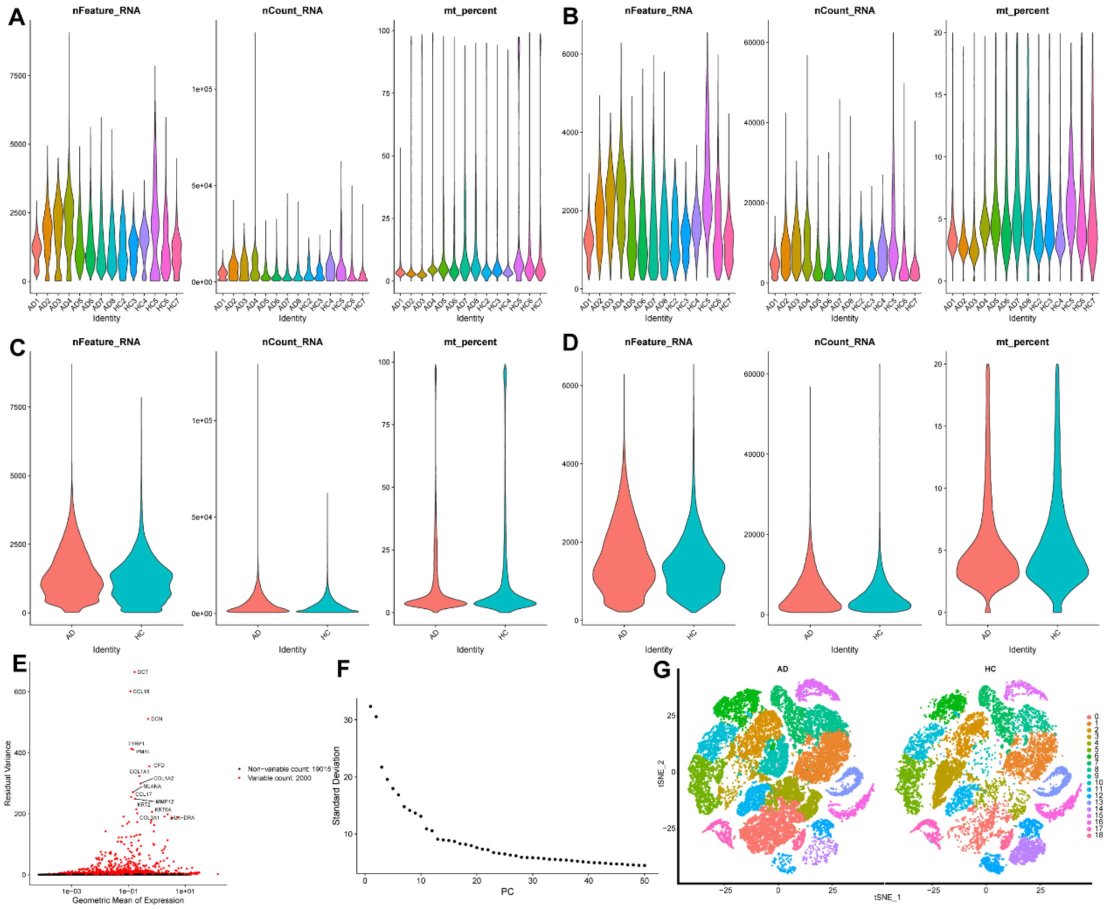
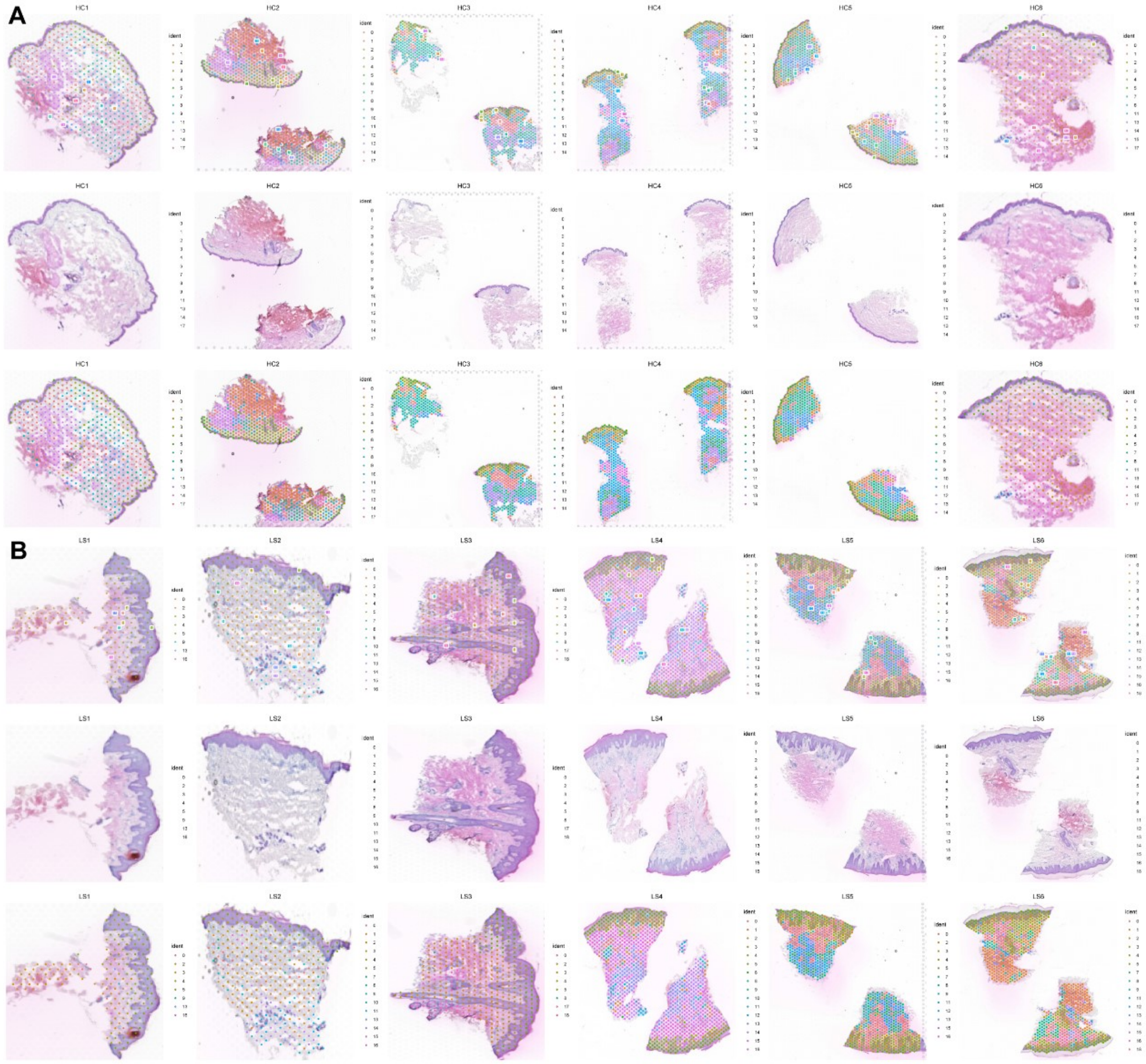
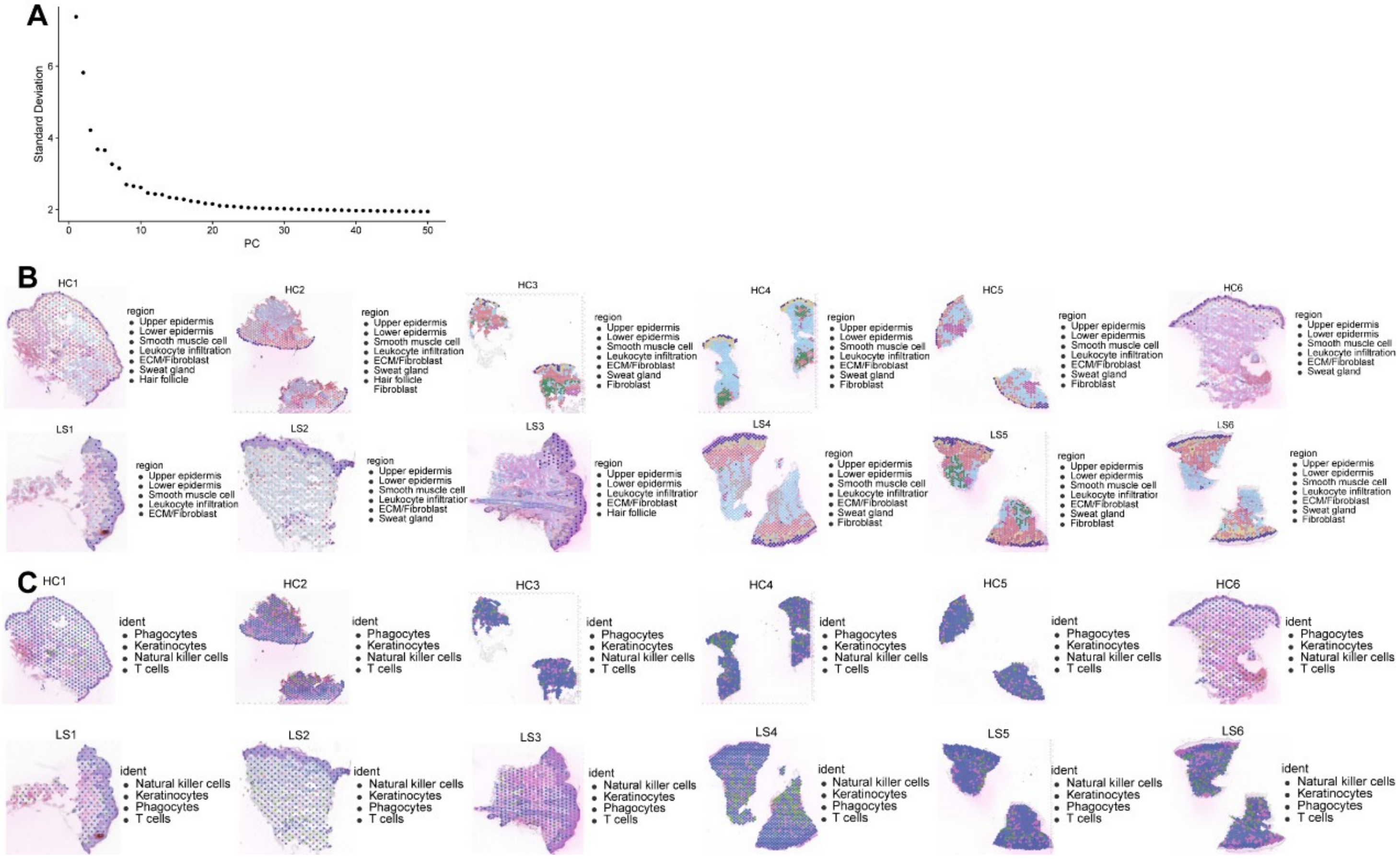


Supplementary Figure S1. ScRNA-seq data processing and clustering. **A, B** – Violin plots illustrating the total gene counts (nFeature_RNA), total gene expression counts (nCount_RNA), and percentage of mitochondrial genes (percent.mt) before (**A**) and after (**B**) cell filtering for each sample. **C, D** – Violin plots displaying the total gene counts (nFeature_RNA), total gene expression counts (nCount_RNA), and percentage of mitochondrial genes (percent.mt) before (**C**) and after (**D**) cell filtering for HC and AD samples. **E** – Volcano plots highlighting the highly variable genes (HVGs). **F** – Elbow plot depicting the principal components (PCs) from principal component analysis (PCA). **G** – t-SNE plots showing the distribution of clusters in HC and AD samples



Supplementary Figure S2. Hematoxylin and Eosin (H&E) Staining and Spatial Clustering of Skin Tissues in HC and AD Samples. A, B – H&E-stained tissue sections and corresponding spatial clusters for HC (**A**) and AD (**B**) skin tissues



Supplementary Figure S3. ST-seq data processing, annotation, and integration with scRNA-seq data analysis. **A** – Elbow plot depicting the principal components (PCs) from principal component analysis (PCA). **B** – Annotation of spatial regions in HC and AD skin tissues. **C** – Mapping of cell types in ST-seq data within HC and AD skin tissues