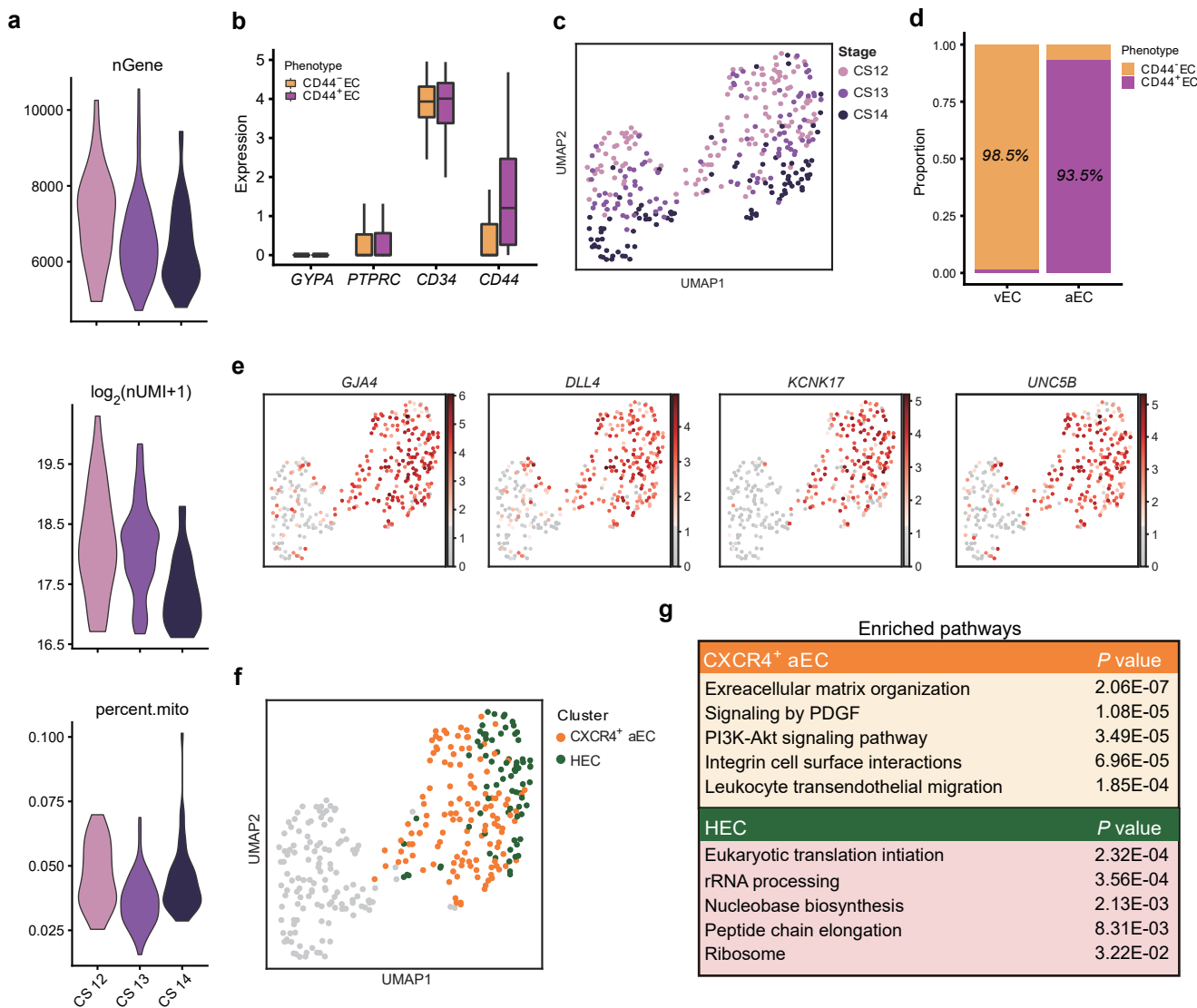




Supplementary Figure 2. Quality of scRNA-seq data of CD44⁺/CD44⁻ ECs and feature of two sub-divided aEC clusters

a. Violin plots displaying gene counts, $\log_2(\text{nUMI}+1)$ and mitochondrial gene percentages of scRNA-seq data generated from CD44⁺/CD44⁻ ECs of CS 12 CH, CS 13 and CS 14 AGM region. **b.** Box plots for the expression of surface markers used for FACS sorting. *GYPA* encodes CD235a and *PTPRC* encodes CD45. **c.** UMAP plot with different sampling stages mapped on it. **d.** Bar plots showing the proportion of immunophenotypic CD44⁺ EC and CD44⁻ EC in aEC and vEC clusters. **e.** UMAP plots showing the expression of several arterial genes. **f.** Mapping of CXCR4⁺ aEC and HEC on the UMAP depicted in Fig. 2b. **g.** Pathways respectively enriched in two aEC sub-clusters.