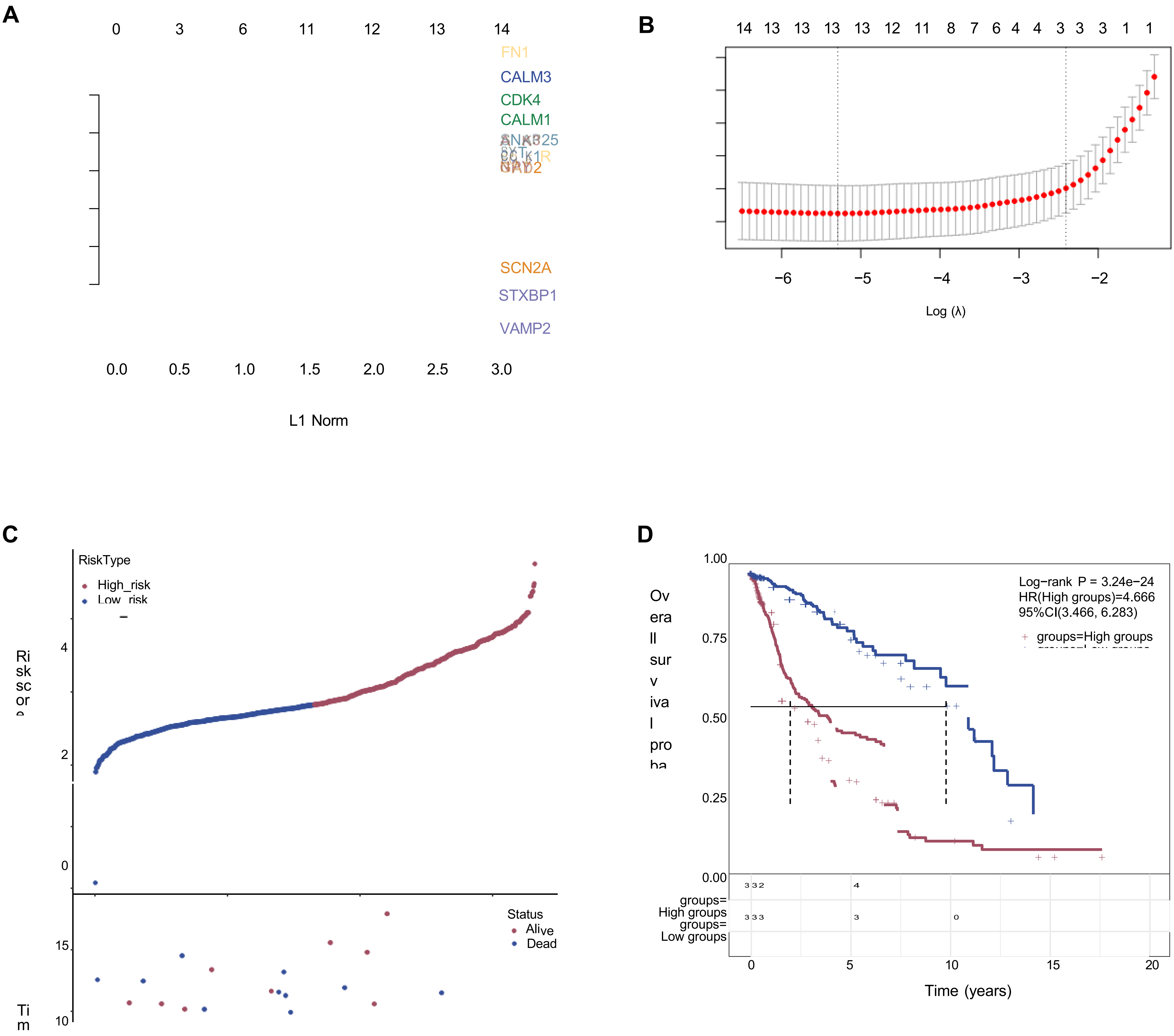
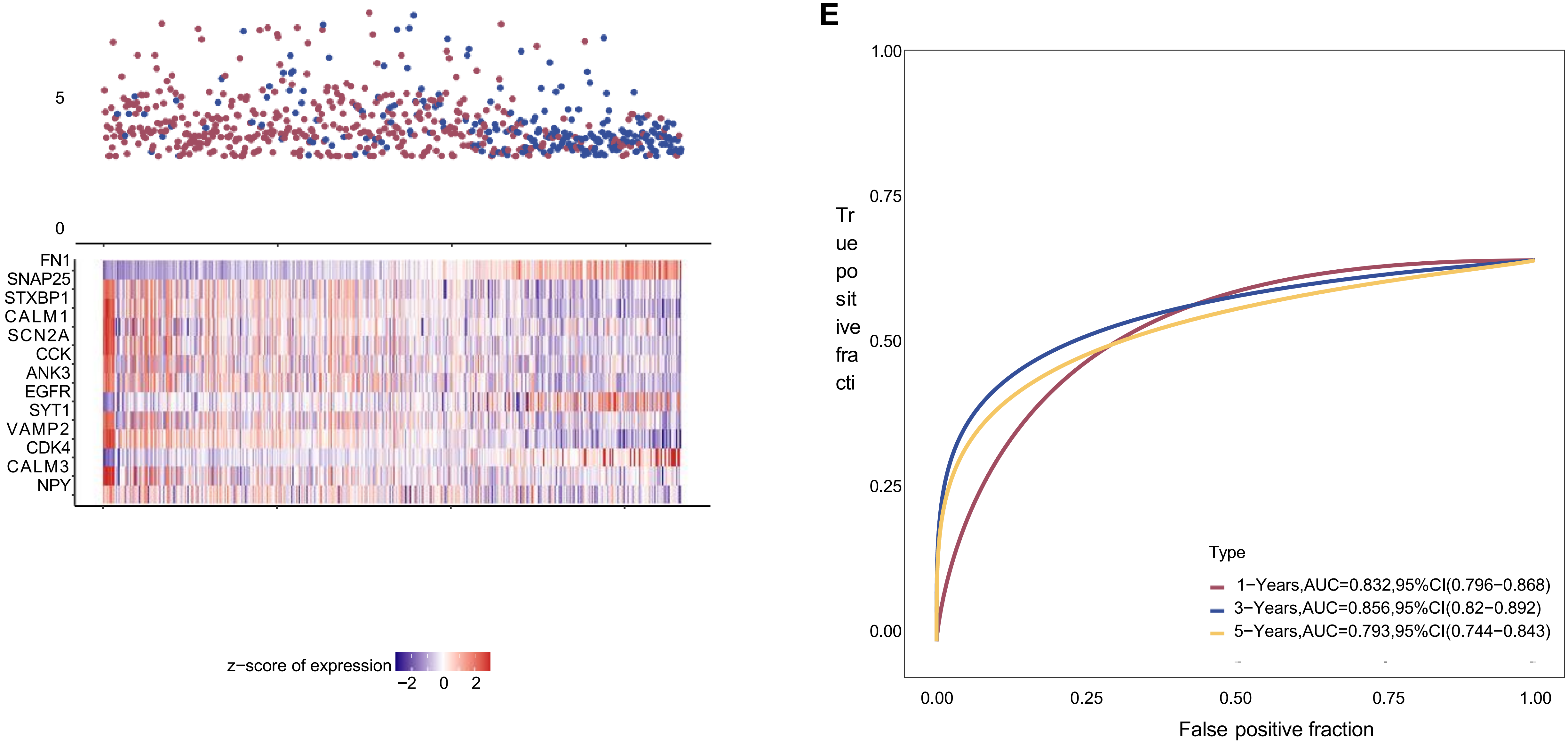

A
0
3
6
11
12
13
14
FN1
CALM3
CDK4
CALM1
SNAP25
OXT
CCK1R
GAD2
SCN2A
STXBP1
VAMP2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
L1 Norm
B
14 13 13 13 13 12 11 8 7 6 4 4 3 3 3 1 1
−6
−5
−4
−3
−2
Log (λ)
C
RiskType
High_risk
Low_risk
Risk score
4
2
0
Status
Alive
Dead
15
10
Tim
D
1.00
0.75
0.50
0.25
0.00
Overall survival proba
Log−rank P = 3.24e−24
HR(High groups)=4.666
95%CI(3.466, 6.283)
groups=High groups
groups=Low groups
332
4
333
3
0
groups=
High groups
groups=
Low groups
0
5
10
15
20
Time (years)



Supplementary Figure S3. Identification and prognostic assessment of 13 characteristic genes of glioma. **A** – least absolute shrinkage and selection operator (LASSO)-Cox regression model analysis of significant genes for OS prognosis. **B** – The relationship between 10-fold cross-validation partial likelihood deviation and log(λ). **C** – Risk model analysis of the selected sample data. The upper panel shows the risk samples, the middle panel shows the survival status, and the lower panel shows the heatmap of the clustering distribution of signature genes. **D** – Kaplan-Meier (KM) survival curve analysis of the two groups in the risk model. The red line indicates the high-risk group and the blue line indicates the low-risk group. **E** – Receiver operating characteristic (ROC) curve analysis on the risk model in patients at 1, 3, and 5 years. The horizontal coordinate is a false positive fraction, and the vertical coordinate is a true positive fraction