

**Single-cell RNA-seq analysis revealed molecular regulation of hematopoietic stem cells fate decisions in response to hypoxia**

Haijing Wang<sup>1, 2, 3, 4</sup>, Zhenyuan Cai<sup>1, 2, 4</sup>, Pengfei Song<sup>1, 2, 4</sup>, Daoxin Liu<sup>1, 2, 4</sup>, Feng Jiang<sup>1, 2, 4</sup>,  
Bo Xu<sup>1, 2, 4</sup>, Tongzuo Zhang<sup>1, 2, 4, \*</sup>

**Affiliation:**

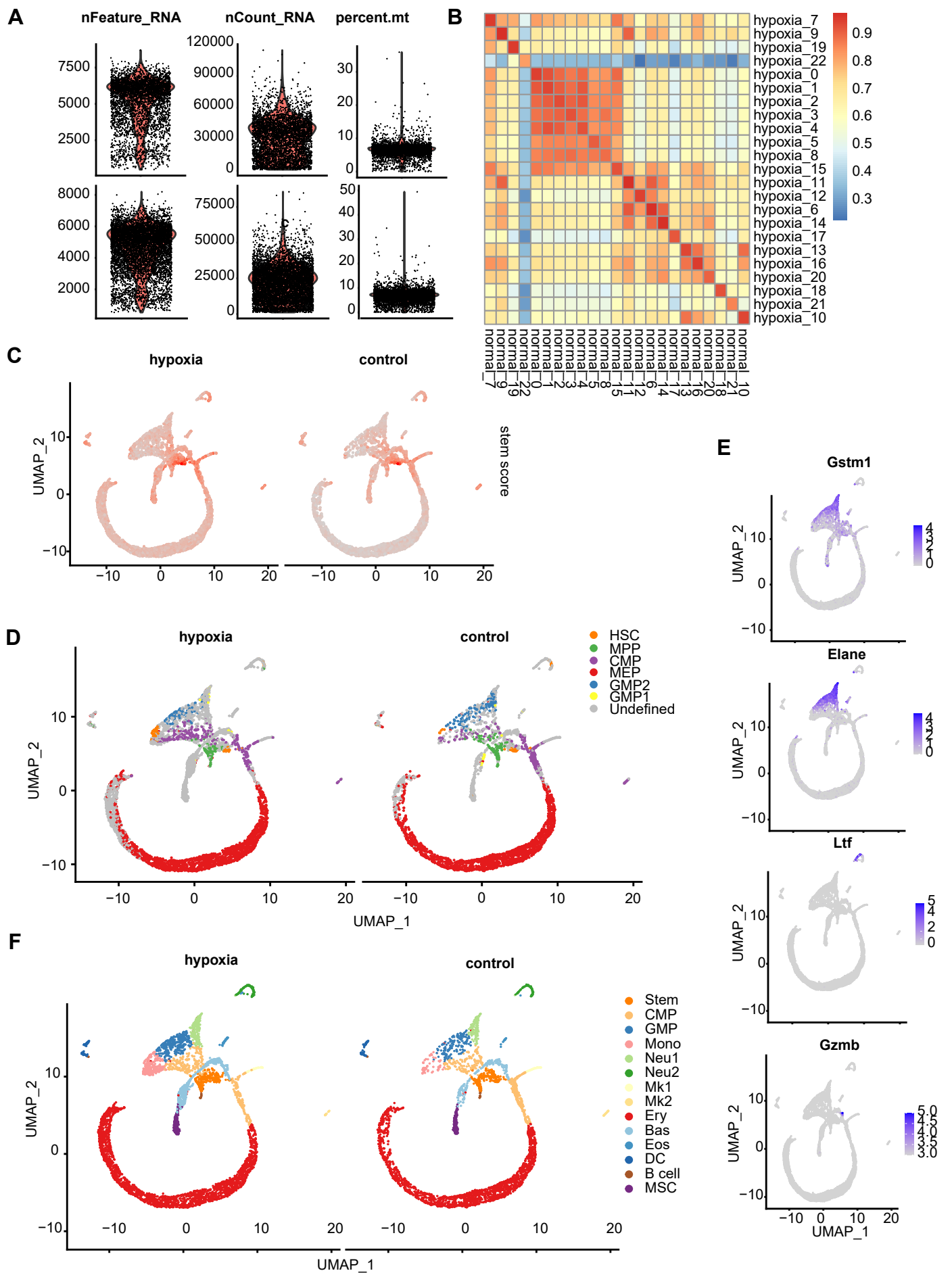
1Key Laboratory of Adaptation and Evolution of Plateau Biota, Northwest Institute of Plateau Biology, Chinese Academy of Sciences, Xining 810001, Qinghai, China;

2 University of Chinese Academy of Sciences, Beijing 100049, China.

3Medical College of Qinghai University, Xining 810016, Qinghai, China;

4Qinghai Provincial Key Laboratory of Animal Ecological Genomics, Xining 810008, Qinghai, China;

\*Corresponding author, E-mail: zhangtz@nwipb.cas.cn.



Supplementary Figure 1

A Quality control for single cell RNA-seq data.

B Heatmap for correlation of 23 clusters between hypoxic group and control.

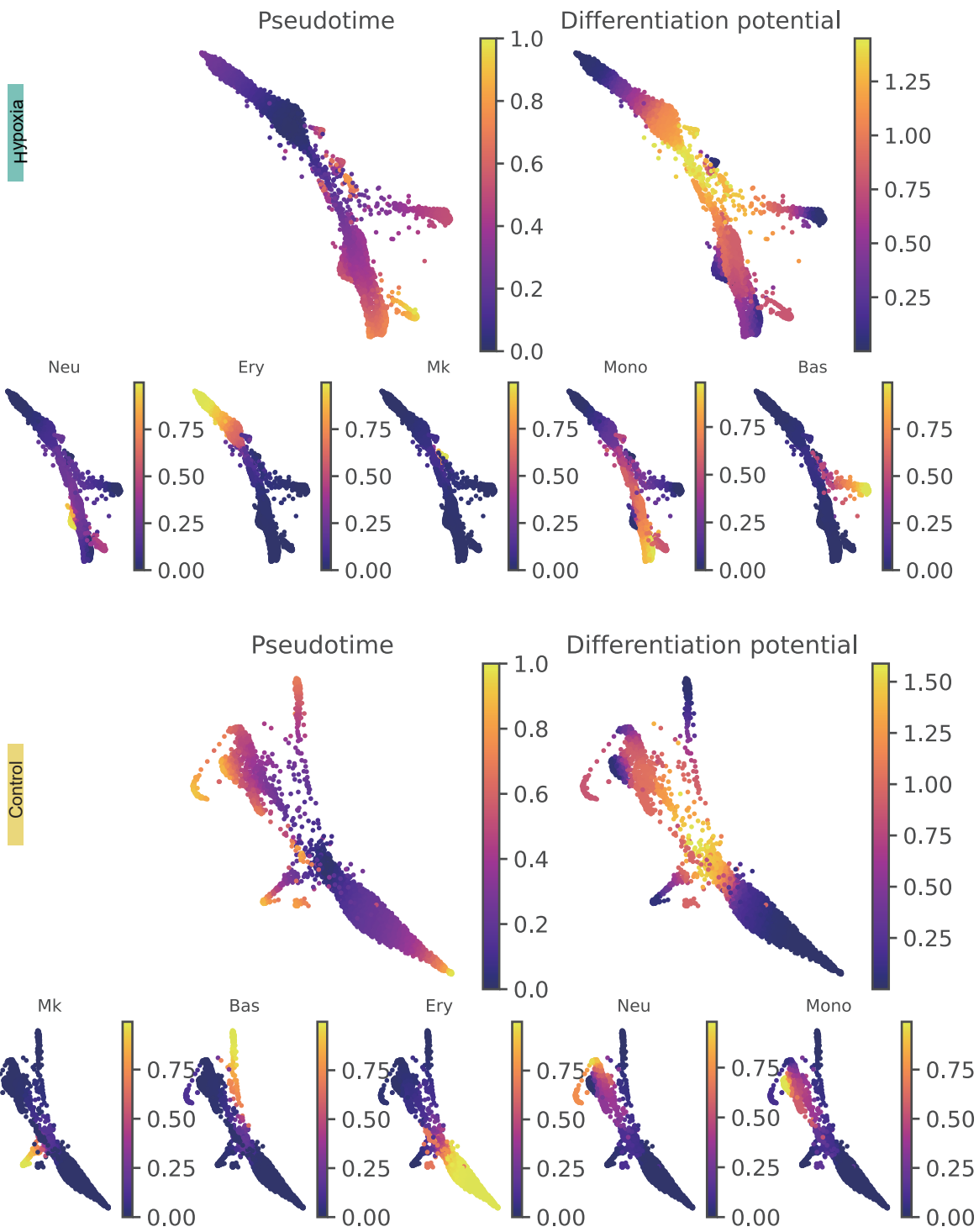
C The stem score was caculated by AUCell in two group.

D Projection of single cells on GSE144273.

E The expression of marker genes in Neu1 and Neu2 clusters

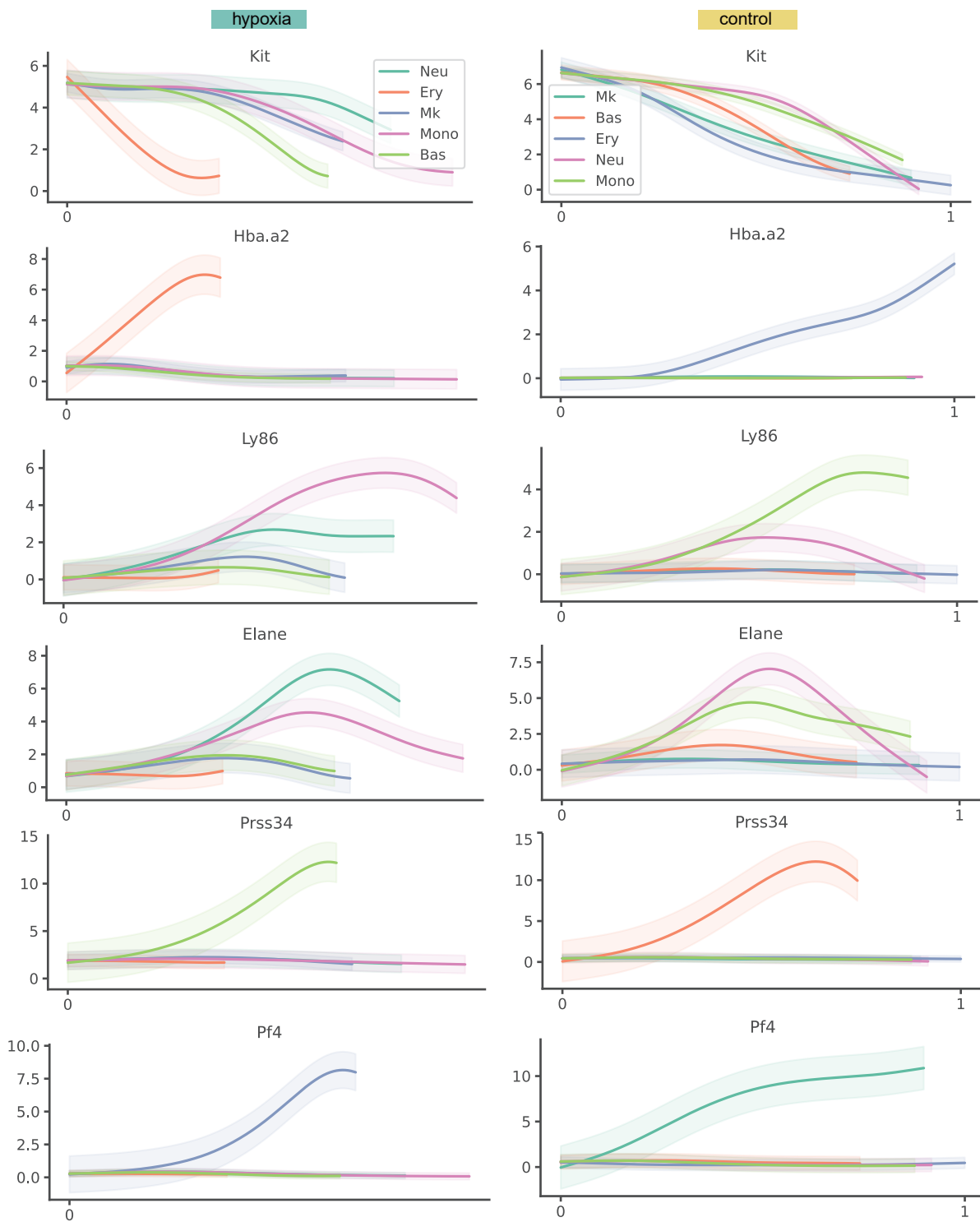
F UMAP representation of cell populations from integration dataset split by treatment (hypoxia and control).





Supplementary Figure 2

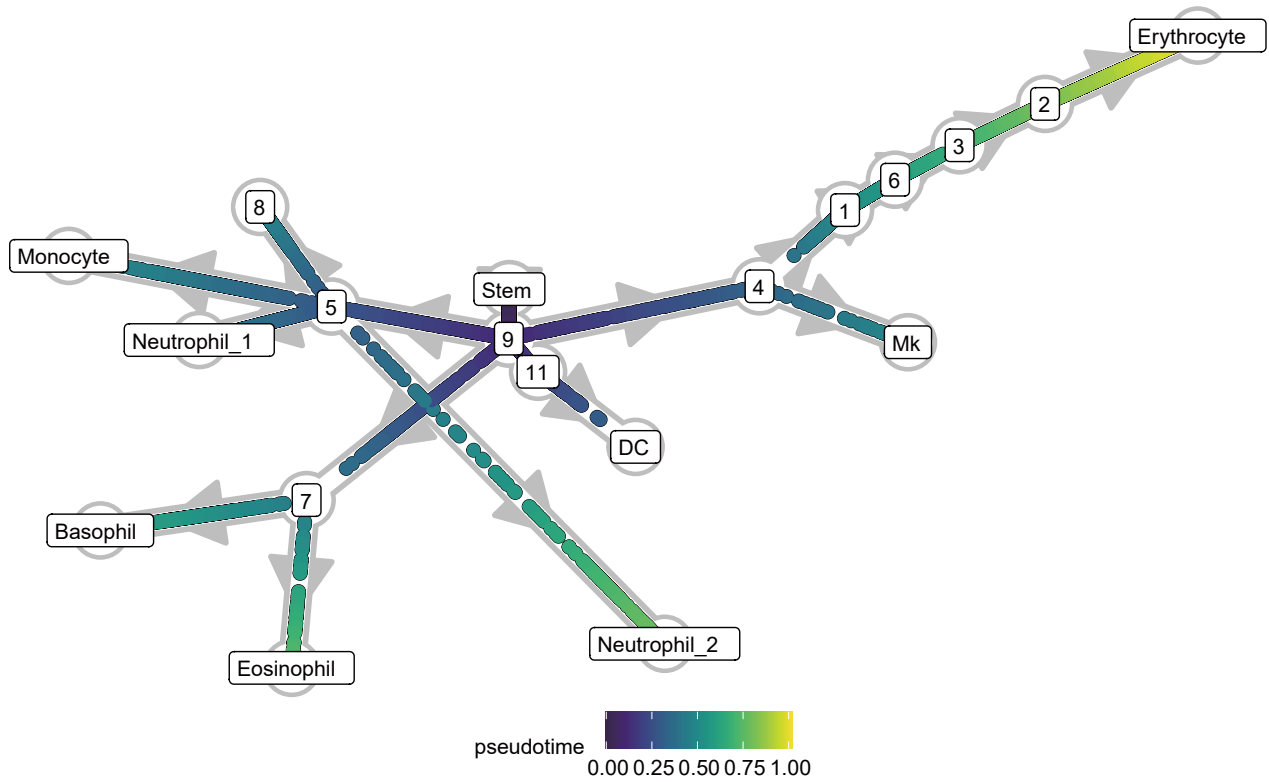
The trajectory identified by Palantir (Top panel: the hypoxia group; bottom panel: the control group).



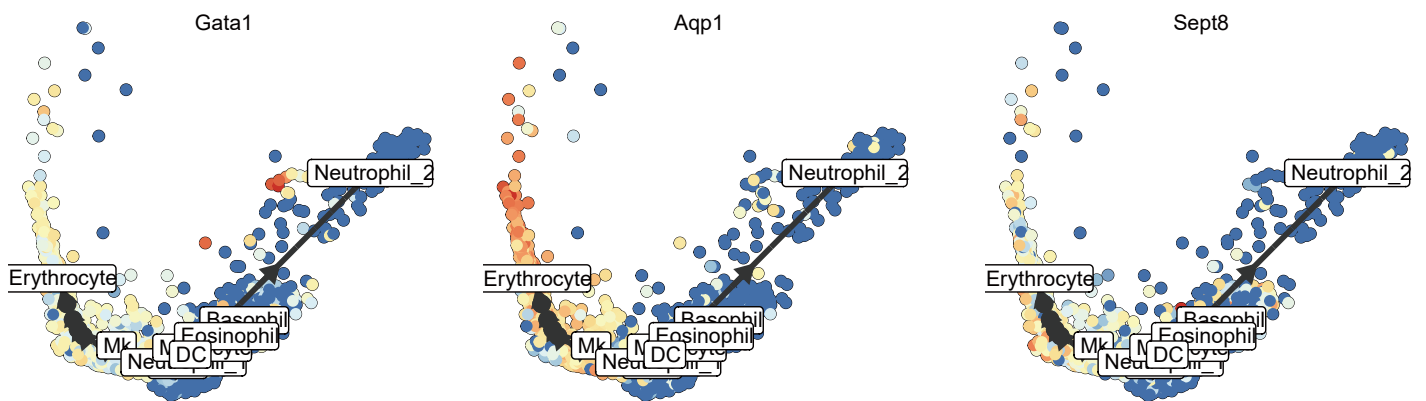
Supplementary Figure 3

The gene expression of selected genes along the trajectory. Different colors represent different lineage development (Left panel: the hypoxia group; right panel: the control group).

A



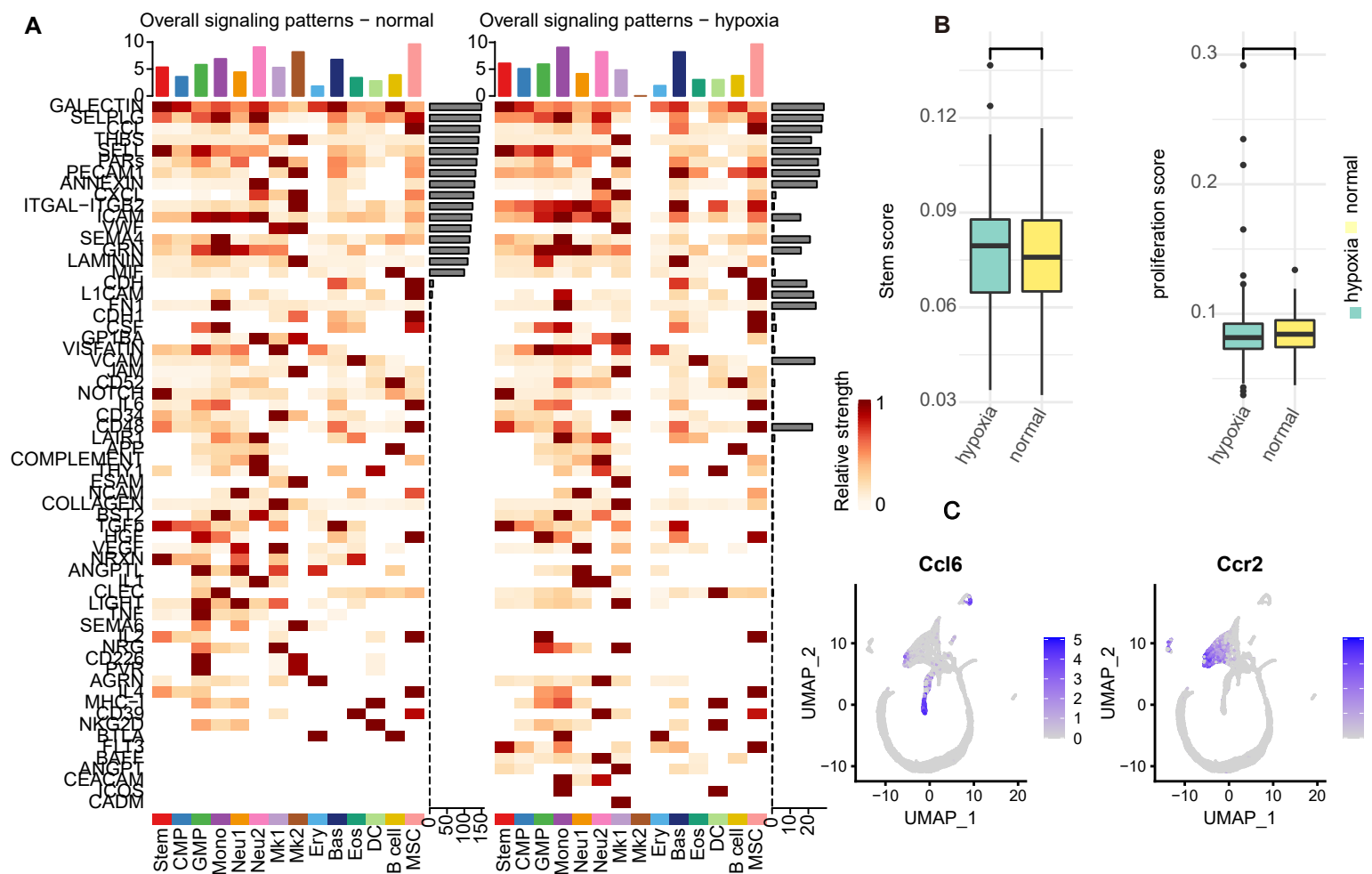
B



Supplementary Figure 4

A Structure of the trajectory during hypoxia. Milestones were labeled and colored by pseudotime.

B Details in Fig. 4E



Supplementary Figure 5

A The overall signalling patterns in hypoxic group and control.

B Boxplot of stemness and proliferation score. Wilcoxon test was conducted and the results showed  $p$  value was 0.40 and 0.23, respectively.

C UMAP representation of the *Ccl6* and *Ccr2* expressing cell cluster.