

Table S1 Clinical information of the subjects

Subject #	Age	Gender	Diagnosis ¹	Experiments ²
1	42	M	Colorectal cancer	(2); (3)
2	35	F	Hepatocellular carcinoma	(2); (3); (4); (5)
3	46	F	Breast cancer	(2); (3); (4)
4	56	F	Colorectal cancer	(1); (4)
5	54	F	Renal cell carcinoma	(1)
6	64	M	Colorectal cancer	(1)
7	59	F	Colorectal cancer	(4)
8	53	F	Colorectal cancer	(5)
9	67	F	Mullerian tumor	(5)
10	36	M	Cholangiocarcinoma	(5)
11	62	M	Colorectal cancer	(5)
12	41	F	Cholangiocarcinoma	(5)

¹Diagnosis: Primary or secondary liver cancer (liver metastases) that led to liver resection surgery.

²Experiments

(1) MTS assay

(2) Fluidigm assay for cell type specific genes

(3) Fluidigm assay for injury response

(4) Histology

(5) Fluidigm assay for Poly-I:C and LPS treatment response

Table S2 Kupffer cell-specific gene candidates

Enriched Fold Change vs HSC ¹	Enriched Fold Change vs LSEC ¹	Gene	Annotation
314.54	247.65	FCN1	ficolin (collagen/fibrinogen domain containing) 1
218.66	235.59	CX3CR1	chemokine (C-X3-C motif) receptor 1
127.59	120.93	S100A12	S100 calcium binding protein A12
113.13	262.18	MNDA	myeloid cell nuclear differentiation antigen
46.26	48.66	ITGA4	integrin alpha 4
38.9	37.63	CCR2	chemokine (C-C motif) receptor 2

Enriched fold change¹ is the average of the fold changes obtained in three patient samples.

Table S3 LSEC-specific gene candidates

Enriched Fold Change vs KC ¹	Enriched Fold Change vs HSC ¹	Gene	Annotation
121.19	124.47	EMCN	endomucin
103.31	112	VWF	von Willebrand factor
88.49	99.4	ADGRL4	adhesion G protein-coupled receptor L4
49.03	66.76	TEK	TEK tyrosine kinase, endothelial

41.01	107.74	CALCRL	calcitonin receptor like receptor
11.96	12.06	CD34	CD34 molecule

Enriched fold change¹ is the average of the fold changes obtained in three patient samples.

Table S4 HSC-specific gene candidates

Enriched Fold Change vs KC ¹	Enriched Fold Change vs LSEC ¹	Gene	Annotation
120.92	148.93	APOB	apolipoprotein B
92.78	63.53	UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7
67.28	44.69	PAH	phenylalanine hydroxylase
37.54	40.09	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5
83.62	31.49	IGFBP1	insulin like growth factor binding protein 1
46.29	27.44	FGFR2	fibroblast growth factor receptor 2
20.65	19.35	AFM	afamin

Enriched fold change¹ is the average of the fold changes obtained in three patient samples.