Supplementary Figure legend

Supplementary Fig. 1. (A) Consensus clustering with consensus matrix k=3 by the unsupervised hierarchical clustering methods. (B) Heatmap of immune related lncRNA patterns in GEO cohorts. Type 1 represents lung adenocarcinoma, type 2 represents lung squamous cell. (C) Random forest and decision tree algorithms for consensus clustering. (D) Gini graph by random forest identifying important variables.

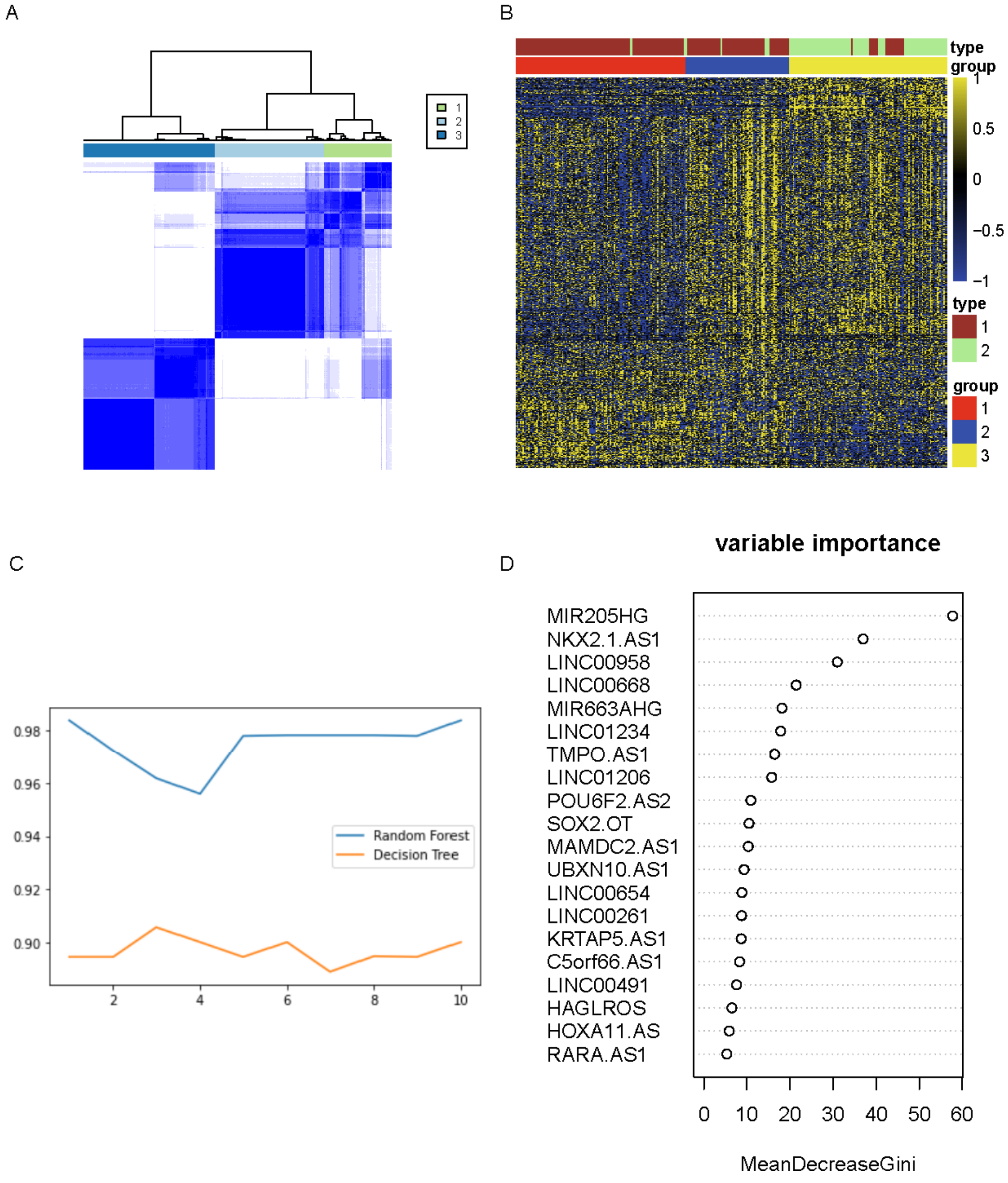
Supplementary Fig. 2 Correlation heatmap between tumor infiltrating immune cells, immune checkpoints, and immune related genes.

Supplementary Fig. 3. (A) Immune infiltrating score estimated by ESTIMATE algorithm. (B -F) Comparison of immune checkpoints, such as IDO1, LAG3, TIGIT, VTCN1 and CD274 among different clusters.

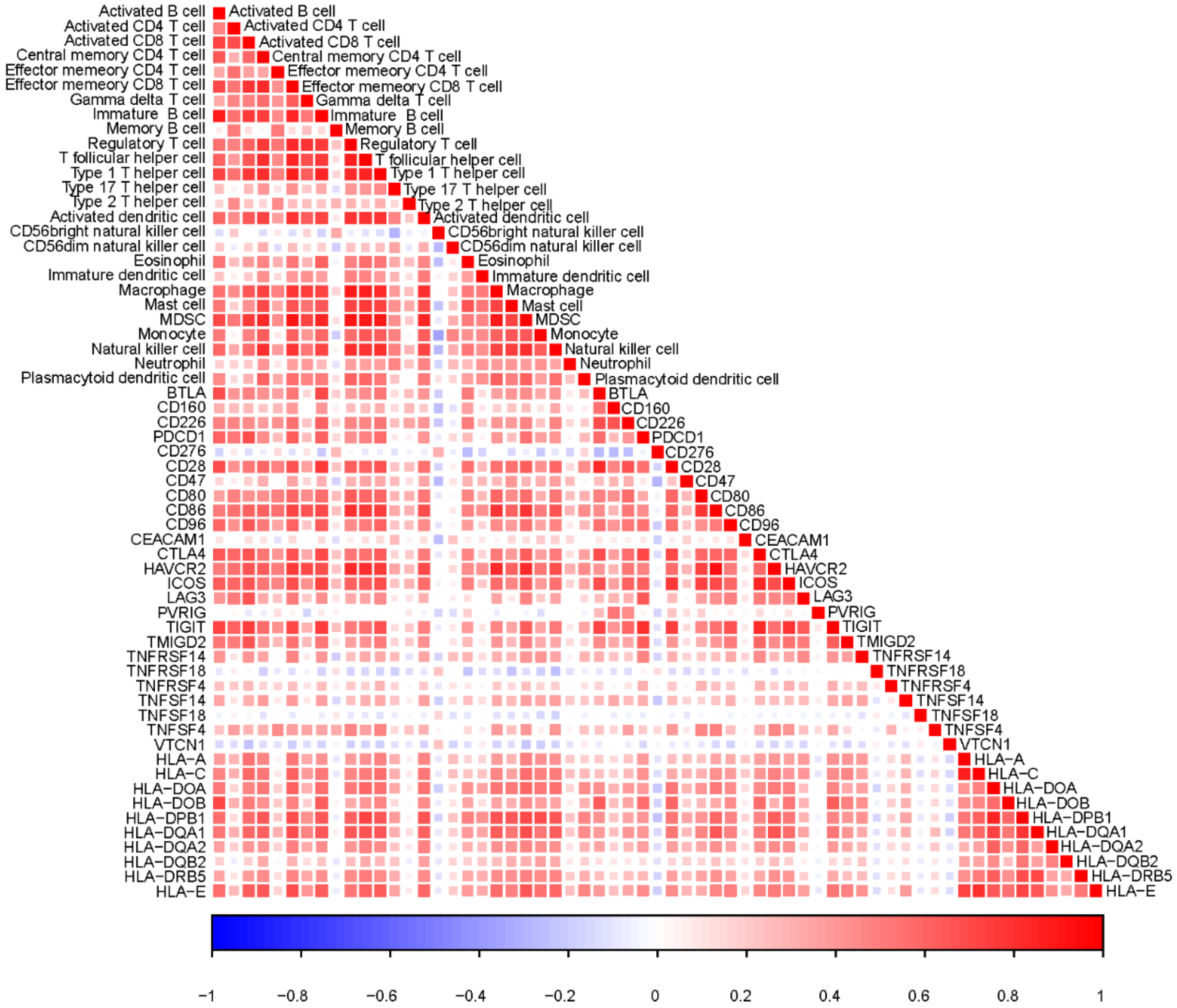
Supplementary Fig. 4. (A) Volcano plot for enrichment pathways of differentially expressed genes between cluster A and cluster C. (B) Volcano plot for enrichment pathways of differentially expressed genes between cluster A and cluster B.

Supplementary Fig. 5. (A -B) Beta values for weighted gene co-expression network analysis. (C) Network heatmap plot through weighted gene co-expression network analysis. (D-E) Eigengene-dendrogram and adjacency heatmap.

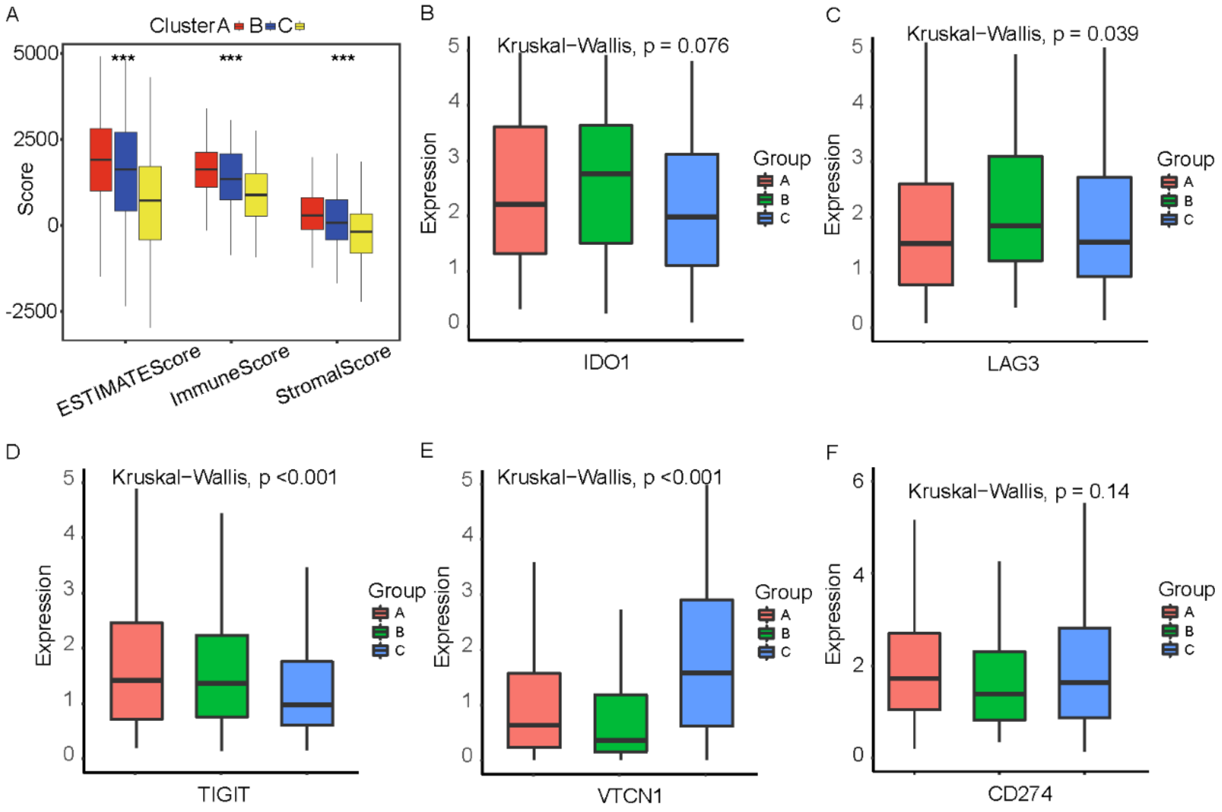
Supplementary Fig. 1



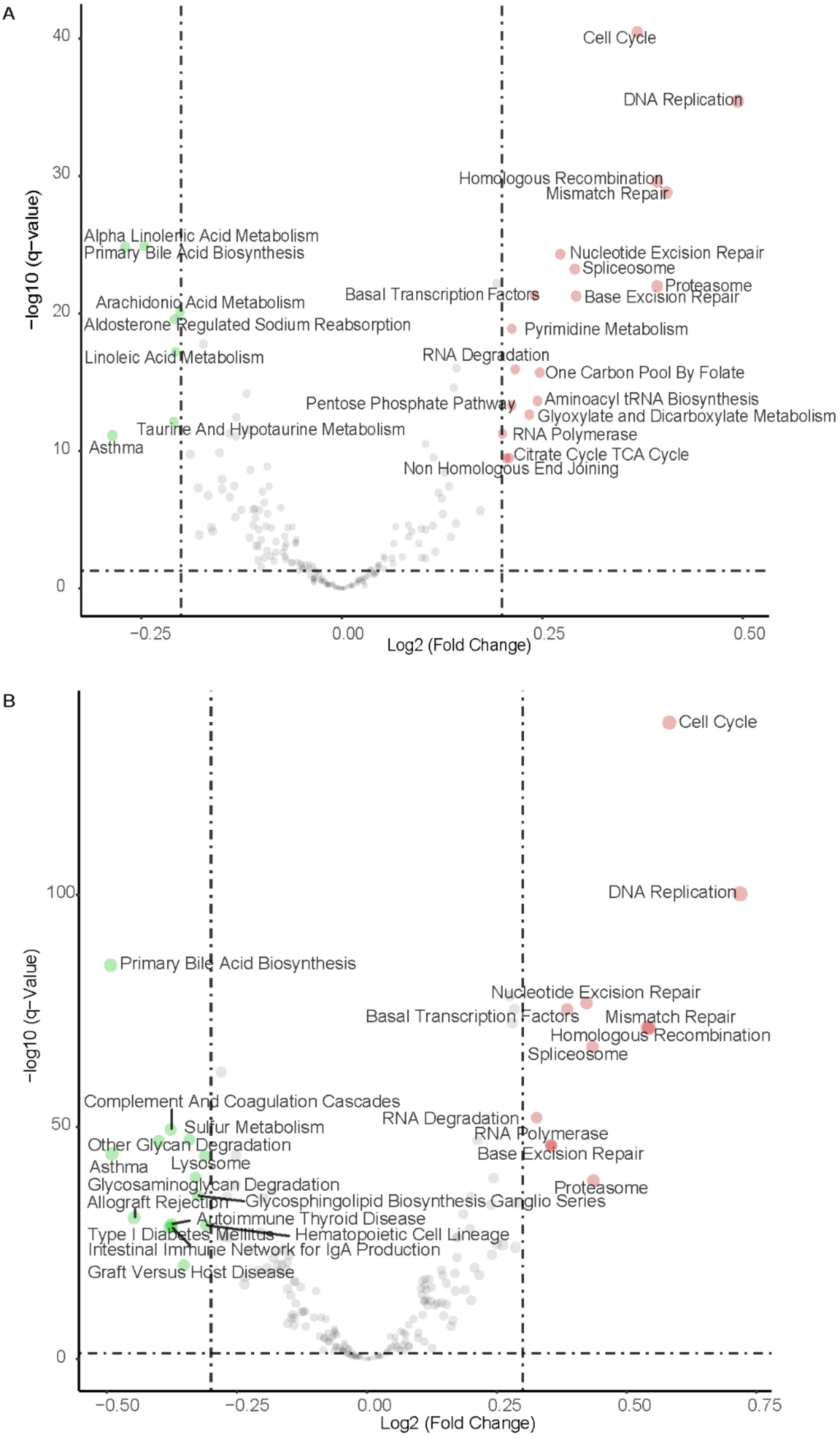
Supplementary Fig. 2



Supplementary Fig. 3



Supplementary Fig. 4



Supplementary Fig. 5