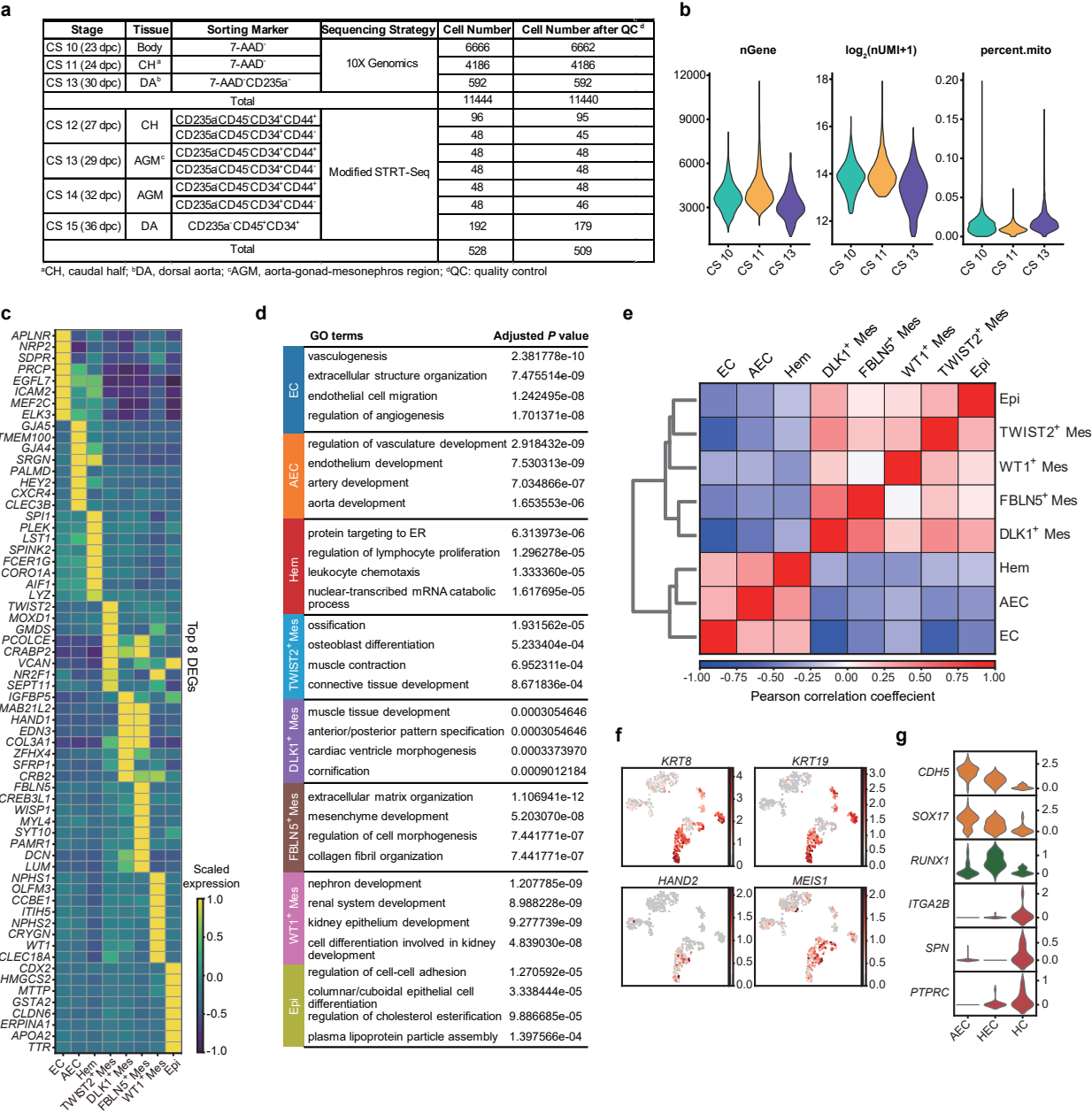




Supplementary Figure 1. Detailed feature of transcriptomically defined cell populations in CS 13 DA

a. Sample information for scRNA-seq data. **b.** Violin plots of cells from 10X-derived datasets (CS 10, CS 11 and CS 13) showing nGene, $\log_2(\text{nUMI}+1)$ and mitochondrial gene expression levels. **c.** Heatmap showing the average expressions of top 8 DEGs for eight clusters. **d.** The enriched major GO:BP terms for each cluster. **e.** Correlation and hierarchical clustering analyses of eight clusters showing that AEC and Hem clusters are more similar with each other, while four mesenchymal populations and Epi cluster correlate more closely to each other. **f.** UMAP plots showing the expression of several featured genes of stromal cells. **g.** Violin plots showing the expression of endothelial and hematopoietic genes in AEC, HEC and HC clusters.