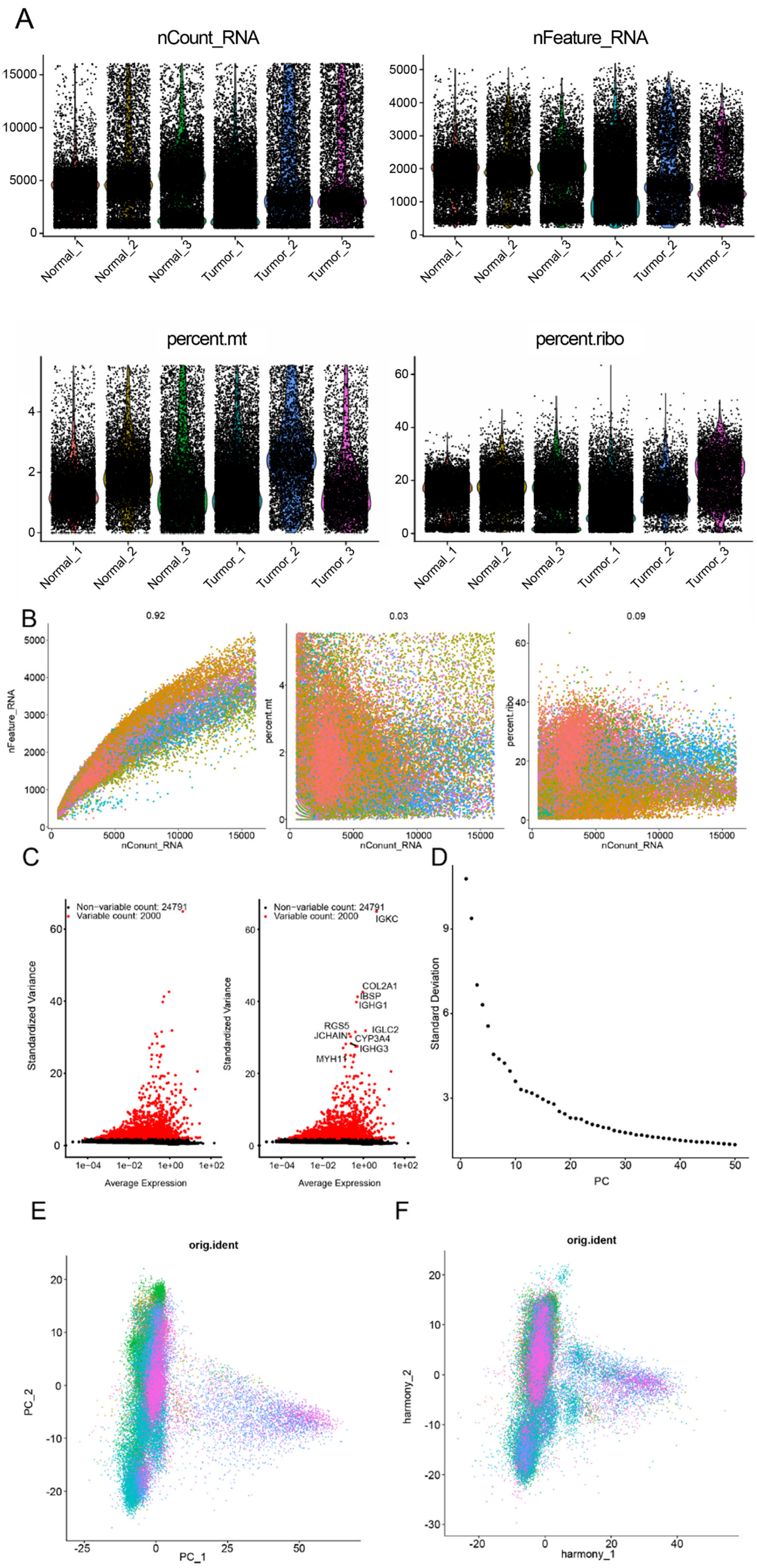

Figure S1 Single-cell data processing and quality control workflow. (A) Distribution of nCount_RNA, nFeature_RNA, percent.mt, and percent.ribo across six samples, including three normal (Normal_1, Normal_2, Normal_3) and three tumor (Tumor_1, Tumor_2, Tumor_3) samples. Each dot represents an individual cell. (B) Scatter plots illustrating the relationships between nCount_RNA and nFeature_RNA, nCount_RNA and percent.mt, and nCount_RNA and percent.ribo. Correlation coefficients are indicated in each plot. (C) Scatter plots depicting the relationship between average expression and standardized variance for all genes (left) and highly variable genes (right). The number of non-variable and variable genes is annotated. (D) Plot showing the relationship between the principal component (PC) and standardized deviation, determining the optimal number of principal components. (E) Principal component analysis (PCA) plot displaying the first two principal components (PC_1 and PC_2) for all cells, color-coded by sample origin (normal or tumor). (F) Harmony batch correction plot showing the first two corrected components (harmony_1 and harmony_2) for all cells, color-coded by sample origin (normal or tumor).

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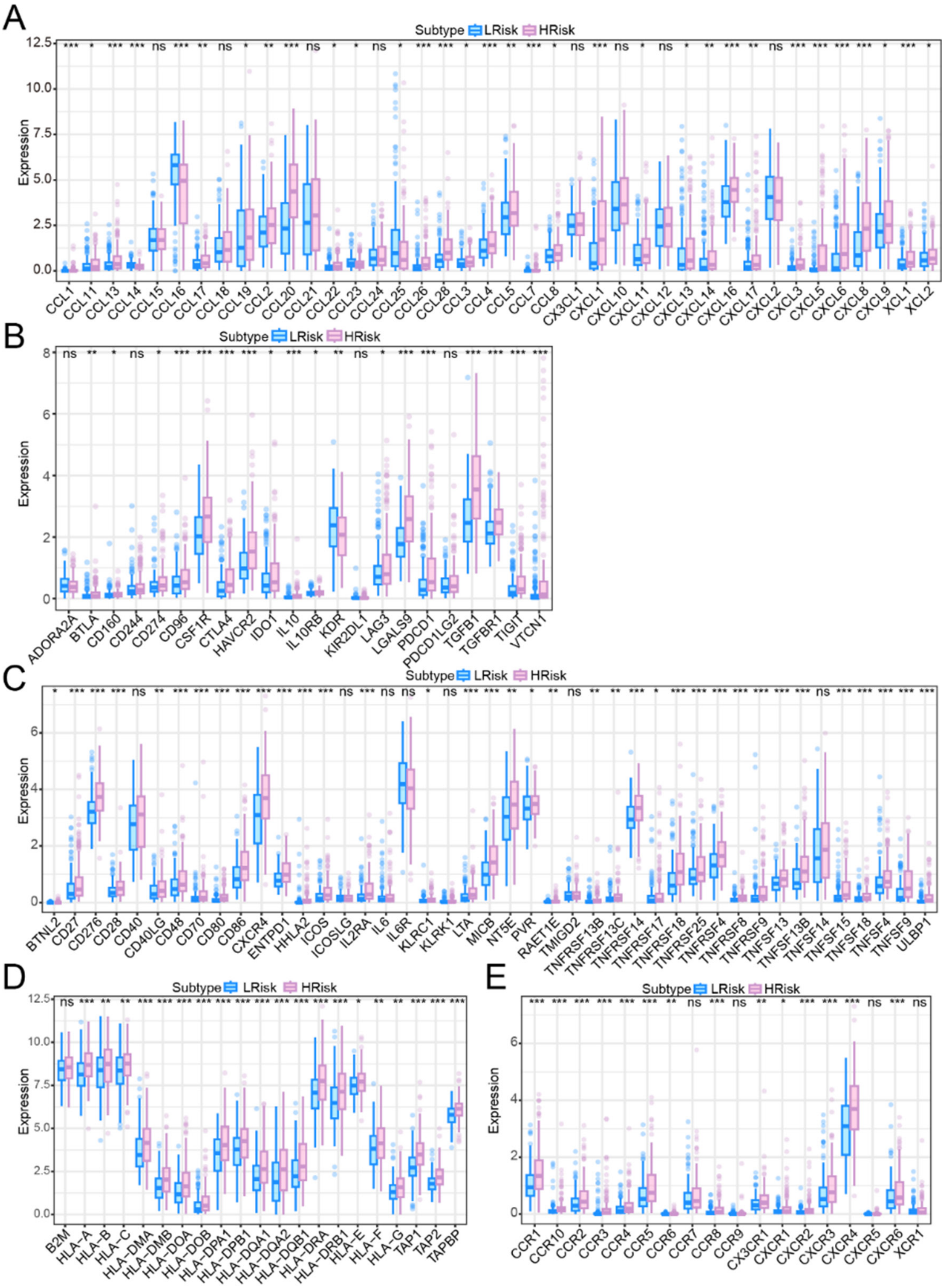

Figure S2 Analysis of immune cell infiltration and gene expression. (A) Box plots depicting the expression levels of immune cell marker genes across different subtypes, categorized by low-risk (LRisk) and high-risk (HRisk) groups. (B) Box plots illustrating the expression levels of immune checkpoint genes in various subtypes, divided between LRisk and HRisk groups. (C) Box plots showing the expression levels of cytokine and chemokine genes across different subtypes, categorized by LRisk and HRisk groups. (D) Box plots representing the expression levels of major histocompatibility complex (MHC) genes in distinct subtypes, separated by LRisk and HRisk groups. (E) Box plots displaying the expression levels of co-stimulatory and coinhibitory genes in various subtypes, classified by LRisk and HRisk groups.

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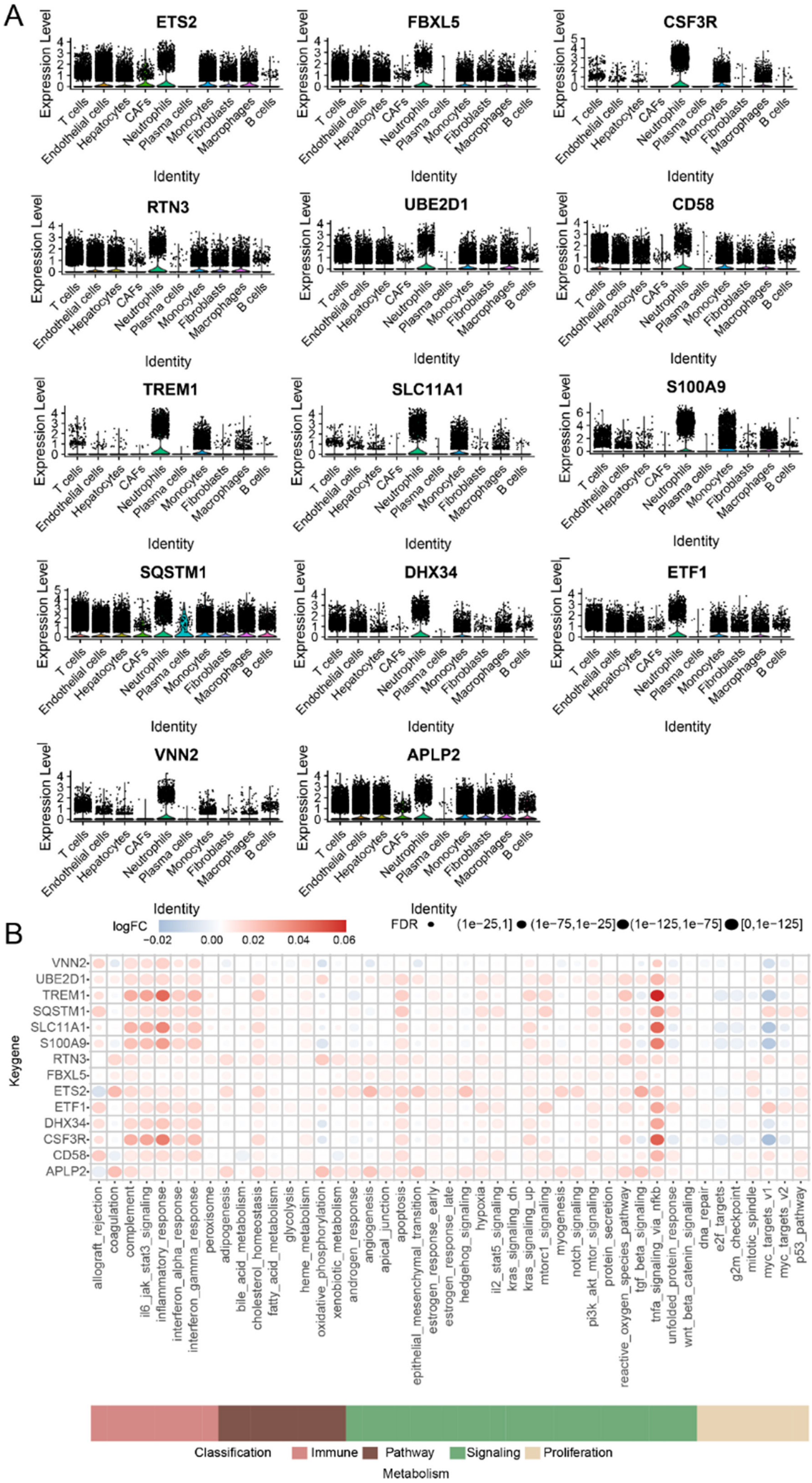

Figure S3 Pathway activity analysis of prognostic signature genes. (A) AUCell pathway activity analysis heatmap displaying the involvement of signature genes in distinct biological processes. (B) Network diagram illustrating the functional associations of signature genes with specific pathways, indicating their roles in immune responses and cellular functions.