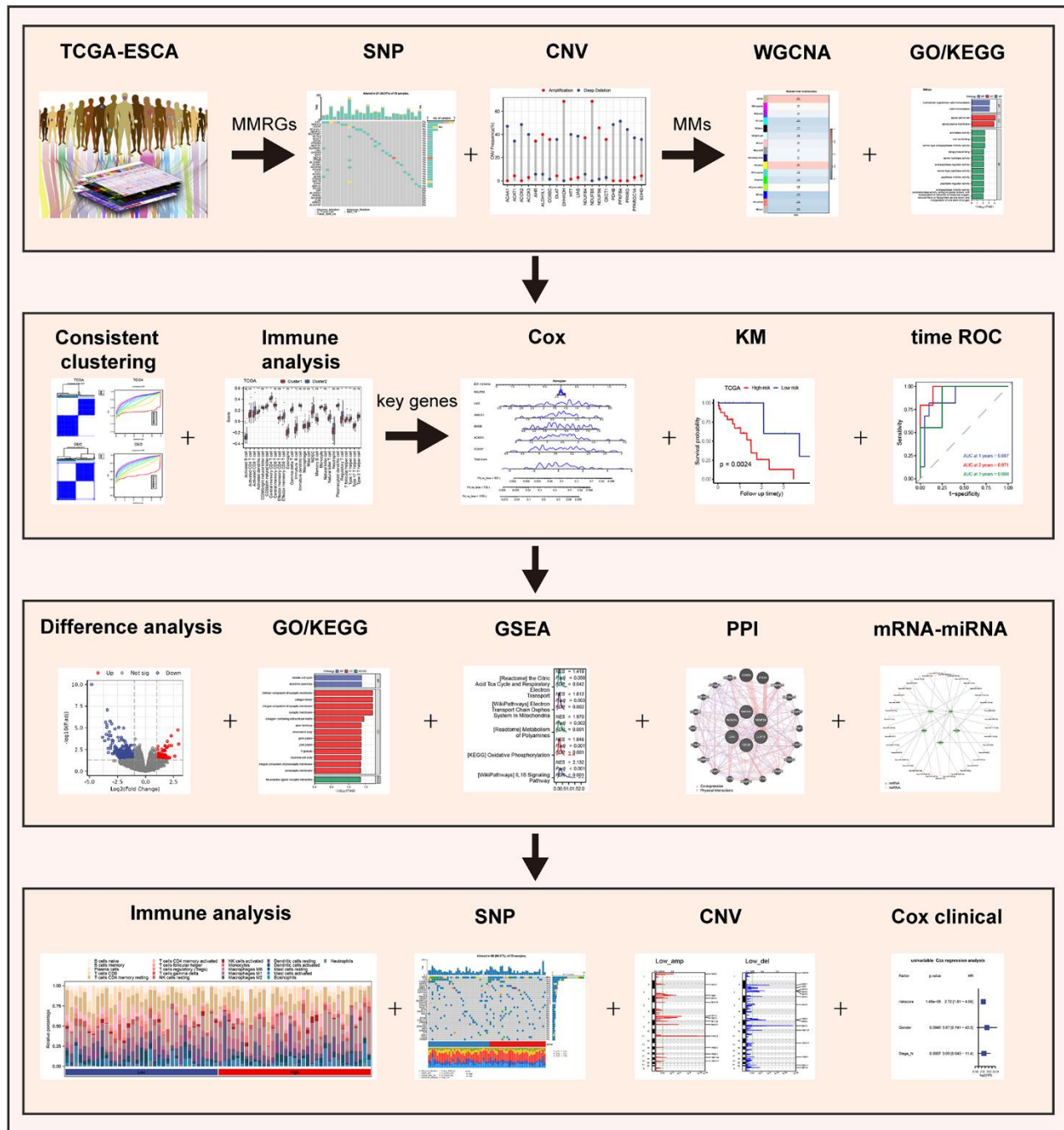
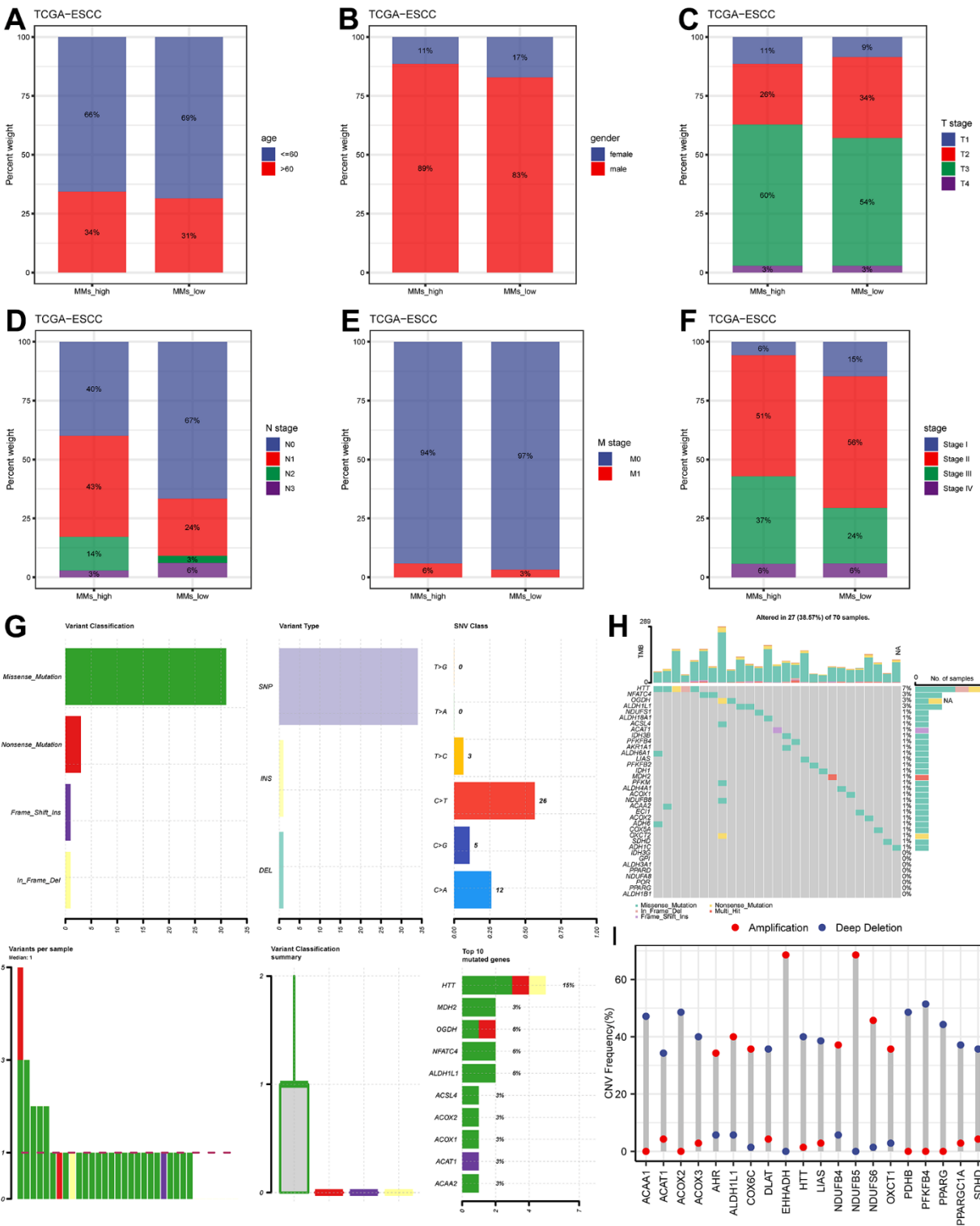


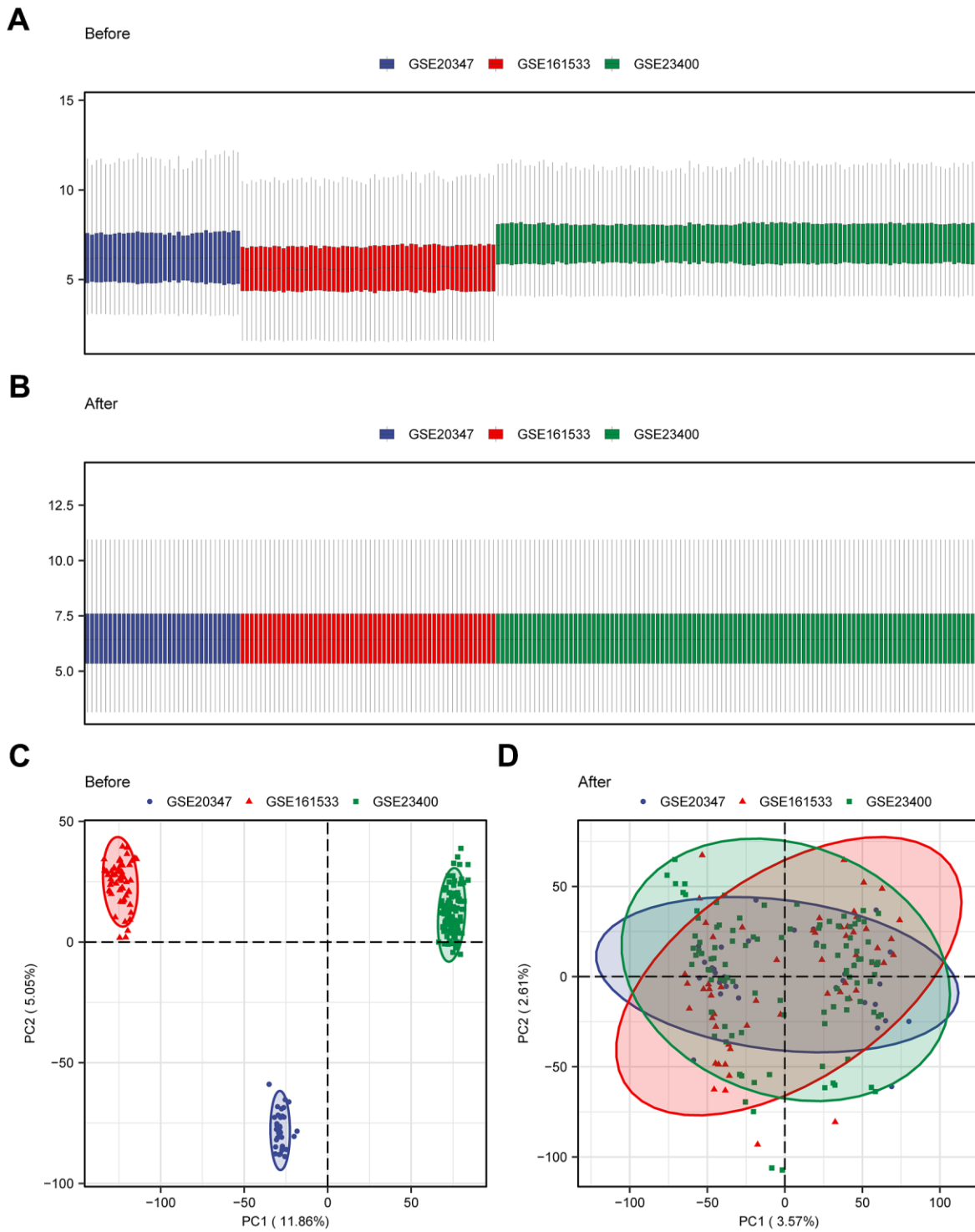
SUPPLEMENTARY FIGURES



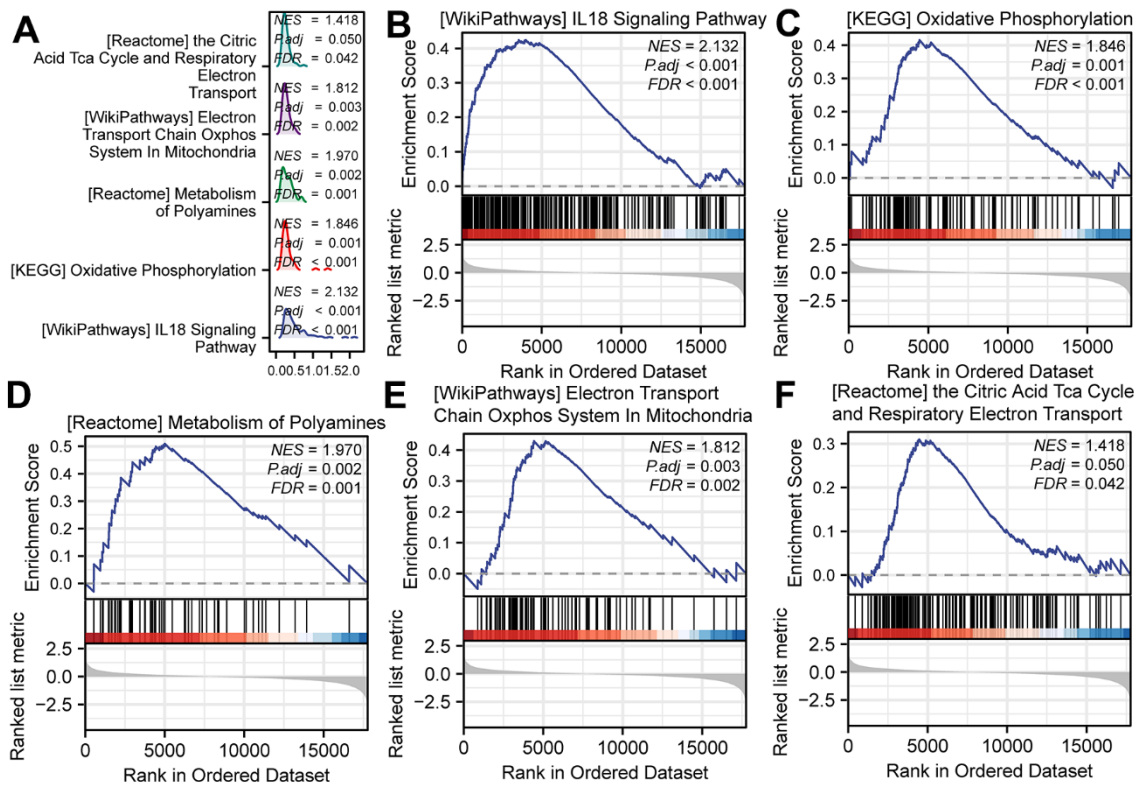
Supplementary Figure 1. Technology roadmap.



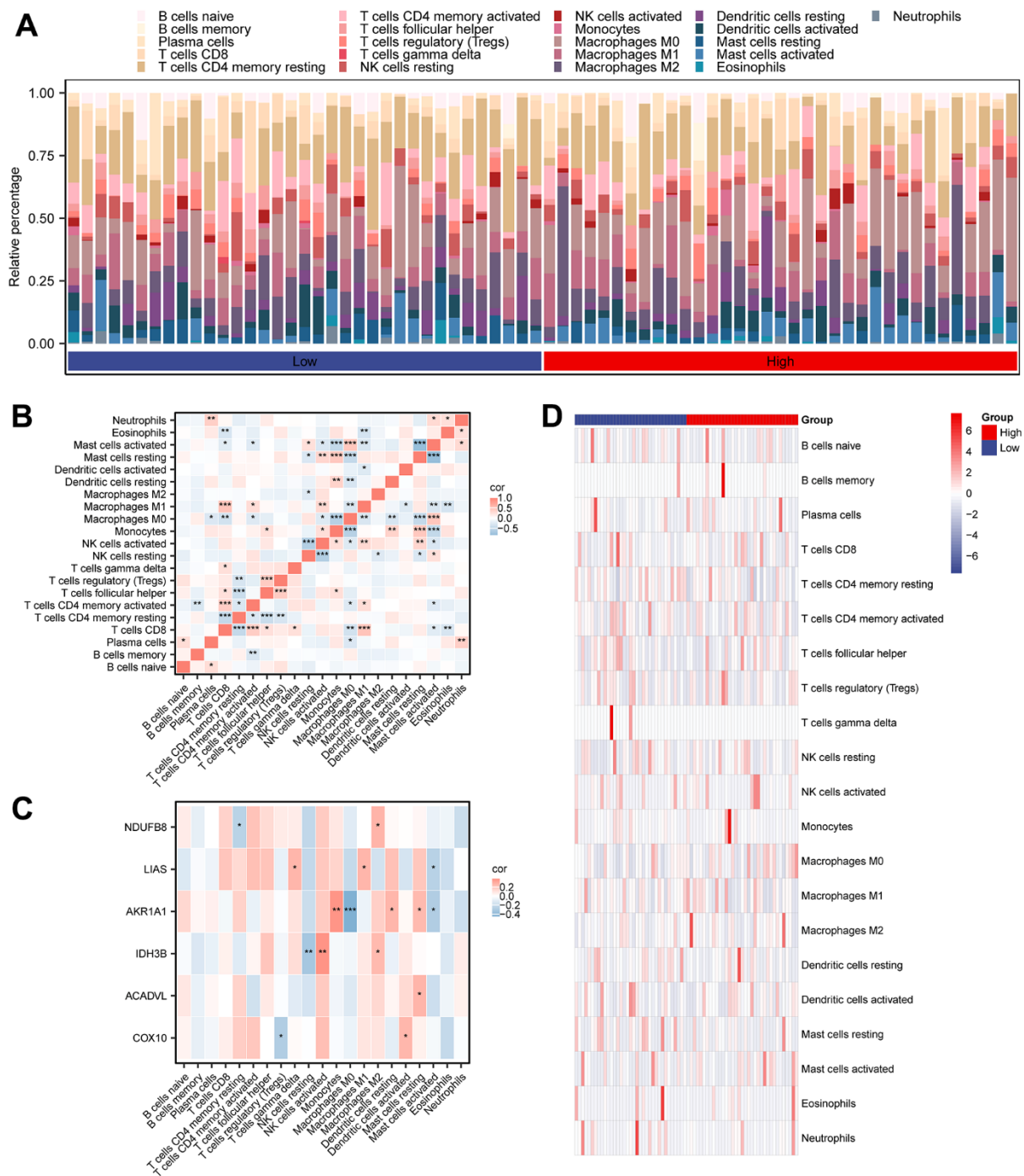
Supplementary Figure 2. Clinical correlation analysis of mitochondrial energy metabolism score and SNP/CNV analysis of MMRGs. (A–F) Clinical correlation analysis of mitochondrial energy metabolism score with Age (A), Gender (B), T stage (C), N stage (D), M stage (E), and Stage (F). (G) Overall SNP analysis of MMRGs in TCGA-ESCC. (H) Mutation waterfall plot of MMRGs in TCGA-ESCC. (I) CNV analysis of MMRGs in TCGA-ESCC. MMRGs, Mitochondrial metabolism-related genes. SNP, single nucleotide polymorphism. CNV, Copy Number Variation.



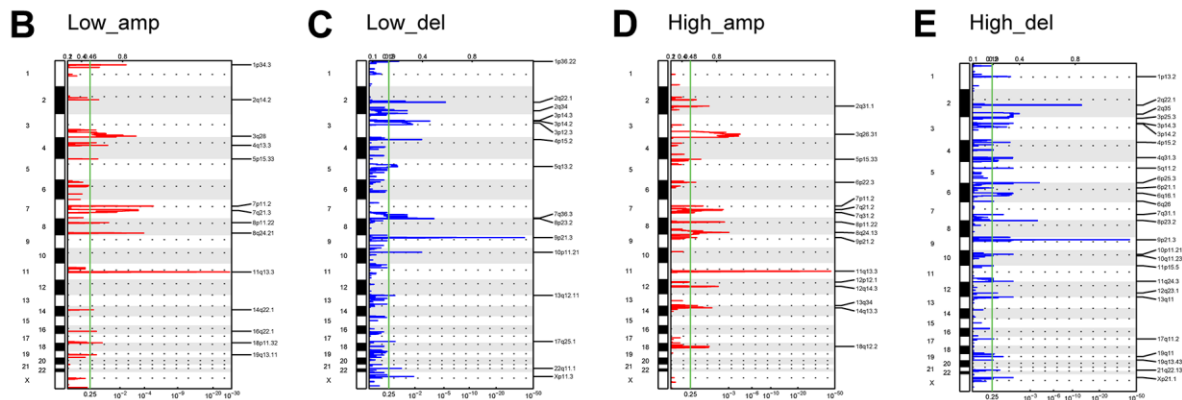
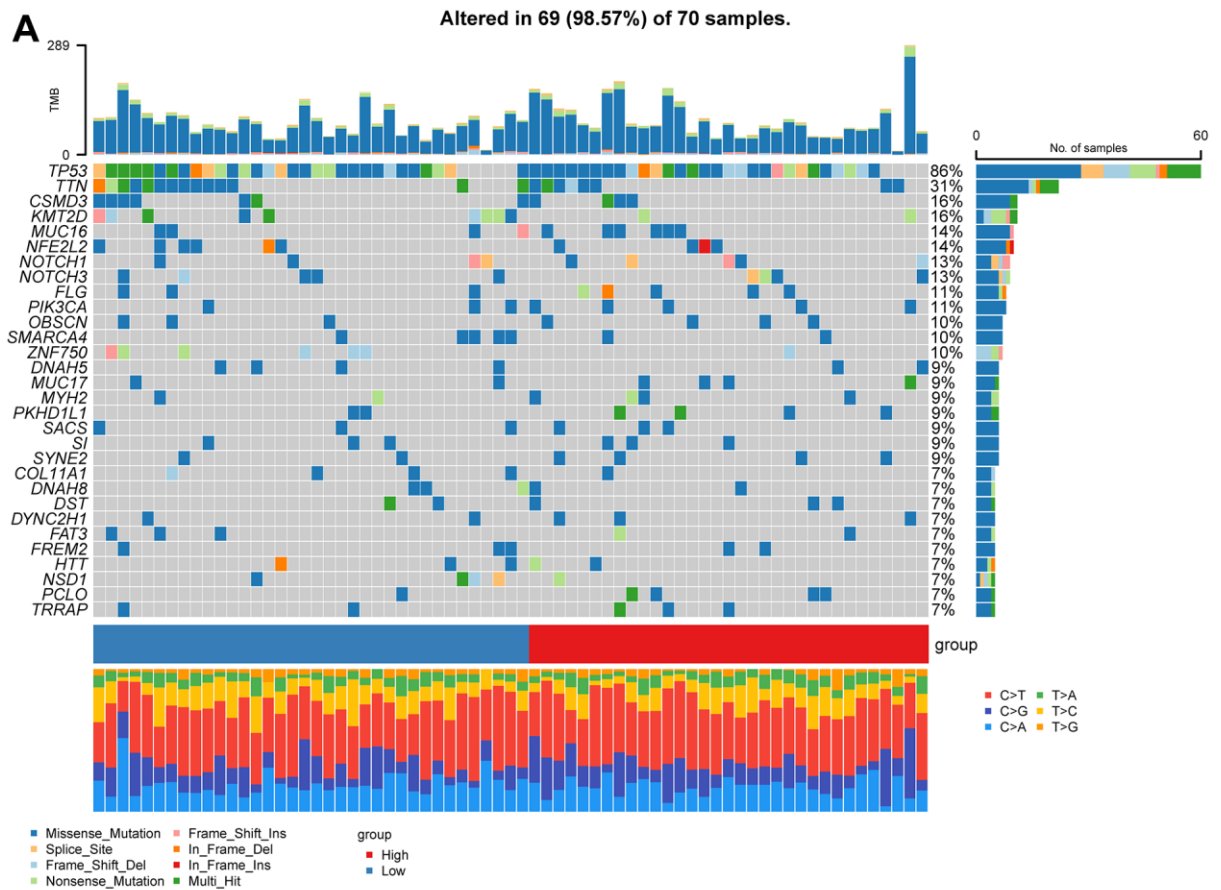
Supplementary Figure 3. Verify set collection and calibrate. (A) The boxplot plot of the merged dataset before removing the batch. (B) The boxplot plot of the merged dataset after removing batches. (C) Merge the PCA plot of the dataset before removing the batch. (D) PCA plot after merging the dataset and removing batches. PCA: Principal Component Analysis.



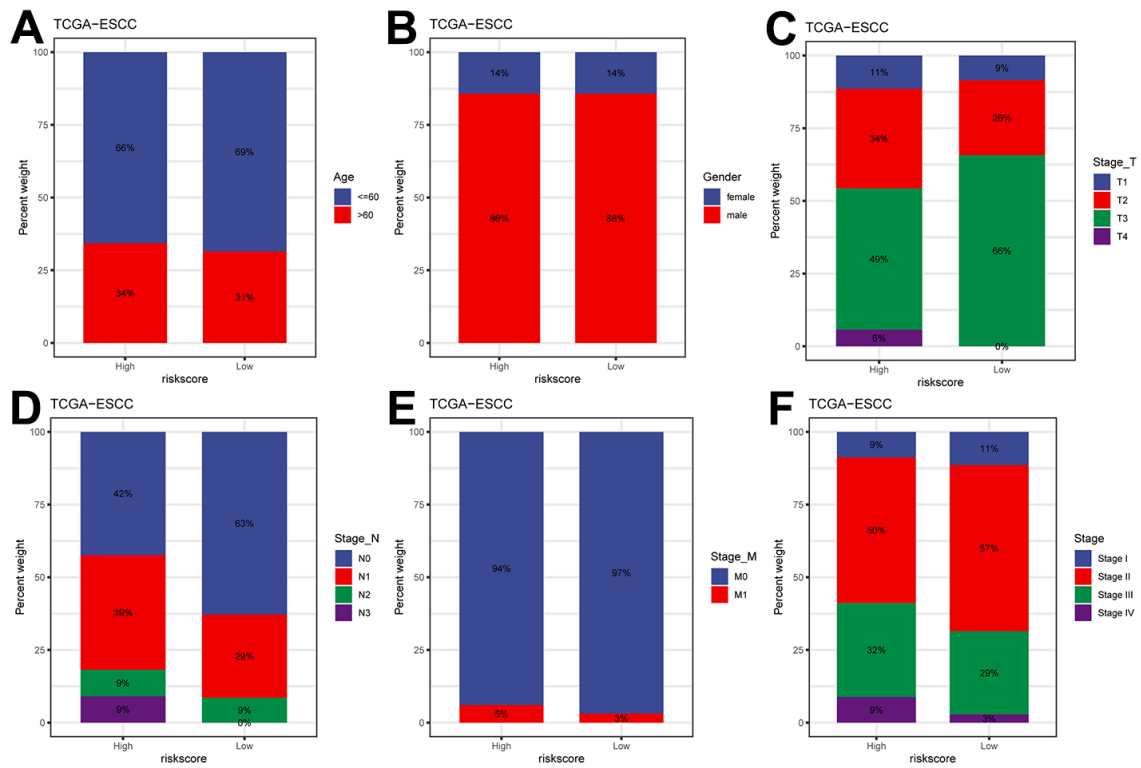
Supplementary Figure 4. The GSEA of the TCGA-ESCC dataset. (A) Volcano plot of the GSEA enrichment analysis of the TCGA-ESCC dataset. (B–F) Pathway maps of the IL 18 Signaling Pathway (B), KEGG Oxidative phosphorylation (C), Metabolism of polyamines (D), Electron transport chain OXPHOS system in mitochondria (E), and Electron Transport (F) pathways.



Supplementary Figure 5. Immune infiltration analysis of the TCGA-ESCC. (A) Stacked bar chart of immune cell infiltration in the High and Low groups of the TCGA-ESCC. (B) Correlation heatmap of immune cells. (C) Correlation heatmap of immune cells and key genes. (D) Heatmap of immune cell infiltration in the TCGA-ESCC.

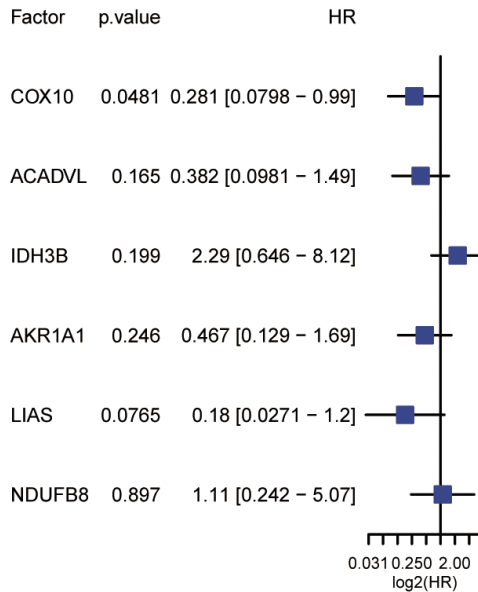


Supplementary Figure 6. SNP and CNV analysis of high-risk and low-risk groups in the Cox model. (A) Waterfall plot of mutation analysis for high- and low-risk groups in the Cox model. **(B, C)** GISTIC analysis of the low-risk group in the TCGA-ESCC dataset. Red indicates CNV amplification **(B)**, while blue denotes CNV deletion **(C)**. **(D, E)** GISTIC analysis of the high-risk group in the TCGA-ESCC dataset. Red represents CNV amplification **(D)**, while blue represents CNV deletion **(E)**.

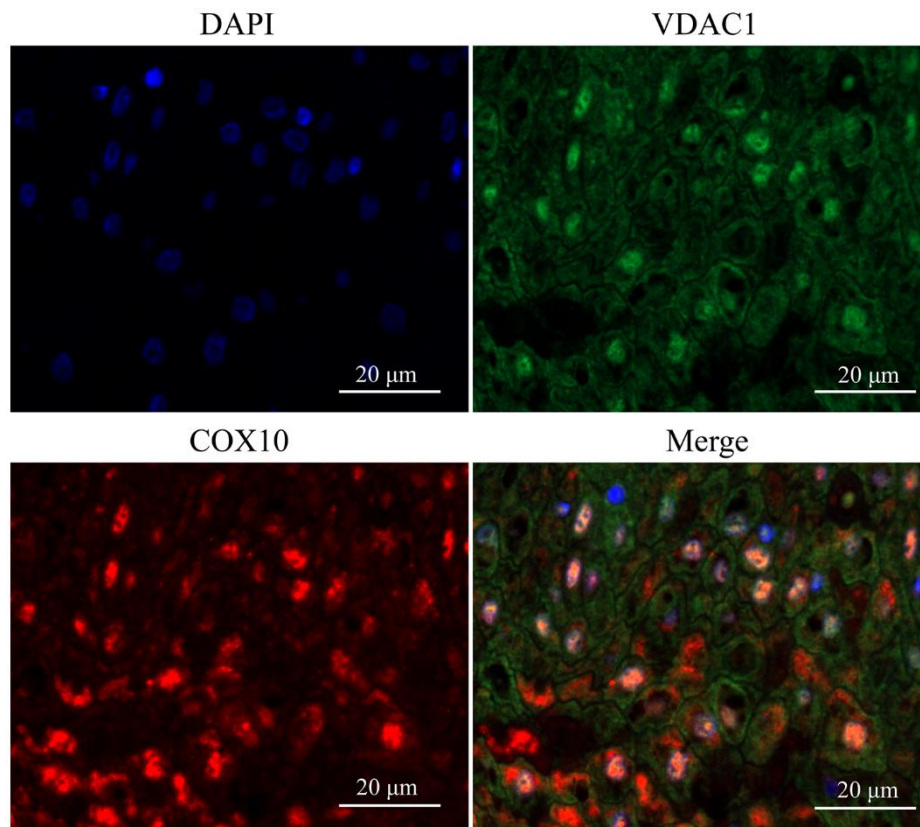


Supplementary Figure 7. Clinical prediction model based on risk score in the TCGA-ESCC dataset. (A–F) Clinical correlation analysis of mitochondrial energy metabolism score with Age (A), Gender (B), T stage (C), N stage (D), M stage (E), and Stage (F).

multifactor Cox regression analysis



Supplementary Figure 8. Risk factor map of MMRGs prognostic model.



Supplementary Figure 9. Immunofluorescence quantitative expression of COX10 in normal oesophageal tissues.