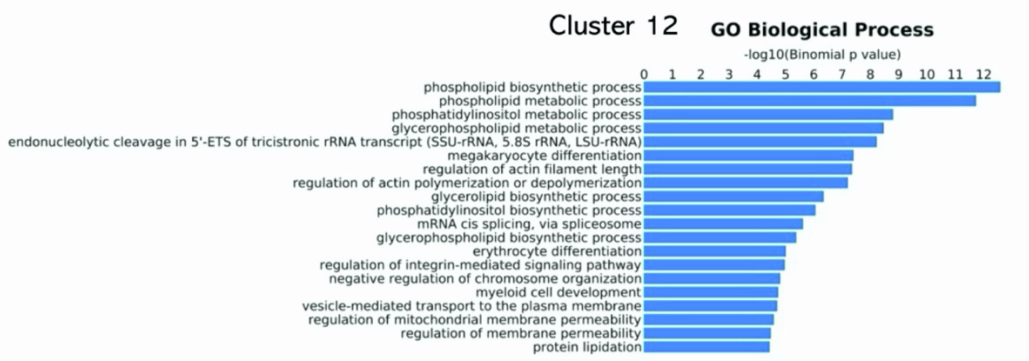
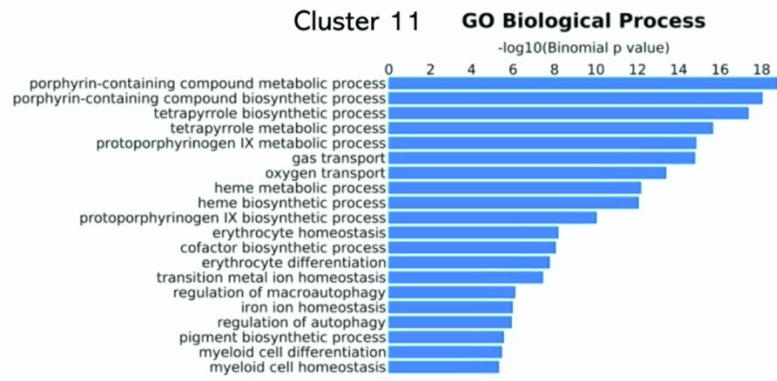
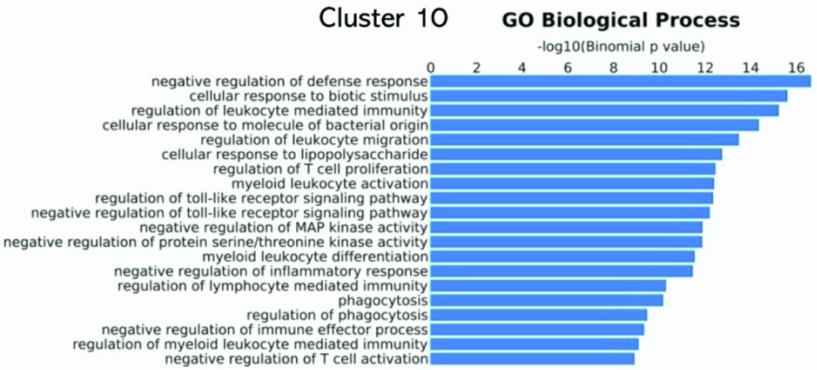
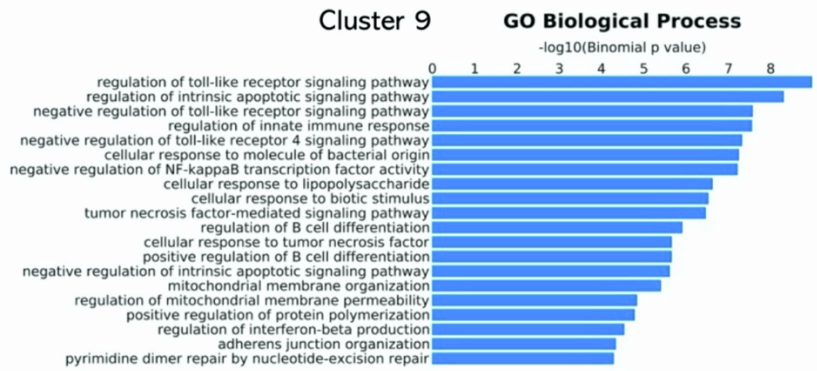


iScience, Volume 25

## **Supplemental information**

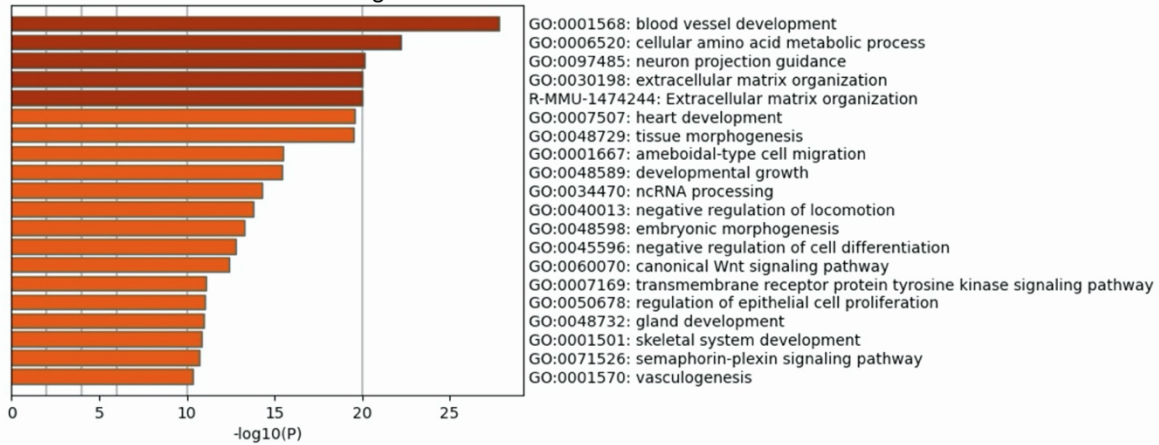
### **Chromatin reconstruction during mouse terminal erythropoiesis**

**Honghao Bi, Ye Hou, Juan Wang, Zongjun Xia, Dongmei Wang, Yijie Liu, Haiyan Bao, Xu Han, Kehan Ren, Ermin Li, Feng Yue, and Peng Ji**

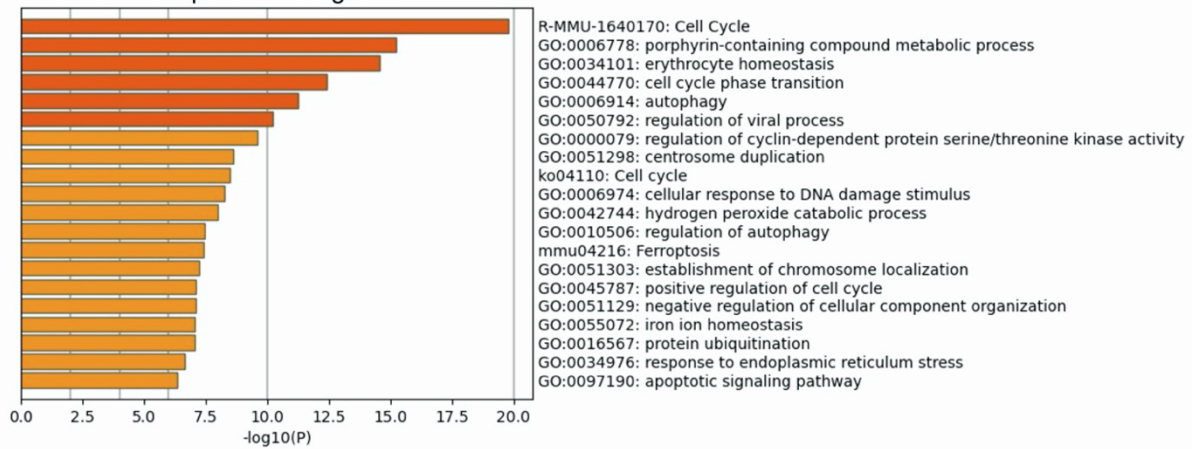


**Supplemental Figure 1. GREAT ontology analysis of the clusters with differential accessibility from the ATAC-seq assay. Related to Figure 3.**

DMSO vs 0 h down 2 fold 1061 genes



DMSO vs 0 h up 2 fold 964 genes



**Supplemental Figure 2. Gene ontology analysis of the genes down or up regulated in DMSO treated cells.** Genes that are down or up regulated 2-fold are included in the analyses.

Related to Figure 4.