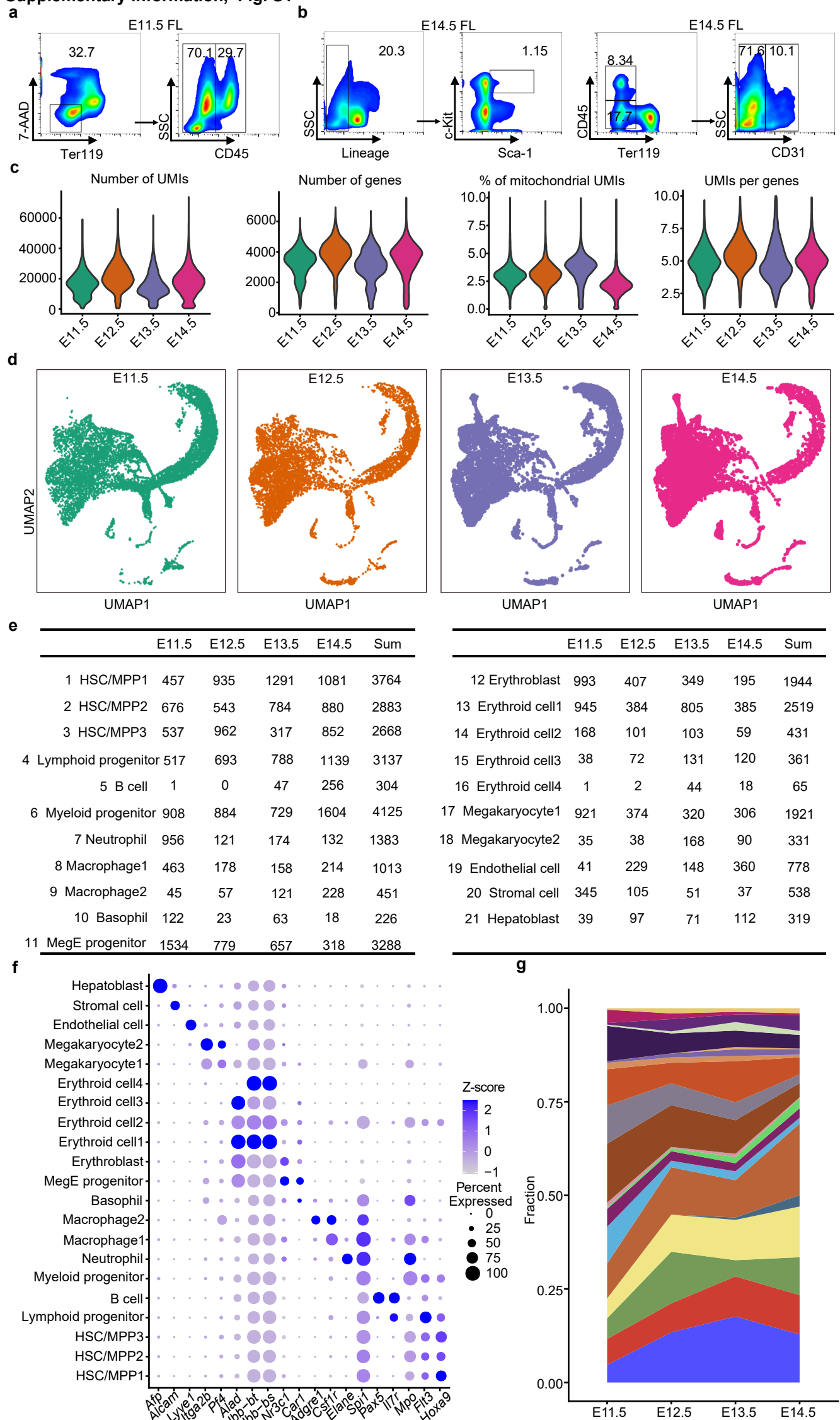


**Supplementary information, Fig. S1**



**Supplementary information, Fig. S1. Sample preparation for scRNA-seq and quality control of scRNA-seq data.** **a** Flow cytometry analysis showing the proportions of CD45<sup>+</sup>Ter119<sup>-</sup>7-AAD<sup>-</sup> hematopoietic cells (HCs) and CD45<sup>-</sup>Ter119<sup>-</sup>7-AAD<sup>-</sup> non-hematopoietic cells (NCs) in E11.5 FL. **b** Flow cytometry analysis showing the proportions of LSK hematopoietic stem cells and multipotent progenitors (HSCs/MPPs), CD45<sup>+</sup>Ter119<sup>-</sup>7-AAD<sup>-</sup> HCs, CD45<sup>-</sup>CD31<sup>+</sup>Ter119<sup>-</sup>7-AAD<sup>-</sup> endothelial cells (ECs), and CD45<sup>-</sup>CD31<sup>-</sup>Ter119<sup>-</sup>7-AAD<sup>-</sup> NCs in E14.5 FL. **c** Violin plots showing the numbers of transcripts, numbers of genes, mitochondria count percentage, and UMI per gene of all cells. **d** UMAP visualization of all cell clusters from E11.5 to E14.5 FL. **e** The cell numbers of 21 cell clusters captured by 10x Genomics in FL. **f** Dot plots showing the expression of known marker genes in all cell types. **g** Percentage of each cell type among the developing FL stages. Colors indicate cell types as shown in (Fig. 1b).