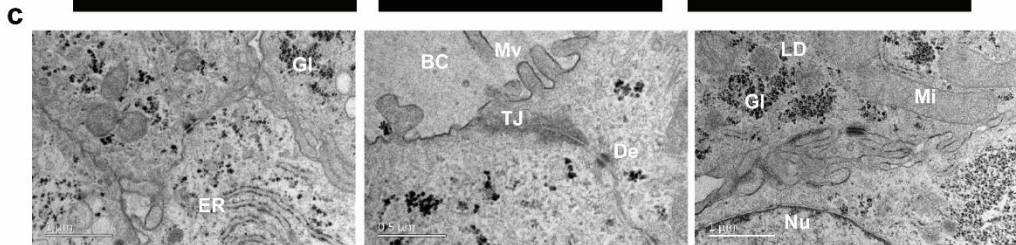
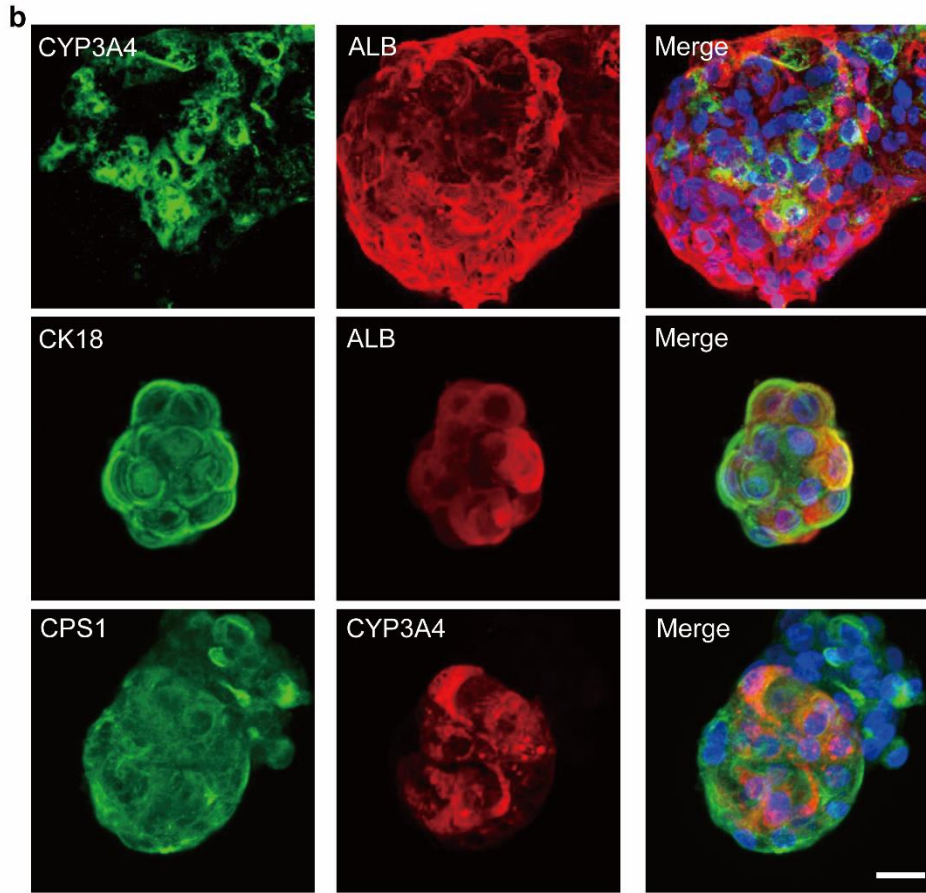
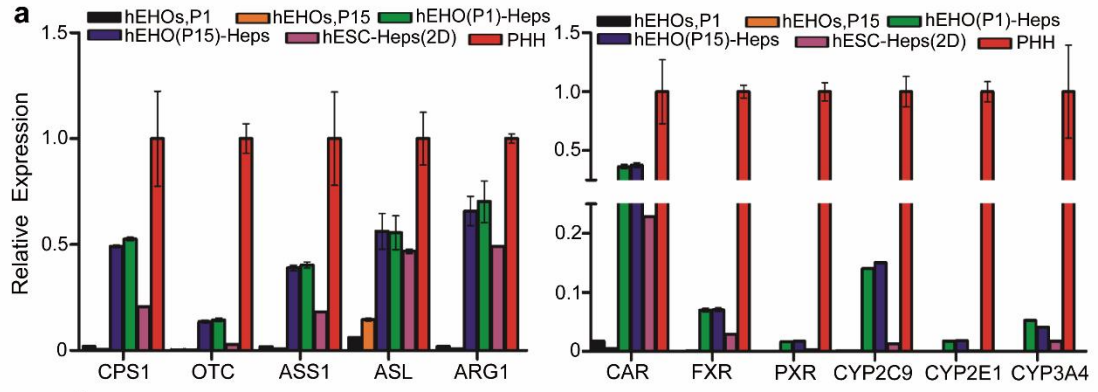


**Fig. S5**



**Supplementary information, Fig. S5 Characterization of hEHO-Heps, related to Fig.4.** (a) qRT-PCR analysis for urea cycle-associated genes (*CPS1*, *OTC*, *ASS1*, *ASL*, *ARG1*) and genes related to drug metabolism (*CAR*, *FXR*, *PXR*, *CYP2C9*, *CYP2E1*, *CYP3A4*) in hEHO-Heps, undifferentiated hEHOs, hESC-Heps(2D) and PHH. Gene expression levels in PHH were normalized to 1. Results are presented as mean  $\pm$  SD from 3 replicates from three independent repeated experiments. (b) Immunostainings for hepatic functional markers ALB, CK18, CPS1 and CYP3A4 in hEHO-Heps. (c) Ultrastructure of hEHO-Heps demonstrated the morphological features of mature hepatocytes, including well-developed organelles and intercellular canaliculi. ER: Endoplasmic Reticulum. Mi: Mitochondria. De: Desmosome. LD: lipid Droplet. TJ: Tight Junction. Mv: Microvilli. Gl: Glycogen. SD, standard deviation. Scale bar: 50 $\mu$ m (b).