# Liver E13.5 Clustering Report

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### 1 Seurat Codes and Parameters

## 2 Clustering and Annotation

### 2.1 Clustering 1

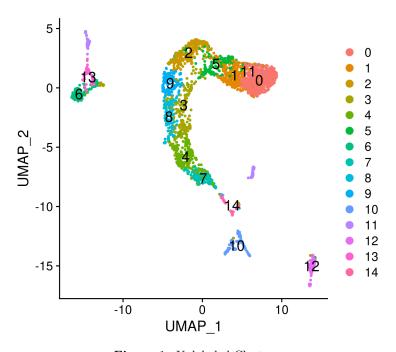


Figure 1: Unlabeled Clusters

Figure 1 is clustering result using 0.8 resolution. RDS file is available in /p200/liujiang\_group/yinyao/Dataset/Seurat/Liver.rds. After extracting markers, some of these clusters can be annotated, but others need further clustering, like C11 (cluster 11, purple), which consists of two parts away form each other.

### 2.2 Annotation 1

Afp, Alb are reported as the markers of hepatocyte or hepatoblast (Gordillo et al., 2015; Chaudhari et al., 2016; Su et al., 2017; Han et al., 2018). Moreover, besides Afp and Alb, hepatocyte also expresses  $Hnf4\alpha$  and

Prox1(Gordillo et al., 2015). Therefore, C6 and C13 are annotated as hepatocyte and hepatoblast, respectively, for their high expression of Afp and Alb, and for expression of  $Hnf4\alpha$  and Prox1 in C13 (**Figure 2**).

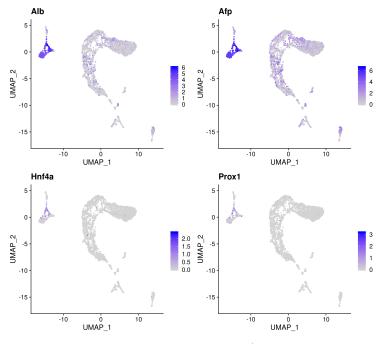


Figure 2: Markers of C6/C13

Cd68, Marco are reported as the markers of macrophage(Su et al., 2017; Han et al., 2018), so C12 is annotated as macrophage. Ppbp, Itga2b are reported as the markers of megakaryocyte(Su et al., 2017), so C14 is annotated as megakaryocyte (Figure 3).

However, in C10, there are two kinds of cell markers, stem cells' and neutrophils'. Similarly, in C11, there are endothelial cells' and mesenchymal cells'. So they need further clustering.

### 2.3 Clustering 2

In order to simply divide one cluster into fewer parts, the resolution used in this part is 0.6.

Cluster 10 C10 is divided into 3 parts (Figure ??), saved as /p200/liujiang\_group/yinyao/Dataset/Seurat /Liver\_C10.rds. Stem cell marker Cd34, Cmtm7(Han et al., 2018) are highly expressed in subcluster 0 of C10. Neutrophil marker S100a9, S100a8(Han et al., 2018) are highly expressed in subcluster 2 of C10. The annotation of subcluster 1 is not defined yet.

Cluster 11 C11 is divided into 2 parts as expected, one of which is annotated as endothelial cell and the other is annotated as mesenchymal cell, due to the endothelial marker Lyve1, Kdr (Gordillo et al., 2015) in subcluster 0, and the mesenchymal marker Pdgfra, Col1a2 (Han et al., 2018) in subcluster 1.()

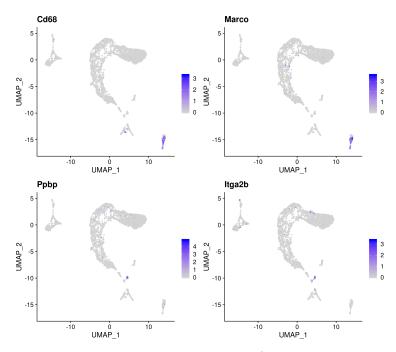


Figure 3: Markers of C12/C14

Figure 4: Subclusters of C10

Figure 5: Stem and Neutrophil Markers in C10

# References

Chaudhari, P., Tian, L., Deshmukh, A., and Jang, Y.-Y. (2016). Expression kinetics of hepatic progenitor markers in cellular models of human liver development recapitulating hepatocyte and biliary cell fate commitment. *Experimental Biology and Medicine*, 241(15):1653–1662.

Gordillo, M., Evans, T., and Gouon-Evans, V. (2015). Orchestrating liver development. *Development*, 142(12):2094–2108. Han, X., Wang, R., Zhou, Y., Fei, L., Sun, H., Lai, S., Saadatpour, A., Zhou, Z., Chen, H., Ye, F., Huang, D., Xu, Y., Huang, W., Jiang, M., Jiang, X., Mao, J., Chen, Y., Lu, C., Xie, J., Fang, Q., Wang, Y., Yue, R., Li, T., Huang, H., Orkin, S. H., Yuan, G.-C., Chen, M., and Guo, G. (2018). Mapping the Mouse Cell Atlas by Microwell-Seq. *Cell*, 172(5):1091–1107.e17. Su, X., Shi, Y., Zou, X., Lu, Z.-N., Xie, G., Yang, J. Y. H., Wu, C.-C., Cui, X.-F., He, K.-Y., Luo, Q., Qu, Y.-L., Wang, N., Wang, L., and Han, Z.-G. (2017). Single-cell RNA-Seq analysis reveals dynamic trajectories during mouse liver development. *BMC Genomics*, 18(1):1–14.

Figure 6: Endothelial and Mesenchymal Markers in C11 Figure 7: Endothelial and Mesenchymal Markers in C11