

SUPPLEMENTARY FIGURE 1. K-M curves of the ccRCC patient subgroups stratified by the expression levels of TLS genes.

(A-Z) K-M analyses for OS of ccRCC patient subgroups based on the RNA expressions of CCL5, CCL8, CCL18, CCL19, CCL20, CCL21, CCR5, CD4, CD5, CD38, CD40, CD200, CSF2, CXCL9, CXCL10, CXCL11, CXCL13, IGSF6, IL1R2, IL2RA, IRF4, MS4A1, SGPP2, SH2D1A, TNFRSF17 and TRAF6.

SUPPLEMENTARY FIGURE 2. Identification of TLS patterns based on the expression levels of the 39 TLS genes.

- (A) Copy number variations (CNVs) frequencies of the 39 TLS genes.
- (B) Frequency of somatic mutations and classification of the 39 TLS genes.
- (C) Distribution of CNVs of 39 TLS genes across 23 chromosomes.
- (D-K) Consensus matrices of ccRCC patients from $k = 2$ to $k = 9$.
- (L-N) The cumulative distribution function (CDF) curves plot, delta plot, and tracking plot corresponding to the consensus matrices from $k = 2$ to $k = 9$.

SUPPLEMENTARY FIGURE 3. Clinicopathological and biological characteristics of three subgroups defined by the 39 TLS genes in ccRCC.

- (A) Principal component analysis (PCA) showing unique dispersion among TLSClusters.
 - (B) Differences in stromal, immune, and ESTIMATE scores among TLSClusters.
 - (C) Heatmap of 39 TLS gene expressions and clinical characteristics among three distinct TLSClusters.
 - (D-F) Gene set variation analysis (GSVA) of activated biological pathways among TLSClusters.
 - (G) Immune cell infiltration differences among TLSClusters.
 - (H) Expressions of ICPs in TLSClusters.
 - (I-L) The distribution of clinical characteristics (age, gender, grade, and stage) among ccRCC patients in TLSClusters.
- *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; ns, not significant.

SUPPLEMENTARY FIGURE 4. Identification of GeneClusters based on the 155 prognosis-related genes.

- (A) The protein-protein interaction (PPI) network illustrating the interactions among the top 50 DEGs within the three TLSClusters.
- (B-C) Functional enrichment analyses of Kyoto encyclopedia of genes and genomes (KEGG) and gene ontology (GO) analyses of DEGs.
- (D-K) Consensus matrices of ccRCC patients from $k = 2$ to $k = 9$.
- (L-N) The cumulative distribution function curves plot, delta plot, and tracking plot corresponding to the consensus matrices from $k = 2$ to $k = 9$.

SUPPLEMENTARY FIGURE 5. Clinicopathological and biological characteristics of GeneClusters.

- (A) Heatmap showing variations in clinical features among GeneClusters.

- (B) Differences in the TME scores among GeneClusters.
 - (C-E) Heatmaps showing varied activation statuses of biological pathways within GeneClusters by GSVA.
 - (F) The abundance of infiltrating immune cell types within GeneClusters.
 - (G) Expressions of ICPs in GeneClusters.
 - (H-K) The distribution of clinical characteristics (age, gender, grade, and stage) among ccRCC patients in GeneClusters.
- *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; ns, not significant.

SUPPLEMENTARY FIGURE 6. TLS-Associated Predictive Signature Development and its correlation between clinical characteristics.

- (A) The ranked dots and scatter plot illustrating the RiskScore distribution and survival status, accompanied by a heatmap depicting the expression profiles of the five chosen genes.
- (B) The receiver operating characteristic (ROC) curves demonstrating the sensitivity and specificity of 1-, 3-, and 5-year OS based on the RiskScore.
- (C) The alluvial diagram illustrating the distribution of patients among different clusters, RiskGroups, and clinical outcomes.
- (D) Disparities in patients' RiskScore among the three TLSClusters.
- (E) Variations in patients' RiskScore among the three GeneClusters.
- (F-G, J-K, and N-O) K-M analyses for OS of patients in high and low RiskGroups stratified by T stage, TNM stage, and tumor grade.
- (H-I, L-M, and P-Q) The distribution of clinical characteristics (T stage, TNM stage, and tumor grade) among ccRCC patients in high and low RiskGroups.

SUPPLEMENTARY FIGURE 7. Establishment of a Prognostic Prediction Nomogram.

- (A) TLS-associated nomogram predicting the 1-, 3-, and 5-year OS of ccRCC patients.
- (B) Calibration curves for validation of the nomogram.
- (C-E) ROC curves for 1-, 3-, and 5-year OS prediction of the nomogram.
- (F-H) Decision curve analysis (DCA) for 1-, 3-, and 5-year OS prediction of the nomogram.

Figure S1

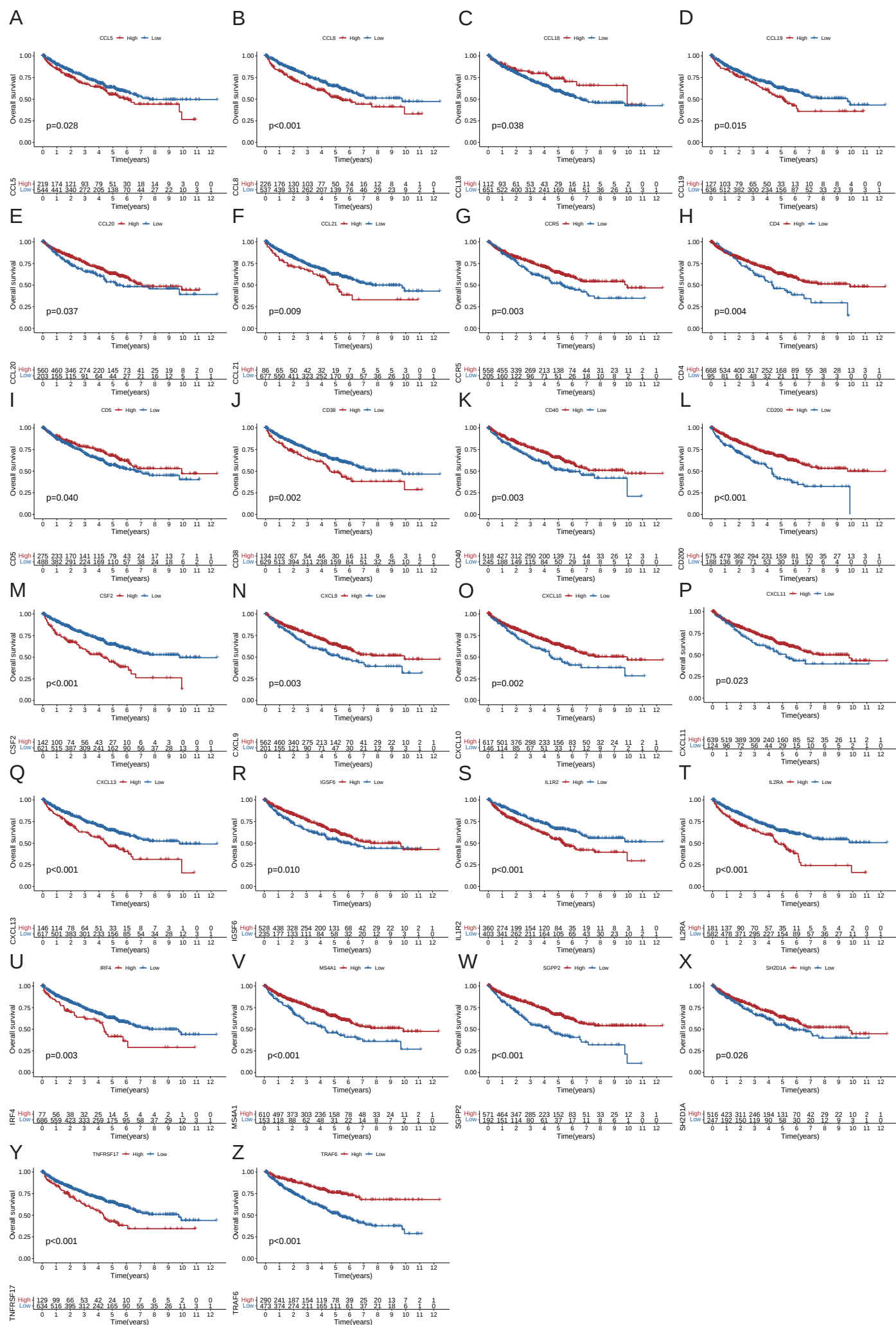


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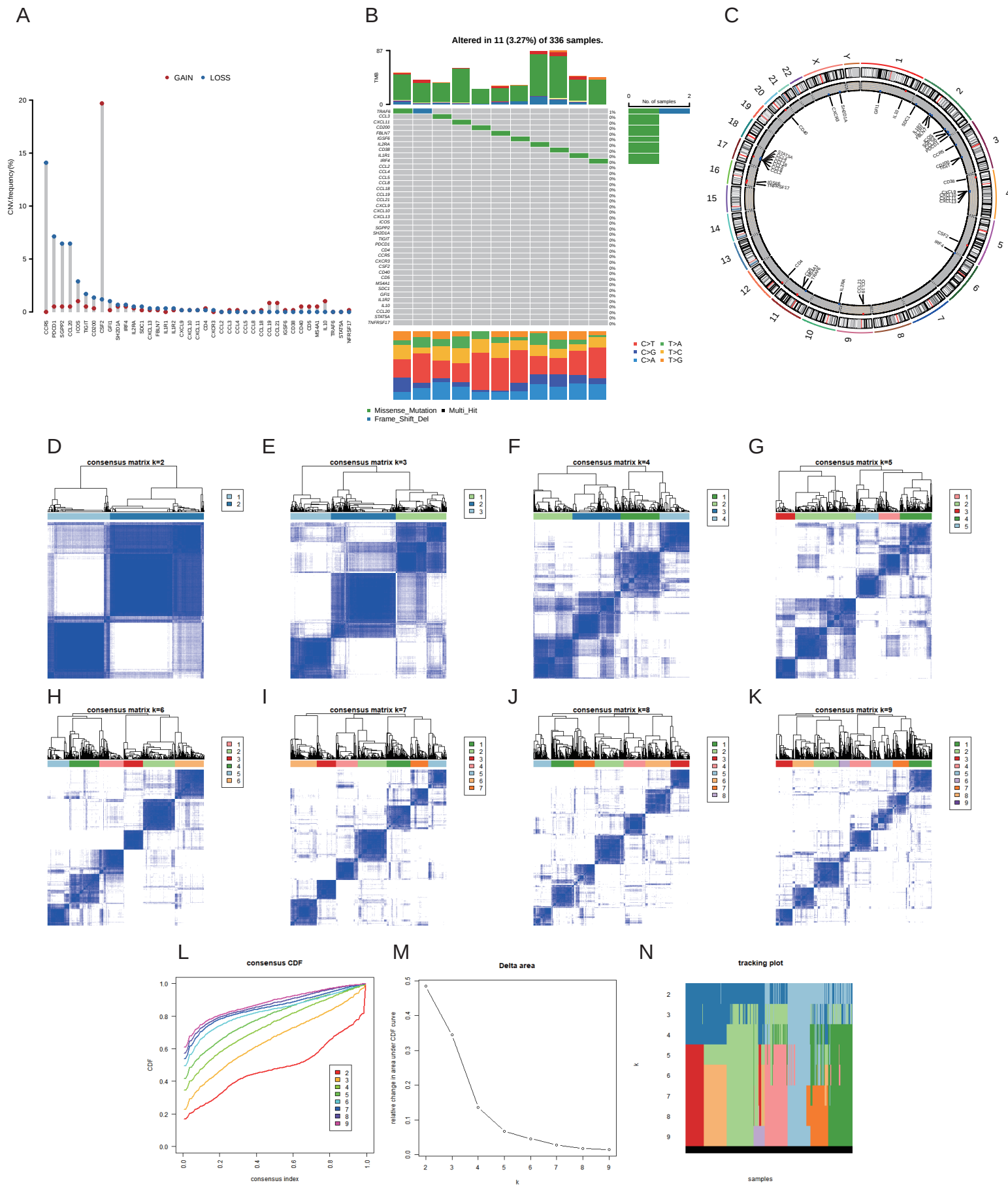


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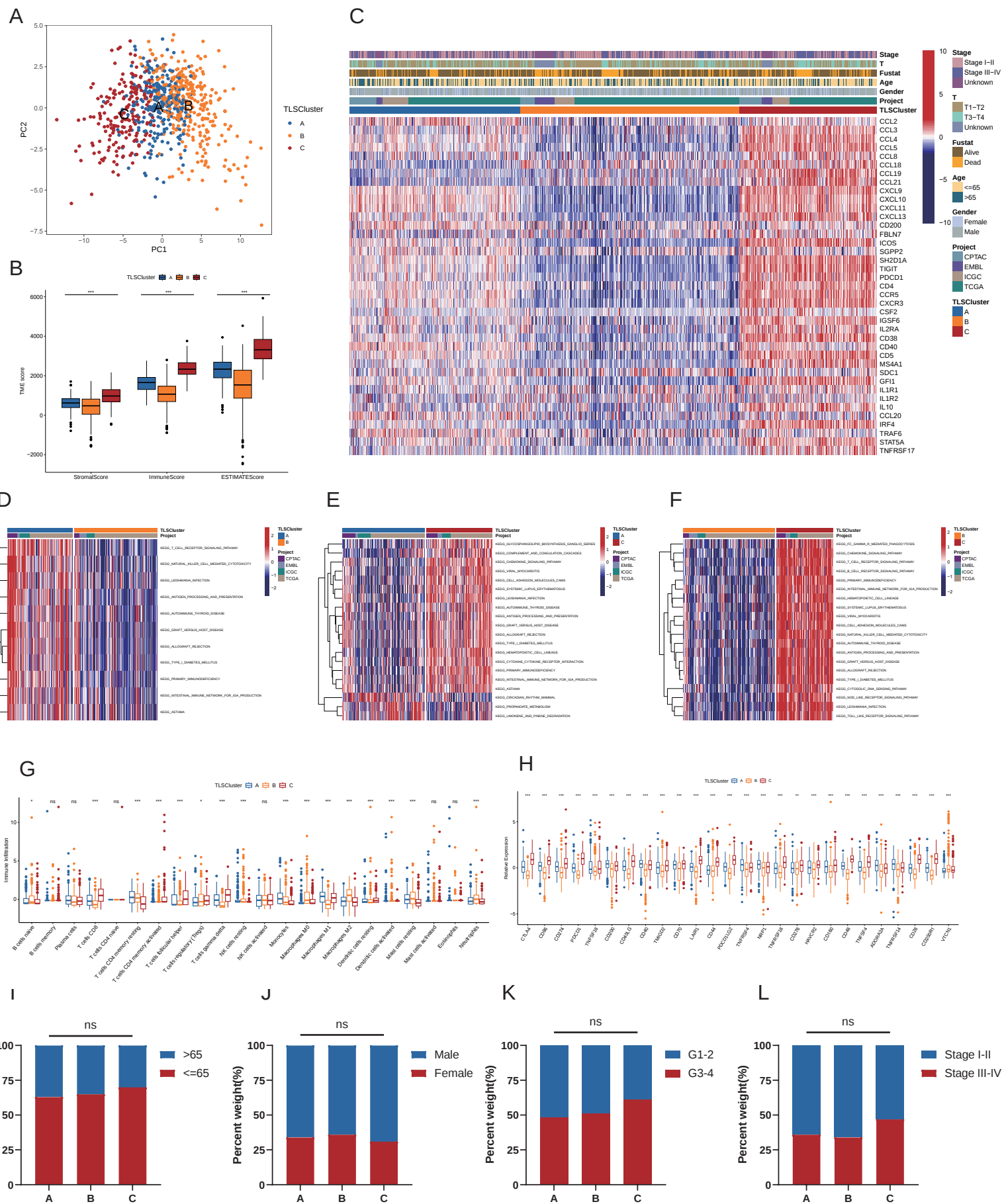


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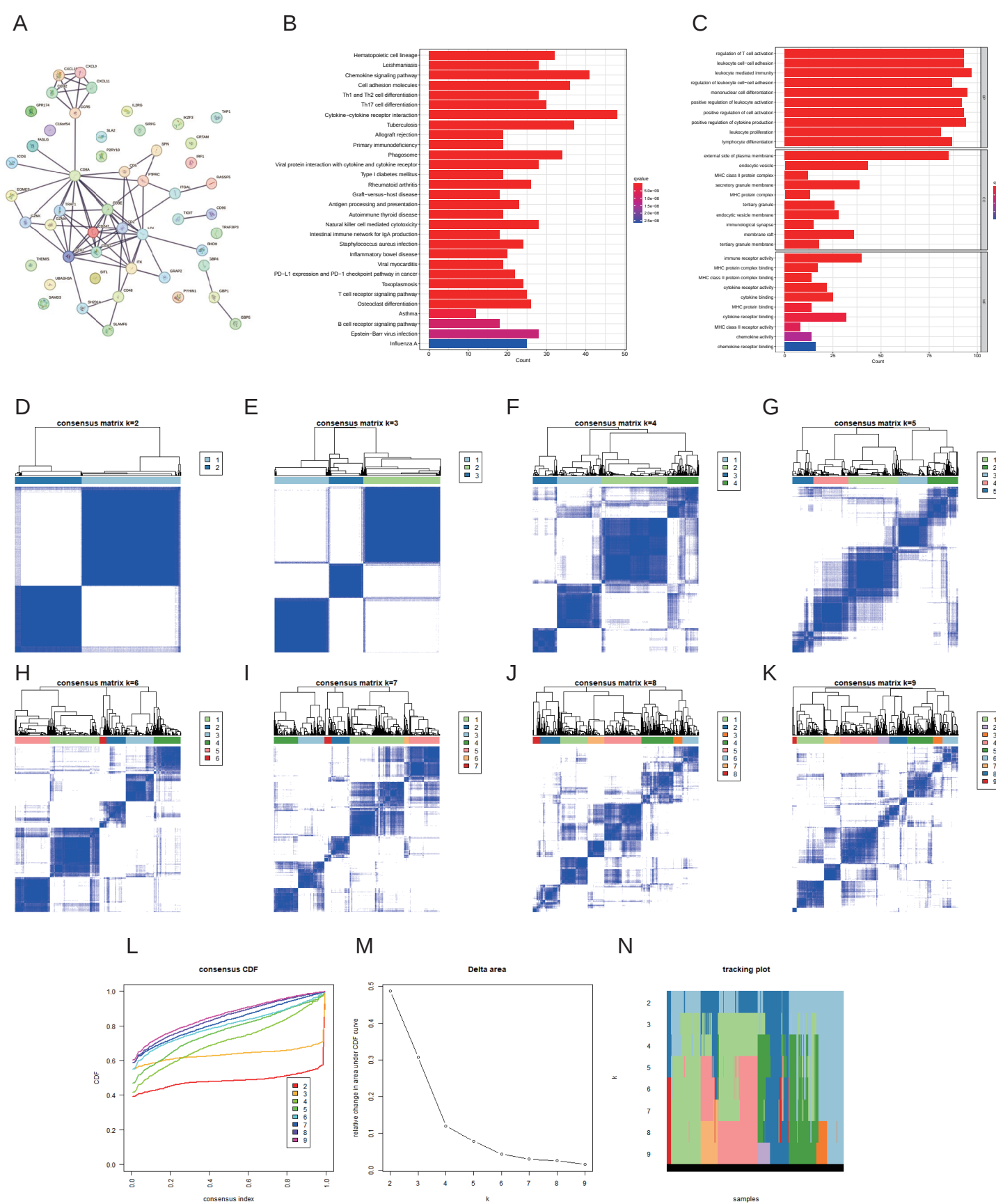


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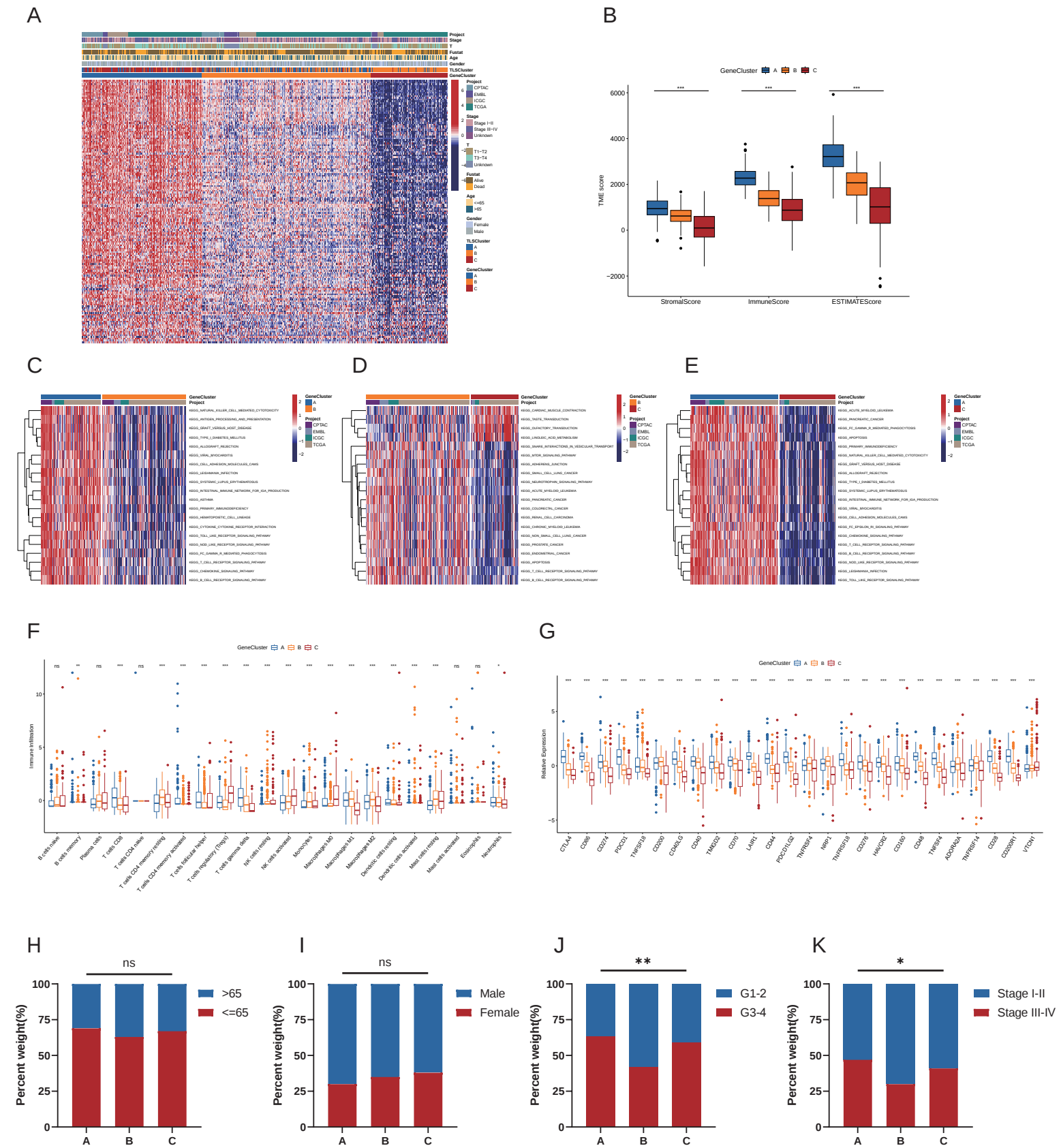


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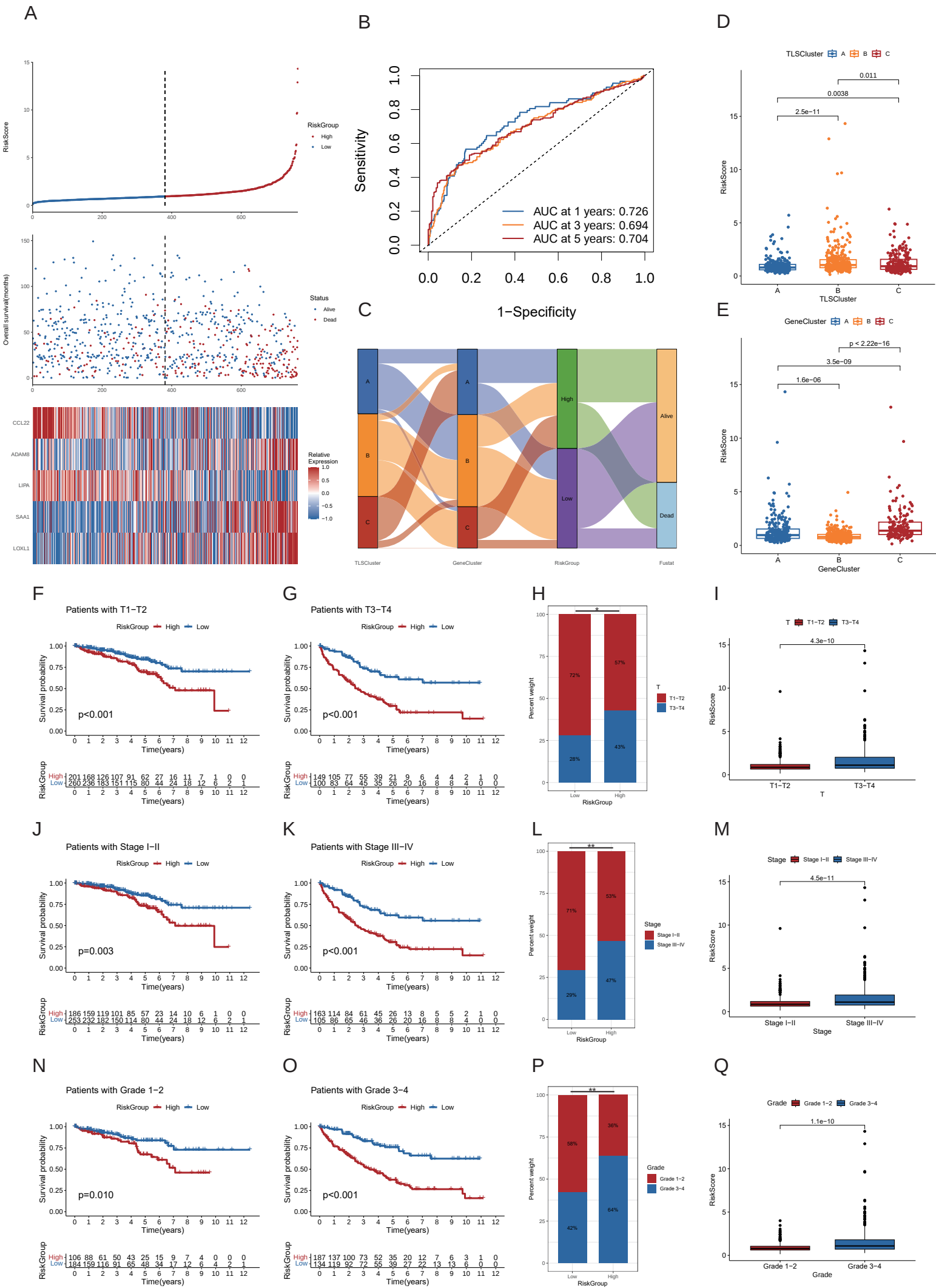
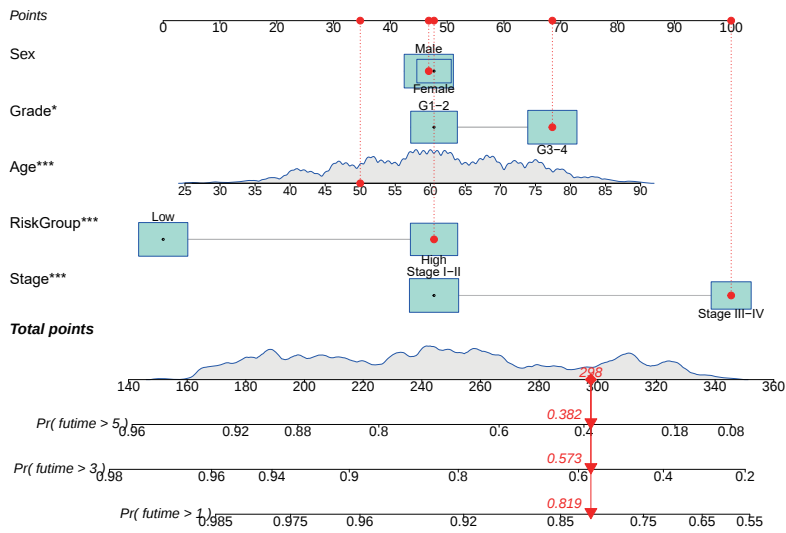
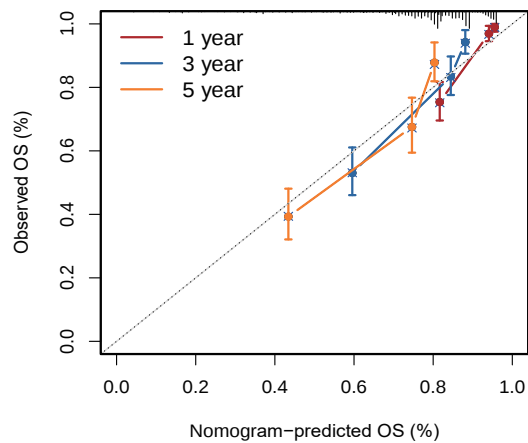


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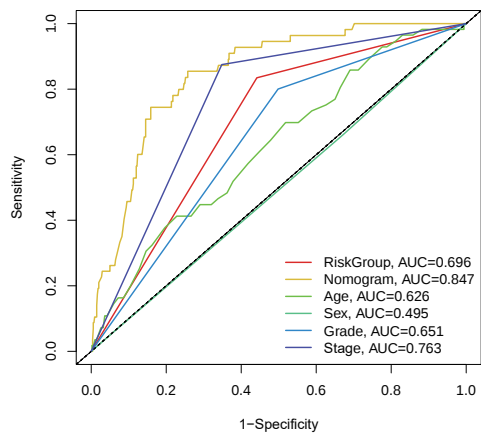
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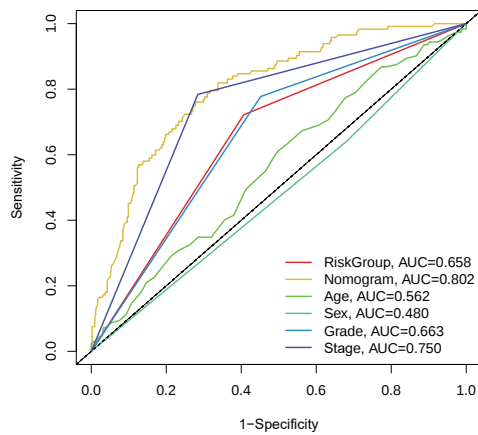
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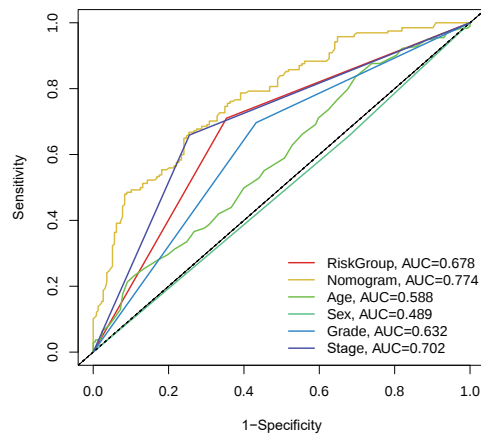
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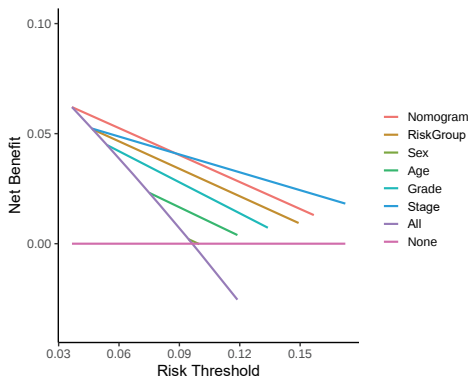
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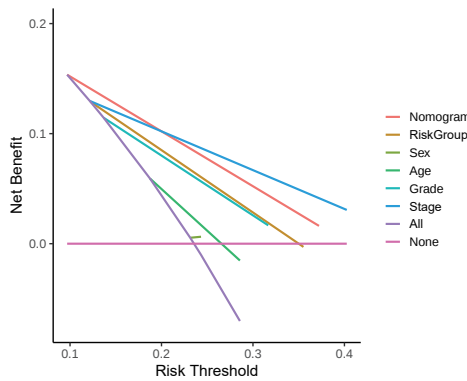
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H

