A Human Liver Cell Atlas: Revealing Cell Type Heterogeneity and Adult Liver Progenitors by Single-Cell RNA-sequencing

The human liver is an essential multifunctional organ, and liver diseases are rising with limited treatment options. However, the cellular composition of the liver remains poorly understood. Here, we performed single-cell RNA-sequencing of ~10,000 cells from normal liver tissue of 9 human donors to construct a human liver cell atlas. Our analysis revealed previously unknown sub-types among endothelial cells, Kupffer cells, and hepatocytes with transcriptome-wide zonation of some of these populations. We reveal heterogeneity of the EPCAM+ population, which comprises hepatocyte-biased and cholangiocyte populations as well as TROP2int bi-potent stem cells with strong potential to form liver organoids. As proof-of-principle, we utilized our atlas to unravel phenotypic changes in hepatocellular carcinoma cells and in human hepatocytes and liver endothelial cells engrafted into a humanized mouse liver. Our human liver cell atlas provides a powerful resource enabling the discovery of previously unknown cell types in the normal and diseased liver.

Date: Monday, November 26, 2018
Time: 16:00 h
Room: Lounge (level 13), Klingelbergstrasse 61 (vis-à-vis Pharmazentrum)
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