

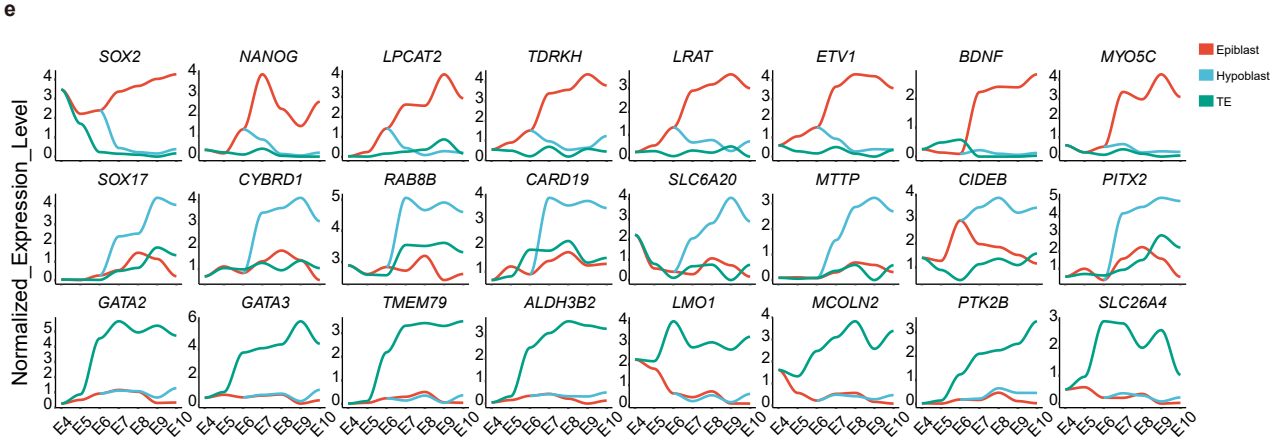
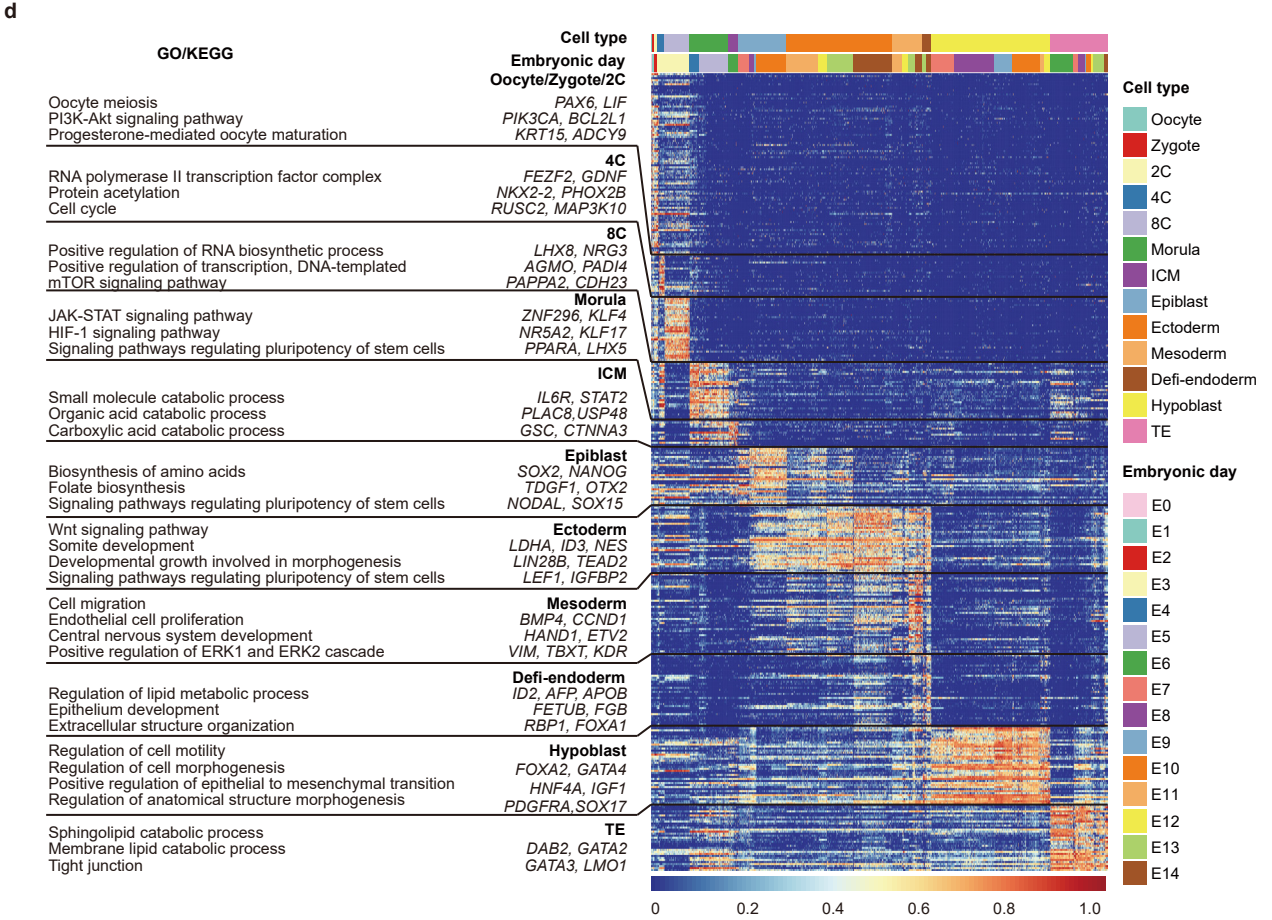
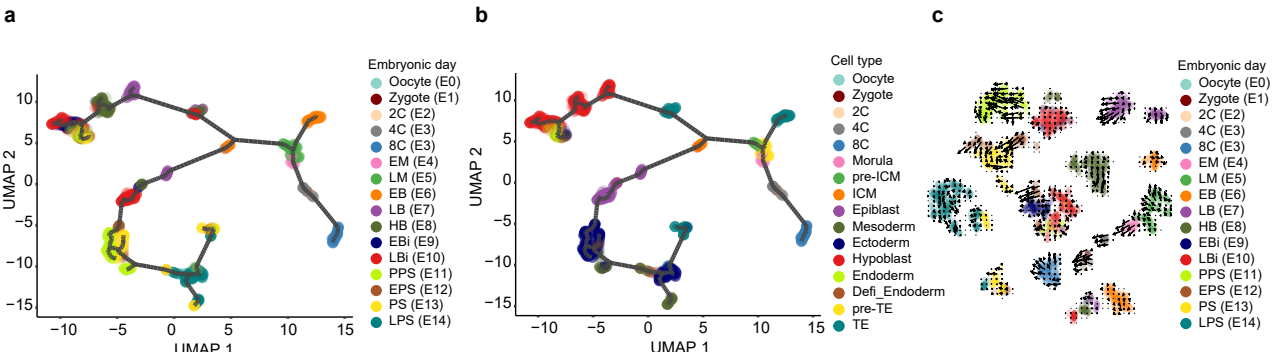


Fig. S1: Single Cell RNA Sequencing of Pig Pre-implantation Embryos, Related to [Fig. 1](#)

a, b Developmental trajectories deduced by pseudotime analysis using monocle 3 and visualized according to embryonic days (**a**) and cell types or lineages (**b**). **c** RNA velocities are visualized on t-SNE plots for the cells at each embryonic stage from E0 to E14. **d** Heat map for the expression of lineage specific genes. The genes were ordered by unsupervised hierarchical clustering (UHC) in each cell type. The representative functional categories that were enriched by relevant genes are shown. **e** Time-course expression profile of canonical and novel lineage markers for epiblast, hypoblast and trophoctoderm.