

Supplementary information

Establishment of human fetal hepatocyte organoids and CRISPR–Cas9-based gene knockin and knockout in organoid cultures from human liver

In the format provided by the
authors and unedited

Establishment of human fetal hepatocyte organoids and CRISPR-Cas9 based gene knock-in and knock-out in organoid cultures from human liver

Delilah Hendriks^{1,*,#}, Benedetta Artegiani^{1,2,3,*,#},
Huili Hu¹, Susana Chuva de Sousa Lopes⁴, Hans Clevers^{1,2,3,#}

¹ Hubrecht Institute, KNAW (Royal Netherlands Academy of Arts and Sciences), Utrecht, The Netherlands

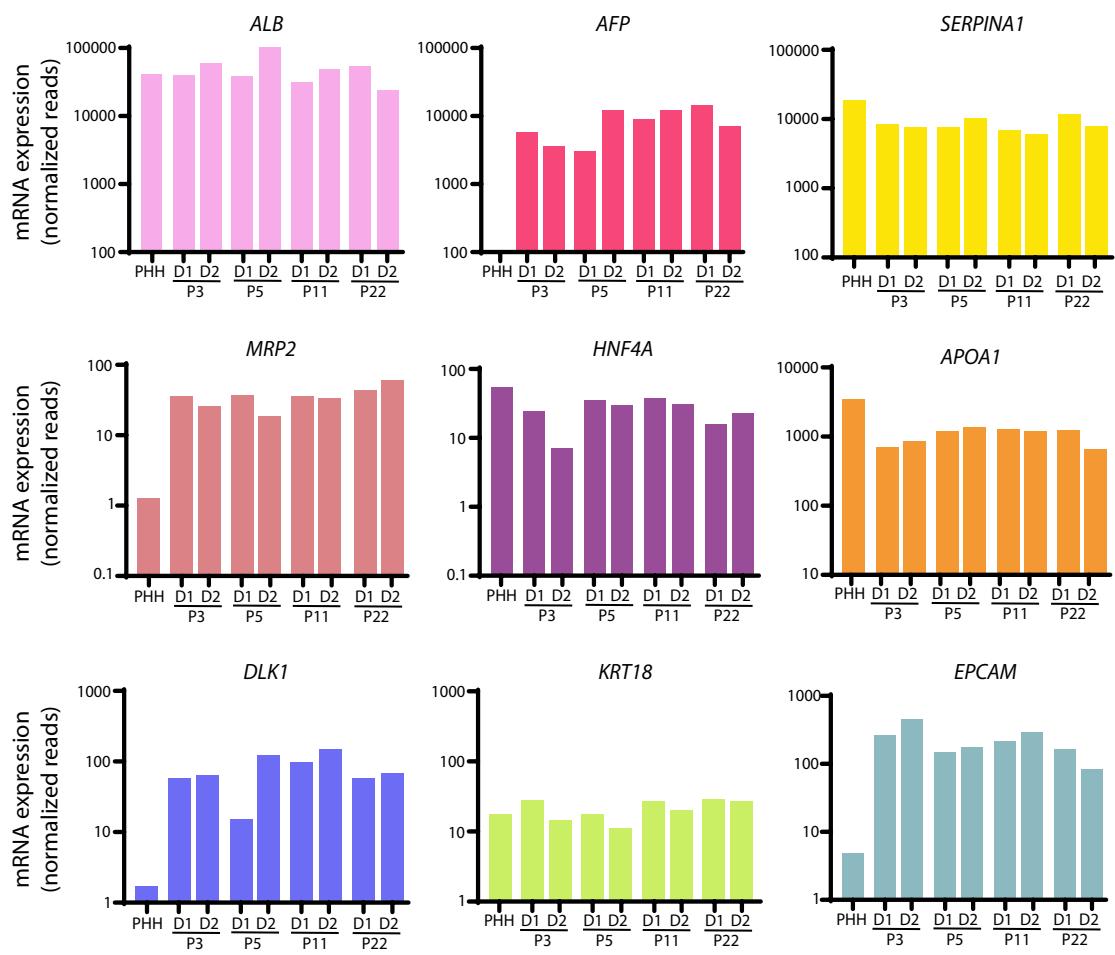
² Oncode Institute, Utrecht, The Netherlands

³ The Princess Maxima Center for Pediatric Oncology, Utrecht, The Netherlands

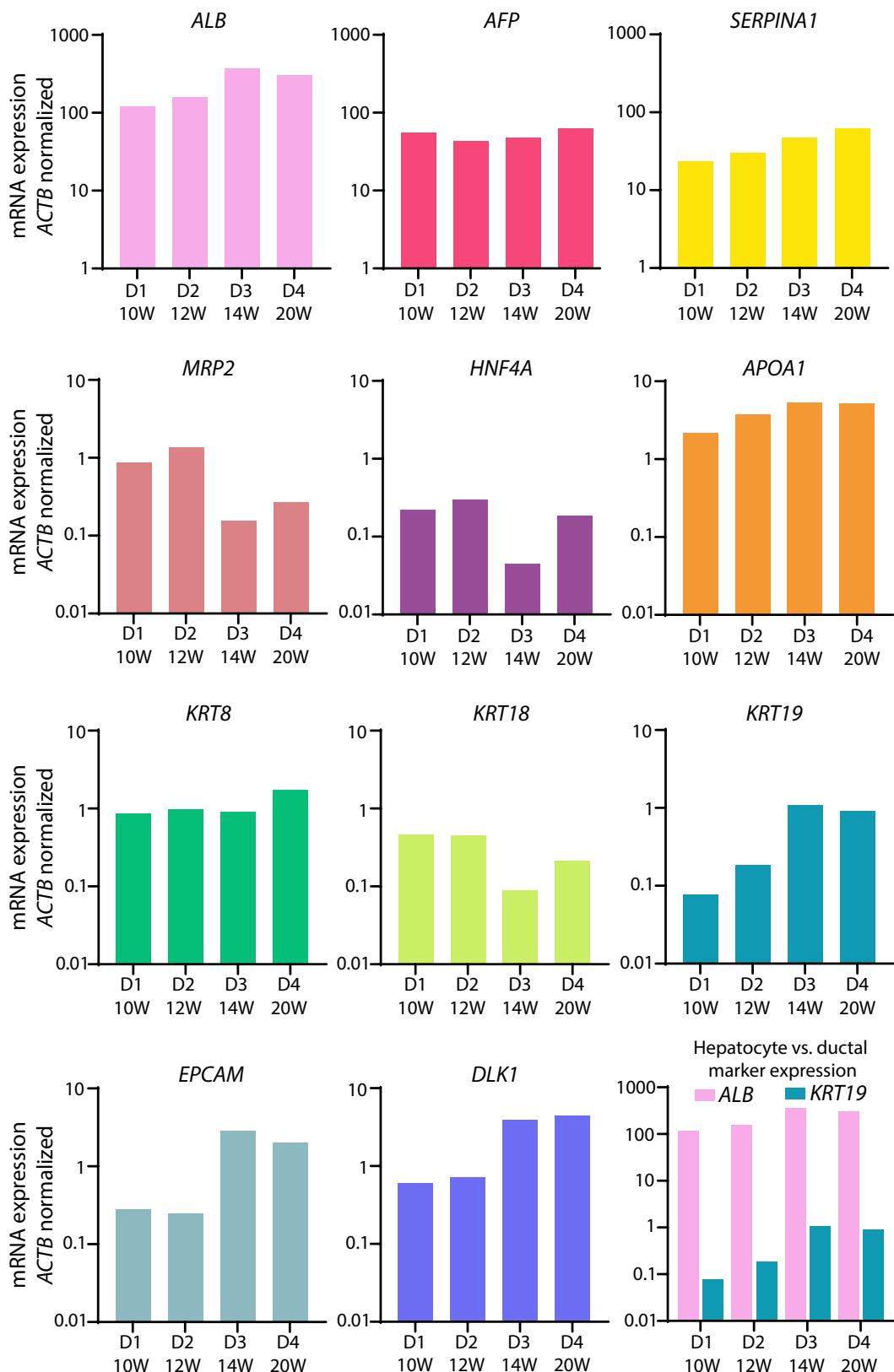
⁴ Anatomy and Embryology, Leiden University Medical Center, Leiden, The Netherlands

* Equal contribution

d.hendriks@hubrecht.eu; b.a.artegiani@prinsesmaximacentrum.nl; h.clevers@hubrecht.eu



Supplementary Figure 1: Hepatic marker expression over passaging of human fetal hepatocyte organoids. Bar plots showing the mRNA expression from bulk RNA-sequencing (read counts normalized) for selected hepatocyte, biliary, and hepatoblast markers in human fetal hepatocyte organoid lines derived from 2 different donors (D1, D2) at early and late passages (ranging from passage 3 to 22) and comparison with expression profiles of adult primary human hepatocytes (PHH). Data presented here is an alternative representation of the data published previously originally (in ref 20) of RNA-sequencing data deposited in GSE111301.



Supplementary Figure 2: Hepatic marker expression of human fetal hepatocyte organoids derived from different gestational ages.

Bar plots showing the mRNA expression from bulk RNA-seq (normalized over the expression of the housekeeping gene *ACTB*) for selected hepatocyte, biliary, and hepatoblast markers in human fetal hepatocyte organoid lines derived from 4 different sources (D1, D2, D3, D4) at 4 different gestational ages (10W, 12W, 14W, 20W).

donors (D1, D2, D3, D4) ranging in age from 10 to 20 gestational weeks. Data from 10W and 12W samples has not been published previously; the data from 14W and 20W is an alternative representation of the RNA-sequencing data described in ref 20 (deposited in GSE111301).