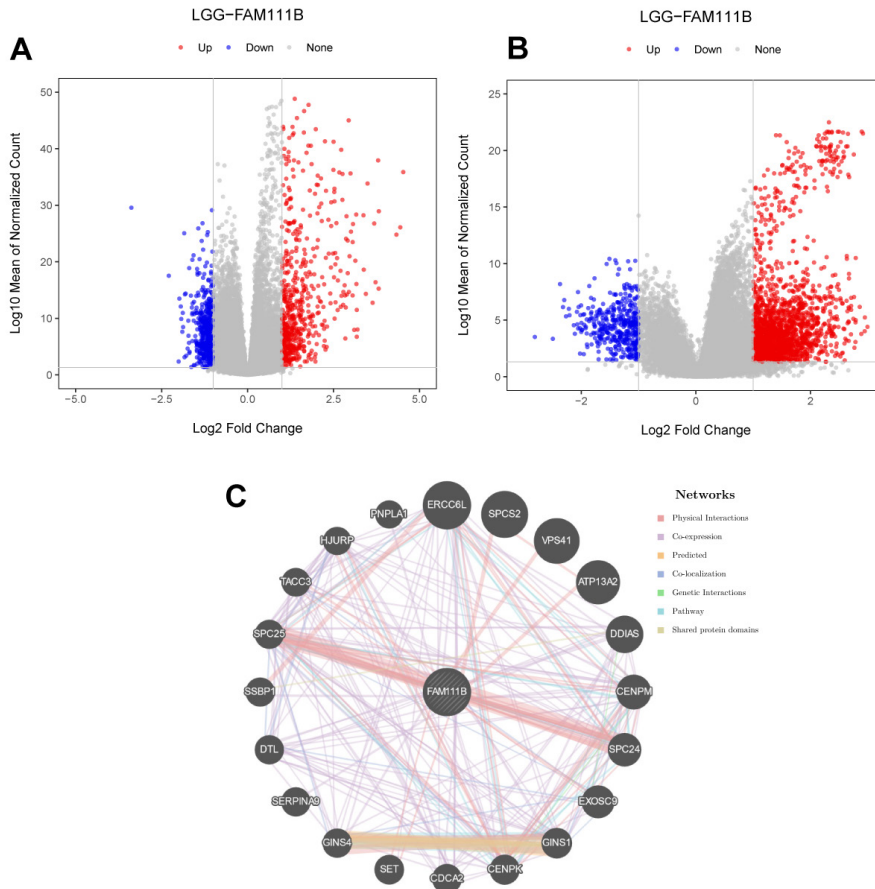


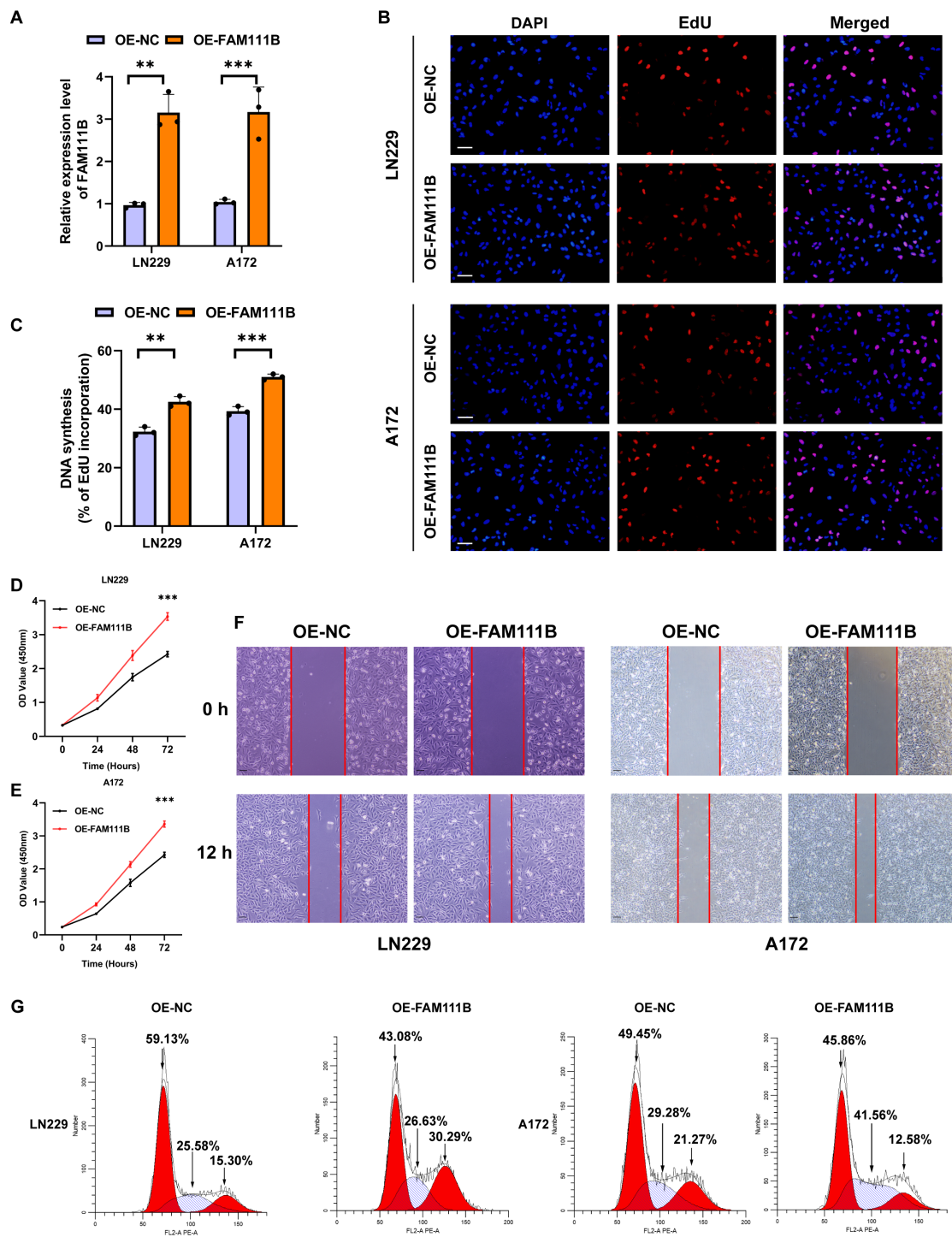
**Figure S1** Expression of FAM111B in different stages of 11 tumor types, including ESAD (A), OSCC (B), PAAD (C), LUAD (D), UCEC (E), THYM (F), THCA (G), MESO (H), KIRP (I), ACC (J), and LIHC (K). ACC, Adrenocortical carcinoma; ESAD, esophageal carcinoma; FAM111B, FAM111 trypsin-like peptidase B; FPKM, fragments per kilobase of transcript per million mapped reads; KIRP, Kidney Renal Papillary Cell Carcinoma; LIHC, Liver Hepatocellular Carcinoma; LUAD, Lung adenocarcinoma; MESO, Mesothelioma; ns, not significant; PAAD, Pancreatic adenocarcinoma; THCA, Thyroid carcinoma; THYM, Thymoma; UCEC, Uterine corpus endometrial carcinoma.



**Figure S2** The disease specific survival (DSS) (A) and progress free interval (PFI) (B) of LGG with different expression levels of FAM111B.



**Figure S3** The differential genes (DEGs) and PPI network analysis. The DEGs in the high and low expression groups of FAM111B in TCGA (A) and CGGA (B) dataset. (C) The potential interaction molecular network of FAM111B was built using the GeneMANIA. CGGA, Chinese Glioma Genome Atlas; TCGA, The Cancer Genome Atlas.



**Figure S4** Effects of FAM111B overexpression on glioma cell proliferation, migration, and cell cycle. (A,C) Real time PCR detected the efficiency of FAM111B overexpression in LN229 and A172 cells. (B) Ethynyldeoxyuridine (EdU) Assay analysis was performed to determine the cell proliferation. Scale bar: 100  $\mu$ m. (D,E) Cell viability was monitored by Cell Counting Kit-8 (CCK8). (F) Scratch test was used to determine the cell migration. Scale bar: 200  $\mu$ m. (G) Flow cytometry was used to detect the cell cycle. Two-tailed Student's *t*-test, \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ .

**Table S1** Sample information from TCGA and CGGA

Characteristics	TCGA	CGGA
n	529	182
Grade, n		
G3	243	79
G2	224	103
IDH status, n		
WT	97	48
Mut	429	133
1p/19q codeletion, n		
Non-codel	358	120
Codel	171	60

CGGA, Chinese Glioma Genome Atlas; IDH, isocitrate dehydrogenase; TCGA, The Cancer Genome Atlas.