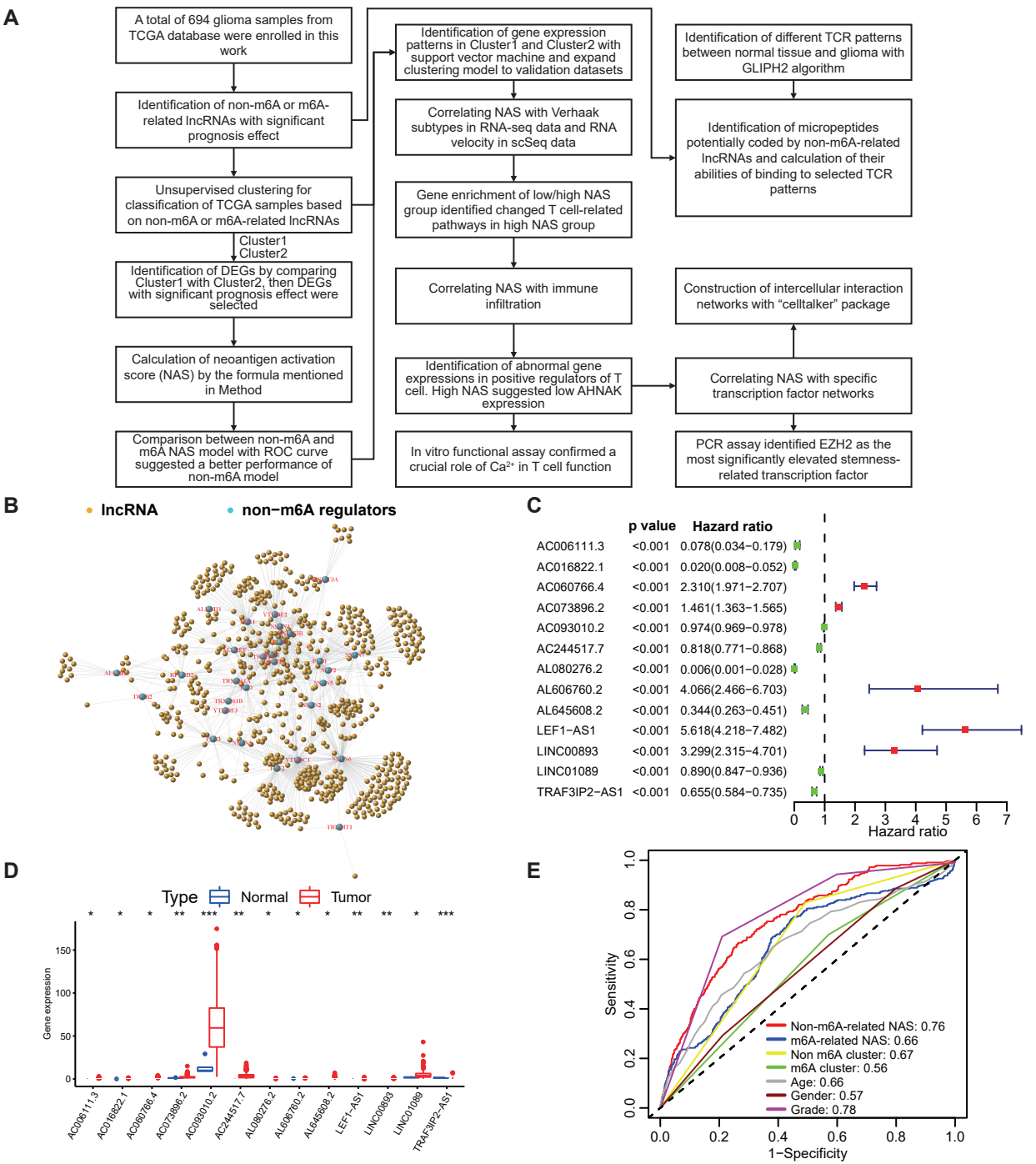
A
A total of 694 glioma samples from TCGA database were enrolled in this work
Identification of non-m6A or m6A-related lncRNAs with significant prognosis effect
Unsupervised clustering for classification of TCGA samples based on non-m6A or m6A-related lncRNAs
Cluster1
Cluster2
Identification of DEGs by comparing Cluster1 with Cluster2, then DEGs with significant prognosis effect were selected
Calculation of neoantigen activation score (NAS) by the formula mentioned in Method
Comparison between non-m6A and m6Â NAS model with ROC curve suggested a better performance of non-m6A model
Identification of gene expression patterns in Cluster1 and Cluster2 with support vector machine and expand clustering model to validation datasets
Correlating NAS with Verhaak subtypes in RNA-seq data and RNA velocity in scSeq data
Gene enrichment of low/high NAS group identified changed T cell-related pathways in high NAS group
Correlating NAS with immune infiltration
Identification of abnormal gene expressions in positive regulators of T cell. High NAS suggested low AHNAK expression
In vitro functional assay confirmed a crucial role of Ca2+ in T cell function
Identification of different TCR patterns between normal tissue and glioma with GLIPH2 algorithm
Identification of micropeptides potentially coded by non-m6A-related lncRNAs and calculation of their abilities of binding to selected TCR patterns
Construction of intercellular interaction networks with “celltalker” package
Correlating NAS with specific transcription factor networks
PCR assay identified EZH2 as the most significantly elevated stemness-related transcription factor
B
lncRNA
non−m6A regulators
C
p value
Hazard ratio
AC006111.3 <0.001 0.078(0.034−0.179)
AC016822.1 <0.001 0.020(0.008−0.052)
AC060766.4 <0.001 2.310(1.971−2.707)
AC073896.2 <0.001 1.461(1.363−1.565)
AC093010.2 <0.001 0.974(0.969−0.978)
AC244517.7 <0.001 0.818(0.771−0.868)
AL080276.2 <0.001 0.006(0.001−0.028)
AL606760.2 <0.001 4.066(2.466−6.703)
AL645608.2 <0.001 0.344(0.263−0.451)
LEF1−AS1 <0.001 5.618(4.218−7.482)
LINC00893 <0.001 3.299(2.315−4.701)
LINC01089 <0.001 0.890(0.847−0.936)
TRAF3IP2−AS1 <0.001 0.655(0.584−0.735)
0 1 2 3 4 5 6 7
Hazard ratio
D
Type
Normal
Tumor
Gene expression
0 50 100 150
AC006111.3
AC016822.1
AC060766.4
AC073896.2
AC093010.2
AC244517.7
AL080276.2
AL606760.2
AL645608.2
LEF1−AS1
LINC00893
LINC01089
TRAF3IP2−AS1
E
Sensitivity
1−Specificity
0.0 0.2 0.4 0.6 0.8 1.0
Non-m6A-related NAS: 0.76
m6A-related NAS: 0.66
Non m6A cluster: 0.67
m6A cluster: 0.56
Age: 0.66
Gender: 0.57
Grade: 0.78