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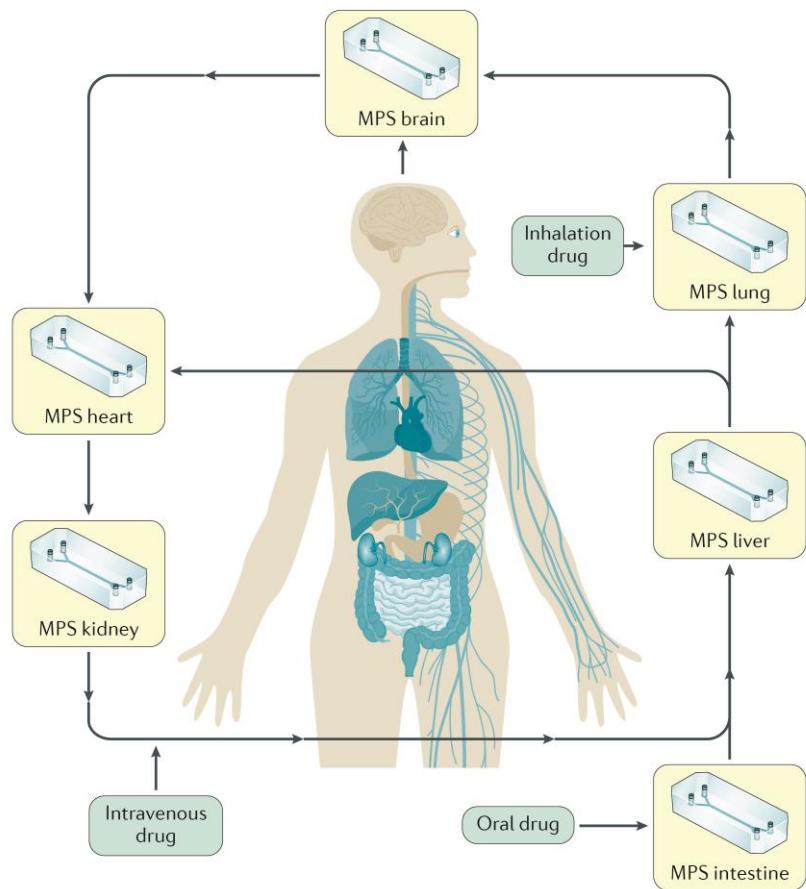
## Supplementary information

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# Human biomimetic liver microphysiology systems in drug development and precision medicine

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**Supplementary Figure 1. Example of a multi-organ MPS.** All integrated multi-organ systems would adhere to known human physiology. In this example, 4 elimination organs (intestine, liver, kidney and lung); 2 barrier layers (intestine, blood brain barrier) and the heart are coupled. 3-drug insertion points are illustrated which demonstrate how this configuration could be used for ADMET. A similar configuration using organ MPS for intestine, liver, pancreas and white adipose tissue would be an integrated multi-organ platform to study complex liver diseases such as NAFLD/NASH and T2DM.

**Supplementary Table 1. Heat Map of the Comparative and Complementary Characteristics of Human Liver Epithelial Organoids, Current human biomimetic-MPS (HBL-MPS), and Next Generation Structured-MPS and Organoid-MPS (Green indicates ability to fulfill the objective and red indicates that the objective cannot be met).**

Characteristics	Epithelial Organoids	Current HBL-MPS	Next Generation: Structured-MPS & Organoid MPS-MPS
<b>Data Acquisition</b>			
Real-Time Imaging Metrics	Yellow	Green	Green
In-Line Sensors of Functions	Red	Green	Green
Temporal and Spatial Content of Read-outs	Red	Green	Green
<b>Controlling the microphysiological state</b>			
Fluidic and Mechanical Cues	Red	Green	Green
Access to Microbiome	Red	Green	Green
Control of Microenvironment (e.g. Zonation, Matrix)	Yellow	Green	Green
Control of Immune Cell Infiltration	Red	Green	Green
Genetic Control of Cell state	Yellow	Red	Green
<b>Cell types and non-epithelial components</b>			
Use of Stem Cells	Green	Yellow	Green
Renewable cell types	Green	Red	Green
Presence of native Cell Types	Yellow	Green	Green
Innervation	Red	Red	Red
Vascularization	Yellow	Green	Green
Extent of Recapitulating Human Liver Acinus Structure	Red	Green	Green
<b>Throughput and heterogeneity</b>			
Homogeneity of individual models	Red	Green	Green
Ease of Production	Yellow	Red	Red
Throughput of studies	Green	Red	Red
Breadth of Applications in Biomedicine	Yellow	Yellow	Green
Key to Characteristics: ■-Missing, □-Partial, ■- Included			

**Supplementary Table 2. Required Functions of Adult, PSC-derived Liver Tissue in HBL-MPS for Physiological & Clinically Relevant Applications.<sup>1-5</sup>**

Functional characteristics	Description
Active transport proteins	NTCP, OATPs, OAT, OCTs, MDR, BSEP, BCR, MRPs
Expression and activity of clinically relevant enzymes	UGT1A1, G-6-Pase, A1AT, OTC, (ATP7B) copper-transporting ATPase 2, (PAH gene) enzyme phenylalanine hydroxylase, branched-chain alpha-keto acid dehydrogenase complex (BCKDC), FAH
Drug Metabolism (Cytochrome activity)	(CYP450) CYP1A2, CYP2A6, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, CYP3A4, CYP7A1
Expression and activity of xenosensors	Ahr, PXR, CAR, XRE,
Expression and transcription of liver specific transcription factors	HNF4a (adult isoform), CEBPa, CEBPb, HNF1a,
Hepatic synthetic functions	Secretion of albumin, A1AT, fibronectin, apoproteins, transthyretin, complement factors, coagulation factors (II, V, VII, IX, X), synthesis of Urea,
Other important metabolic function	Synthesis of cholic acid and chenodeoxycholic acid, Formation of 7α-hydroxycholesterol,
Absence of markers associated with fetal stage	LGR5, OCT4, CD133, AFP, CYP3A7
Morphological features of liver cellular complexity	Liver tissue tight junctions (Claudin-1, 10, occluding, ZO1), liver specific gap junctions (e.g. Cx32, Cx26, Cx43)
Bile duct (cholangiocytes) functions	Transport functions, CFTR (Cl <sup>-</sup> secretion), ASBT (bile acid absorption), SGLT1 (glucose and amino acids absorption), AQP1 (water channel), secretin-induced release of bicarbonate, AE2 (Cl <sup>-</sup> / bicarbonate exchanger)
Liver sinusoidal endothelial cell system functions <sup>215</sup>	CD4, CD32, ICAM1, Fenestrae, blood flow regulation, permeable barrier of different molecules, endocytosis, immune modulators
Functions of liver sinusoids	oxygen and biochemical zonation

**Supplemental Table 3: Example phenotypic, functional and genomic metrics of biomimetic MPS for liver metabolic syndrome disease models**

Readout	MPS Live Measurements	Clinical Relevance
<b>Secretome</b>		
<b>Albumin secretion</b>	ELISA <sup>7</sup>	Metabolic competence, overall hepatocyte function
<b>Urea secretion</b>	Colorimetric <sup>7</sup>	Metabolic competence, overall hepatocyte function
<b>LDH release<sup>+</sup></b>	Colorimetric <sup>7</sup>	Hepatocellular injury corresponding with ALT and AST
<b>Glucose secretion</b>	AmplexRed Glucose Assay <sup>8</sup>	Glucose regulation
<b>β-hydroxybutyrate</b>	Colorimetric <sup>9</sup>	Fatty acid oxidation
<b>Lactate secretion</b>	Colorimetric <sup>10</sup>	Glycolysis
<b>Cytokine release</b>	Human Cytokine Panel <sup>11</sup>	Liver stress/injury response
<b>Fatty acid secretion</b>	Mass spectroscopy <sup>12</sup>	Fatty acid metabolism
<b>TNFα secretion</b>	ELISA <sup>7</sup>	Kupffer activation, innate inflammatory response
<b>Bile acids (BA)</b>	BA profile by Mass spectroscopy <sup>13</sup>	NAFLD, NASH altered plasma BA profile corresponds
<b>Exosomes (proteins/RNA/microRNA)</b>	antibody (α-SK1), qRT-PCR <sup>14</sup>	Circulating extracellular vesicles containing SK1, miRNA-122 & -21 as markers for NAFLD, NASH, HCC
<b>Biosensors</b>		
<b>Hepatocyte Apoptosis</b>	Biosensor <sup>7,15</sup>	Hepatocellular injury/death
<b>ROS (Hepatocytes &amp; Kupffer)</b>	Biosensor <sup>7,15</sup>	Hepatocellular injury, Kupffer cell activation
<b>DAG (Hepatocytes)</b>	Biosensor <sup>16</sup>	Insulin resistance marker
<b>ER stress/UPR Hepatocytes</b>	Biosensor <sup>16</sup>	Hepatocellular damage
<b>Insulin resistance (Hepatocytes)</b>	Biosensor <sup>17,18</sup>	Loss suppression of glucose production
<b>Cell Tracking (stellate &amp; Kupffer)</b>	Biosensor <sup>15</sup>	Morphology of early liver injury, proliferation
<b>JNK activity</b>	Biosensor <sup>19</sup>	Contributes to inflammation, fibrosis, cancer growth, and metabolic diseases of the liver
<b>Imaging Measures</b>		
<b>Steatosis</b>	Brightfield & LipidTox <sup>20</sup>	Normal and/or pathological fat storage in hepatocytes
<b>PMN Infiltration</b>	Imaging labeled PMNs <sup>21</sup>	Adaptive inflammatory response
<b>Mitochondrial Function</b>	TMRE <sup>20</sup>	Hepatocellular health and function
<b>Glucose Uptake</b>	6-NBDG <sup>22</sup>	Hepatocellular insulin resistance marker
<b>Endpoint Measurements</b>		
<b>Glycogen</b>	Antibody <sup>23</sup> or PAS stain <sup>24</sup>	Glucose regulation
<b>Hepatocyte Ballooning</b>	Cytokeratin, anti-CK8/18	A key indication of NASH <sup>25</sup>
<b>LSEC Activation</b>	ICAM antibody – IF <sup>26</sup>	Regulates fibrosis and inflammation responses
<b>Fibrosis (Stellate Activation &amp; Collagen Synthesis)</b>	α-SMA, COL1A2 IF <sup>7</sup>	Early fibrosis indicator and direct measure of fibrosis
<b>RNAseq</b>	RNA sequencing, multiple methods <sup>27</sup>	Comparison to patient results <sup>28,29</sup>

\*Based on known clinical data; α-SK1 = sphingosine kinase 1 ; α-SMA = alpha smooth muscle actin; COL1A2 = collagen type 1, alpha 2; 6-NBDG- fluorescent glucose probe; DAG diacylglycerol

**Supplementary Table 4: Examples of potential gene-based or secreted clinically relevant biomarkers in HBL-MPS<sup>30-37</sup>**

Disease	Relevant genes			Secreted molecule(s)
	Variant	Transcription factor	Other	
<b>NAFLD (Steatosis vs NASH)</b>	PNPLA3 MBOAT7 GCKR TM6SF2 TCF7L2	FXR HNF4a SREBP CEBPa PPAR $\alpha$		cytokeratin 18 caspase-cleaved fragments, IL-6, adiponectin, TNFa, IL-8, pyroglutamate, Fibroblast growth factor (FGF) 21 in combination with cytokeratin 18 cleavage fragments, miR-34a, miR-122, miR-192, miR-21, miR-375, miR-16, miR-222
<b>Fibrosis</b>	PNPLA3 MBOAT7 GCKR TM6SF2 TCF7L2	SMAD3 STAT3 YAP1 GLI2 AP-1 SOX9 MRTF-A	MMPs TIMPs	Procollagen Type III (PIIINP), precursor C3-protein (PRO-C3), hyaluronic acid, TIMP-1 circulating DNA methylation of PPAR $\gamma$ promoter
<b>Alpha1 Antitrypsin Deficiency</b>	<b>Genetic variants of SERPINA1</b>			Alpha1 Antitrypsin
	c.187C > T c.194C > T c.226_228delTTC c.230C > T c.551_552delC c.647G > T c.721A > T	c.739C > T c.839A > T c.863A > T c.1096G > A c.1130_1131insT c.1156_1157insC c.1178C > T		
<b>Phenylketonuria</b>	>950 phenylalanine hydroxylase (PAH) gene variants. Most common variants (c.1222C>T, c.1066-11G>A) (23% and 6% of all mutations, respectively)			phenylalanine (Phe)

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