

File name: Supplementary Data 1

Description: The FPKM information of Bulk RNA-seq samples during primed-to-naive transition process. Information regarding K-means clustering of Bulk RNA-seq on gene expression and differential analysis in subpopulations of cells at day 6 and 8.

File name: Supplementary Data 2

Description: Gene lists for human epiblast-specific genes, primed-specific genes, TE, EPI, PrE, DE and TSC signatures used in this study.

File name: Supplementary Data 3

Description: ATAC-seq peak annotation in CAD for cells towards naive pluripotency.

File name: Supplementary Data 4

Description: ATAC-seq peak annotation in CAD for transitioning intermediates remaining RFP-negative.

File name: Supplementary Data 5

Description: The FPKM information of Bulk RNA-seq samples during TSC derivation from RFP+ and RFP-intermediates and prolonged 5iLAF induction process toward naive pluripotency.