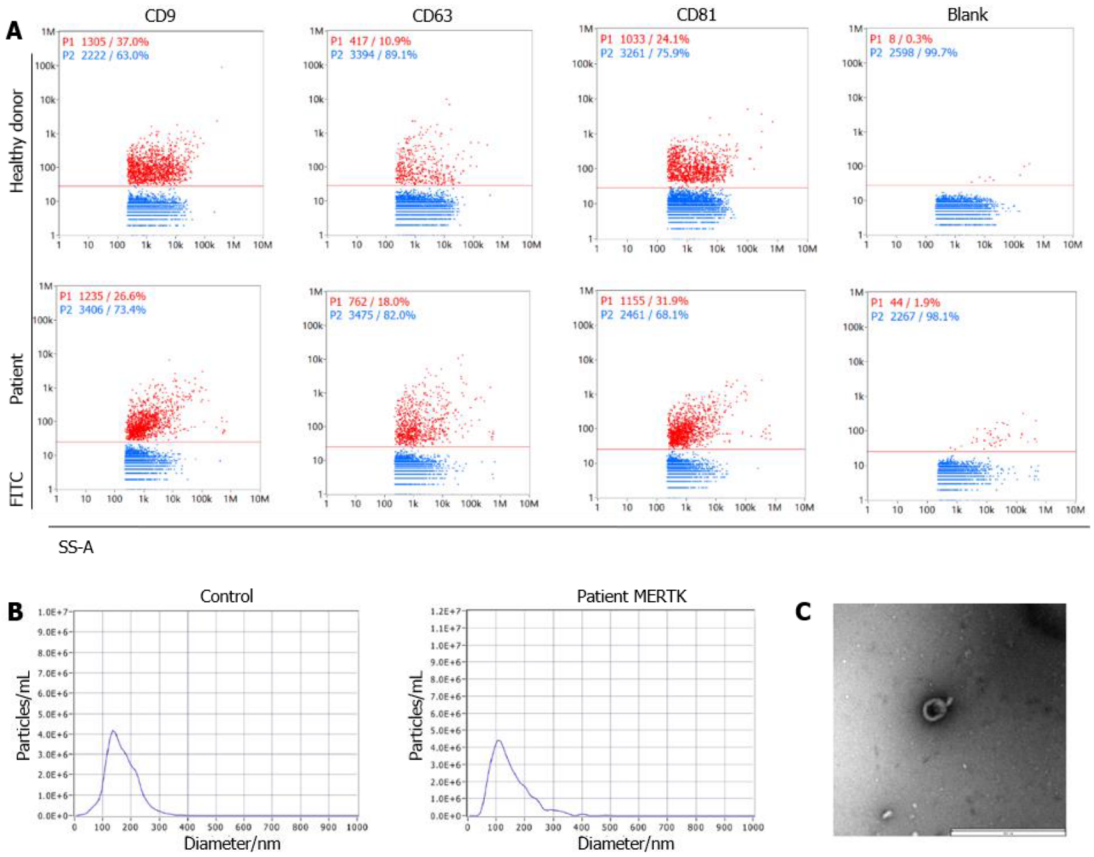
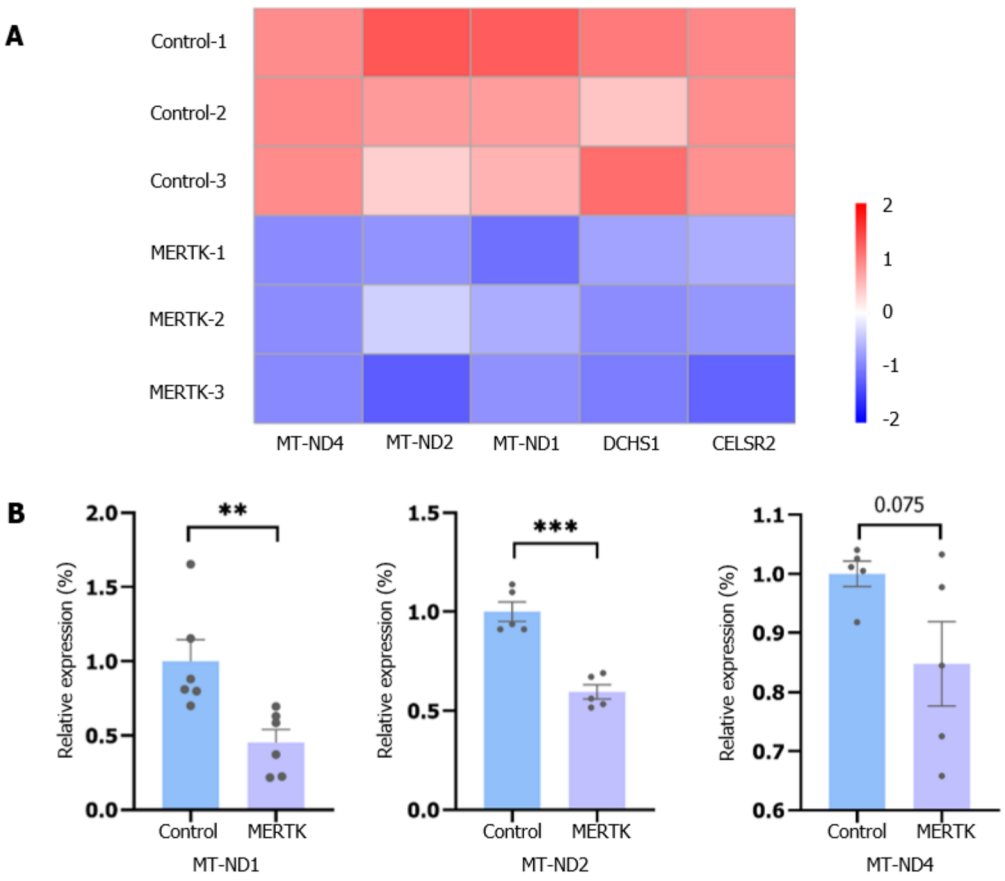
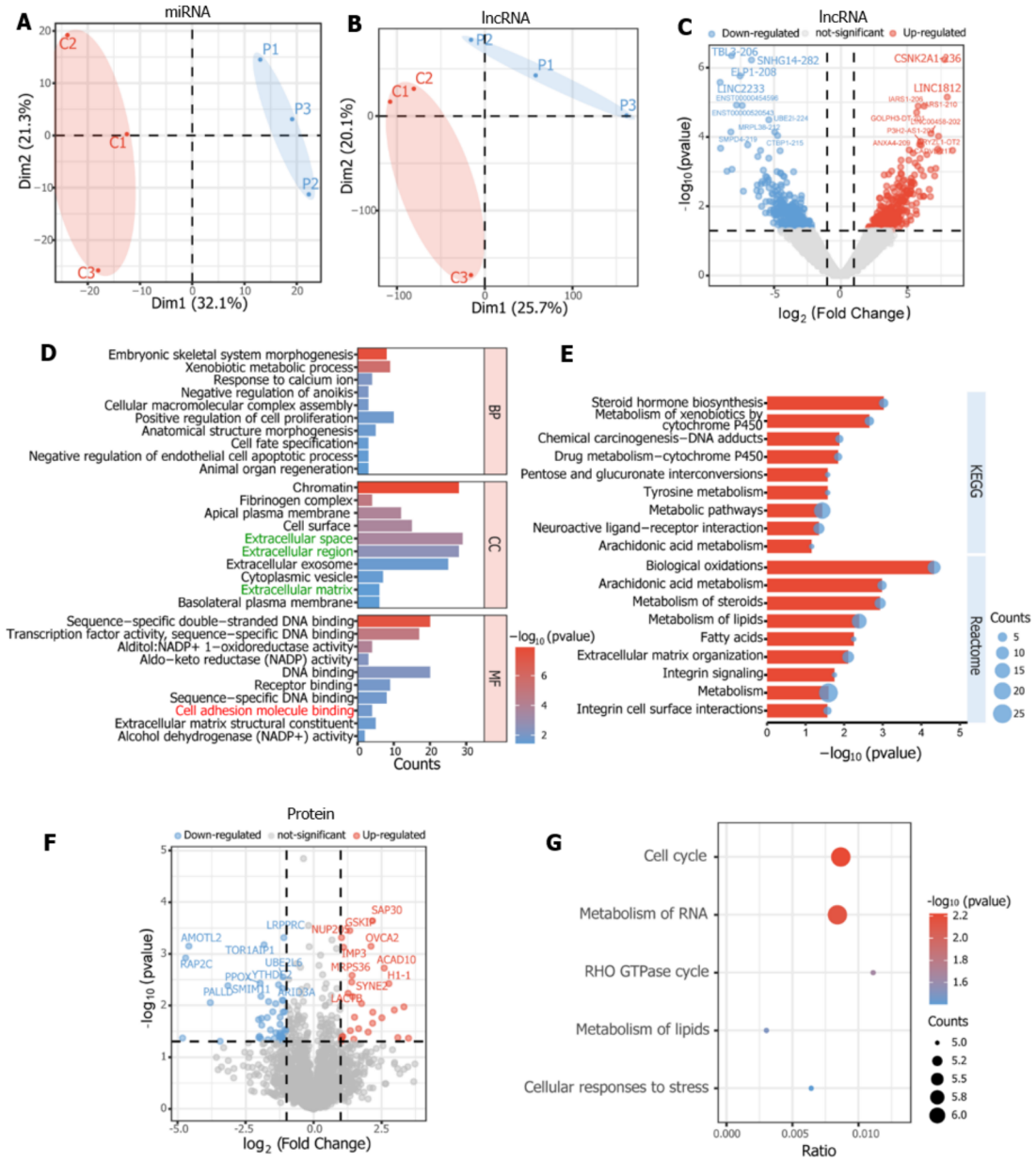


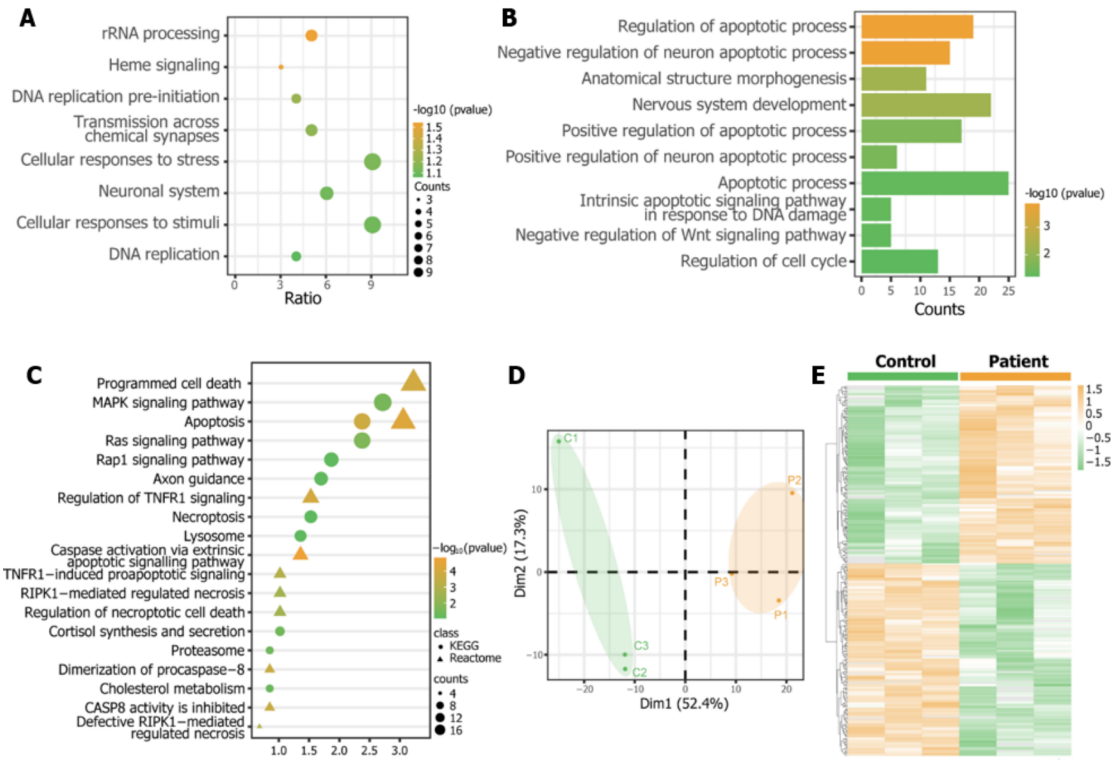
Supplementary Figure 1 Isolation and identification of EVs. A: Nano FCM of surface markers CD9, CD63, CD81 of EVs. B: Nanoparticle Tracking Analysis of isolated EVs. C: Transmission electron microscopyimage of isolated EVs.



Supplementary Figure 2 Expressions of representative mitochondrial genes and cadherin subfamily members. A: Expression heatmap of mitochondrial genes MT-ND1, MT-ND2, MT-ND4, and cadherin subfamily members DCHS1 and CELSR2. B: Relative expressions of MT-ND1, MT-ND2, and MT-ND4 between two groups. Two-tailed t-test, **P < 0.01, ***P < 0.001.



Supplementary Figure 3 Transcriptomic and proteomic analyses identified the differences in cell adhesion, extracellular components, and metabolism between patient iPSCs and control iPSCs. A, B: PCA of miRNA and lncRNA expressions. C: Differentially expressed lncRNAs between patient iPSCs and control iPSCs. D: GO enrichment analysis of differentially expressed lncRNA target genes. E: KEGG and REACTOME enrichment analysis of differentially expressed lncRNA target genes. F: PCA of protein expression. G. KEGG enrichment analysis of differentially expressed proteins.



Supplementary Figure 4 Transcriptomic and proteomic analysis indicated that iPSC-derived EVs helped regulate the cell cycle, response, and neuronal development. A: REACTOME enrichment analysis of differentially expressed lncRNA target genes. B: GO-biological process enrichment analysis of differentially expressed lncRNA target genes. C: KEGG enrichment analysis of differentially expressed lncRNA target genes. D: PCA of iPSC-derived EVs protein cargos. E. Heatmap of iPSC-derived EVs protein expression.