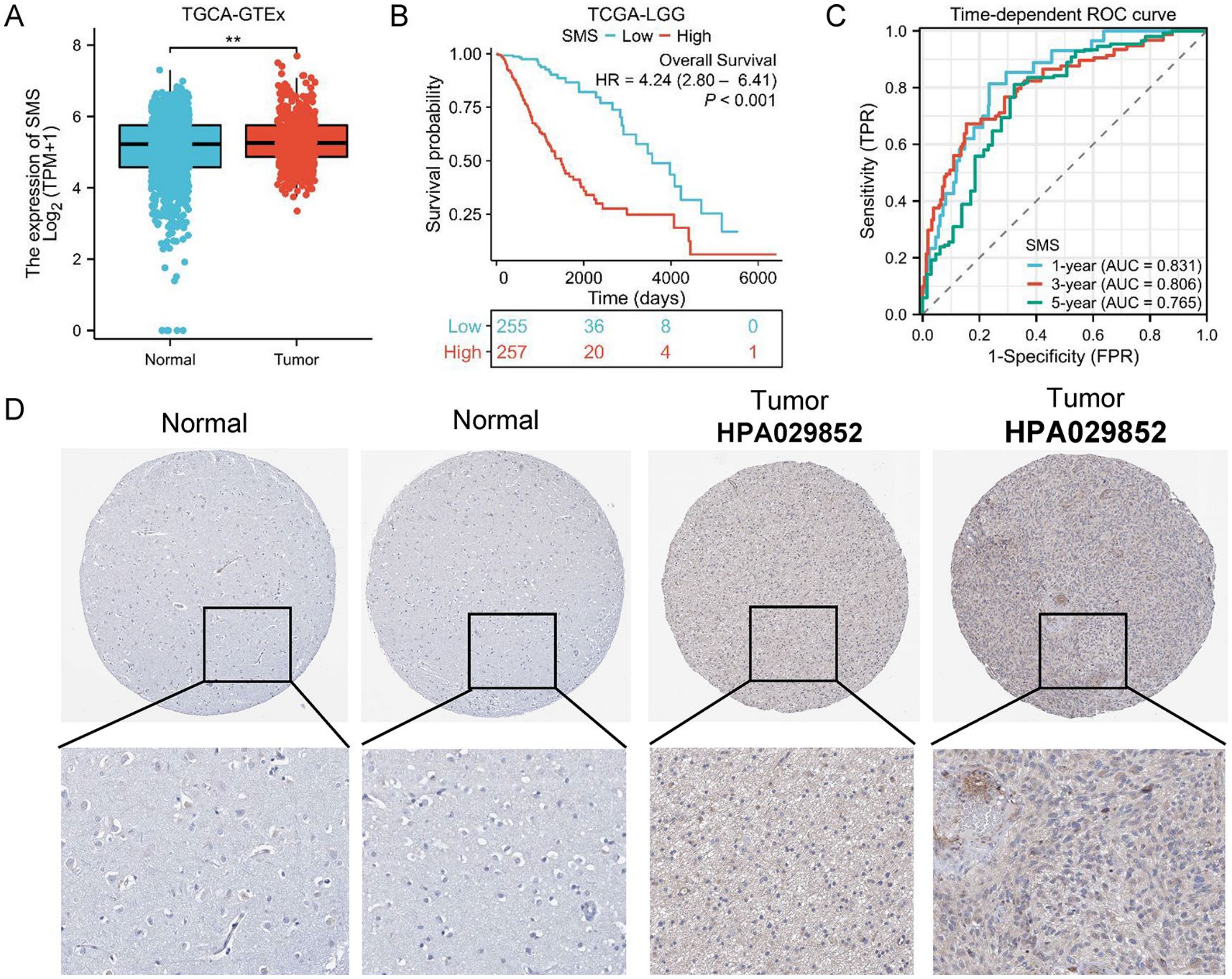

Figure S1 (A) Differential mRNA expression of SMS in tumor and normal tissues. (B) Prognostic differences between high and low expression subgroups of SMS in the TCGA-LGG cohort. (C) Time-dependent ROC curves at 1,3,5 years for predicting LGG patients based on SMS expression. (D) SMS in both normal and tumor tissues sourced from the Human Protein Atlas database (https://www.proteinatlas.org/). Image credit goes to The Human Protein Atlas. The links to the individual normal and tumor tissues of each protein are provided for SMS. SMS-Normal (https://www.proteinatlas.org/ENSG00000102172-SMS/tissue/cerebral+cortex#img), SMS-Tumor (https://www.proteinatlas.org/ENSG00000102172-SMS/cancer/glioma#img), respectively. Visualized with DAB, and counter-stained with hematoxylin, 20×, magnification.

Table S1 Polyamine metabolism genes

Reactome metabolism of polyamines
AGMAT
AMD1
AZIN1
AZIN2
NQO1
OAZ1
OAZ2
OAZ3
ODC1
PAOX
PSMA1
PSMA2
PSMA3
PSMA4
PSMA5
PSMA6
PSMA7
PSMA8
PSMB1
PSMB10
PSMB11
PSMB2
PSMB3
PSMB4
PSMB5
PSMB6
PSMB7
PSMB8
PSMB9
PSMC1
PSMC2
PSMC3
PSMC4
PSMC5
PSMC6
PSMD1
PSMD10
PSMD11
PSMD12
PSMD13
PSMD14
PSMD2
PSMD3
PSMD4
PSMD5
PSMD6
PSMD7
PSMD8
PSMD9
PSME1
PSME2
PSME3
PSME4
PSMF1
SAT1
SEM1
SMOX
SMS
SRM

https://dx.doi.org/10.21037/tcr-2025-776