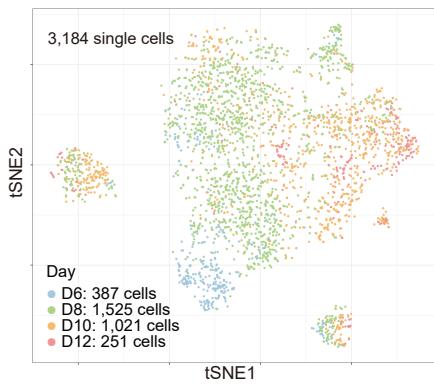
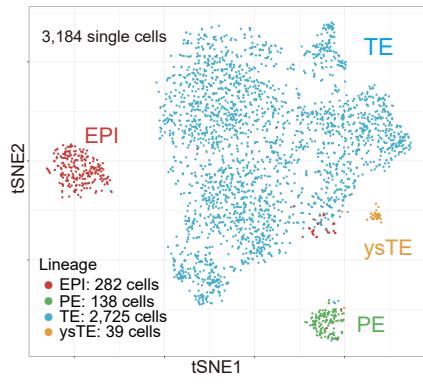
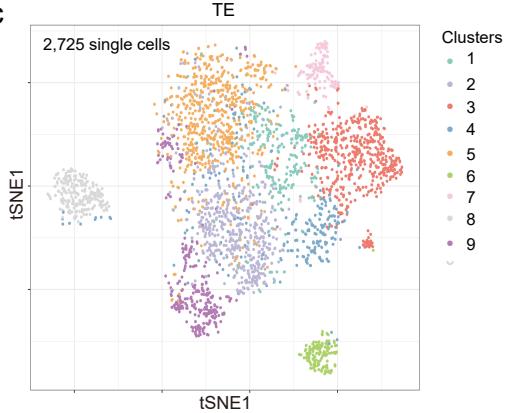
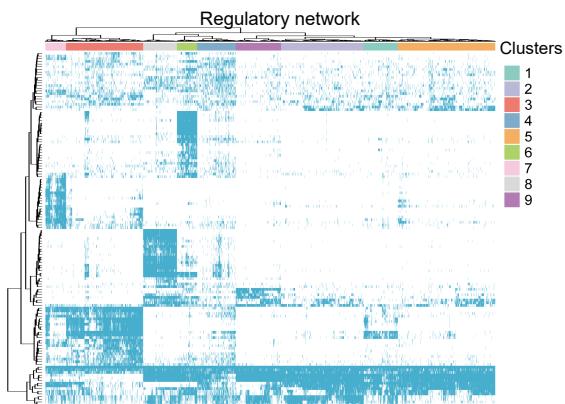
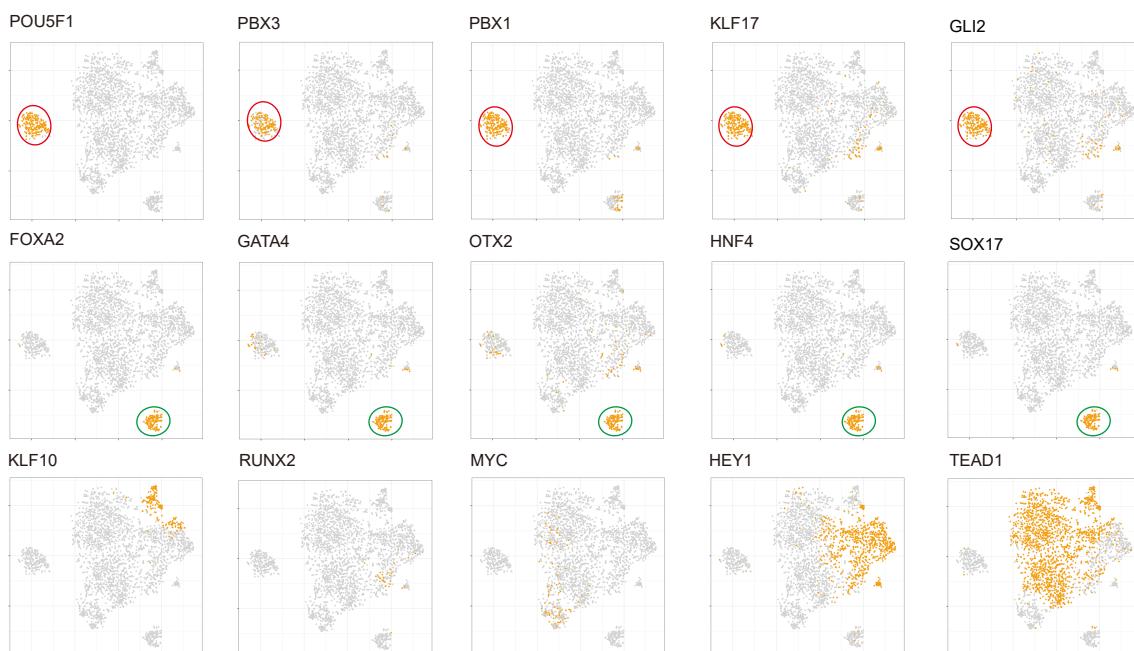
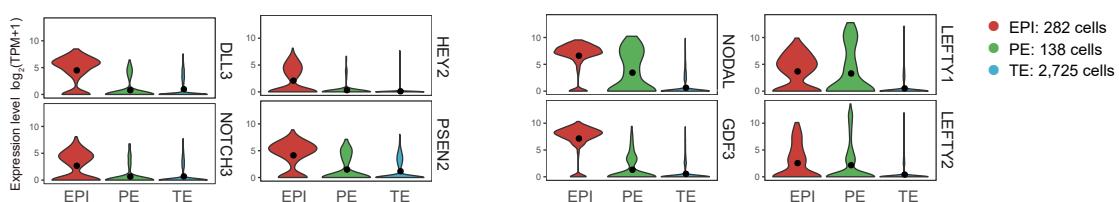


a**b****c****d****e****f**

Transcription factor networks among three lineages.

(a-b) The t-SNE plot on binary regulon activity matrix. Cells are colored according to embryonic stage (a). The t-SNE plot on both the expression matrix and regulon activity matrix have similar lineage clusters. Cells are colored according to the previously defined lineage based on transcriptome expression (b). 3,184 single cells were included. D6: 387, D8: 1,525, D10: 1,021, D12: 251 (a). EPI: 282, PE: 138, TE: 2,725, ysTE: 39 (b).

(c) The t-SNE plot on the binary regulon activity matrix. Cells are clustered by k-means with the binary regulon activity matrix. TE cells were divided into seven clusters based on regulation networks. 3,184 single cells were included.

(d) Heatmap showing the clustered regulon activity matrix, revealing that the different cell types in panel c have distinct regulatory network patterns. The color bar above the heatmap indicates the cell type identified in panel (c)

(e) Selected regulon activity on the t-SNE map. 3,184 single cells were included.

(f) Violin plot showing the expression levels of Notch and Nodal signaling pathway-associated genes in three lineages. Scale="width", all violins have the same maximum width. 3,145 cells were included. EPI: 282 cells, PE: 138 cells, TE: 2,725 cells.