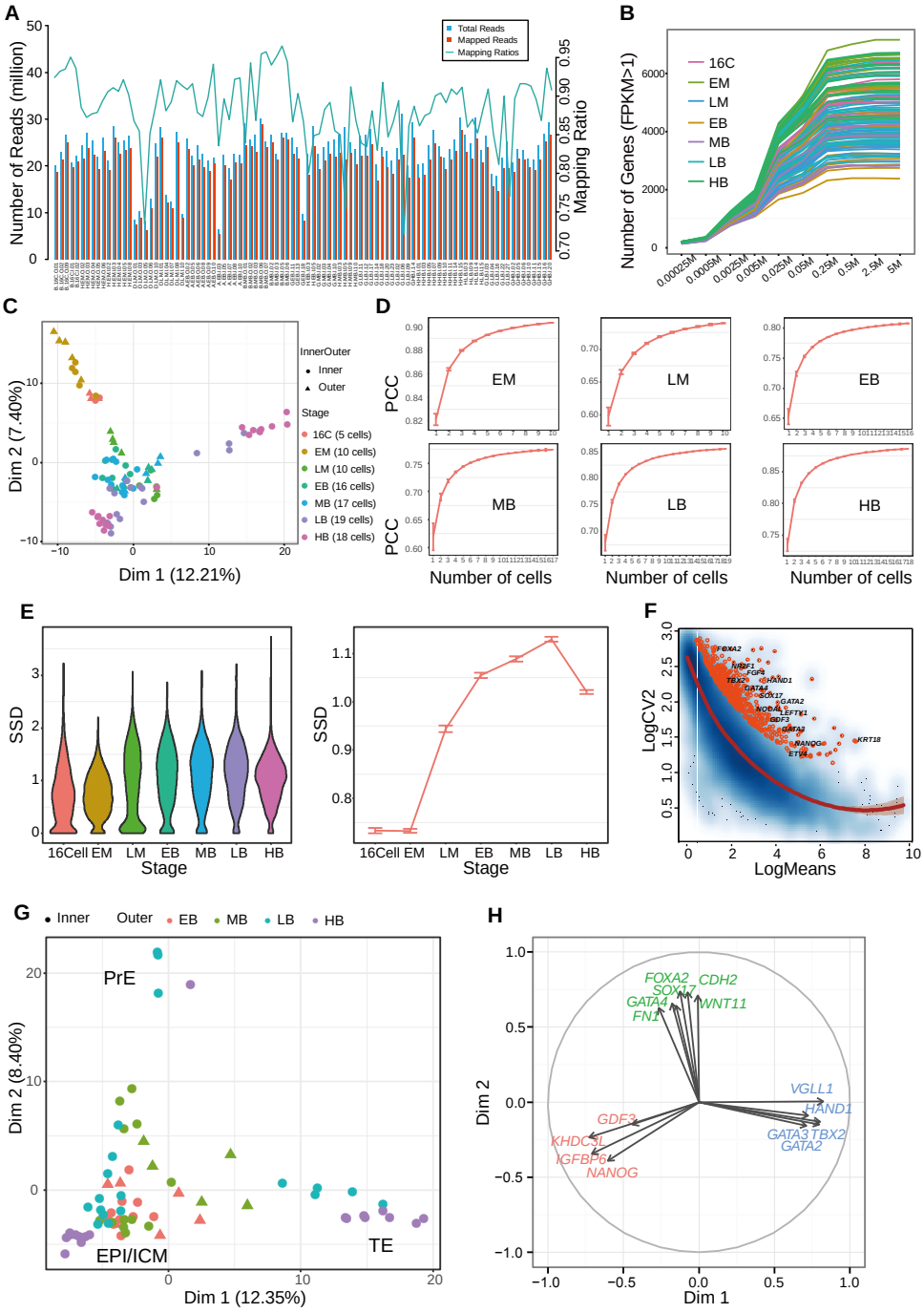
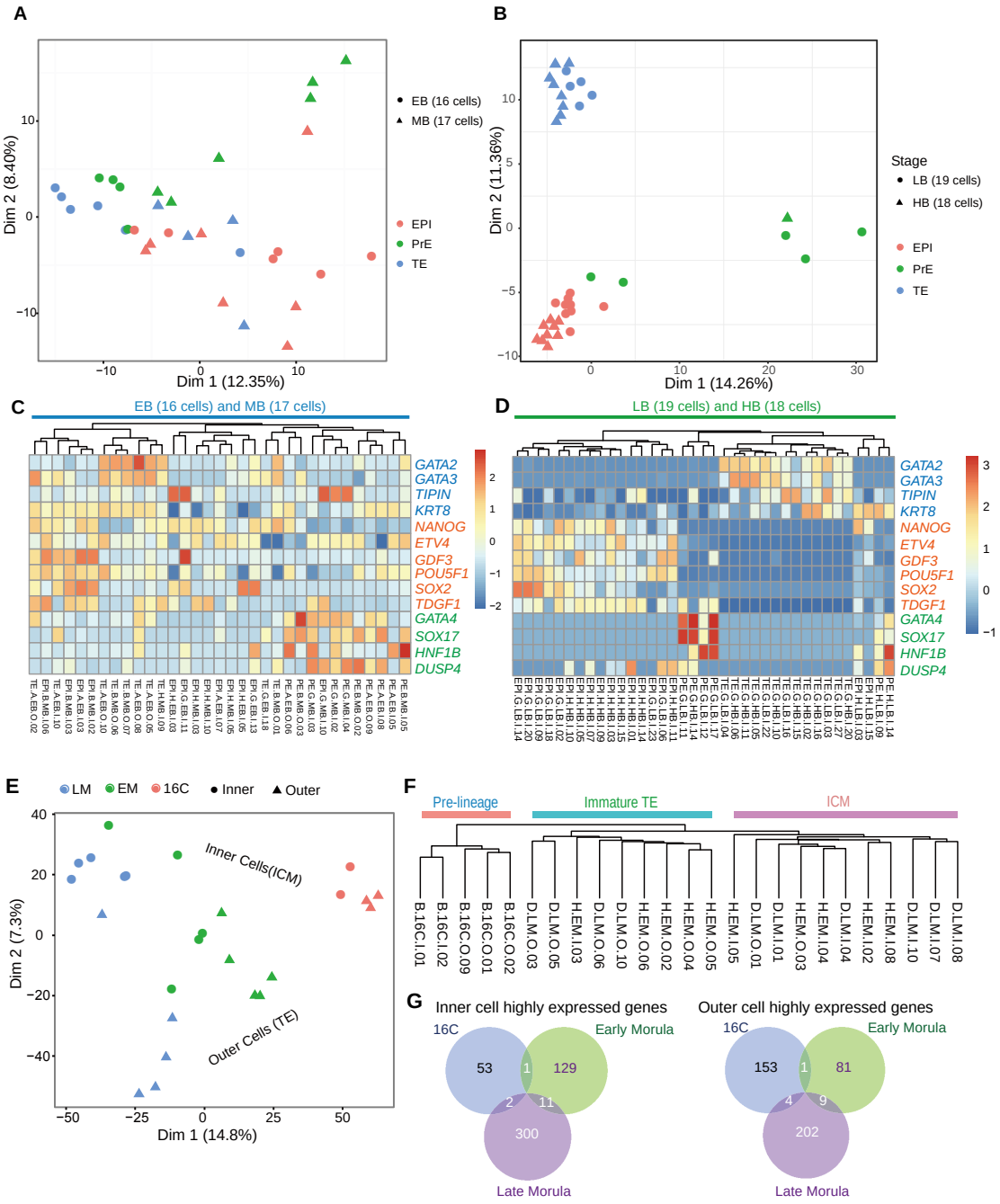
Supplemental Figures



Supplemental Fig. S1. Single cell RNA-sequencing data are of high quality and suitable to define the cell fates.

(A) Summary of total reads, mapped reads and mapping ratios of each single cell. (B) Saturation curve of sequencing and 0.5 million reads are sufficient for single cell gene

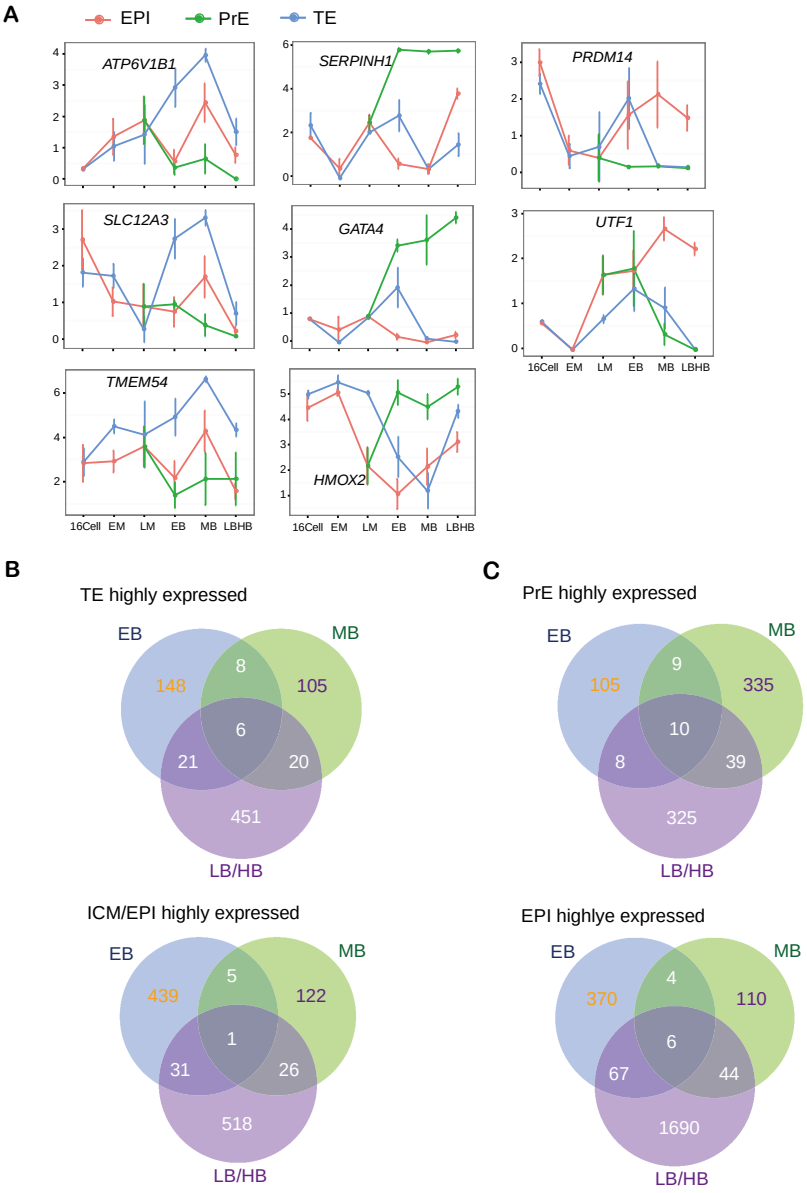
expression quantification. X-axis is represented as the number of random selected reads, and Y-axis is the number of detected genes. (C) PCA result of all single cells. (D) Saturation curve analysis of cell fates. X-axis is the number of single cells for calculating the average expression level. Y-axis is the Pearson correlation coefficient (PCC) between the average expression of random selected single cells and single embryo RNA-sequencing at matching stage. Data are represented as mean ± SEM after sampling for 10 times. (E) Degree of SSD within each stage visualized by Violin plot and line plot. Data are represented as mean ± SEM. (F) The most variable genes identified for downstream lineage construction analysis. Some known marker genes are labeled. (G) PCA analysis also reveals three groups of samples from EB through to HB stages. (H) Genes that have the most loadings in PC1 and PC2. These genes contain some known lineage marker genes, such as *GATA2*, *GATA3*, *TBX2*, *GATA4*, and *SOX17*. Data were performed on batch 1 samples.



Supplemental Fig. S2. Cell lineage specification in rhesus monkey early embryos.

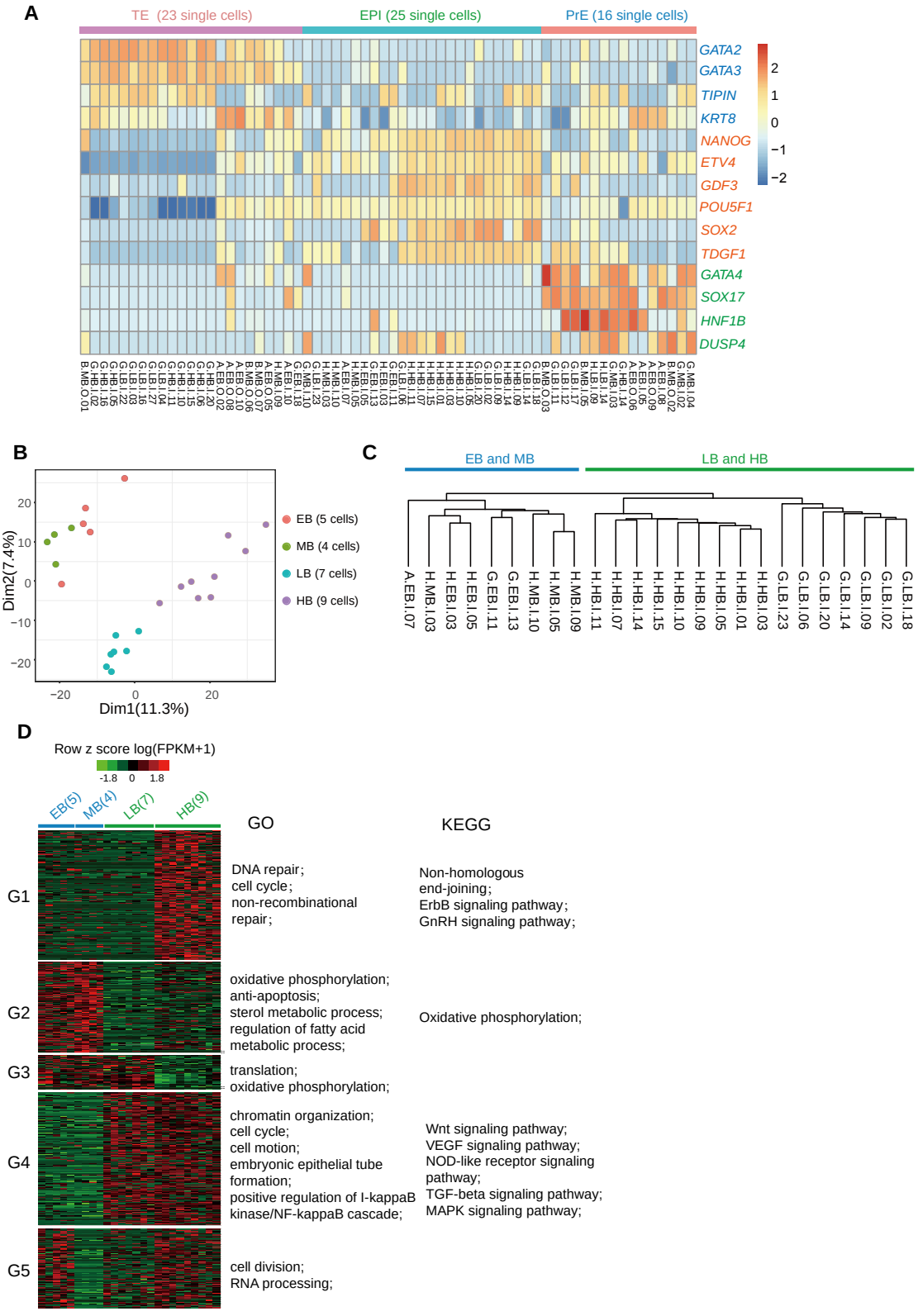
PCA analysis of blastomeres from EB and MB stages (A) and LB and HB stages (B), based on the most variable genes of corresponding stages. (C) Expression of typical lineage marker genes in blastomeres collected from EB and MB. (D) Expression of typical lineage marker genes in blastomeres from LB and HB. (E) PCA analysis of

single blastomeres from 16-cell embryos, EM and LM. (F) Hierarchical clustering of single blastomeres from 16-cell embryos, EM and LM. (G) Numbers of genes highly expressed in inner cells and outer cells at stages of 16-cell, EM and LM (FDR < 0.05). Data were from batch 1 samples.



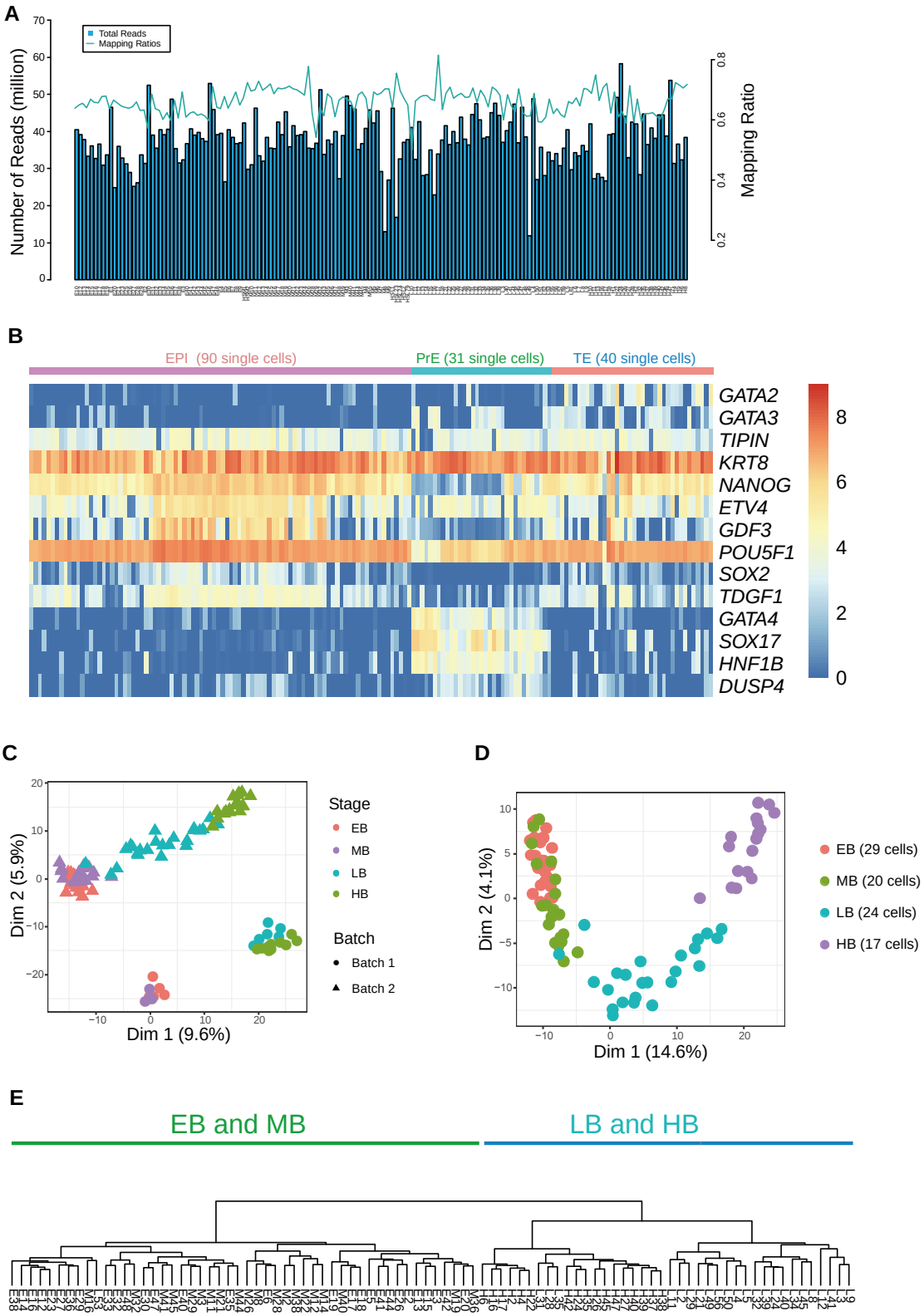
Supplemental Fig. S3. Lineage specific genes at differential blastocyst stages.

(A) Examples of lineage specific genes for TE, EPI and PrE (FDR < 0.01). Data were shown as mean ± SEM. (B) Numbers of the genes highly expressed in TE or ICM from EB through to HB stages (FDR < 0.05). (C) Numbers of genes highly expressed in PrE or EPI from EB through to HB stages (FDR < 0.05). Data were from batch 1 samples.



Supplemental Fig. S4. Analyses of protein coding genes revealed the Naïve-Primed transition during the monkey pre-implantation embryo development.

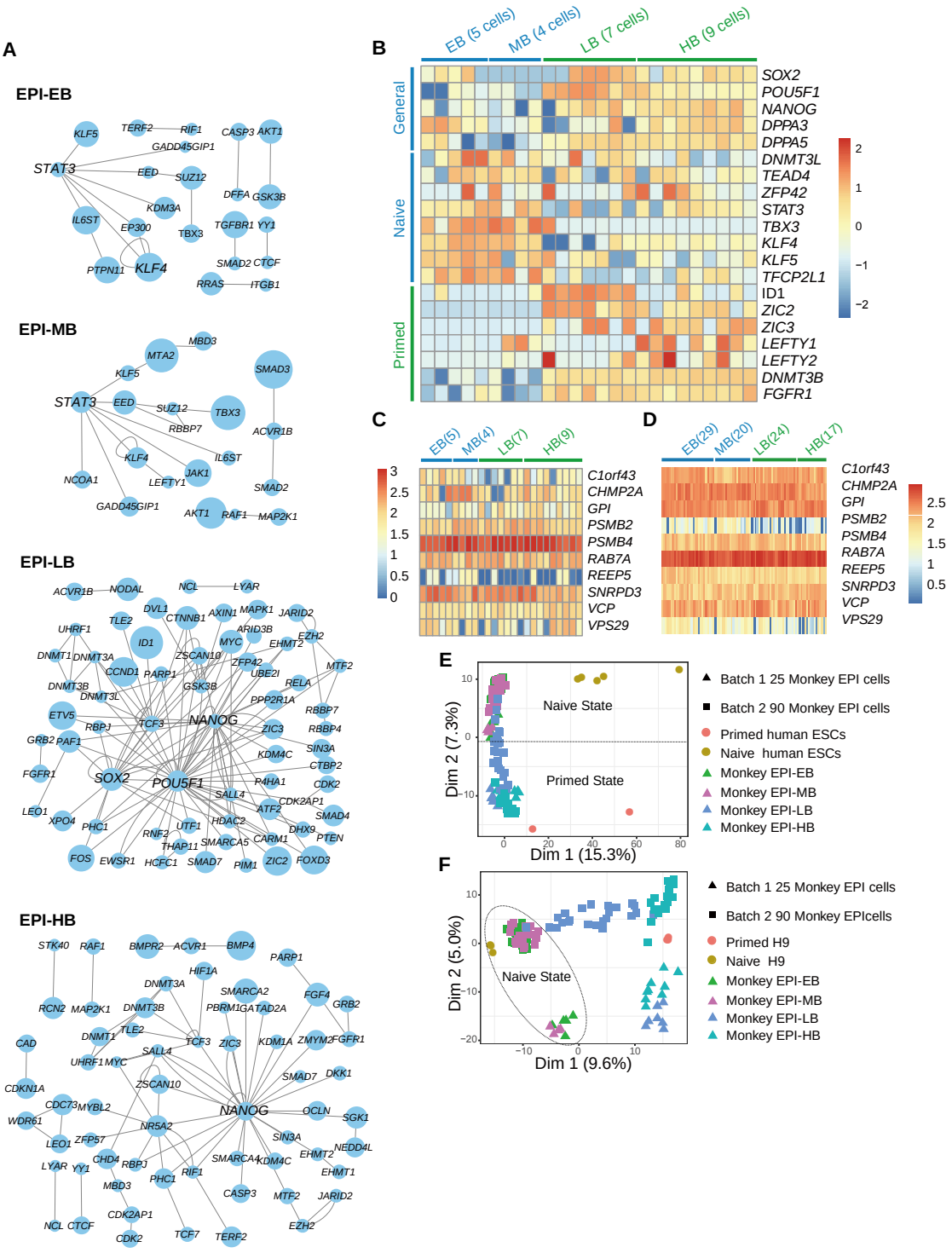
(A) Clustering based on the conserved lineage marker genes identified 25 batch 1 EPI cells for further analysis. PCA (B) and Hierarchical clustering (C) analyses based on the protein coding gene expression revealed the two clusters of batch 1 EPI cells from EB through to HB stages. (D) BICSKmeans clustering of differential expressed genes (DEGs) (FDR < 0.01) in batch 1 EPI cells from EB through to HB stages. The GO terms and KEGG enrichment of each group of DEGs were shown.



Supplemental Fig. S5. Quality control of the batch 2 single cells.

(A) Summary of total reads, mapped reads and mapping ratios of 161 batch 2 single cells. (B) Clustering based on the conserved lineage marker genes identified 90 batch

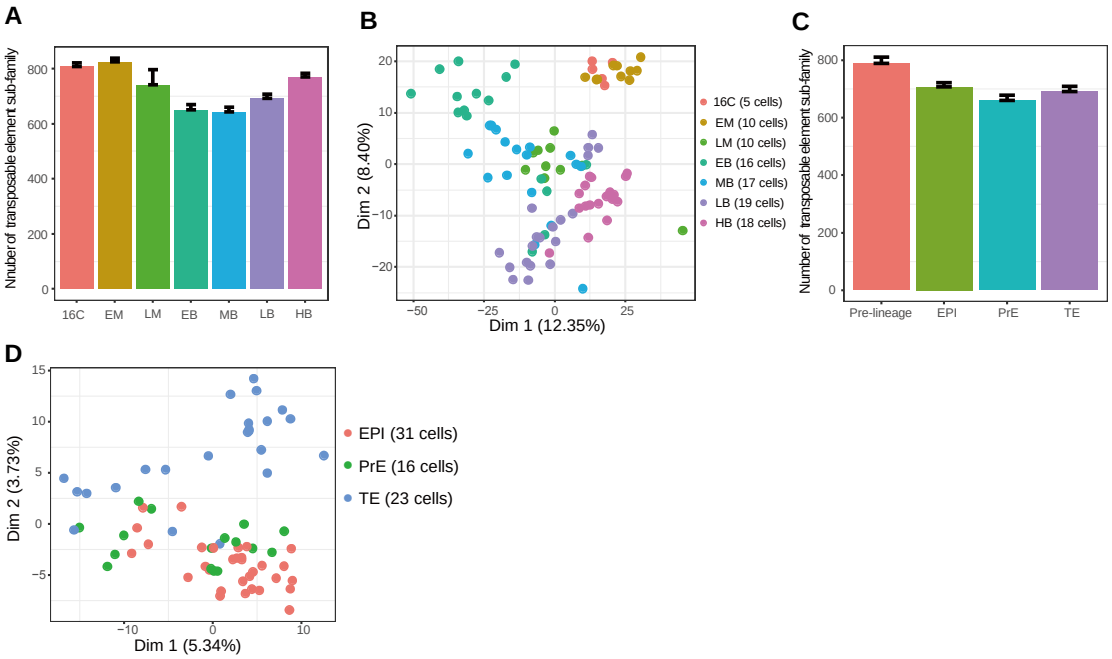
2 EPI cells for further analysis. (C) PCA analysis on the batch 1 and batch 2 EPI cells revealed the consistent segregation pattern. PCA analysis (D) and hierarchical clustering (E) of the batch 2 EPI cells revealed the dynamic change of cellular state.



Supplemental Fig. S6. Distinct pluripotent states exist in rhesus monkey pre-implantation embryos.

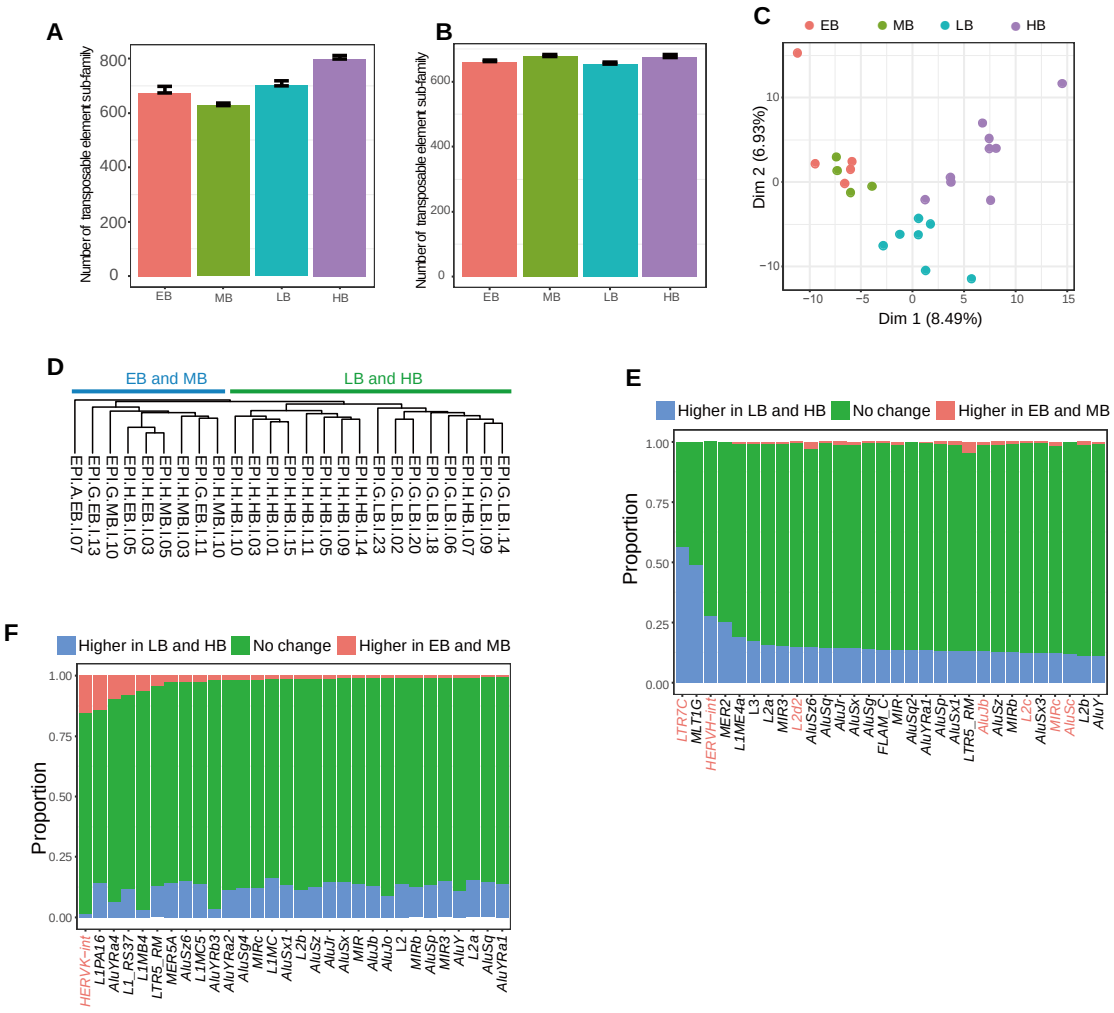
(A) PluriNetWork analysis on batch 1 EPI cells from four blastocyst stages revealed a transition of network topology from mid- to late- blastocyst stage. (B) Expression

pattern of marker genes for naïve pluripotency, primed pluripotency and general pluripotency in batch 1 EPI cells of EB, MB, LB, and HB in rhesus monkey. Expression pattern of house-keeping genes in batch 1 (C) and batch 2 (D) EPI cells from EB through to HB. (E, F) Comparative transcriptome analysis between our rhesus monkey EPI cells and human naïve/primed ESCs. Human ESC transcriptome data were from Theunissen et al. 2014 (E) or from Takashima et al. 2014 (F).



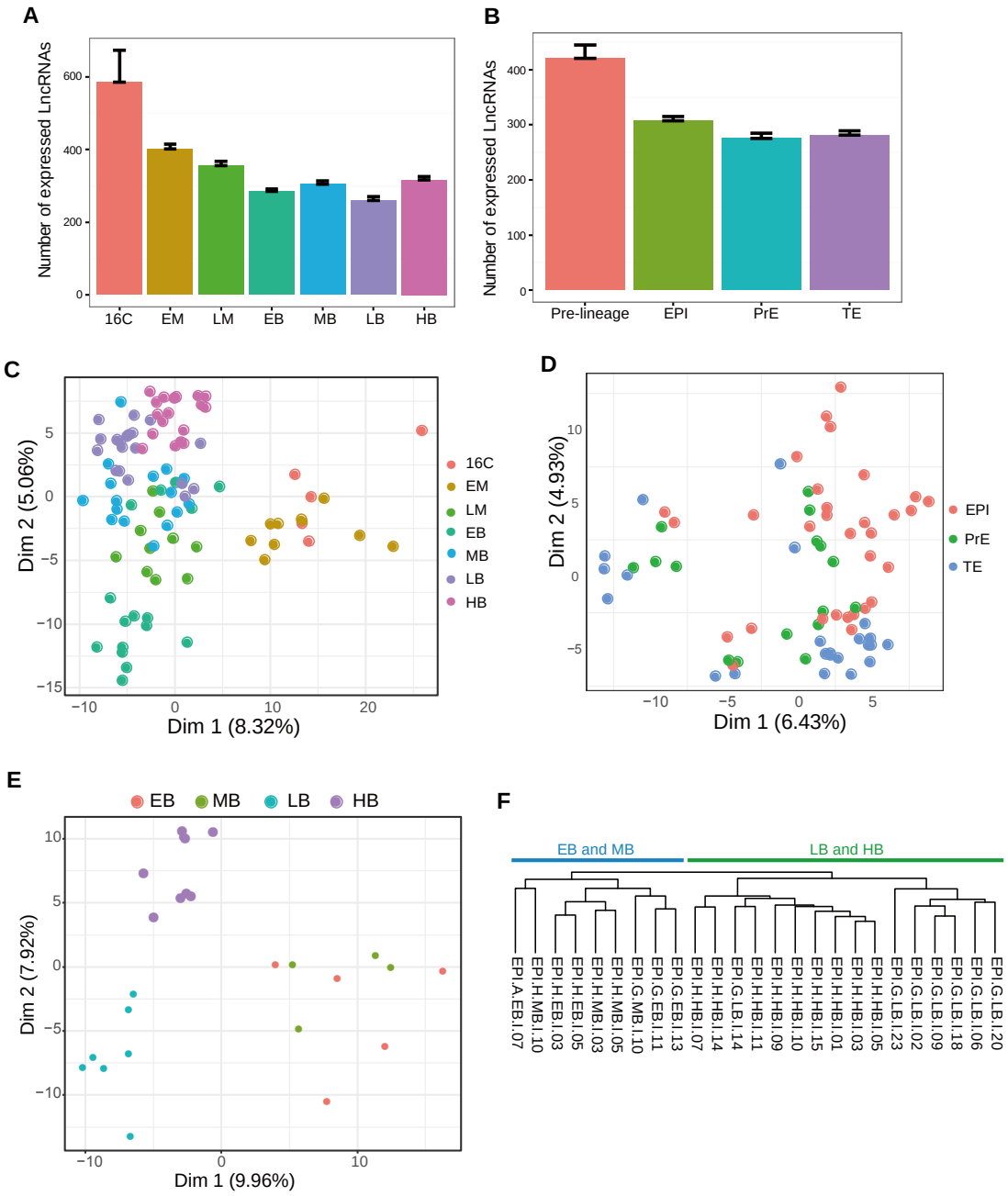
Supplemental Fig. S7. Expression of transposable element subfamilies in rhesus monkey pre-implantation embryos.

(A) The numbers of expressed transposable element subfamilies (FPKM > 1) at different developmental stages. Data were shown as mean ± SEM. (B) The expression profiles of transposable element could well separate the samples of differential development stages. (C) The numbers of expressed transposable element subfamilies (FPKM > 1) in different cell lineages. (D) The expression profiles of transposable element could separate the samples of different lineages. Data were from batch 1 samples.



Supplemental Fig. S8. Dynamic changes of transposable element expression in EPI cells of four blastocyst stages.

The numbers of expressed transposable element subfamilies in batch 1 (A) and batch 2 (B) EPI cells of four blastocyst stages. PCA (C) and hierarchical clustering (D) could well separate the batch 1 EPI cells into two clusters (EB-MB cluster and LB-HB cluster). (E) Summary of the transposable elements that showed higher expression in LB and HB stages in batch 1 EPI cells. (F) Summary of the transposable elements that showed higher expression in EB and MB stages in batch 1 EPI cells.



Supplemental Fig. S9. Dynamic changes of lncRNA expression in EPI cells from four blastocyst stages.

The numbers of expressed lncRNAs (FPKM>1) in blastomeres collected from differential developmental stages (A) and cell lineages (B). The expression profiles of lncRNAs could separate the samples of different developmental stages (C) and cell lineages (D). PCA (E) and Hierarchical clustering (F) analyses based on lncRNA

expression profiles well separated the EPI cells of EB and MB stages from those of LB and HB stages. Data were from batch 1 samples.