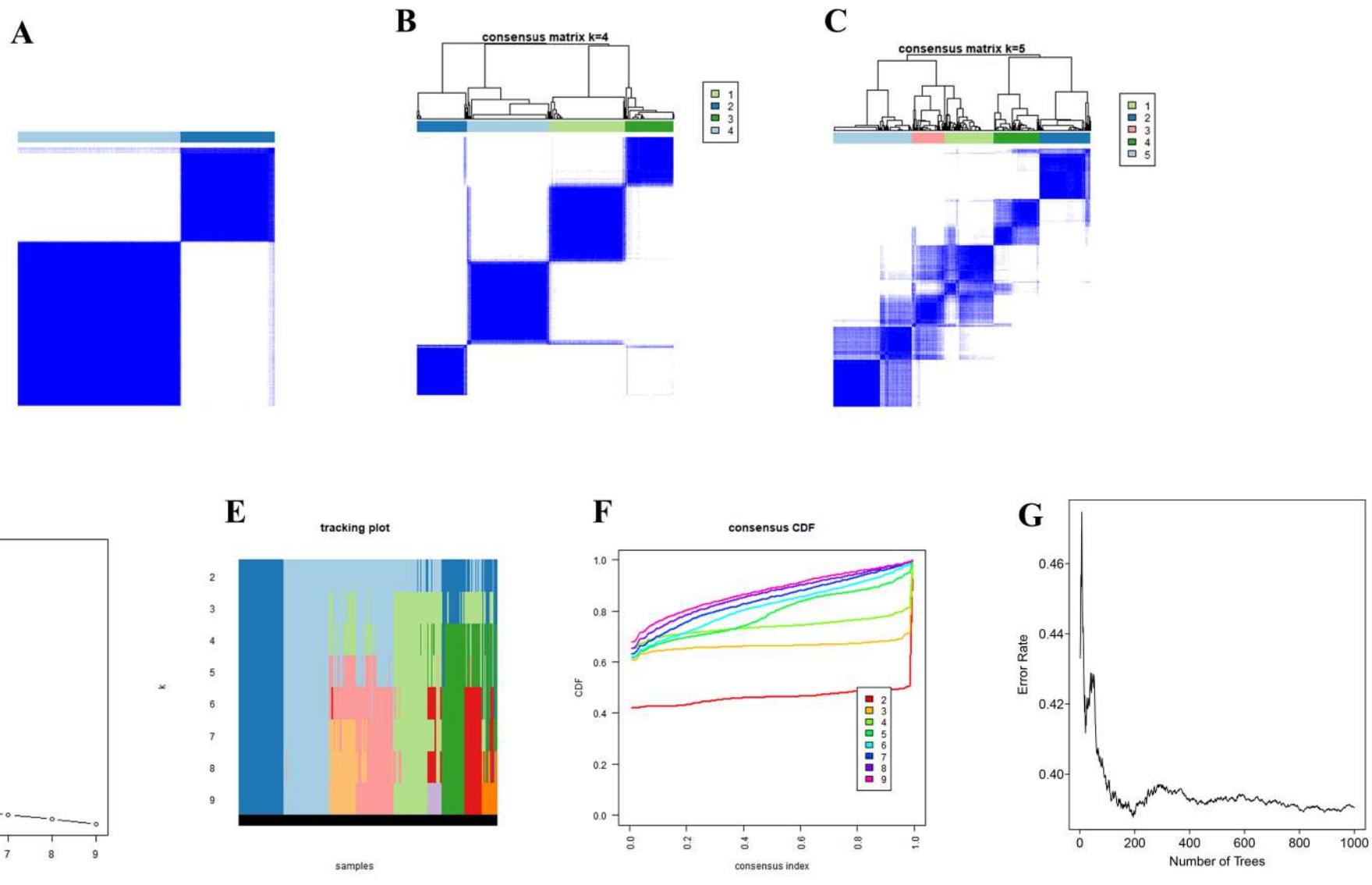
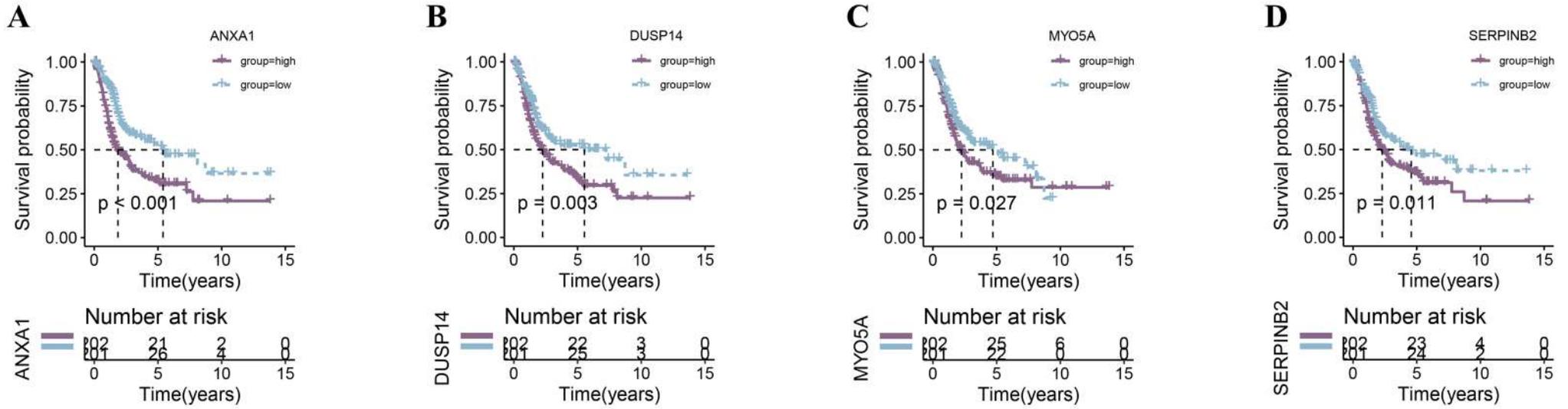


# Supplementary Figure S1.



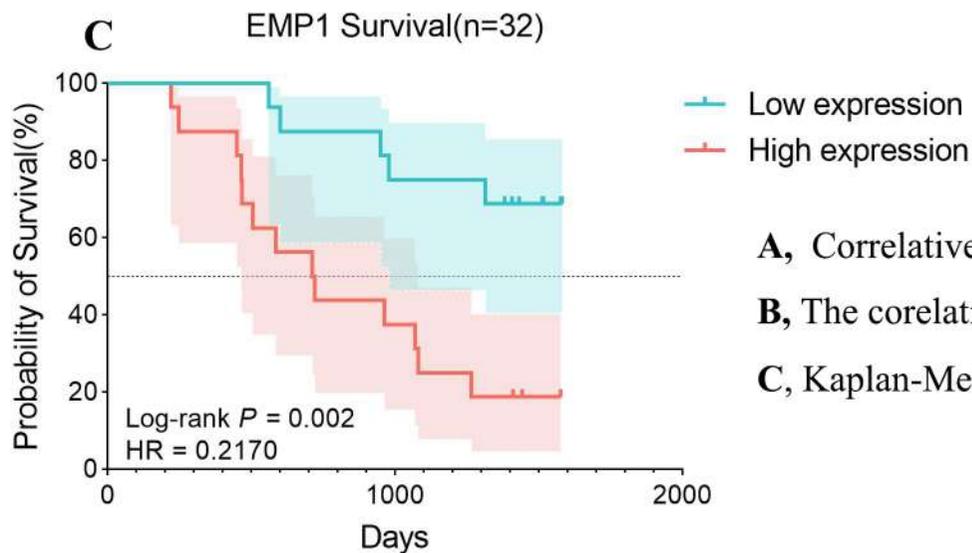
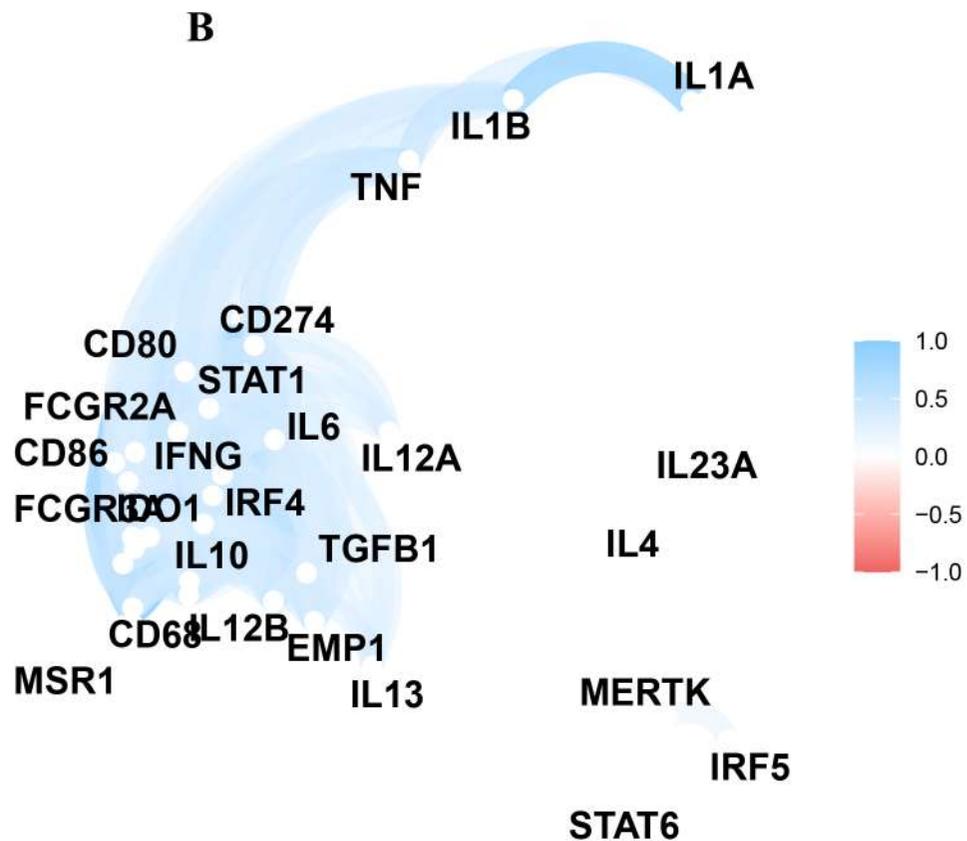
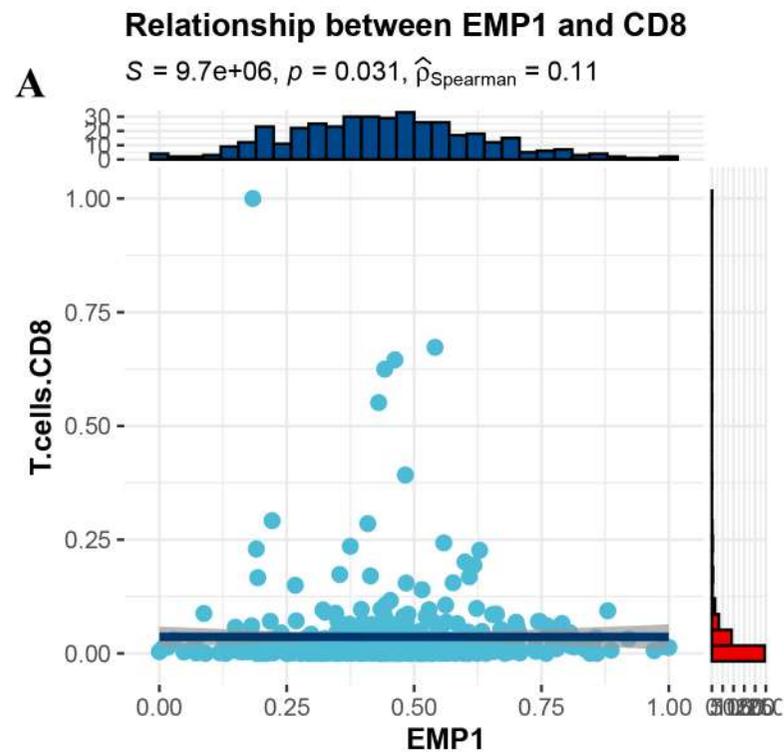
**A-C**, Consensus matrixes of the TCGA . **D**, Optical clustering chosen by delta area. **E-F**, Tracking plot and cumulative distribution function (CDF) curve describing the distribution of random variables. **G**, The change of error rate with the increasing number of trees.

# Supplementary Figure S2.



**A-D**, Survival plot showing the prognostic value of 4 out of the 8 essential genes.

# Supplementary Figure S3.

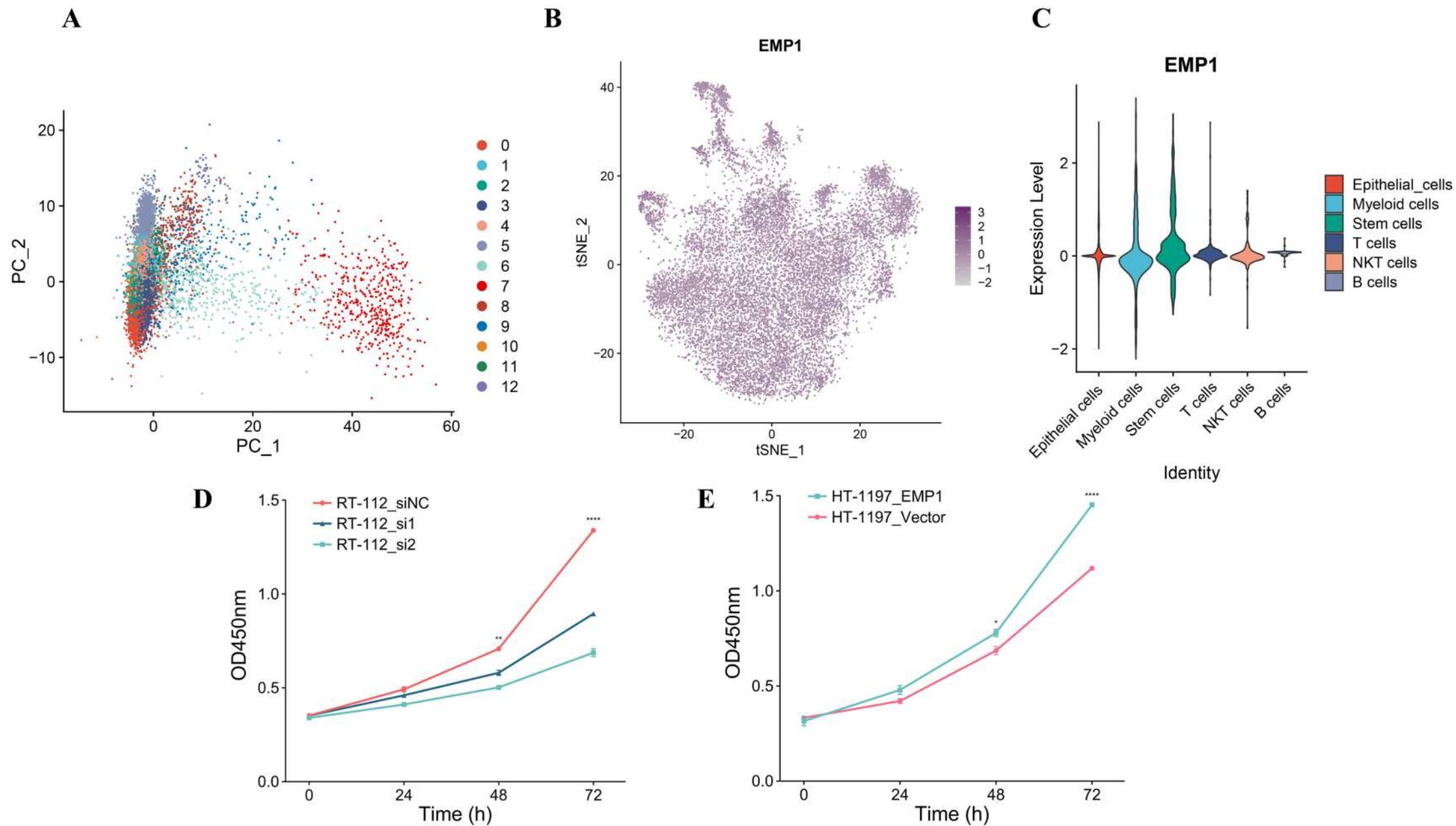


**A**, Correlative plot showing the correlation between EMP1 level and quantity of CD8+ T cells.

**B**, The correlation between expression of M1 or M2 related markers and EMP1 level.

**C**, Kaplan-Meier curve presenting the survival difference between EMP1 High and Low group.

## Supplementary Figure S4.



**A**, PCA analysis of the scRNA data. **B**, The distribution of EMP1 expression on all kinds of clusters.

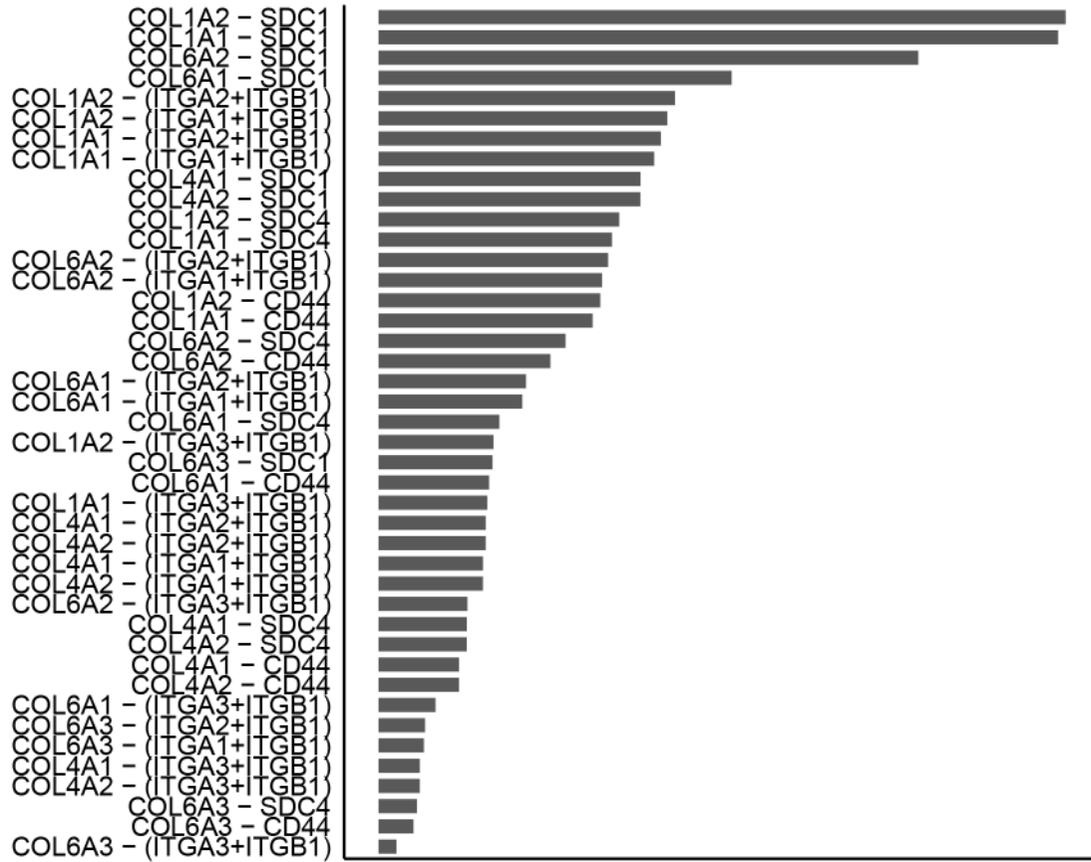
**C**, Violin plot showing the EMP1 level on these 6 kinds of cells.

**D**, **E**, CCK8 assay plotting the efficacy of EMP1 in promoting Cancer cells proliferation.

# Supplementary Figure S5.

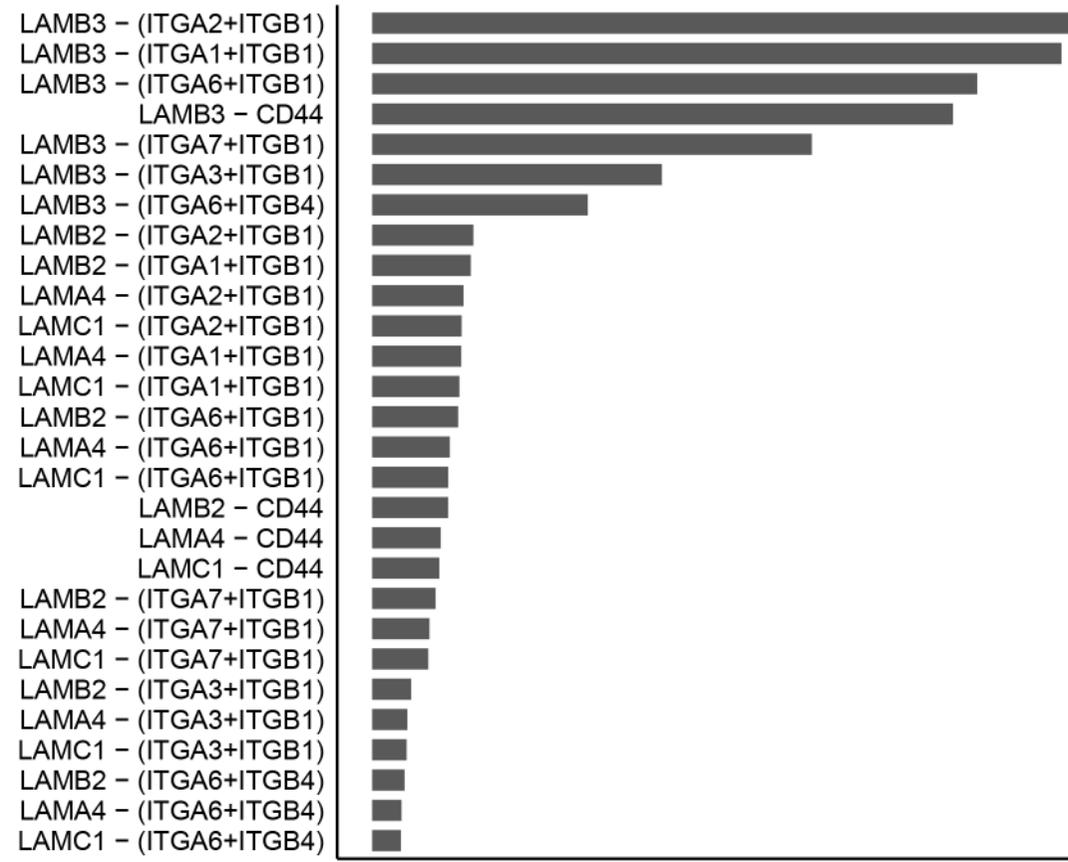
**A**

Contribution of each L-R pair



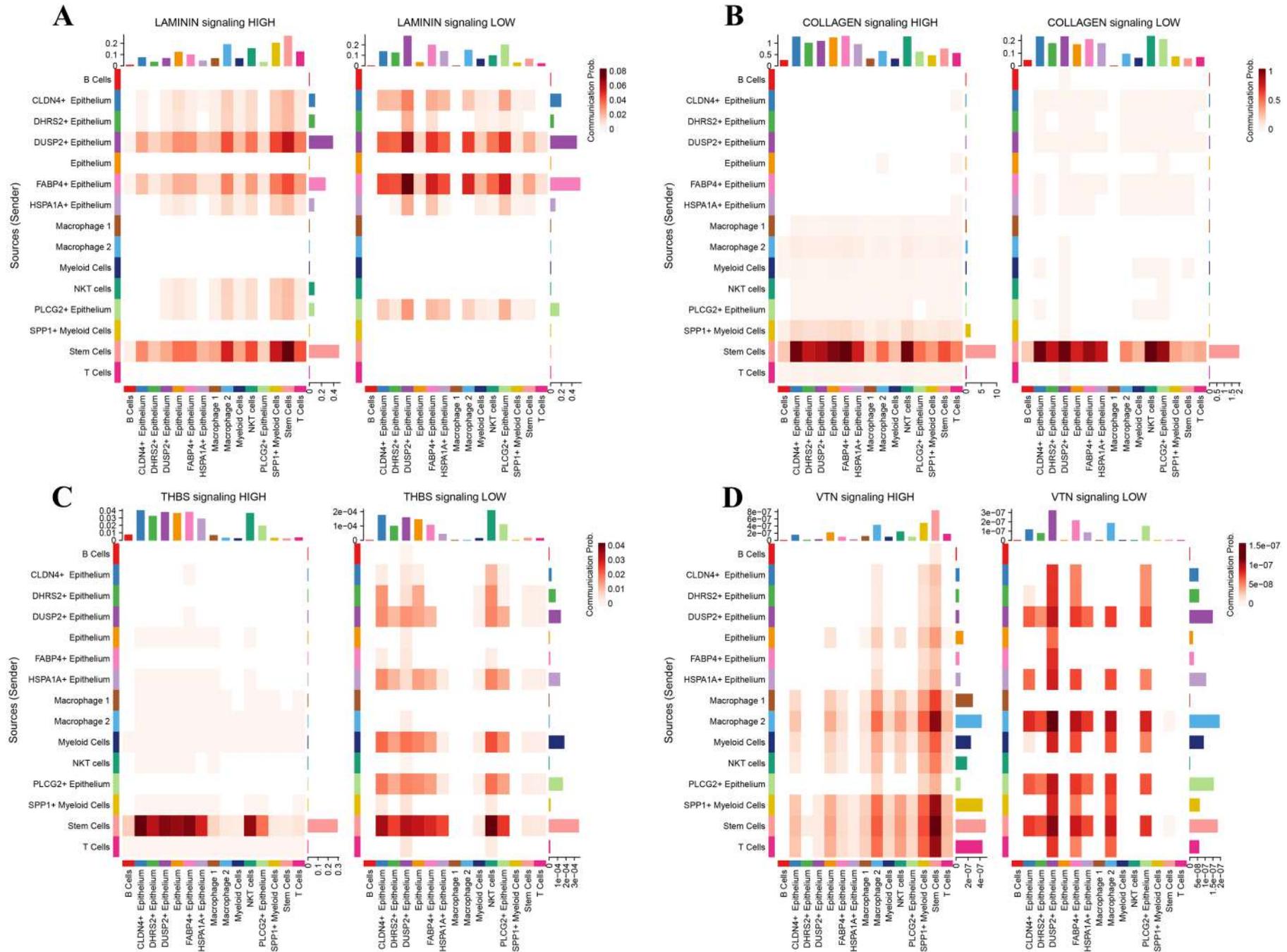
**B**

Contribution of each L-R pair



**A, B,** The contribution of each L-R pair in Collagen and LAMININ networks respectively.

# Supplementary Figure S6.



**A-D**, Heatmap exhibiting the different communication activity between EMP1 high and low group based on the four ECM relevant networks.