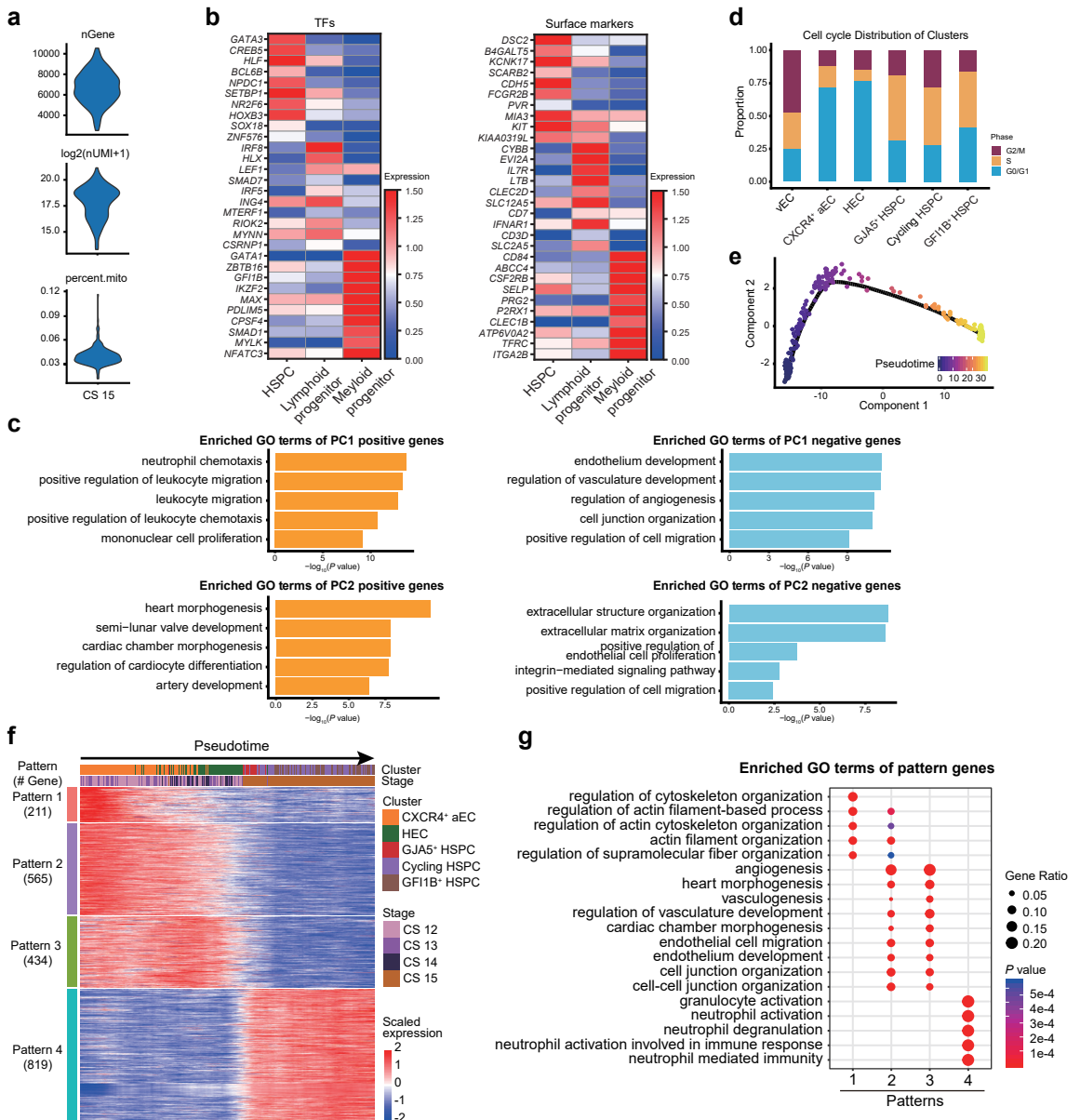




Supplementary Figure 3. Different gene expression patterns and cell cycle status of the cells along the endothelial-to-HSPC transition

a. Violin plots displaying gene counts, $\log_2(nUMI+1)$ and mitochondrial gene percentages of scRNA-seq data generated from CD45⁺CD34⁺ cells of CS 15 DA. **b.** Heatmaps of the scaled average expressions of top 10 differentially expressed TFs (left) and surface markers (right) in HSPC (HSPC1/2/3), Myeloid progenitor and Lymphoid progenitor clusters. **c.** The enriched GO:BP terms for PC 1 (upper) and PC 2 (lower) positive (left) and negative (right) genes from PCA shown in Fig. 3f. **d.** Cell cycle distribution in vEC, CXCR4⁺ aEC, HEC and three HSPC clusters (GJA5⁺ HSPC, Cycling HSPC and GF11B⁺ HSPC). **e.** Pseudotime analysis by Monocle 2. **f.** Heatmap showing the scaled expressions of pattern genes along the trajectory axis inferred by Monocle 2 (smoothed over 20 adjacent cells). Note four patterns are revealed with the number of genes of each pattern is shown. **g.** The enriched GO terms of genes of four different expression patterns.