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**Portal fibroblasts with mesenchymal stem cell features form a reservoir of proliferative myofibroblasts in liver fibrosis**

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4 **proliferative myofibroblasts in liver fibrosis**  
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57 sequencing; SLIT2.  
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**Abbreviations:** ABCB4, ATP-binding cassette B4;  $\alpha$ -SMA, alpha-smooth muscle actin; CK19, cytokeratin 19; CCl<sub>4</sub>, carbon tetrachloride; CDAA, choline-deficient, L-amino acid-defined; CFU-F, colony forming unit-fibroblast; CSAA, choline-sufficient, L-amino acid-defined; DDC, 3,5-diethoxycarbonyl-1,4-dihydrocollidine; DEG, differentially expressed gene; EC, endothelial cell; ECM, extracellular matrix; FISH, fluorescent *in situ* hybridization; GO, gene ontology; HSC, hepatic stellate cell; HUVEC, human umbilical vein endothelial cell; LSEC, liver sinusoidal endothelial cell; MSC, mesenchymal stem cell; NAFLD, non-alcoholic fatty liver disease; NASH, non-alcoholic steatohepatitis; NCD, normal chow diet; PCA, principal component analysis; PMSC, portal fibroblast with mesenchymal stem cell features; PSC, primary sclerosing cholangitis; ROBO, Roundabout; RT-qPCR, Reverse transcription-quantitative PCR; scRNAseq, single-cell RNA-sequencing; *t*-SNE, *t*-distributed stochastic neighbor embedding; VSMC, vascular smooth muscle cell.

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14 J.Gu., T.F., T.H.K., B.H., R.M., E.G-S., C.G., V.R., J.Ga., T.J. acquired experimental  
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16 and clinical data; L.L., A.B., H.E.M., J.Gu., S.L., P.C., F.T., T.J., C.H., A.C. analyzed  
17  
18 and interpreted the data; L.L., S.L., A.C., C.H. drafted the manuscript, with critical  
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20 revision from all authors.  
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## Abstract

**Background & Aims:** In liver fibrosis, myofibroblasts derive from hepatic stellate cells (HSCs) and as yet undefined mesenchymal cells. We aimed to identify portal mesenchymal progenitors of myofibroblasts. **Approach & Results:** Portal mesenchymal cells were isolated from mouse bilio-vascular tree and analyzed by scRNAseq. Thereby, we uncovered the landscape of portal mesenchymal cells in homeostatic mouse liver. Trajectory analysis enabled inferring a small cell population further defined by surface markers used to isolate it. This population consisted of portal fibroblasts with mesenchymal stem cell features (PMSCs), *i.e.*, high clonogenicity and tri-lineage differentiation potential, that generated proliferative myofibroblasts, contrasting with non-proliferative HSC-derived myofibroblasts (-MFs). Using bulk RNAseq, we built oligogene signatures of the two cell populations, that remained discriminant across myofibroblastic differentiation. SLIT2, a prototypical gene of PMSC/PMSC-MF signature, mediated pro-fibrotic and angiogenic effects of these cells, whose conditioned medium promoted HSC survival and endothelial cell tubulogenesis. Using PMSC/PMSC-MF 7-gene signature and *SLIT2* FISH, we showed that PMSCs display a perivascular portal distribution in homeostatic liver and largely expand with fibrosis progression, contributing to the myofibroblast populations that form fibrotic septa, preferentially along neo-vessels, in murine and human liver disorders, irrespective of aetiology. We also unraveled a 6-gene expression signature of HSCs/HSC-MFs that did not vary in these disorders, consistent with their low proliferation rate. **Conclusions:** PMSCs form a small reservoir of expansive myofibroblasts, which in interaction with neo-vessels and HSC-MFs that mainly arise *via* differentiation from a preexisting pool, underlie the formation of fibrotic septa in all types of liver diseases.

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5 Mesenchymal cells are key players in tissue homeostasis and wound healing. In the  
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7 liver, mesenchymal cells comprise hepatic stellate cells (HSCs), that reside in  
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9 sinusoids, and perivascular cells including vascular smooth muscle cells (VSMCs) and  
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11 fibroblasts, that reside in the portal tracts and around central veins. Genetic-based  
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13 lineage-tracing analyses have demonstrated that HSCs and perivascular  
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15 mesenchymal cells as well as mesothelial cells all derive from the septum transversum  
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17 during liver development (1). Over the past 30 years, HSCs have been extensively  
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19 investigated for their capacity to undergo myofibroblastic differentiation, and have been  
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21 identified as a major source of myofibroblasts in liver fibrosis (2). However, the other  
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23 liver mesenchymal cells, particularly portal mesenchymal cells have gained increasing  
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25 interest as evidence has accumulated that indicates they could also generate  
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27 myofibroblasts (3-6). The portal tracts contain three main structures referred to as the  
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29 portal triad, *i.e.*, the portal vein, hepatic artery and bile duct, surrounded by a  
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31 mesenchyme, which has remained poorly defined so far. Little is known regarding the  
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33 identity, spatial distribution or functions of portal mesenchymal cells and how they  
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35 contribute to fibrosis. A major limitation has been the lack of markers, especially  
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37 surface markers that would allow to isolate portal mesenchymal cells or track them *in*  
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39 *vivo*. Using a model of outgrowth from fragments of the bilio-vascular tree isolated from  
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41 rat liver, we previously showed that portal cells distinct from HSCs could generate  
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43 myofibroblasts, that we referred to as portal myofibroblasts, characterized by  
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45 COL15A1 expression, a high proliferation rate and pro-angiogenic properties (4, 7, 8).  
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47 However, the precursors of portal myofibroblasts have not been truly identified in these  
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49 studies. In the present study, we isolated portal mesenchymal cells from mouse liver  
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51 as a single-cell preparation and analyzed their diversity using single-cell RNA-  
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3 sequencing (scRNAseq). A minimal set of surface markers enabled us to isolate a  
4 subset of portal fibroblasts with mesenchymal stem cell features (PMSCs) and the  
5 ability to generate myofibroblasts. Markers of PMSCs were discovered and used to  
6 examine the expansion potential of these cells in murine and human liver fibrosis.  
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## 14 **Experimental procedures**

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16 Details are provided in Supplementary material.

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18 **Animals.** Male mice of C57BL/6J or FVB.129 genetic background, were used at the  
19 age of 8-12 weeks for cell isolation and liver fibrosis models, in compliance with  
20 ARRIVE guidelines.  
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26 **Cell isolation and culture.** The bilio-vascular tree was isolated from mouse liver, by  
27 adapting a procedure we previously described in rat (7), and further processed using  
28 cell sorting and flow cytometry analysis to collect and analyze mesenchymal cells.  
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**RNAseq.** ScRNAseq of the bilio-vascular tree Lin-negative cells (gated as Epcam<sup>+</sup>  
CD31<sup>-</sup>CD45<sup>-</sup>CD11b<sup>-</sup> cells), was performed using the 10X Genomics 3' v3 kit (10×  
Genomics). NextSeq500 (Illumina) device was used for single-cell and bulk RNAseq.  
ScRNAseq analyses were performed using CellRanger, Seurat and Monocle, and bulk  
RNAseq analyses, using STAR, RSEM and edgeR R package.

**Human liver samples.** Fresh and frozen samples of normal and pathological liver  
tissue were collected with the approval of ethical committees, from patients who gave  
written informed consent.

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3 **Reverse transcription-quantitative PCR (RT-qPCR), Immunofluorescence and**  
4 **fluorescent *in situ* hybridization (FISH).** Primers, antibodies and probes are listed in  
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6 Table S1-3.  
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10 **Microarray analyses.** Pangenomic analysis of frozen liver tissue samples, was  
11 performed using the Affymetrix human gene 1.0 st microarray.  
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14 **SLIT2-mediated functions analyses.** The conditioned medium of PMSC-derived  
15 myofibroblasts (PMSC-MFs) was tested for potential effects on the viability of the LX-  
16 2 HSC cells, and the tubulogenesis of human umbilical vein endothelial cells  
17 (HUVECs). In these experiments, SLIT2 signaling was blocked using siRNA,  
18 CRISPR/Cas9, anti-ROBO1 antibody or a recombinant ROBO1/Fc chimera.  
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26 **Statistical analyses.** Unless otherwise stated, statistical analyses were performed  
27 using Graphpad Prism v6.0 and R. Unpaired two-sided Wilcoxon test and ANOVA with  
28 a Scheffe post-hoc test were used to compare differences between two groups, and  
29 more than two groups, respectively. A significant difference was defined as  $p < 0.05$ .  
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## 38 **Results**

### 39 **Landscape of the portal mesenchyme revealed by scRNAseq**

40 Portal mesenchymal cells represent a small cell population. They are tightly bound to  
41 the portal triad, relying on basement membranes. This makes them more difficult to  
42 isolate than hepatocytes or sinusoidal cells, which reside in a loose, basement  
43 membrane-free, extracellular matrix (ECM). In the present study, we set up a specific  
44 procedure to isolate portal mesenchymal cells, for scRNAseq analysis. We adapted a  
45 method we previously established for the culture of rat portal myofibroblasts (7), to  
46 isolate fragments of the bilio-vascular tree from mouse liver. The bilio-vascular tree  
47 fragments were submitted to enzymatic digestion, resulting in a single-cell suspension,  
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3 which was depleted in cells expressing the lineage (Lin) markers of cholangiocytes  
4 (EpCAM), endothelial cells (CD31), and hematopoietic cells (CD45 and CD11b) using  
5 cell sorting. Lin-negative single-cell suspension was then processed to generate a  
6 scRNAseq cDNA library (Fig. 1A). We captured 4,976 sequenced cells that met quality  
7 control metrics (Fig. S1A) from healthy mouse liver. Unsupervised clustering identified  
8 16 distinct clusters that were assigned to fibroblast (5 clusters), VSMC (5 clusters),  
9 endothelial (4 clusters), HSC (1 cluster) and mesothelial (1 cluster) identities (Fig. 1B).  
10 The hierarchical clustering of gene expression profiles supported this classification  
11 except for the very small cluster of VSMC-5 (Fig. 1C). The most selective expressed  
12 genes that allowed to segregate cell clusters are shown in Fig. 1D, Fig. S2 and Table  
13 S4. In all clusters, the expression of cell cycle-related genes, e.g., *Mki67*, was at the  
14 limit of detection, as expected from resting cells in homeostatic liver (Fig. S3).  
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### ***The non-mesenchymal components: mesothelial and endothelial cells***

33 Mesothelial cells display an intermediate phenotype between epithelial and  
34 mesenchymal cells and form a single layer that covers the liver surface (9). The liver  
35 capsule also covers the intrahepatic parenchyma surrounding the Glissonian pedicles  
36 including bile ducts (10), which can explain the presence of mesothelial cells in our cell  
37 suspension. Genes expressed in these cells included previously reported mesothelial  
38 markers, among which the most specific were *Msln* and *Upk1b* as well as epithelial  
39 markers, such as *Krt8* and *Krt19*, and mesenchymal markers, such as *Vim* but almost  
40 no *Pdgfrb*. Additional putative markers restricted to this cluster included *Fxyd3*, *Myl7*  
41 and *Slpi* (Fig. S4A).  
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55 We identified four clusters of endothelial cells (ECs), enriched in markers such as  
56 *Pecam1*, *Cdh5*, *Kdr* and *Egfl7* (Fig. S4B). The PECAM1 protein (alias CD31) has been  
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3 shown to be intracellular in liver sinusoidal endothelial cells (LSECs) (11), which  
4 explains, at least partly, why ECs escaped our negative selection according to the  
5 membrane antigen CD31. Moreover, even though cells from the bilio-vascular tree  
6 were preferentially retrieved by our method, basement membrane-free LSECs adhere  
7 to other cell types and are prone to be collected during isolation procedures, as  
8 previously reported (12). As shown in Fig. S5, we found markers of EC zonation in the  
9 liver, *i.e.*, of peri-central LSECs in EC-1, of peri-portal LSECs and/or portal vascular  
10 ECs in EC-2, of lymphatic ECs in EC-3, and of hepatic arterial ECs in EC-4 (12, 13).  
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### ***The mesenchymal components: fibroblasts, HSCs and VSMCs***

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25 Our single-cell analysis revealed five clusters of fibroblasts (Fig. 1B-D), which  
26 predominantly expressed genes involved in vascular ECM such as *Mmp19*, *Col6a5*,  
27 *Col6a6* or *Col15a1*, and also expressed genes of interstitial collagens such as *Col1a1*,  
28 *Col1a2*, *Col3a1* at higher levels than other clusters. Both fibroblasts and HSCs  
29 expressed *Pdgfra*, whereas *Eln* previously reported as a marker of portal fibroblasts  
30 (5), was expressed in many other clusters (Fig. S4C). Fib-3 highly expressed *Ptn* (Fig.  
31 1D), a pericyte-derived trophic factor for ECs (14), suggesting a particular interaction  
32 of this cluster with portal vessels, whereas Fib-5 was enriched in HSC markers, such  
33 as *Lrat* (2) and *Reln* (5) (Fig. S4D), which was not driven by doublets (Fig. S1B), and  
34 may thus represent an intermediate population between fibroblasts and HSCs. All five  
35 fibroblast clusters were enriched in the gene ontology (GO) terms “ECM organization”  
36 and “Wound healing” (Fig. S6, Table S5). Individual clusters were also enriched in  
37 terms related to cell (including leucocyte) chemotaxis (Fib-1), epithelial cell proliferation  
38 and migration (Fib-2), tissue development or morphogenesis (Fib-3, Fib-4, Fib-5).  
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3 Cells of cluster 8 were recognized as HSCs. They were enriched in GO terms related  
4 to immunity and cell differentiation (Fig. S6). Among classical markers of HSCs, *Lrat*  
5 and *Reln* (2, 5) appeared to be not fully specific, being expressed notably in Fib-2 and  
6 Fib-5 (Fig. S4D). Like others (2, 15), we found virtually no expression of *Gfap*, whereas  
7 *Des* and *Cygb* (2, 3), were expressed at variable levels in virtually all clusters. Among  
8 HSC markers newly identified by scRNAseq (15-18) or bulk RNAseq (19), our analysis  
9 confirmed that some of them were restricted to HSCs, such as *Tmem56*, *Colec10*,  
10 *Mapt* or *Bco1*. Others such as *Fcna* or *Angptl6*, although not fully specific, were largely  
11 overexpressed in HSCs, whereas yet others such as *Rgs5*, *Pcdh7*, *Adamtsl2*,  
12 *Gucy1a1/b1* or *Colec11* were expressed at relatively high levels in several other  
13 mesenchymal cells, in addition to HSCs. Both *Ngfr* and *I134* on one hand, *Vipr1* and  
14 *Pth1r* on the other one, previously reported to preferentially mark peri-portal and peri-  
15 central HSCs, respectively (15), were expressed in the HSC cluster, indicating that this  
16 cluster was representative of all HSCs (Fig. S4D).

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18 We identified 5 clusters of VSMCs that expressed at highest levels markers such as  
19 *Myh11*, *Cnn1*, *Acta2* or *Tagln* (13, 15) (Fig. S4E). VSMC clusters were enriched in GO  
20 terms related to muscle functions but also to “Inflammatory response” (Fig. S6).

### 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 **Identification of PMSCs**

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47 As a first approach to assess differentiation potency of the different clusters, we  
48 computed single-cell entropy, an approximation of single-cell differentiation potency  
49 based on predicted signalling promiscuity (20). Of all clusters, Fib-3 displayed the  
50 highest differentiation potency as suggested by the highest entropy value (Fig. 2A).  
51 We also examined the differentiation dynamics among mesenchymal cells, and  
52 analyzed all cells except mesothelial and endothelial cells, using Monocle 2 (21). This  
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analysis showed a common trajectory of mesenchymal cells with one bifurcation and three branches defining states (Fig. 2B). On the basis of entropy analysis, the branch containing Fib-3 was defined as the root state. As shown in Fig. 2B, the root state was mainly populated by Fib-3 and Fib-4 cells, which were consequently assumed to be progenitor cells, contrasting with the two other states populated by VSMCs, notably VSMC-1, and HSCs, both well-differentiated cell types with high pseudotime values. Consistent with this assumption, GO terms related to development were concentrated in Fib-3 and Fib-4, suggesting multilineage potential of these two clusters (Fig. 2C). Genes previously reported to demarcate universal fibroblasts in mouse tissues, *i.e.* *Pi16* and *Col15a1* (22), or portal fibroblasts/myofibroblasts, *i.e.*, *Col15a1* (4), *Cd34* (6, 15), *Thy1* alias CD90 (6, 23, 24), *Gli1* (19, 25), *Clec3b* (15), *Fbln2* (26) and *Entpd2* (27), were mainly expressed in these two clusters (Fig. 2D). *Pi16*<sup>+</sup> cells, were recently shown to serve as resource fibroblasts that would pass through *Col15a1*<sup>+</sup> fibroblasts able to secrete basement membrane proteins, before developing into specialized fibroblasts, in all steady-state mouse tissues (22). In addition, CD34, Thy1 and Gli1 are all considered as stem cell markers. To further analyze Fib-3 and Fib-4 clusters, we defined a minimal set of surface markers enabling to isolate them together. As shown in Fig. 2E, a high expression of *Pdgfra*, *Cd34* and *Cd9* combined with a low expression of *Cd200* appeared to discriminate Fib-3 and Fib-4 from other Lin-negative cells. We FACS-sorted Lin (Epcam/CD31/CD45/CD11b)-negative, PDGFR $\alpha$ /CD34/CD9-positive, and CD200-low cells (Gate 4 in Fig. 2F) and examined this population for stem cell features. The percentage of cells recovered was approximately 0.03 % of total liver cells. The cells of this population were highly clonogenic (80 colony forming unit-fibroblast (CFU-F) per 2,000 cells) (Fig. 2G) irrespective of whether they were Thy1-positive or negative (Fig. S7). They also

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3 displayed the expression of classical mesenchymal stem cell (MSC) markers, *i.e.*,  
4 CD105, Sca-1, CD29 (Fig. 2H), and the ability to undergo trilineage (adipogenic,  
5 osteogenic and chondrogenic) differentiation, in culture (Fig. 2I). Taken together, the  
6 cells isolated by our gating strategy displayed MSC attributes and were designated  
7 PMSCs. When cultured on a stiff substratum (Fig. 2J, bottom panels), PMSCs  
8 proliferated and gave rise to cells phenotypically similar to portal myofibroblasts  
9 expressing COL15A1 (4), here referred to as PMSC-MFs. This phenotypic change was  
10 accompanied by the expected up-regulation of *Acta2*, the gene encoding alpha-  
11 smooth muscle actin ( $\alpha$ -SMA), no change in *Col1a1* expression, and a down-regulation  
12 of *Col15a1* (Fig. 2K). Despite such down-regulation, *Col15a1* demarcates both PMSCs  
13 and portal myofibroblasts (4). It was possible to maintain PMSCs in a resting state by  
14 cultivating them in spheroids, on ultra-low attachment plates, in which case the  
15 expression of  $\alpha$ -SMA was not induced and that of Col15a1, less reduced (Fig. 2J-K).  
16 Overall, these data indicate that our screening strategy and isolation procedure  
17 enabled identifying portal fibroblasts with MSC properties and high collagen expression  
18 as precursors of portal myofibroblasts.

### Specific phenotypes and molecular profiles of PMSCs, HSCs and derived myofibroblasts

19 The isolation of PMSCs provided a unique opportunity to compare them with HSCs,  
20 and uncover specific markers of the two cell populations and of their myofibroblastic  
21 progenies. We performed transcriptomic analyses using bulk RNAseq, to compare  
22 PMSCs with ultrapure HSCs (28), as ascertained by vitamin A fluorescence (Fig. S8A).  
23 We identified 3,273 genes expressed at higher levels in PMSCs, and 3,122, in HSCs  
24 (Fig. 3A, upper panel). Projections onto *t*-SNE plot (Fig. 3A, lower panel), showed that  
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3 the top 10 differentially expressed genes in PMSCs included common markers of portal  
4 fibroblasts, as expected from a comparison with HSCs, but were expressed at highest  
5 levels in Fib-3/Fib-4, indicating that PMSCs comprised mainly if not exclusively Fib-  
6 3/Fib-4 fibroblasts. The top 10 differentially expressed genes of HSCs included  
7 common markers with ECs, but none with the other mesenchymal cells. Consistent  
8 with the GO analyses of scRNAseq (Fig. S6, Table S5), bulk RNAseq analysis showed  
9 enrichment in pathways related to “Extracellular matrix organization” in PMSCs and  
10 “Immunity” in HSCs, and further highlighted pathways related to “Angiogenesis” in  
11 PMSCs and to “Metabolism of fat-soluble vitamins” in HSCs (Fig. 3B).

12 Both PMSCs (Fig. 2J-K), and HSCs (3, 4), undergo phenotypic changes into  
13 myofibroblasts in primary culture. Phenotypically, the major difference we observed  
14 between the two cell populations, was an intense proliferation in PMSCs as they  
15 became myofibroblastic, whereas HSCs differentiated into myofibroblasts without  
16 dividing (Fig. S8A, D-E including videomicroscopy). We extended bulk RNAseq  
17 analyses to the myofibroblasts derived from both cell populations in culture, including  
18 an early and late stage of differentiation for PMSC-MFs (Table S6). Principal  
19 component analysis (PCA) showed a clear discrimination of PMSCs and HSCs from  
20 their myofibroblastic progenies according to PC1, while PMSC-MFs were  
21 discriminated from HSC-derived myofibroblasts (HSC-MFs) according to PC2 (Fig.  
22 3C). The molecular profiles of PMSCs and HSCs became more similar as they  
23 differentiated into myofibroblasts. Yet, they retained specificities at the stage of  
24 myofibroblasts as confirmed by GO analysis (Fig. 3D). When fully differentiated into  
25 myofibroblasts, *i.e.*, after 7 days of culture, both cell populations were enriched in  
26 themes related to muscle differentiation, whereas additionally, PMSC-MFs were  
27 enriched in themes related to axonogenesis and ECM organization. To a large extent,  
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3 PMSCs/PMSC-MFs overexpressed genes encoding fibrillar collagens (*Col1a1*,  
4 *Col1a2*, *Col3a1*), *Timp1* and *Acta2*, the hallmarks of liver fibrosis, whereas *Col4a1*, a  
5 major component of sinusoidal ECM was overexpressed in HSC-MFs (Fig. S9). At an  
6 early stage of myofibroblastic differentiation, *i.e.*, after 3 days of culture, PMSC  
7 transcriptome was highly enriched in pathways related to cell proliferation (Fig. 3D). At  
8 a later stage of myofibroblastic differentiation, *i.e.*, after 7 days of culture, PMSC-MFs  
9 compared to HSC-MFs still markedly overexpressed genes involved in cell  
10 proliferation, consistent with videomicroscopy and CFU-F assays, showing that only  
11 PMSCs as opposed to HSCs were clonogenic and divided in culture (Fig. S8B-E).

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24 Next, we looked for gene expressions that would demarcate the two cell populations  
25 both in their resting and myofibroblastic states, and that could thus be used in fibrotic  
26 liver tissue analyses to assess if PMSCs/PMSC-MFs were more expansive than  
27 HSCs/HSC-MFs, also *in vivo*. Altogether, comparative analyses of gene expressions  
28 indicated that 100 genes in PMSCs (or Fib-3/Fib-4) and 112 genes in HSCs, i) were  
29 overexpressed according to both scRNAseq and bulk RNAseq analyses, and ii)  
30 remained differentially expressed in these cells throughout myofibroblastic  
31 differentiation (Fig. 3E). Among such genes, we selected those that combined the  
32 highest differential expression (>3.5-fold), a relatively high expression (CPM>40) in the  
33 demarcated cell population, limited variation with myofibroblastic differentiation, and  
34 no or little expression in the other liver cell types, to build an oligogene expression  
35 signature of PMSCs/PMSC-MFs (7 genes) and HSCs/HSC-MFs (6 genes) (Fig. 3F-  
36 G). Projection of the two signatures onto current (Fig. 1B) and previous scRNAseq  
37 datasets (15, 18) showed that the PMSC/PMSC-MF signature demarcated liver  
38 fibroblasts, with highest intensity in Fib-3/Fib-4 (Fig. S10A) and in liver fibroblasts  
39 accumulating in liver fibrosis induced either by carbon tetrachloride (CCl<sub>4</sub>) or bile duct  
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3 ligation (BDL) (Fig. S10B-C), with little or no signal in other liver cell types. The  
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5 HSC/HSC-MF signature demarcated the HSC cluster (Fig. S10A), as well as the vast  
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7 majority of HSCs in mouse liver, including in CCl<sub>4</sub>- and BDL-induced liver fibrosis, and  
8  
9 virtually no other liver cell populations except a small portion of ECs (Fig. S10B-C).  
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### 14 **Implication of PMSCs and PMSC-MFs in liver fibrosis**

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16 Our transcriptome analyses highlighted *Slit2* as a prototypical gene of PMSC/PMSC-  
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18 MF signature. Its expression was particularly stable in PMSCs throughout their  
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20 myofibroblastic differentiation and virtually absent from all other liver cell types  
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22 including HSCs/HSC-MFs (Fig. 4A, left panel). Using FISH, we confirmed that PMSC-  
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24 MFs in culture were distinguishable from HSC-MFs by *Slit2* expression (Fig. 4A, right  
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26 panel). SLIT2 is an axon guidance molecule, which was previously shown to trigger  
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28 HSC activation and fibrosis (29-31) as well as angiogenesis, in the liver (32). However,  
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30 so far, the endogenous source of SLIT2 in the liver, had not been accurately identified.  
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35 Our scRNAseq data showed that *Slit2* expression was concentrated in Fib-3/Fib-4,  
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37 whereas its roundabout (ROBO) receptors were mainly expressed in the HSC and EC  
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39 clusters, and to a lesser extent in the fibroblast clusters (Fig. 4B). Therefore, previous  
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41 and current findings suggested that PMSCs had the potential to signal towards HSCs  
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43 and ECs via *Slit2*, to promote their pro-fibrotic and pro-angiogenic activity, respectively.  
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45 Supporting such mechanisms, PMSC-MF conditioned medium prevented the  
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47 decrease in cell viability induced by an oxidative stress in the LX-2 HSC cell line and  
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49 this effect was abolished by silencing *Slit2* via SiRNA in PMSC-MFs (Fig. 4C). PMSC-  
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51 MF conditioned medium also increased tubulogenesis in HUVECs and this effect was  
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53 largely SLIT2-dependent. It was prevented in the presence of anti-ROBO1 antibody or  
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55 recombinant ROBO1/Fc chimera that entraps soluble SLIT2 and it was reduced by  
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3 Slit2 depletion via CRISPR/Cas9 in PMSC-MFs (Fig. 4D). We used SLIT2 FISH to  
4 demarcate PMSCs/PMSC-MFs and address their connections with other cell types in  
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6 normal and cirrhotic human liver. In normal liver, SLIT2<sup>+</sup> cells were scarce, although  
7  
8 more abundant in large portal tracts than in the small ones. They were virtually  
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10 restricted to portal tracts and displayed a perivascular distribution (Fig. 4E, left panel,  
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12 Fig. S11, upper panel). In cirrhotic liver, irrespective of aetiology (i.e., alcoholic liver  
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14 disease, non-alcoholic steatohepatitis (NASH) or chronic hepatitis C), SLIT2<sup>+</sup> cells  
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16 were much more abundant than in normal liver (Fig. 4E, middle and right panels). They  
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18 were mainly located in the fibrotic septa, displayed  $\alpha$ -SMA expression and were thus  
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20 identified as PMSC-MFs. Within fibrotic septa, SLIT2<sup>+</sup>/ $\alpha$ -SMA<sup>+</sup> PMSC-MFs were  
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22 intermingled with, and outnumbered by SLIT2<sup>-</sup>/ $\alpha$ -SMA<sup>+</sup> myofibroblasts, and were  
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24 frequently located in the surrounding of vascular lumens (Fig. 4E, middle panel).  
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26 Consistent with PMSC/PMSC-MF interacting with HSCs/HSC-MFs and ECs, we found  
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28 that in cirrhosis, SLIT2<sup>+</sup> PMSC-MFs often lined up along CD31<sup>+</sup> neo-vessels, and thus  
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30 appeared as a scaffold for the accumulation of abundant SLIT2<sup>-</sup>/ $\alpha$ -SMA<sup>+</sup>  
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32 myofibroblasts, most likely largely derived from HSCs (Fig. 4F). Both in normal and  
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34 cirrhotic human livers, SLIT2<sup>+</sup> cells were clearly distinct from cytokeratin 19 (CK19)-  
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36 labeled cholangiocytes (Fig. S11).

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45 To further ascertain that PMSCs/PMSC-MFs accumulated in liver fibrosis, we  
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47 measured SLIT2 mRNA levels in mouse and human injured livers. We found that the  
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49 hepatic expression of *Slit2* increased in mouse models of either cholestatic diseases,  
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51 *i.e.*, 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC), *Abcb4*<sup>-/-</sup>, or NASH, *i.e.*, choline-  
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53 deficient, L-amino acid-defined (CDAA) and cytotoxic injury, *i.e.*, CCl<sub>4</sub> (Fig. S12), along  
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55 with those of fibrosis markers (*Acta2*, *Col1a1*) in all models, and of an angiogenesis  
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57 marker (*vWF*) in the cholestatic models (Fig. 5A and S13). The complete  
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3 PMSC/PMSC-MF 7-gene signature was increased in the DDC, *Abcb4*<sup>-/-</sup> and CDAA  
4 models, whereas the HSC/HSC-MF 6-gene signature that was tested in the DDC and  
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6  
7 CDAA models, was not (Fig. 5A and [S13](#)). The analysis of a cohort of patients with  
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10 non-alcoholic fatty liver disease (NAFLD) showed that the expression of *SLIT2* was  
11  
12 increased in the group with advanced fibrosis, *i.e.* F3-F4 according to the SAF score  
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14 (33) (Fig. 5B). We also examined the microarray data of liver tissue samples from  
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16 patients with NASH, primary sclerosing cholangitis (PSC) and other chronic liver  
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18 diseases (alcoholic liver disease, haemochromatosis, primary biliary cholangitis,  
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20 autoimmune hepatitis), for *SLIT2* expression and the oligogene expression signatures  
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22 of PMSCs/PMSC-MFs and of HSCs/HSC-MFs. This analysis showed that *SLIT2*  
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24 expression and the 7-gene expression signature of PMSCs/PMSC-MFs were both  
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26 significantly increased in the liver of patients with all types of chronic liver diseases, as  
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28 compared to normal liver (Fig. 5C-D, left panels and [S14A](#)). *SLIT2* expression and the  
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30 7-gene expression signature were both similarly correlated with *ACTA2*, *COL1A1* and  
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32 *vWF* expression in these samples (Fig. 5C-D). The analysis of the microarray data also  
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34 indicated that in contrast to the PMSC/PMSC-MF 7-gene signature, the 6-gene  
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36 expression signature of HSCs/HSC-MFs was not significantly different between any  
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38 group of diseased livers and normal livers (Fig. 5E and [S14B](#)). This finding is consistent  
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40 with a low proliferation rate of HSCs and further supports the assumption that HSC-  
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42 MFs would primarily derive from myofibroblastic differentiation of the HSC preexisting  
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44 pool. We concluded from these results that PMSCs give rise to a highly expansive  
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46 population of myofibroblasts in liver fibrosis irrespective of the cause.  
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## 56 Discussion

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3 In the present study, we provide a detailed atlas of portal mesenchymal cells, that were  
4 obtained *via* dissociation of the bilio-vascular tree. While being consistent with previous  
5 scRNAseq studies of the liver, notably from a *Pdgfrb*-GFP reporter mouse (15), our  
6 analysis revealed the existence of several clusters of fibroblasts. Among them, the Fib-  
7 3 and Fib-4 clusters, displayed relatively low levels of *Pdgfrb* expression compared to  
8 the other clusters of liver mesenchymal cells (Fig. S4A), and thus may have been  
9 underestimated in the study of PDGFR $\beta$ <sup>+</sup> cells (15). Fib-3 and Fib-4 were highlighted  
10 as potential progenitor cells on the basis of entropy, GO and trajectory analyses as  
11 well as the expression of stem cell markers. Thus, Fib-3 and Fib-4 appeared as the  
12 most primitive of liver mesenchymal cells, which form a continuum of cells with  
13 overlapping markers, along a gradient of differentiation that bifurcates towards mature  
14 VSMCs on one hand and HSCs on the other one. In this context, PMSCs were isolated  
15 as a cell population, that primarily comprised Fib-3 and Fib-4. MSCs were first  
16 identified in the bone marrow as clonogenic, multipotent cells, able to differentiate into  
17 lineages of mesenchymal tissues including osteoblasts, chondrocytes and adipocytes  
18 in culture (34). Subsequently, cells with similar properties were identified in multiple  
19 organs and also referred to as MSCs (35), although a controversy over the MSC  
20 terminology has been fueled by studies showing that MSCs from different tissues  
21 exhibited different differentiation capacities (36). Yet, MSCs from different tissues  
22 share common features including a small cell population, clonogenicity, the ability to  
23 differentiate into the afore-mentioned mesenchymal cell lineages *in vitro* and a frequent  
24 perivascular distribution (35, 36). PMSCs displayed all these characteristics. Thy1 and  
25 Gli1, two stem cell markers predominantly expressed in Fib-3, as well as fibulin-2 and  
26 ENTPD2, predominantly expressed in Fib-4, were previously immunolocalized in the  
27 portal tracts of homeostatic liver, with a perivascular or periductal distribution (19, 23-  
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3 25, 27, 37-39). We found that the sub-populations of Thy1<sup>+</sup> and Thy1<sup>-</sup> PMSCs were  
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5 equally clonogenic (Fig. S7), implying that both Fib-3 and Fib-4 are resource fibroblasts  
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7 in the liver. COL15A1 (4) and SLIT2, that we identified as PMSC markers, are  
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9 expressed in both clusters, and also display a perivascular or periductal distribution in  
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11 the homeostatic liver. As formerly proposed for other MSCs, e.g., in the skeletal muscle  
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13 (36), we suggest that Fib3 and Fib4 represent subsets of the same original population,  
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15 recruited to the surface of nascent portal blood vessels or later, of developing bile  
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17 ducts.  
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24 The lack of markers that would enable to differentiate HSC-derived from non-HSC-  
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26 derived myofibroblasts has been a major hurdle so far, to gain insight into the  
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28 specificities of the different types of liver myofibroblasts and their contributions to liver  
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30 fibrosis. The isolation of PMSCs allowed us to gain such insight and seek invaluable  
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32 markers of the two populations. The comparison of transcriptional profiles indicated  
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34 that in their resting state, PMSCs primarily ensure ECM organization and vasculature  
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36 integrity whereas HSCs are mainly involved in immunity and the metabolism of vitamin  
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38 A. A striking difference between the two cell populations as they transform into  
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40 myofibroblasts *in vitro*, is that PMSCs intensely proliferate whereas HSCs do not  
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42 divide. In addition, whereas the expression of  $\alpha$ -SMA is induced in both cell types, that  
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44 of ECM genes such as *Col1a1*, is up-regulated in HSCs but not in PMSCs, so that they  
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46 both converge towards more similar phenotypes. As a result, most of gene expressions  
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48 that could demarcate the two cell populations in their resting state are lost or no longer  
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50 discriminant between their myofibroblastic progenies. Thus, among markers of  
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52 PMSCs, the expression of *Gli1* or *Entpd2* is totally suppressed in PMSC-MFs, whereas  
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54 that of *Fbln2* expression is induced in HSC-MFs (Fig. S15). Our strategy was to build  
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3 oligogene expression signatures, which included only markers of the two cell  
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5 populations that maintained high differential expression, with limited variation (average  
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7 fold-change of approximately one), throughout their myofibroblastic differentiation.  
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9 Specificity of the cell signatures for liver fibroblasts and HSCs *in vivo*, was attested by  
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11 their projection onto previous scRNAseq datasets of mouse liver fibrosis (15, 18).  
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13 PMSC gene signature was predominantly expressed in Fib-3/Fib-4, but also to a lesser  
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15 extent in other fibroblast clusters (Fig. S10A), which therefore could also proliferate in  
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17 liver injury.  
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24 *Slit2*, known as a profibrotic and proangiogenic factor in the liver (29-32), is a  
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26 prototypical gene of PMSC/PMSC-MF signature. From the present data, we may  
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28 postulate that following liver injury, SLIT2, produced by proliferating PMSCs/PMSC-  
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30 MFs, promotes the formation of new vessels and the survival of HSC-MFs. Supporting  
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32 this view, FISH analyses showed that *SLIT2*<sup>+</sup> PMSCs/PMSC-MFs accumulated along  
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34 neo-vessels in the fibrotic septa of cirrhotic livers, surrounded by *SLIT2*  
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36 myofibroblasts, likely mostly HSC-derived. As we previously showed for *COL15A1* (4),  
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38 the hepatic expression of *SLIT2* increased in injured liver in correlation with that of  
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40 *COL1A1* and *vWF*, in all types of liver fibrosis. Akin to *SLIT2*, the complete  
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42 PMSC/PMSC-MF 7-gene signature increased, indicating that this cell population  
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44 expanded in mouse and human liver fibrosis of multiple causes. As they expand,  
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46 PMSCs/PMSC-MFs may promote liver fibrosis *via* several mechanisms including the  
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48 SLIT2/ROBO axis, but also the production of *COL15A1*, a multiplexin that anchors  
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50 interstitial collagen to basement membranes forming a scaffold for fibrosis progression  
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52 (4, 40), the overproduction of *COL1A1* and *COL1A2*, that form the major interstitial  
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54 collagen in liver fibrosis, and of *LOXL1*, which promotes elastin cross-linking, among  
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3 others. ScRNAseq analysis of human liver mesenchymal cells in cirrhosis (13),  
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5 previously identified a cluster distinguished by PDGFRA expression that expanded in  
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7 cirrhotic livers and was annotated scar-associated mesenchymal cells. We found that  
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9 the expression of all PMSC/PMSC-MF signature genes is largely predominant in this  
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11 population (Fig. S16), supporting the clinical relevance of our findings and our  
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13 conclusion regarding the expansion of PMSC-MFs in liver fibrosis. In a previous study,  
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15 a 122-gene HSC signature was shown to be increased in experimental and human  
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17 liver fibrosis (41). However, this latter signature was designed in comparison with other  
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19 liver cell types that did not include other liver mesenchymal cells, and highlighted  
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21 genes such as *Pcdh7* that were herein found to be expressed not only in HSCs/HSC-  
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23 MFs but also in PMSCs/PMSC-MFs (Fig. S4D and S15). Our HSC/HSC-MF 6-gene  
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25 expression signature did not increase in human fibrosis, which is consistent with a low  
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27 proliferation rate of HSCs/HSC-MFs *in vitro*, as shown here and *in vivo*, in recent  
28  
29 scRNAseq analysis of HSCs/HSC-MFs in mouse models of liver fibrosis (17, 18).  
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31 Despite little or no proliferation, HSC-MFs that derive from the large preexisting pool  
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33 of HSCs, likely form the major part of liver myofibroblasts. However, as they proliferate  
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35 and expand within the lobule, PMSC-MFs may develop interactions with ECs and  
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37 HSCs anticipated to play crucial roles in fibrosis progression.  
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52  
53 Pierre-Emmanuel Rautou (CRI, Université de Paris) for their contributions.  
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3 Data availability: All sequencing data are deposited in the Gene Expression Omnibus  
4 (GEO) with the accession numbers GSE163777 (scRNAseq), GSE164037 (bulk  
5 RNAseq) and GSE159676 (microarrays).  
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8 Author names in bold designate shared co-first authorship  
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## 11 12 13 **Figure legends**

### 14 15 **Fig. 1. ScRNAseq profiling of mesenchymal cells from the bilio-vascular tree.** (A)

16 Outline of the experimental procedure for preparation of Lin  
17 (EpCam,CD31,CD45,CD11b)-negative cells from the mouse bilio-vascular tree for  
18 scRNAseq analysis. (B) *t*-SNE projection of 4,976 single cells from one healthy liver,  
19 revealing 16 clusters (color-coded), identified by their expression profiles and ordered  
20 according to the number of cells they comprise. (C) Dendrogram showing the  
21 relationships of clusters. (D) Dot plot of two selective differentially expressed genes in  
22 each cluster.  
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### 36 **Fig. 2. Characterization of PMSCs.** (A) Single-cell entropy of all clusters. (B)

37 Inference of sequenced mesenchymal cells by Monocle 2 reverse graph embedding  
38 (pseudotime along differentiation trajectory in inset). (C) Heatmap of GO enrichment  
39 related to development. (D) Dot plot of genes previously reported to demarcate  
40 progenitor fibroblasts (red frame) or portal (myo)fibroblasts (black frame). (E) Dot plot  
41 of genes encoding surface markers *Pdgfra/Cd34/Cd9* and *Cd200*. (F) FACS plot  
42 showing the gating strategy for Fib-3/Fib-4 cell sorting (Gate 4). (G) CFU-F formed by  
43 sorted cells from gates as defined in F (n=3-9). (H) Flow cytometry analysis of MSC  
44 surface markers in cells from gate 4 (n=4-10). (I) Trilineage differentiation of cells from  
45 gate 4 (PMSCs), towards adipocytes (Oil red O), osteoblasts (Alizarin red S) and  
46 chondrocytes (Alcian blue). (J) Immunofluorescence of Col15A1 and  $\alpha$ -SMA in PMSC  
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spheroids (upper panel) or grown into PMSC-MFs on stiff substratum (lower panel). (K) *Col15a1*, *Acta2* and *Col1a1* expression in PMSCs (freshly isolated or cultured as in J) (n=3). Means  $\pm$  SEM; \*\* $p$ <0.01; \*\*\* $p$ <0.001; \*\*\*\* $p$ <0.0001 (Wilcoxon test); Scale bars=50  $\mu$ m.

**Fig. 3. Transcriptomic features of PMSCs/PMSC-MFs compared to HSCs/HSC-MFs.** (A,B) Bulk RNAseq analysis of PMSCs and HSCs, A) Volcano plot (upper panel) showing 3,273 and 3,122 DEGs (FDR  $\leq$  0.05, fold-difference  $\geq$  2) in PMSCs and HSCs, respectively. Top 10 DEGs are labeled and their average expression, projected on *t*-SNE plot of scRNAseq (lower panel); (B) Gene Set Enrichment Analysis (GSEA) of all genes overexpressed in PMSCs or HSCs. (C) Overview of cell preparations (n=4 per condition), analyzed by bulk RNAseq and PCA of variance of read counts (ellipses: 95% CI). (D) K-means clustering of 5,000 genes with highest variance showing enriched GO terms. (E) Venn diagram showing DEGs in PMSCs (or Fib-3/Fib-4) and in HSCs, both in bulk RNAseq and scRNAseq and maintaining high differential expression after myofibroblastic differentiation (-MFs-7d). (F-G) Heatmaps of PMSC and HSC oligogene expression signatures assessed by F) bulk RNAseq or G) RT-qPCR analyses of PMSCs, HSCs, derived myofibroblasts (-MFs-7d), and other liver cell types. KCs, Kupffer cells.

**Fig. 4. Slit2 marker in PMSCs/PMSC-MFs and its functional analysis.** (A) *Slit2* RT-qPCR in PMSCs, HSCs, their derived myofibroblasts (-MFs-d7), and other liver cell types (n=3) (left panel); Slit2 FISH and  $\alpha$ -SMA immunofluorescence in PMSC-MFs-d7 and HSC-MFs-d7 (right panel). (B) *t*-SNE plot of *Slit2* and its Robo receptors in scRNAseq clusters. (C) PMSC-MFs that were transfected with *Slit2* or scramble (Scr)

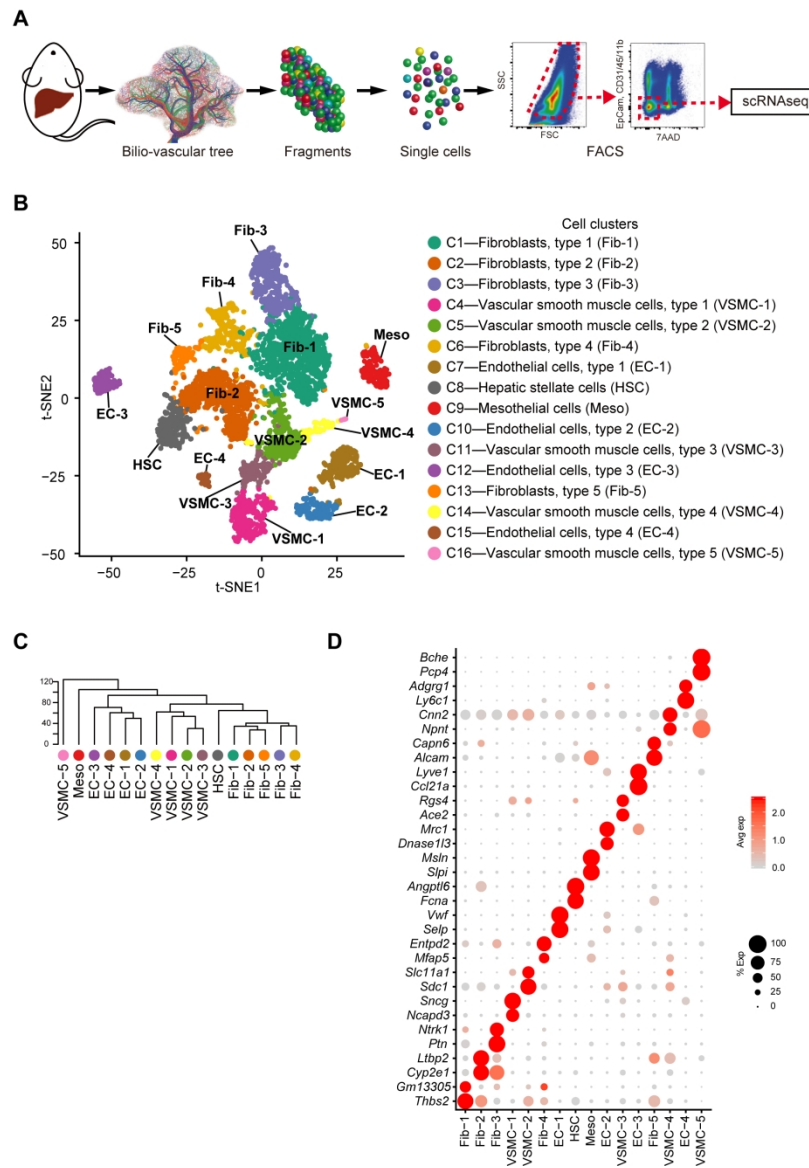
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3 siRNA, were examined for *Slit2* and *Acta2* expression by RT-qPCR, and their  
4 conditioned medium (CM) tested towards the cell viability, assessed by MTT, of LX-2  
5 cells exposed to H<sub>2</sub>O<sub>2</sub> (n=5-8). (D) Tube formation was evaluated in HUVECs  
6 incubated with PMSC-MF CM in the absence (n=6) or presence of ROBO1/Fc (n=5)  
7 or anti-ROBO1 antibody (n=5), or with control (CTL) serum-free medium (n=9); and in  
8 HUVECs incubated with the CM of PMSC-MFs infected with a lentivirus expressing  
9 Cas9 and a gRNA targeting the first exon of *Slit2* (LV*Slit2*, n=8) or a control lentivirus  
10 expressing Cas9 and a scramble gRNA (LV, n=8), or with CTL serum-free medium  
11 (n=3). After 6 hours, pictures were taken and the number of junctions, counted, using  
12 the Angiogenesis Analyzer tool Fiji. (E, F) *SLIT2* FISH and  $\alpha$ -SMA or CD31  
13 immunofluorescence in normal and cirrhotic human liver; E) In normal liver (left panel),  
14 a small number of *SLIT2*<sup>+</sup> PMSCs (arrowheads) are visible in portal tracts (perivascular  
15 *SLIT2*<sup>+</sup> PMSCs, distinct from  $\alpha$ -SMA<sup>+</sup> VSMCs, shown in insets), representative of n=2  
16 (CV, central vein; PV, portal vein). In cirrhosis (middle panel), *SLIT2*<sup>+</sup> are intermingled  
17 with *SLIT2*<sup>-</sup> myofibroblasts in fibrotic septa (FS) (*SLIT2*<sup>+</sup>,  $\alpha$ -SMA<sup>+</sup> PMSC-MF, shown in  
18 inset); right panel: quantification of labeled areas; F) *SLIT2*<sup>+</sup> PMSC-MFs (red  
19 arrowheads) line up along CD31<sup>+</sup> neo-vessels (white arrowheads), surrounded by  
20 several layers of  $\alpha$ -SMA<sup>+</sup> myofibroblasts that populate the entire fibrotic septa (dashed  
21 green line) (merge shown in inset), representative of cirrhosis of alcoholic (n=3), NASH  
22 (n=1) or hepatitis C (n=1) origins (Scale bars=50  $\mu$ m). Means  $\pm$  SEM; \**p*<0.05;  
23 \*\**p*<0.01; \*\*\*\**p*<0.0001 (One-way ANOVA in A, Wilcoxon test in C and D).

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55 **Fig. 5. Expression of *SLIT2*, PMSC/PMSC-MF and HSC/PMSC-MF oligogene**  
56 **signatures in liver fibrosis.** Hepatic expression of *SLIT2*, *ACTA2*, *COL1A1*, *vWF*,  
57 PMSC/PMSC-MF or HSC/HSC-MF oligogene signatures assessed by (A,B) RT-qPCR,  
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3 A) in liver tissue from mice fed normal chow diet (NCD, n=12) or DDC (n= 8) for 4  
4 weeks (upper panels), or fed CSAA (n=5) or CDAA (n=17) for 8 weeks (lower panels),  
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7 B) in liver biopsy from patients with NAFLD, at stages of fibrosis F0 (n=26), F1 (n=15),  
8 F2 (n=12), F3-F4 (n=7). (C) by Affymetrix microarray analysis of normal human liver  
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10 (n=5 patients) and of liver tissue samples from patients with NASH (n=7 patients), PSC  
11 (n=6 patients, 2 biopsies/patient) or other liver diseases (n=8 patients) (left panel); (D)  
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PMSC/PMSC-MF and (E) HSC/HSC-MF oligogene signatures assessed by Affymetrix microarray analysis of human liver tissue samples as in C. Correlations between *SLIT2* or PMSC 7-gene signature and *ACTA2*, *COL1A1*, or *vWF* expression are shown in C and D right panels. Individual values and means  $\pm$  SEM are shown; \* $p < 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p < 0.001$ ; \*\*\*\* $p < 0.0001$ ; ns, non-significant (Wilcoxon test in A, C-E; one-way ANOVA in B); r values are Pearson correlation coefficients.

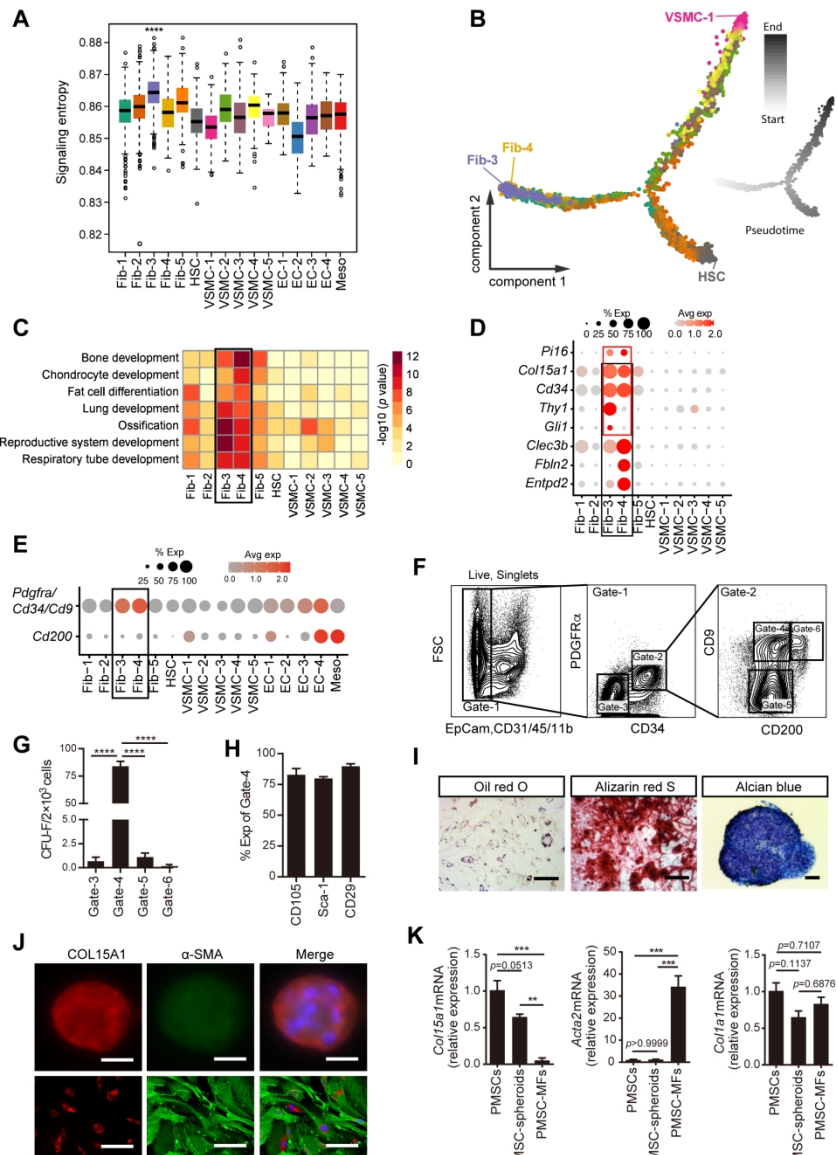
Figure 1



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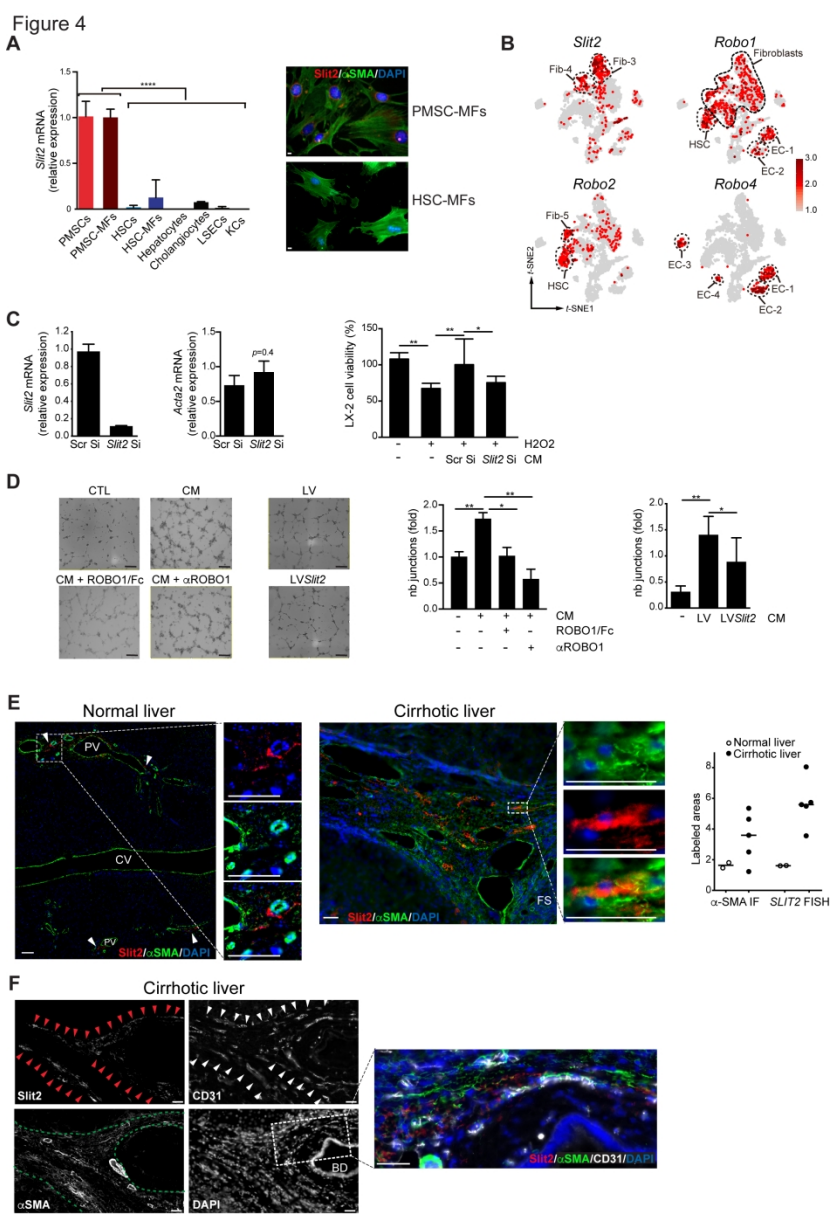


Figure 2

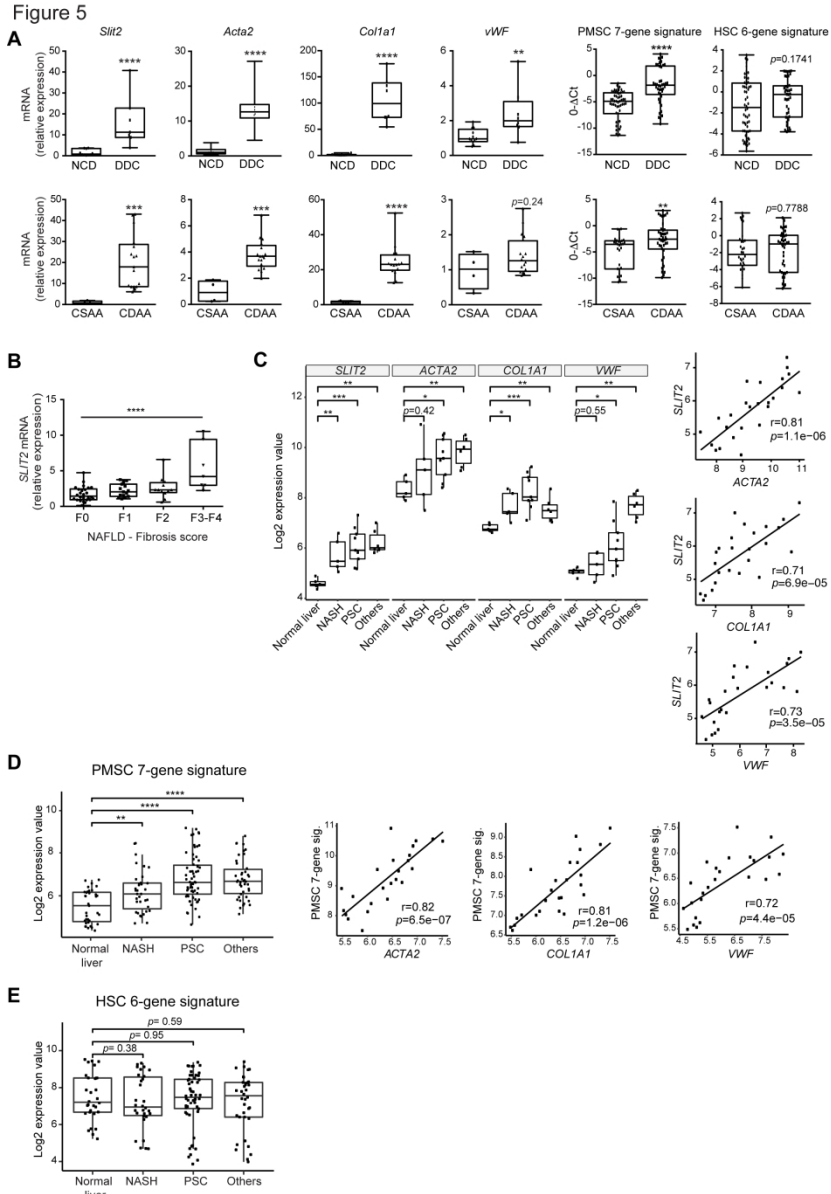


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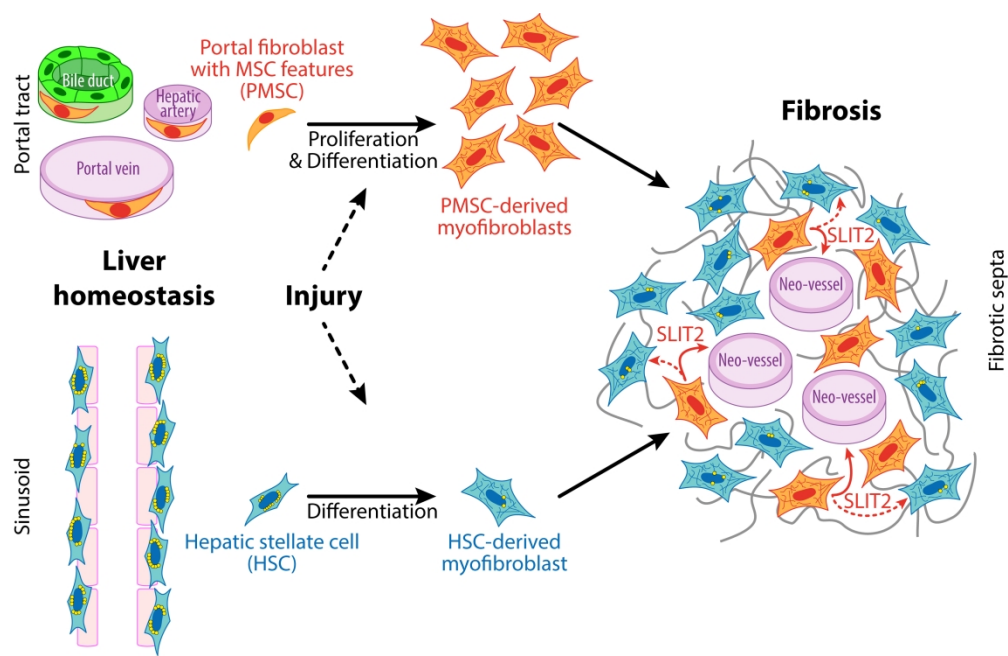


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**Portal fibroblasts with mesenchymal stem cell features form a reservoir  
of proliferative myofibroblasts in liver fibrosis**

Lin Lei, Alix Bruneau, Haquima El Mourabit, Justine Guégan, Trine Folseraas, Sara Lemoine, Tom Hemming Karlsen, Bénédicte Hoareau, Romain Morichon, Ester Gonzalez-Sanchez, Claire Goumard, Vlad Ratziu, Pierre Charbord, Jérémie Gautheron, Frank Tacke, Thierry Jaffredo, Axelle Cadoret\*, Chantal Housset\* (\*co-senior authorship).

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## Supplementary Experimental procedures

### **Animal experiments.**

Animal experiments were conducted in the CRSA animal facility (DDPP agreement No. C 75-12-01) and were approved under Nos. 2018060418401070v2, 2018102211507258, 2019090307246392v3 and 2018072719352187v1 by the Ethics Committee of Animal Experiments, Charles Darwin No. 5, Paris. Animals, all males, were housed in a temperature-controlled, specific pathogen-free environment, on a 12-hour light-dark cycle, with free access to chow and water. *Abcb4*<sup>-/-</sup> mice and their wildtype *Abcb4*<sup>+/+</sup> littermates were bred, using *Abcb4*<sup>+/-</sup> heterozygous mice on an FVB/N genetic background (FVB.129P2-*Abcb4*tm1Bor/J) provided by Sanofi R&D (Chilly-Mazarin, France). Liver fibrosis was also induced in C57BL/6J male mice, by 3 methods: 1) 10-week-old mice were fed a diet containing 0.1% DDC (Sigma, 137030) or a normal control diet (NCD), for 4 weeks; 2) 8-week-old mice were fed a CDAA or CSAA diet (Ssniff spezialdiäten GmbH, Soest, Germany), for 8 weeks; 3) 8-week-old mice received i.p. injections of CCl<sub>4</sub> (1 μL/g body weight) diluted at 50% (V/V) in mineral oil or mineral oil (vehicle), twice a week for 6 weeks.

### **Cell isolation.**

*Cell collection from the bilio-vascular tree.* *In situ* retrograde perfusion of the liver was performed through the inferior vena cava with Ca<sup>2+</sup>,Mg<sup>2+</sup>-free HBSS (Gibco, 14170-088)/1% EDTA (Sigma, 03690) for 5 minutes at 37°C, and then with HBSS containing Ca<sup>2+</sup>,Mg<sup>2+</sup> (Gibco, 24020117)/0.15 mg/mL collagenase P (Sigma, 11213873001) for 20 minutes at 37°C. Next, the liver was collected and placed in L15 Leibovitz medium (Sigma, L5520) at 4°C. The liver parenchyma was mechanically detached and discarded. The remaining bilio-vascular tree was minced and incubated in MEM (Gibco, 21090-022) containing 0.075 mg/mL collagenase P, 0.02 mg/mL DNase (Sigma, DN25), 3% FBS (FBS; Gibco, 10270-098), 1 mg/mL BSA (Sigma, A7030), 1% HEPES (Gibco, 15630) and 1% Penicillin-Streptomycin (Gibco, 15140-122), under agitation for 15 minutes at 37°C. The bilio-vascular fragments were collected on top of a 40-μm cell strainer and centrifuged at 1,500 rpm, for 5 minutes at 4°C. The cell pellet was resuspended in 0.05% Trypsin-EDTA (Invitrogen, 25300-054) with 0.02 mg/mL DNase and incubated under agitation for 15 minutes at 37°C, and the dissociated cells were filtered three times through a 20-μm cell strainer. Following red blood cell lysis with ACK lysis buffer, the cell suspension was centrifuged at 1,500 rpm, for 5 minutes at 4°C, and the cell pellet was resuspended in a FACS buffer composed of PBS with 2% FBS, 1% HEPES and 1% Penicillin-Streptomycin, at a concentration of 1 × 10<sup>7</sup> cells/mL for cell sorting. For cholangiocyte isolation, cells were incubated with an anti-Epcam-FITC antibody (BioLegend, Clone: G8.8) for 30 minutes at 4°C and cells were sorted using a FACSAria II cell sorter (BD Biosciences).

*Hepatocyte, Kupffer cell, LSEC and HSC collection.* Hepatocytes, LSECs and Kupffer cells were isolated as previously described (1), with modifications. For

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hepatocyte isolation, the liver was perfused *in situ* with HBSS containing 0.15 mg/mL collagenase P for 20 minutes at 37°C. The cell suspension was filtered through a 70- $\mu$ m strainer and centrifuged twice at 400 rpm, for 5 minutes at 4°C, to eliminate non-parenchymal cells. LSEC and Kupffer cell isolation was performed by *ex situ* dissociation of the liver using a gentleMACs dissociator (Miltenyi) and magnetic selection using CD146 microbeads (Miltenyi, 130-092-007) and anti-F4/80 microbeads (Miltenyi, 130-110-443), respectively. For HSC isolation, the liver was perfused *in situ*, with HBSS containing 0.4 mg/mL pronase (Sigma, 10165921001) for 5 minutes at 37°C, and then with 0.05 mg/mL collagenase P for 15 min at 37°C. The liver was collected, minced and further digested in HBSS containing 0.044 mg/mL collagenase P, 0.5 mg/mL pronase and 0.02 mg/mL DNase, under agitation for 15 minutes at 37°C. The resulting cell suspension was submitted to density gradient-centrifugation at 1,380 g for 17 minutes, in GBSS (Gibco)/Histodenz (Sigma, D2158) at 4°C. HSCs were collected from the interface and resuspended in FACS buffer for further purification by cell sorting based on retinoid autofluorescence, as previously described (2).

### **Cell sorting and flow cytometry analysis**

Cells isolated from the bilio-vascular tree were incubated with 1% anti-mouse CD16/CD32 antibody (BD Pharmingen, 553141) for 10 minutes on ice, to block Fc receptors before incubation with anti-Epcam-FITC, anti-CD31-FITC, anti-CD45-FITC and anti-CD11b-FITC antibodies, all at concentrations of 1:100, for 30 minutes at 4°C. Dead cells were stained with 7-aminoactinomycin D (7-AAD; BD Biosciences, 559925) immediately before cell sorting was performed, using a FACSAria II cell sorter (BD Biosciences). Lin-negative cells, gated as Epcam<sup>+</sup>CD31<sup>+</sup>CD45<sup>+</sup>CD11b<sup>-</sup> cells, were collected and subjected to scRNAseq analysis. To isolate PMSCs from the bilio-vascular tree, cells were labeled with anti-Epcam-, anti-CD31-, anti-CD45- and anti-CD11b-FITC antibodies as above, and anti-PDGFR $\alpha$ -PE, anti-CD34-APC, anti-CD9-BV421 and anti-CD200-APC-R700, all at concentrations of 1:100 except for anti-PDGFR $\alpha$ -PE (1:50). PMSCs were gated as Lin<sup>-</sup>PDGFR $\alpha$ <sup>+</sup>CD34<sup>+</sup>CD9<sup>+</sup>CD200<sup>low</sup> cells. To sort Thy1<sup>-</sup>, Thy1<sup>low</sup> and Thy1<sup>high</sup> PMSCs, cells from the bilio-vascular tree were labeled with anti-Epcam-FITC, anti-CD31-FITC, anti-CD45-FITC, anti-CD11b-FITC, anti-PDGFR $\alpha$ -PE, anti-CD34-APC, anti-CD9-BV421, anti-CD200-APC-R700 antibodies as above, and anti-Thy1-PE-Cy7 antibody at a concentration of 1:100. For flow cytometry analysis, freshly isolated PMSCs were labeled either with anti-CD105-BV510, anti-Sca1-BV510 or anti-CD29-PE/Cy7, all at concentrations of 1:100. Analyses were performed using BD FACSDiva™ and FlowJo (Tree Star) software. All antibodies are listed in [Table S1](#).

### **Cell culture.**

PMSCs and HSCs were seeded in 6-well plates at a density of 20,000 cells/cm<sup>2</sup> and cultured in DMEM containing 20% FBS, 1% HEPES and 1% Penicillin-Streptomycin to obtain PMSC-MFs and HSC-MFs, respectively. To maintain PMSCs in a resting state, cells were seeded in 96-well ultra-low attachment



(ULA) round-bottomed plates. The LX-2 human HSC cell line (provided by Human HepCell, IHU-ICAN) was cultured in DMEM containing 10% FBS, 1% HEPES and 1% Penicillin-Streptomycin. HUVECs were grown in EndoGRO™-VEGF complete medium (Millipore).

### **Cell clonogenicity and differentiation assays.**

Cell clonogenicity was examined by CFU-F assay, as follows: 2,000 sorted cells were plated onto a 10-cm plastic dish and maintained in DMEM/20% FBS. The presence of more than 50 cells in a cluster after 14 days in culture, was counted as a colony. The capacity of PMSCs to differentiate towards adipogenic, osteogenic or chondrogenic lineages was analyzed using specific protocols. For adipogenic and osteogenic differentiation, sorted PMSCs were plated in 48-well plates coated with matrigel (Corning, 356231) at a density of 5,000 cells/cm<sup>2</sup> in DMEM/20% FBS until subconfluence. Then, the culture medium was changed for adipogenic (R&D Systems, CCM011) or osteogenic (R&D Systems, CCM009) differentiation medium. After 21 days, cells were fixed with 4% paraformaldehyde and stained using Oil Red O (Sigma) or Alizarin Red solution (Sigma), respectively. For chondrogenic differentiation, 50,000 sorted PMSCs were plated in ULA plate in chondrogenic differentiation medium (R&D Systems, CCM006) to form spheroids. After 21 days, the spheroids were fixed in 4% paraformaldehyde, embedded in OCT (Sakura Finetek) and cryosections (8 μm) were stained with Alcian blue (Santa Cruz Biotechnology) and counterstained with nuclear fast red (Vector).

### **Videomicroscopy.**

PMSCs and HSCs were seeded in 24-well plates at densities of 5,000 and 50,000 per well, respectively, and cultured in standard conditions. Twenty-four hours after seeding, the cells were placed in the CellVivo Incubation System (Pecon GmbH, Ernah, Germany) driven by a high-end inverted microscope IX83 (Olympus Corporation, Tokyo, Japan). One picture has been taken every hour, using a 10X UPLFN 0.3NA PH1 objective lens and ORCA-Flash 4 LT digital (Hamamatsu Photonics KK, Tokyo, Japan) driven by Cellsens dimension 1.16 (Olympus). The movies have been built using the open source software Fiji (3).

### **ScRNAseq.**

Cells were loaded onto a GemCode instrument (10x Genomics) to generate single-cell barcoded droplets, *i.e.*, gel beads in emulsion (GEMs). Sequencing libraries were constructed using the Chromium Single-cell 3' Library Kit (10x Genomics) according to the manufacturer's protocol and sequenced on a NextSeq 500 device (Illumina). Average read depth of the sample was 79,199 reads/cell. Reads were then aligned to the mouse genome mm10/Grcm38 using the Cell Ranger 3.0.2 software. Subsequent analysis was performed in R using the filtered barcode and count matrices produced by Cell Ranger. The data were analyzed using Seurat 3.6.1 (4). Genes expressed in less than 6 cells, as well as cells with less than 500 or more than 25,000 unique molecular identifiers (UMIs), were filtered out. Any single-cell with more than 10% UMIs

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1 mapped to mitochondrial genes was also removed. Seurat SCTransform  
2 function (5) was used to normalize and scale the data  
3 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE163777>).  
4

5 Dimensionality reduction was performed through PCA on the gene expression  
6 matrix and using the first 30 PCs for clustering and visualization. Unsupervised  
7 shared nearest neighbor clustering was performed using Seurat FindClusters  
8 function at the resolution of 0.6 and visualization was achieved using spectral  
9  $t$ -SNE of the principal components as implemented in Seurat. Cluster  
10 dendrogram was constructed using BuildClustertree built-in function of the R  
11 package Seurat which used cluster averaged PCs for calculating a PC distance  
12 matrix. The cell clusters identified were evaluated for differential genes  
13 expression (DGE), using Seurat FindAllMarkers function. All genes considered  
14 for cell-type classification were determined with  $p$  value  $< 0.01$  and log (fold-  
15 change)  $> 0.25$  as cutoff by performing DGE analysis between the clusters  
16 using Wilcoxon rank sum test and Benjamini and Hochberg procedure for  $p$ -  
17 values adjustment. Single-cell entropy was calculated using LandSCENT v.  
18 0.99.3, as previously described. Doublet analysis was performed, using two  
19 methods, *i.e.*, DoubletFinder, R package v 2.0 and Scrublet, python library v0.1.  
20 Thereby, we identified 334 and 103 potential doublets, respectively. They  
21 included 66 doublets in common, that were plotted on  $t$ -SNE projection (Fig.  
22 S1B). The Monocle version 2.14.0 R package (6) was used to organize cells in  
23 pseudotime and infer cell trajectories from the Seurat dataset. We ran  
24 reduceDimension with  $t$ -SNE as the reduction method, num\_dim=12,  
25 norm\_method="log" and max\_components = 2. Cells were clustered with the  
26 density peak clustering algorithm by setting P to 2 and  $\Delta$  to 4 (and  
27 skip\_rho\_sigma = T to facilitate the computation). The top 1000 significantly  
28 differentially expressed genes between clusters were selected as the ordering  
29 genes and used in Monocle for clustering and ordering cells using the DDRTree  
30 method and reverse graph embedding.  
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#### 40 **Bulk RNAseq.**

41 RNA was extracted using Rneasy Micro Kit (Qiagen). Libraries were generated  
42 from total RNA and paired-end sequencing was performed on a NextSeq 500  
43 device (Illumina). Raw sequencing data were quality-controlled with the FastQC  
44 program. Paired reads were aligned to the mouse reference genome (mm10  
45 build) with the STAR software v2.5.3a (option for no multihits). Mapping results  
46 were quality-checked using RNASEQC. Gene counts were obtained by using  
47 RSEM tools v1.2.28 (rsem-calculate-expression, option for paired-end and  
48 stranded). Expected gene counts were first normalized using TMM method in  
49 the edgeR R package and genes with a count per million (CPM)  $< 1$  in 20% of  
50 samples, were removed  
51

52 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164037>).  
53

54 Differential gene expression analysis was performed using DEseq2. A  $\log_2$  of  
55 fold change of 1 and a Benjamini-Hochberg adjusted  $p$  value cutoff  $< 0.05$  (FDR)  
56 was set to determine significant differentially expressed genes.  
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## GO enrichment and Gene Set Enrichment Analysis.

Symbol gene IDs were first converted to Entrez gene IDs using the clusterProfiler R package (7). Functional enrichment in GO biological processes of differentially expressed genes was performed using EnrichGO built-in function of the clusterProfiler version 3.14 with default parameters. The comparison of enriched functional enrichment among mesenchymal cell populations was performed using clusterProfiler CompareCluster function (7). Heatmap of enriched term was generated in R. GSEA was implemented using the R package ReactomePA with default parameters (8).

### ***Import of previously published data sets.***

We downloaded the raw scRNAseq data of i) 23,291 Pdgfrb-GFP+ mesenchymal cells from uninjured and fibrotic (6 weeks CCl<sub>4</sub>) mouse livers published and deposited in the GEO by Dobie *et al.* (GSE137720), ii) 47,752 liver cells of all types from uninjured oil-treated (10,636) and fibrotic (CCl<sub>4</sub> 3 weeks, 18,185; BDL 10 days, 18,931) mouse livers published and deposited in the GEO by Yang *et al.* (GSE171904).

### ***Slit2 silencing by siRNA and LX-2 survival.***

*Slit2* and scramble siRNA (SMARTpool: ON-TARGETplus *Slit2* siRNA L-058235-00-0005, ON-TARGETplus Non-targeting Pool D-001810-10-05) were purchased from Dharmacon. PMSC-MFs at passage 1 in 6-well plates were transfected with siRNA (50 nmol/L) using Dharmafect1. Forty-eight hours after transfection, the cells were incubated with serum-free DMEM for 24 hours to generate conditioned medium. LX-2 cells were seeded in 96-well plates (7,000/well) and 24 hours later, were incubated in serum-free DMEM containing H<sub>2</sub>O<sub>2</sub> (200 μmol/L) for 30 min. Thereafter, the medium was replaced by serum-free DMEM or conditioned medium from transfected PMSC-MFs and 24 hours later, cell viability was assessed using MMT assay. Absorbance was quantified at 540 nm (TECAN).

### ***Slit2 deletion by CRISPR/Cas9.***

The lentiviral plasmid plentiCRISPRv2, a gift from Zhang lab (Addgene, MA, USA; plasmid #52961), contains hSpCas9, a guide RNA (gRNA), and a puromycin resistance sequence. The gRNA targeting exon 1 of *Slit2* was designed using <http://cistrome.org/SSC>, that ensures specificity and high cleavage efficiency.

Its sequence was sense, 5' CTTGAACAAGGTGGCGCCGC 3', antisense, 5' GCGGCGCCACCTTGTTCAAG 3'. The web-based tool, CRISPOR (<http://crispor.tefor.net>) that predicts the risk of off-target sequences by providing a cutting frequency determination (CFD) specificity score ranging from 1 to 100, was used to avoid off-target sequences. Guides with a CFD specificity score > 50 are recommended by Doench JG *et al.* (9). The gRNA we used to target *Slit2* exon 1 has a CFD score of 98. This gRNA did not perfectly match any other genomic region. One off-target with three mismatches was found in an intronic region of *Mapk4* and 40 off-targets were found with four

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mismatches, making unlikely that these off-targets were involved in the effect caused by *Slit2* ablation. Lentiviruses dedicated to *Slit2* knockout (LV*Slit2*) and a control lentivirus (LV) expressing Cas9 and a scramble gRNA were produced by the VVTG platform (Federative Research Institute, Necker, France). Sub-confluent PMSC-MFs at day 7 of primary culture, were infected with viral particles at a minimal titer of  $10^8$  units per mL. Forty-eight hours post-infection, the culture medium was discarded and conditioned medium was prepared by incubating the cells with serum-free medium for 24 hours.

### **Tube assay.**

HUVECs (15,000 cells/well) were plated in 15-well  $\mu$ -slide angiogenesis Ibidi plates (Clinisciences) previously coated with 50  $\mu$ l of growth factor-reduced Matrigel (BD Biosciences) and incubated in the presence of PMSC-MF conditioned medium (harvested from cells incubated with serum-free medium for 24 hours) or serum-free medium as a control. To assess the contribution of SLIT2 secreted by PMSC-MFs in angiogenesis, HUVECs were incubated with PMSC-MF conditioned medium a) in the presence of 100 ng/mL of recombinant rat ROBO1/Fc chimera protein (R&D Systems, #1749B) (10), b) after they had been preincubated for 1 hour with 10  $\mu$ g/mL of anti-human ROBO1 antibody (R&D Systems, #AF7118), or c) with the conditioned medium from PMSC-MFs infected with a lentivirus expressing Cas9 and a gRNA targeting the first exon of *Slit2*, dedicated to *Slit2* knockout (LV*Slit2*) or a control lentivirus (LV) expressing Cas9 and a scramble gRNA. HUVECs were placed in the CellVivo Incubation System as for videomicroscopy (described above) and tube formation was evaluated after 6 hours of incubation using the Angiogenesis Analyzer tool (Fiji software).

### **Human liver tissue samples.**

Samples of normal liver from patients undergoing liver resections for focal lesions (n=2 patients), and of cirrhotic livers from patients with NASH (n=1), chronic hepatitis C (n=1) or alcoholic liver disease (n=3) undergoing liver resection or transplantation, were provided by Human HepCell platform (IHU-ICAN, Declaration No. AC-2020-3861) for FISH. Frozen samples of liver biopsy from subjects with a suspicion of non-alcoholic fatty liver disease at stages of fibrosis F0 (n=26), F1 (n=15), F2 (n=12), F3-F4 (n=7), were provided by the Biological Resource Center, BIO-ICAN, Paris, France, with ethical approval from the Persons Protection Committee (CPP Ile de France VI) for RT-qPCR analyses. The RNA used for microarray experiments was extracted from frozen tissue obtained from explanted livers or diagnostic liver biopsies from i) normal human liver tissue (tumor-free tissue from livers with colorectal cancer metastasis) (n=5 patients) and ii) liver tissue from patients with chronic liver diseases, including PSC (n=6 patients, 2 biopsies/patient), NASH (n=7 patients) and other liver diseases including autoimmune hepatitis (n=3), primary biliary cholangitis (n=2), alcoholic liver disease (n=1), haemochromatosis (n=1) and sarcoidosis (n=1). The liver specimens were provided by the Norwegian biobank for primary sclerosing cholangitis, Oslo, Norway with ethical approval

1 from the Regional Committee for Medical and Health Research ethics of South  
2 East Norway. All subjects gave written informed consent before to allow the use  
3 of the samples.  
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### 6 **RT-qPCR.**

7 Total RNA was extracted from frozen liver tissue samples or harvested cells  
8 using the RNeasy Mini Kit or Micro Kit (Qiagen), respectively. The cDNA was  
9 synthesized using the MMLV-RT (Invitrogen, 28025013) or SuperScript™ II  
10 (Invitrogen, 18064014) and real-time PCR was performed using the LightCycler  
11 480 SYBR Green I Master Kit on an LC480 device (Roche Diagnostics). Target  
12 gene mRNA levels were normalized using HPRT or 18S as a reference gene  
13 and expressed as relative levels ( $2^{-\Delta\Delta Ct}$  method). Normalized values ( $\Delta Ct$ )  
14 were used for oligogene signature analysis and presented as  $0-\Delta Ct$ , so that  
15 higher values indicate higher expression levels. The primers (Table S2) were  
16 designed using the primer software from Roche Diagnostics.  
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### 22 **Immunofluorescence and FISH.**

23 For immunofluorescence, cell preparations were fixed in 4% paraformaldehyde  
24 at 4°C for 15 minutes, and incubated with primary antibodies against COL15A1  
25 (Abcam, ab58717, 1:200) or  $\alpha$ -SMA (Agilent, M085129-2, 1:100) at 4°C  
26 overnight. Nuclear staining was performed using Draq5 (Abcam). Cells were  
27 examined with a SP2 confocal microscope (Leica, Bannockburn, IL, USA).  
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29 For co-labeling by FISH and immunofluorescence, cell preparations and tissue  
30 samples were fixed in 4% paraformaldehyde at 4°C for 20 minutes and 4 hours,  
31 respectively. Tissue samples were then transferred to 30% sucrose in PBS at  
32 4°C until sinking and then placed in a plastic mold filled with O.C.T. that was  
33 immersed in 2 methyl-butane maintained at -70°C, and stored at -80°C. Tissue  
34 sectioning was performed at -25°C and 10- $\mu$ m cryosections were mounted on  
35 SuperFrostPlus™ slides that were kept on dry ice. Before processing, tissue  
36 sections were thawed in 100% ethanol for 5 minutes, followed by 1 minute in  
37 TBS buffer. Cell preparations or tissue sections were then transferred to pre-  
38 warmed hybridization buffer (5X SSC / 1% BSA / 10% Formamid / 0,1% (w/v)  
39 SDS) at 75°C for 20 minutes. The probes, directed at *SLIT2* or Scramble (Table  
40 S3), conjugated to Fam-6 or Atto-633, respectively, were diluted at 50 ng/ $\mu$ L  
41 and denatured at 85°C for 5 minutes while the samples were dried and  
42 denatured on a preheated plate at 85°C for 2 minutes. The probes (100 $\mu$ L) were  
43 added to tissue sections then covered with a coverslip and sealed with glue. In  
44 the following steps the samples were kept in the dark. They were incubated at  
45 75°C overnight in a dark wet chamber. After removal of the coverslip, the slides  
46 were transferred to freshly prepared hybridization buffer at 75°C for 15 minutes.  
47 The slides were washed with TBS for 5 minutes, and then with TBS-Triton x100  
48 0.3% for 15 minutes, at room temperature. After a 5-minute TBS wash at room  
49 temperature, the slides were blocked for 60 minutes with 2% Normal Goat  
50 Serum (Thermo Fisher) in TBS-T (0.1%). Tissue sections were incubated with  
51 anti- $\alpha$ -SMA (1:100, M085129-2, Agilent) in blocking buffer, overnight at 4°C.  
52 Slides were washed with TBS 3 times for 5 minutes at room temperature and  
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1 incubated with secondary antibody (Goat anti-mouse IgG Alexa Fluor 555  
2 Conjugate, CellSignaling #4409, 1:500) and DAPI 2 $\mu$ g/mL (Sigma-Aldrich).  
3 Large field imaging acquisition was performed on a Zeiss Axio Observer 7. For  
4 image processing, the large field images were stitched and background was  
5 subtracted, using the default settings of ZEISS software ZEN 3.1 (blue edition).  
6 Exported single channel grayscale in .tiff were later processed in Fiji. The  
7 background due to FISH staining was assessed using the scramble probe and  
8 this autofluorescence was subtracted from the *SLIT2* channel using image  
9 calculator module. For quantification, binary masks of at least two independent  
10 experiments were generated using the trainable classification software Ilastik  
11 (v 1.3.3). Marked areas were then measured using Fiji. The plugin Color pixel  
12 counter was used to count the number of pixels on the image of a specific color.  
13 Results are expressed as a percentage of pixels in the Region of Interest.  
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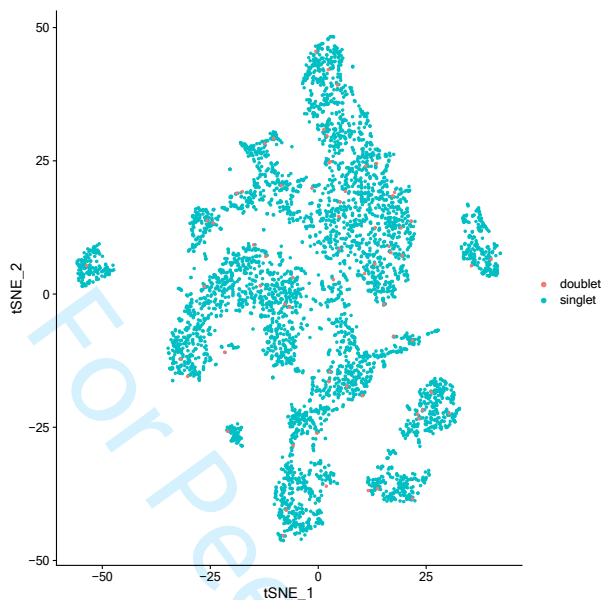
### 19 **Microarray analyses.**

20 Pangenomic analysis of frozen liver tissue samples, was performed using the  
21 Affymetrix human gene 1.0 st microarray. Analysis was conducted using  
22 R. *oligo* bioconductor package to import raw data CEL files in an ExpressionSet  
23 object and *rma* function to normalize the data. After normalization,  
24 summarization was performed because transcripts are represented by multiple  
25 probes, on the Affymetrix platform. For each gene, the background-adjusted  
26 and normalized intensities of all probes were summarized into one estimated  
27 amount proportional to the amount of RNA transcripts. Summarized data have  
28 been annotated with hugene10sttranscriptcluster.db bioconductor package  
29 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE159676>).  
30 Statistical analysis was performed using non-parametric Wilcoxon test.  
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	nCounts (transcripts)	nFeatures (genes)	% mitochondrial genes
Mean per cell	10539	2951	3.14 %

B



**Fig. S1: scRNAseq (A) Quality control metrics; (B) Analysis of doublets (plotted on *t*-SNE).**

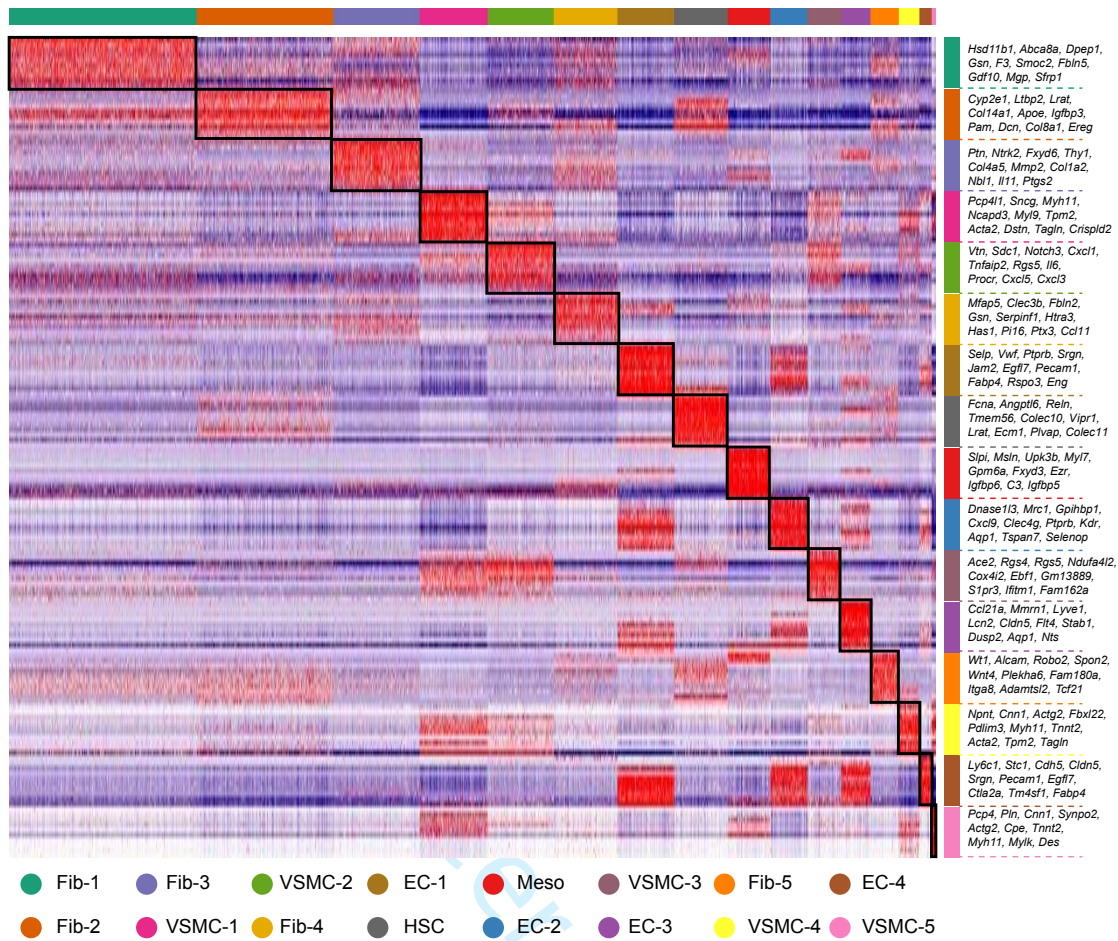


Fig. S2: Heatmap of the top 10 differentially expressed genes in scRNAseq clusters. (see also Table S4).

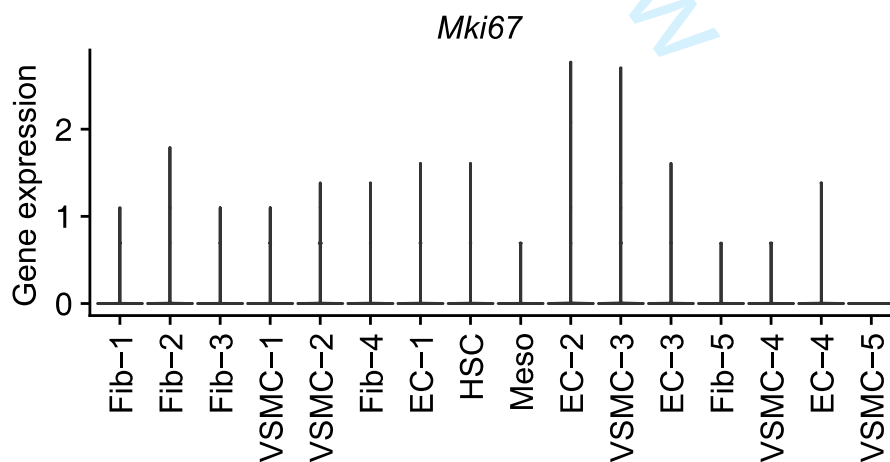
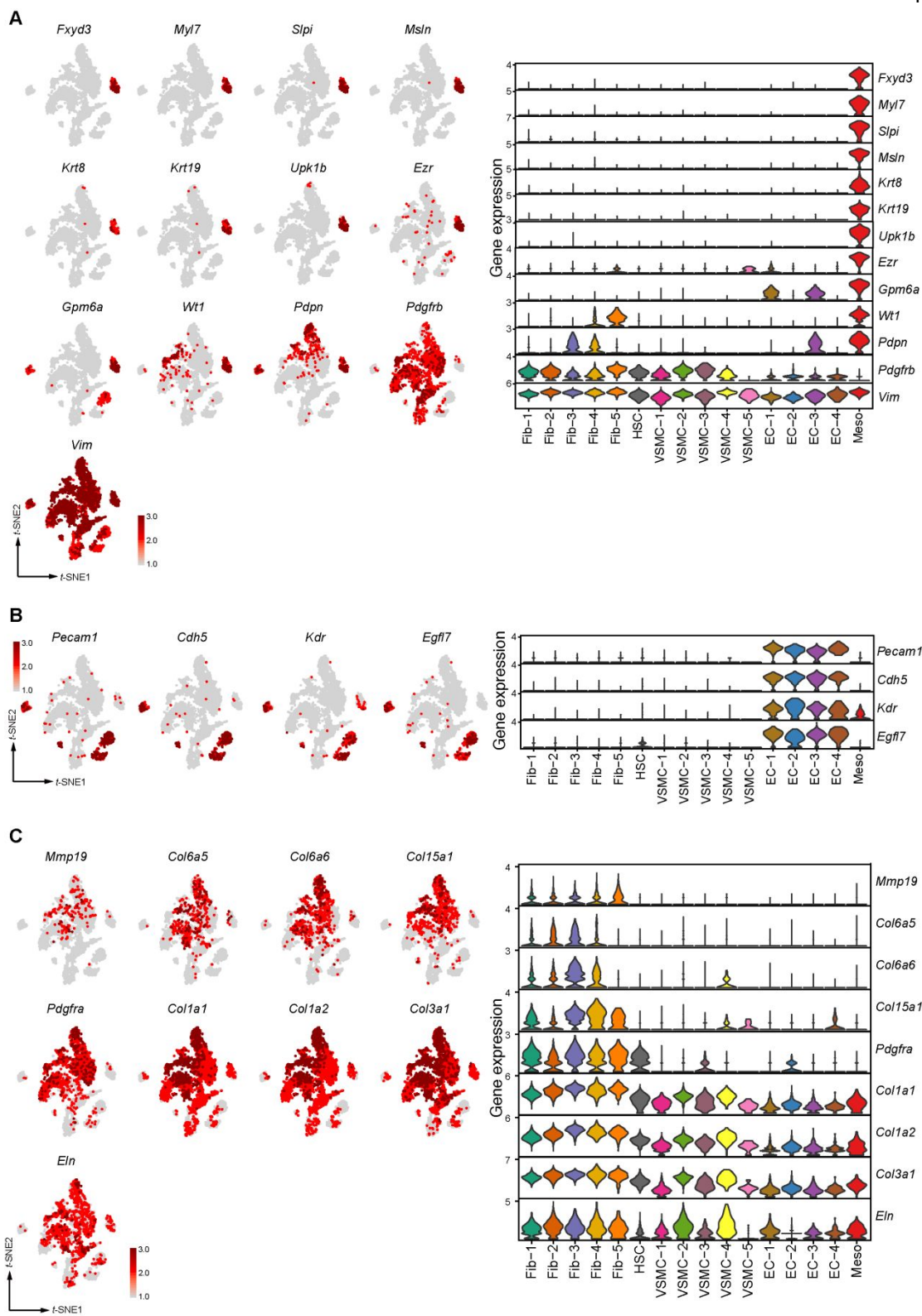
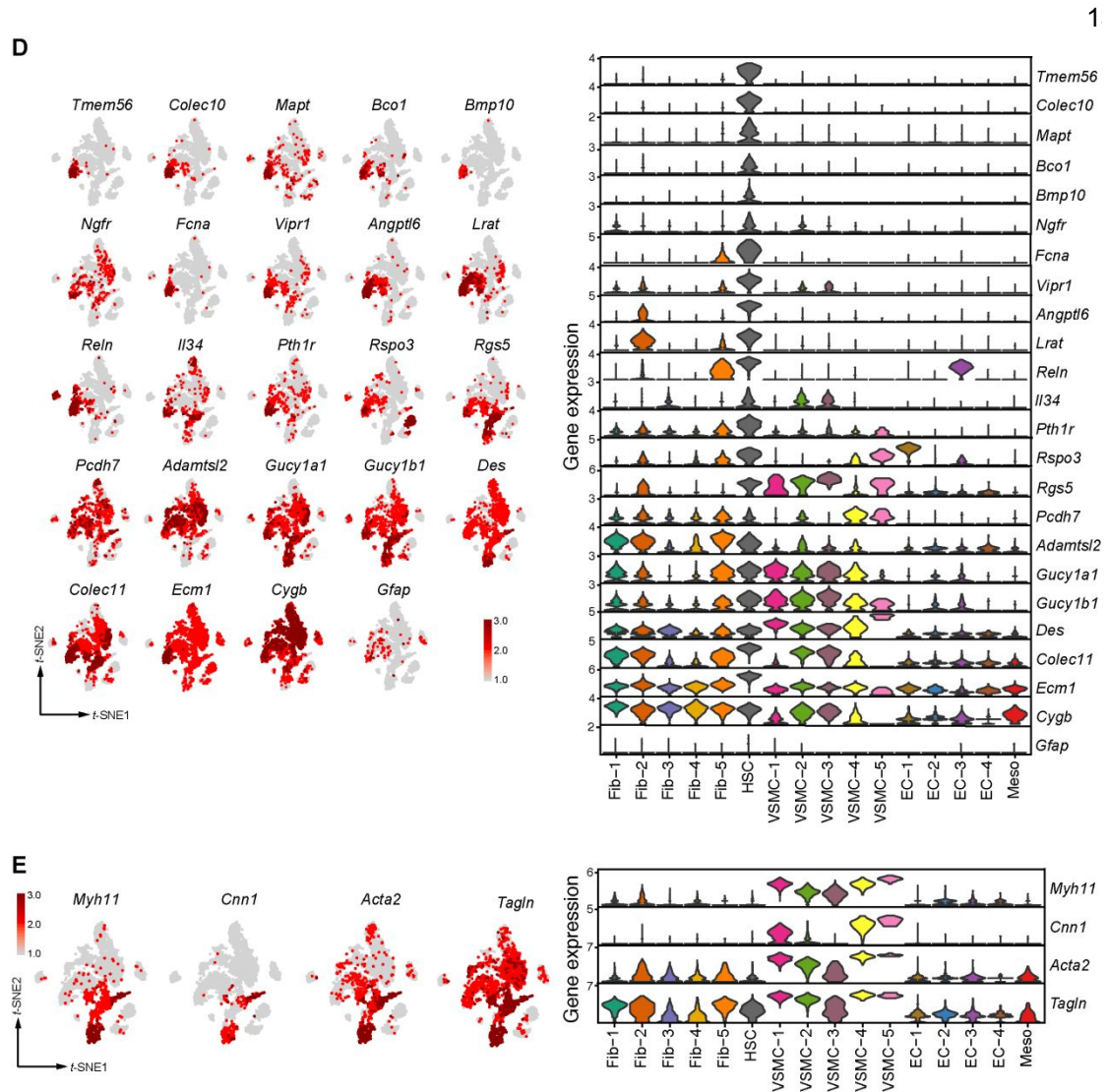


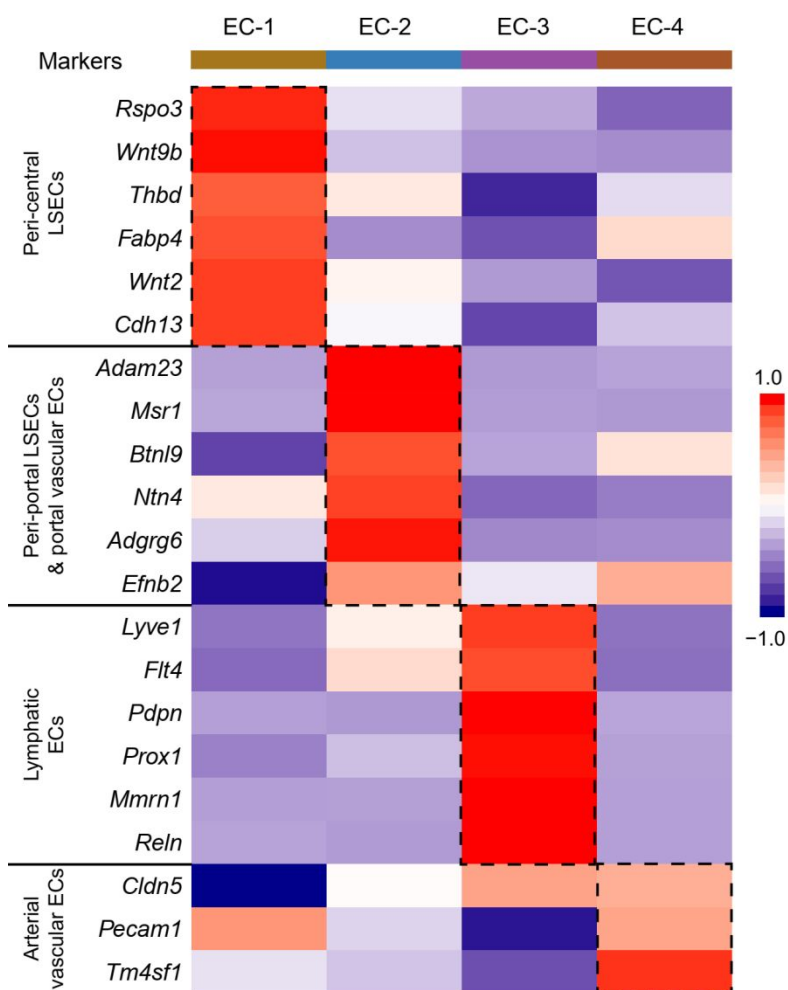
Fig. S3: Violin plots showing the expression of the proliferation marker *Mki67* across all scRNAseq clusters.





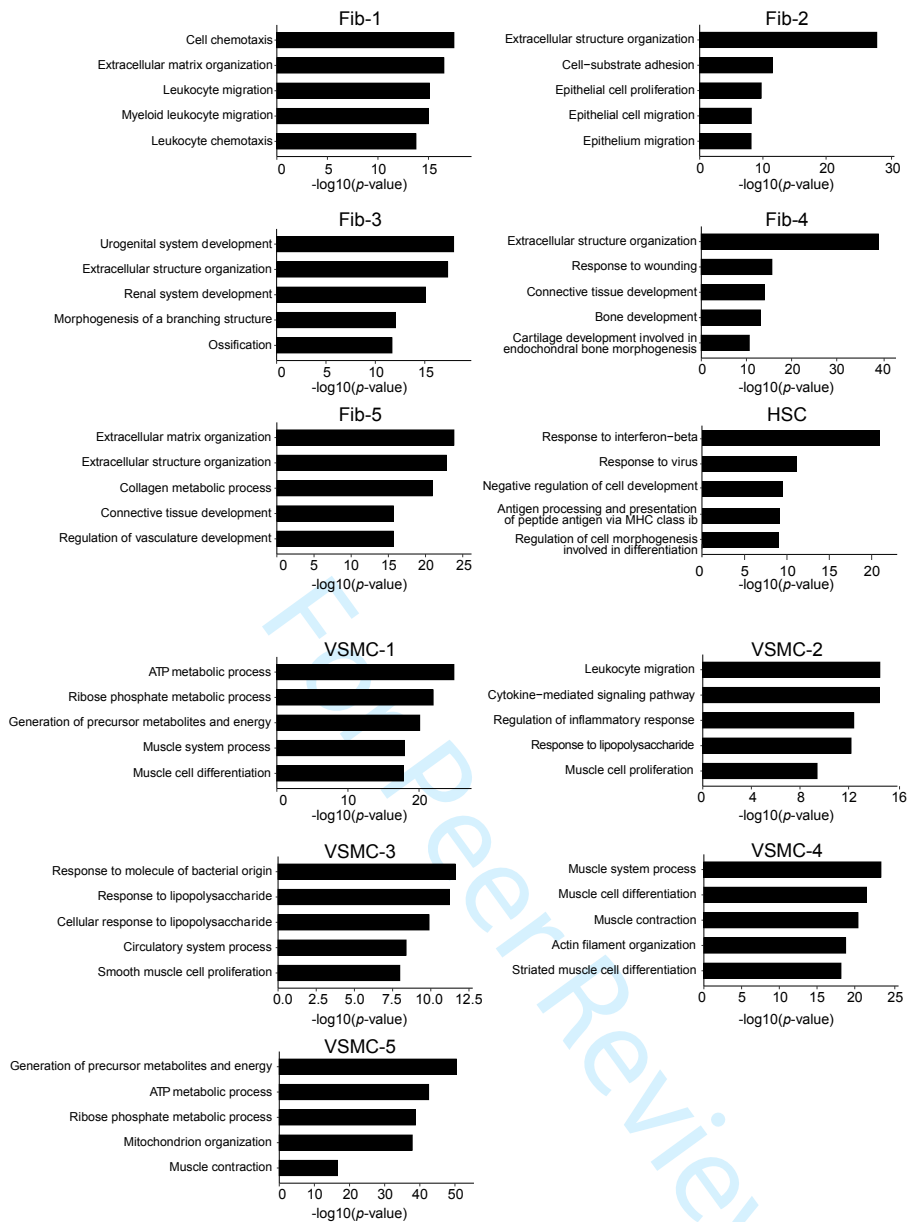


**Fig. S4: *t*-SNE and Violin plots across all scRNAseq clusters of gene expressions, that were previously or herein reported to demarcate the following cell types: (A) mesothelial cells (Meso), (B) endothelial cells (EC), (C) fibroblasts (Fib), (D) hepatic stellate cells (HSC), (E) vascular smooth muscle cells (VSMC).**

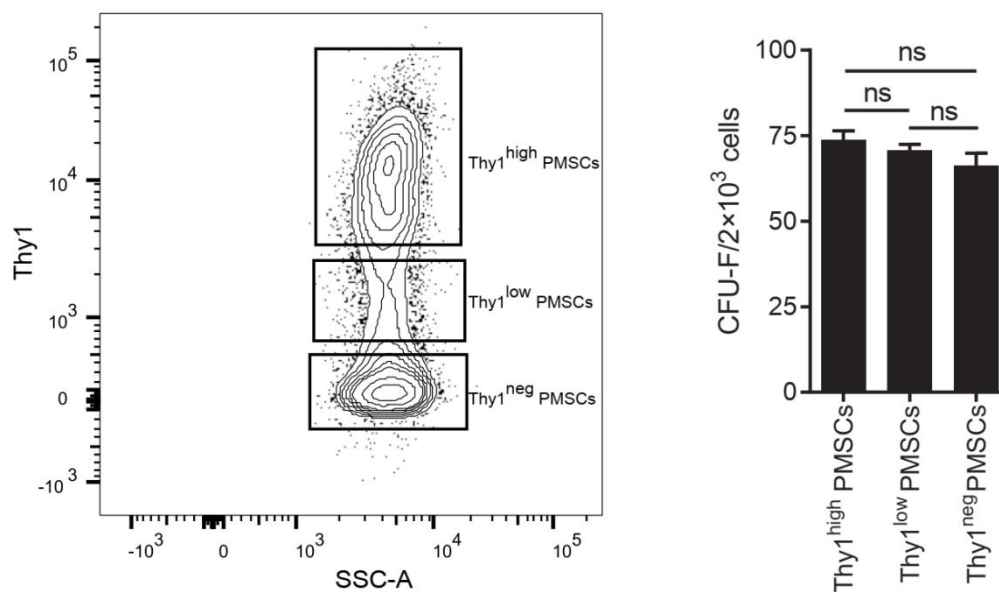


**Fig. S5: Heatmap depicting representative genes expressed in the endothelial cell (EC) clusters of the scRNAseq.**

Color scale represents the average expression level across all cells within each cluster. LSECs, liver sinusoidal endothelial cells.



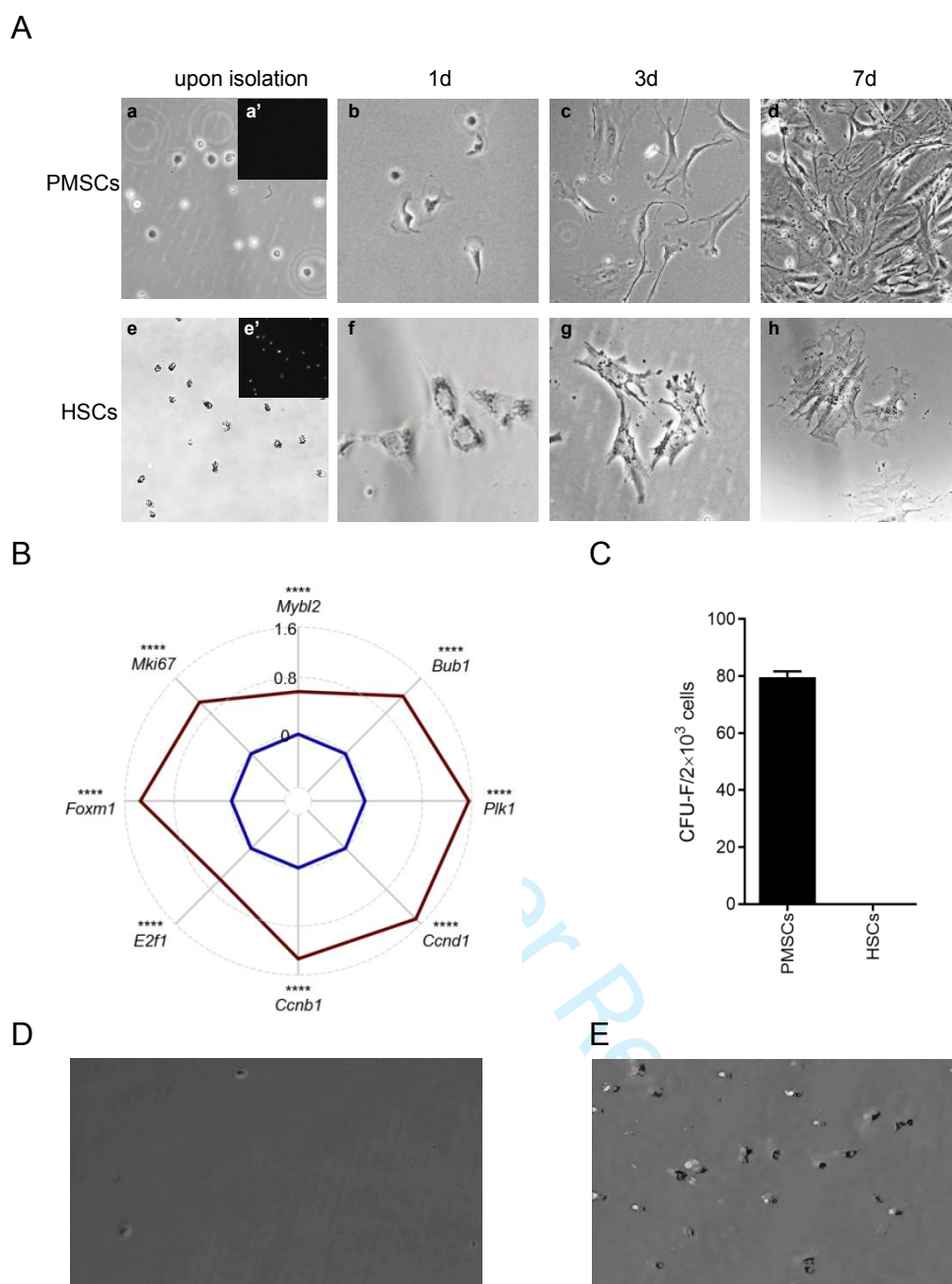
**Fig. S6: GO enrichment of genes significantly overexpressed in the different mesenchymal cell clusters of the scRNAseq. (see also Table S5).**



**Fig. S7: Clonogenicity of PMSCs according to Thy1 expression.**

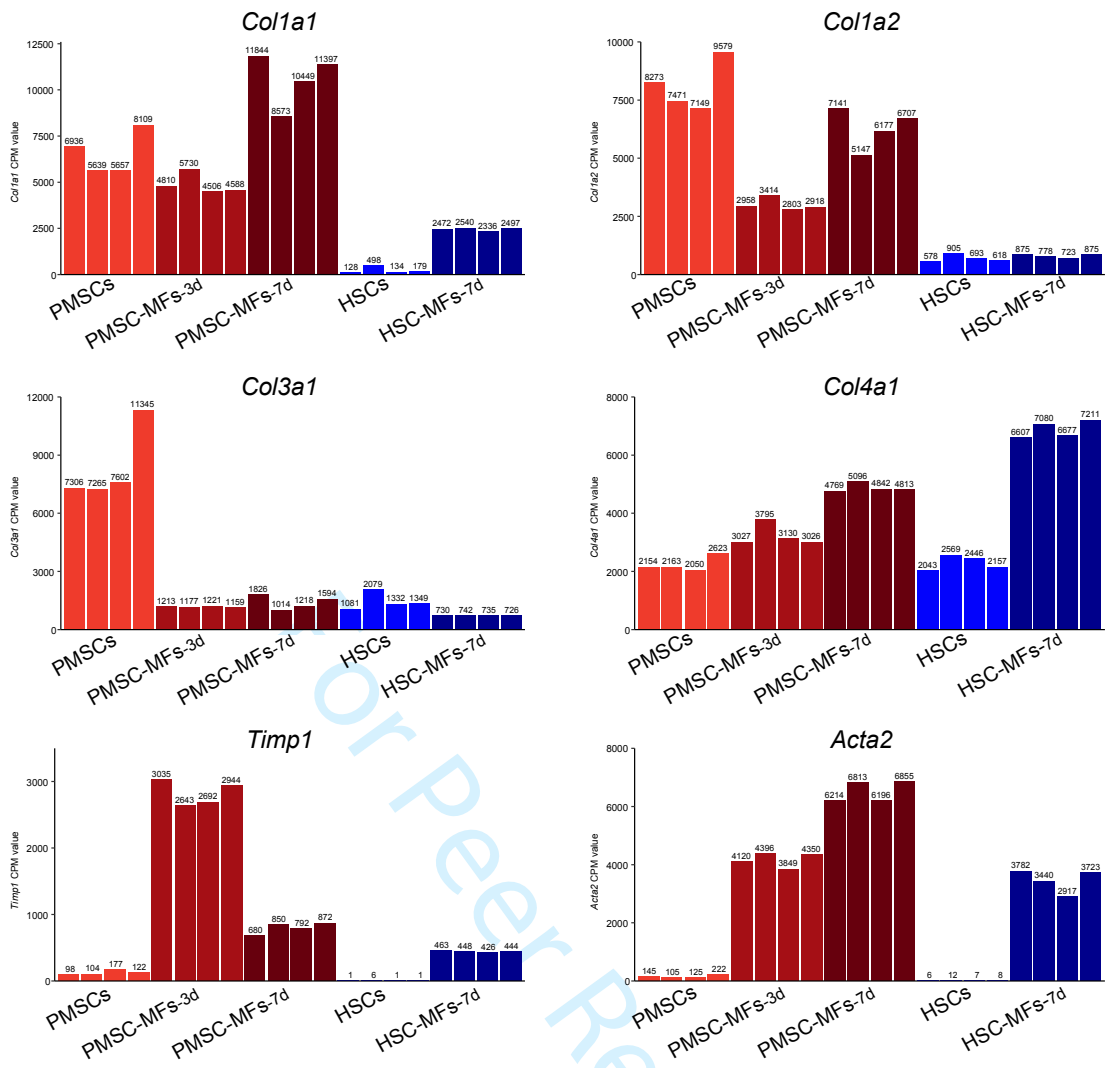
Left panel: Representative flow cytogram of Thy1 expression on PMSCs. Right panel: CFU-F formed by Thy1<sup>neg</sup>, Thy1<sup>low</sup> and Thy1<sup>high</sup> PMSCs. Data represent means  $\pm$  SEM (n=3). Statistical significance was evaluated using one-way ANOVA; ns, non-significant.

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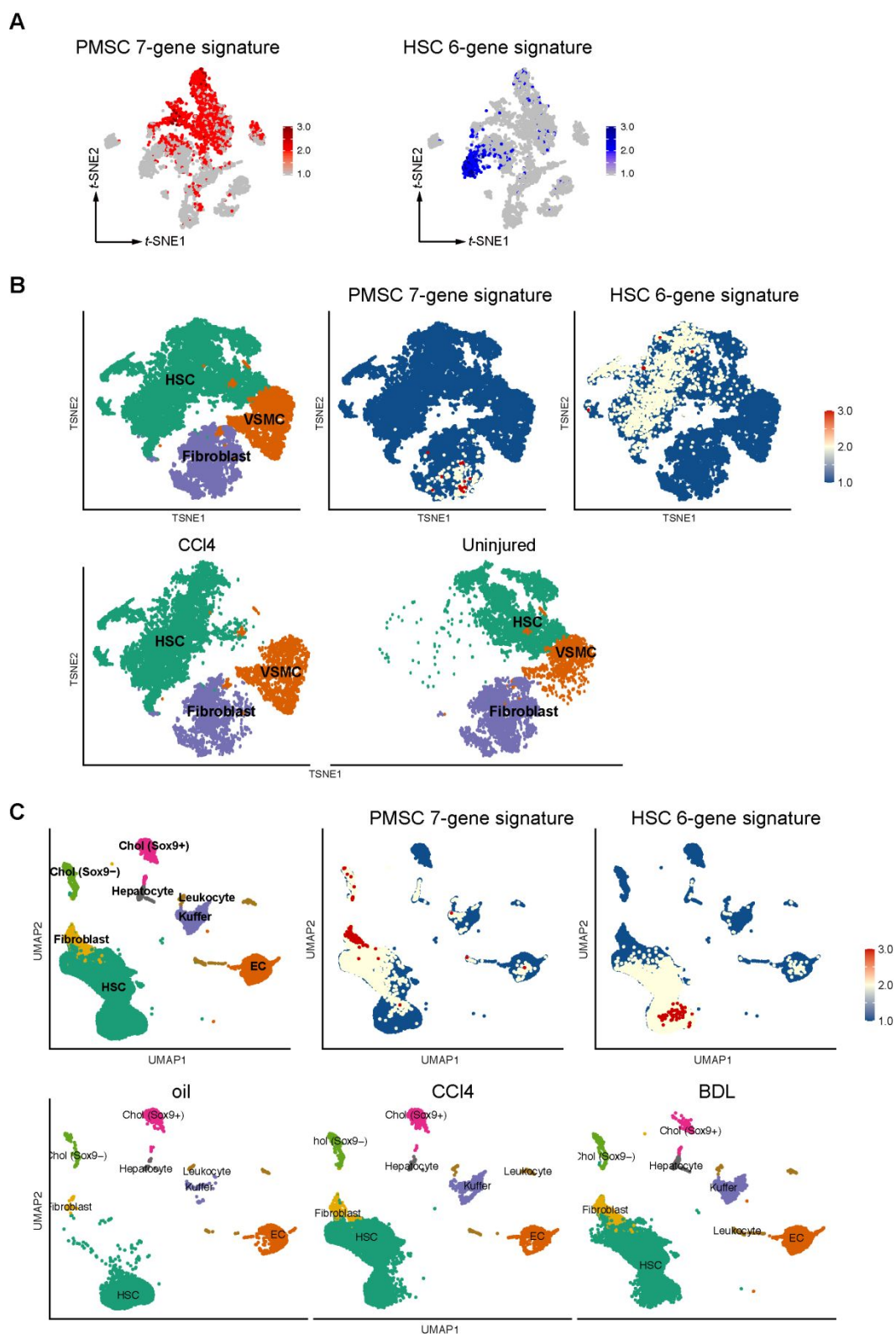
**Fig. S8: Phenotypic comparison of PMSCs/PMSC-MFs and HSCs/HSC-MFs.**

(A) Microscopic appearance: Cells were observed under phase-contrast microscopy (fluorescence microscopy under 328-nm ultraviolet excitation in insets) (a,e) immediately after cell sorting, (b-d, f-h) at the indicated days (d) of primary culture. (B-E) Proliferative properties: B) Proliferation-related gene expressions in PMSC-MFs vs. HSC-MFs. Radar plot showing the log<sub>2</sub> fold-difference in the expression of cell proliferation-related genes in bulk RNAseq analysis of PMSC-MFs (red line) and HSC-MFs (blue line) after 7 days in culture. Statistical significance was evaluated using Wilcoxon test; \*\*\*\*p<0.0001; C) CFU-F formed by sorted PMSCs and HSCs (Means ± SEM, n=8); Videomicroscopy (provided separately) of D) PMSCs and E) HSCs between day 1 and day 5 of primary culture (representative of 2 random fields).



**Fig. S9: Expression of pro-fibrotic genes in PMSCs and HSCs, in resting or myofibroblastic states after 3 days (-MFs-3d) or 7 days (-MFs-7d) in primary culture. CPM, counts per million.**

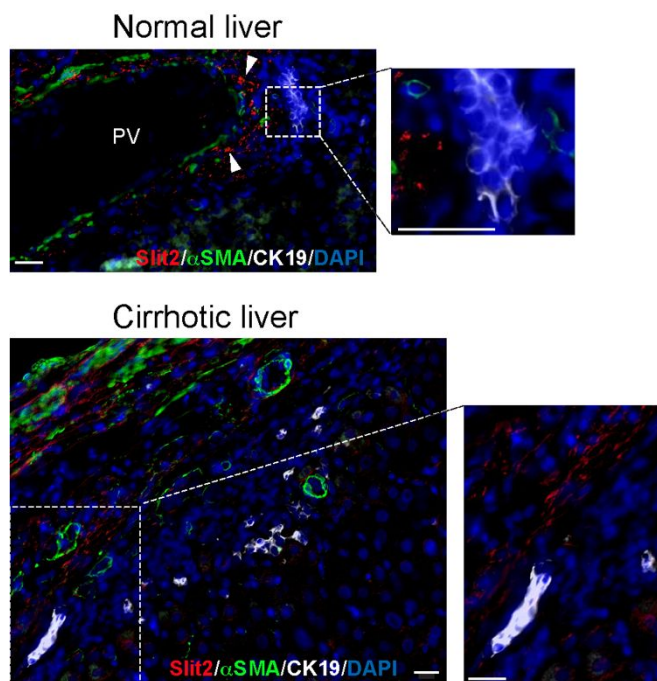
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**Fig. S10: PMSC/PMSC-MF and HSC/HSC-MF oligogene signatures projected onto (A) current and (B, C) previous scRNAseq data sets.**

A) Clustering of portal mesenchymal cells from uninjured mouse liver as in Fig. 1B; B) Clustering of *Pdgfrb*-GFP<sup>+</sup> mesenchymal cells from uninjured and fibrotic (6 weeks CCl<sub>4</sub>) mouse livers from *Dobie et al.* (GSE137720); C) Clustering of all liver cells from uninjured (oil) and fibrotic (3 weeks CCl<sub>4</sub>, 10 days BDL) mouse livers from *Yang et al.* (GSE171904). Chol, cholangiocytes.

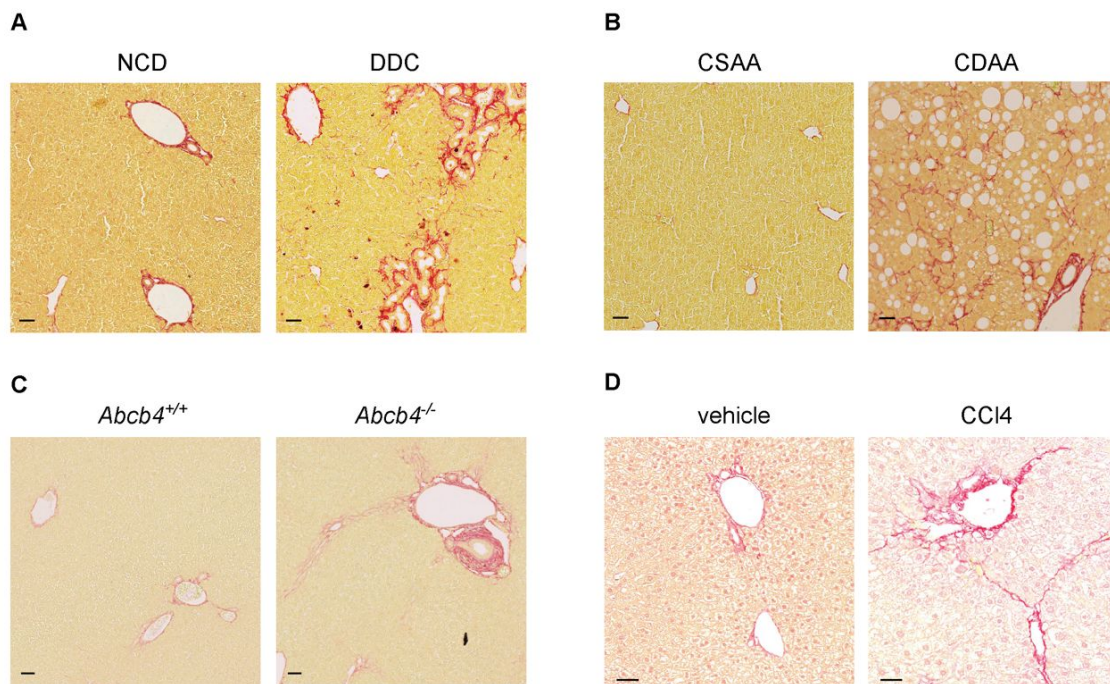




**Fig. S11: Distinct localization of *SLIT2*<sup>+</sup> cells and cholangiocytes.**

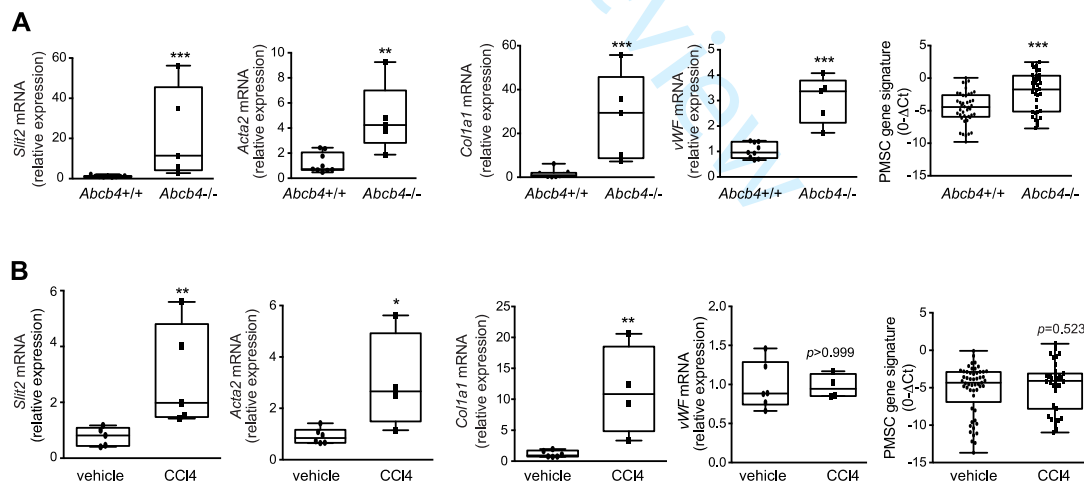
*SLIT2* FISH and  $\alpha$ -SMA or CK19 immunofluorescence were performed on normal and cirrhotic human liver tissue sections. In normal liver (upper panel), perivascular *SLIT2*<sup>+</sup> cells (arrowheads) in a large portal tract are distinct from  $\alpha$ -SMA<sup>+</sup> VSMCs and from CK19<sup>+</sup> cholangiocytes (higher magnification in inset), representative of n=2 (PV, portal vein). In cirrhotic liver (lower panel), *SLIT2*<sup>+</sup> intermingled with *SLIT2*<sup>-</sup> myofibroblasts in fibrotic septa, are distinct from CK19<sup>+</sup> cholangiocytes (higher magnification in inset), representative of cirrhosis of alcoholic (n=3), NASH (n=1) or hepatitis C (n=1) origins (Scale bars=50  $\mu$ m).

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**Fig. S12: Mouse models of liver fibrosis.**

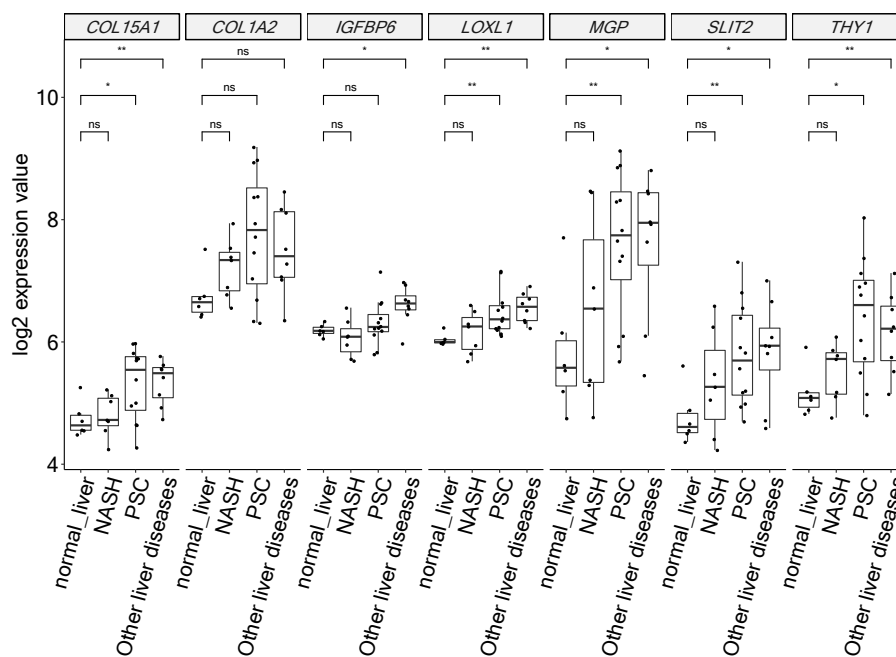
Sirius red staining of the liver from (A) mice fed NCD or DDC diet for 4 weeks; (B) mice fed CSAA or CDAA diet for 8 weeks; (C) *Abcb4*<sup>+/+</sup> and *Abcb4*<sup>-/-</sup> mice at the age of 8 weeks; (D) vehicle- or CCl<sub>4</sub>-i.p.-injected mice for 6 weeks. NCD, normal chow diet; DDC, 3,5-diethoxycarbonyl-1,4-dihydrocollidine; CSAA, choline-sufficient L-amino acid-defined; CDAA, choline-deficient L-amino acid-defined diet. Representative of 5 to 17 animals per group. Scale bars=50  $\mu$ m.



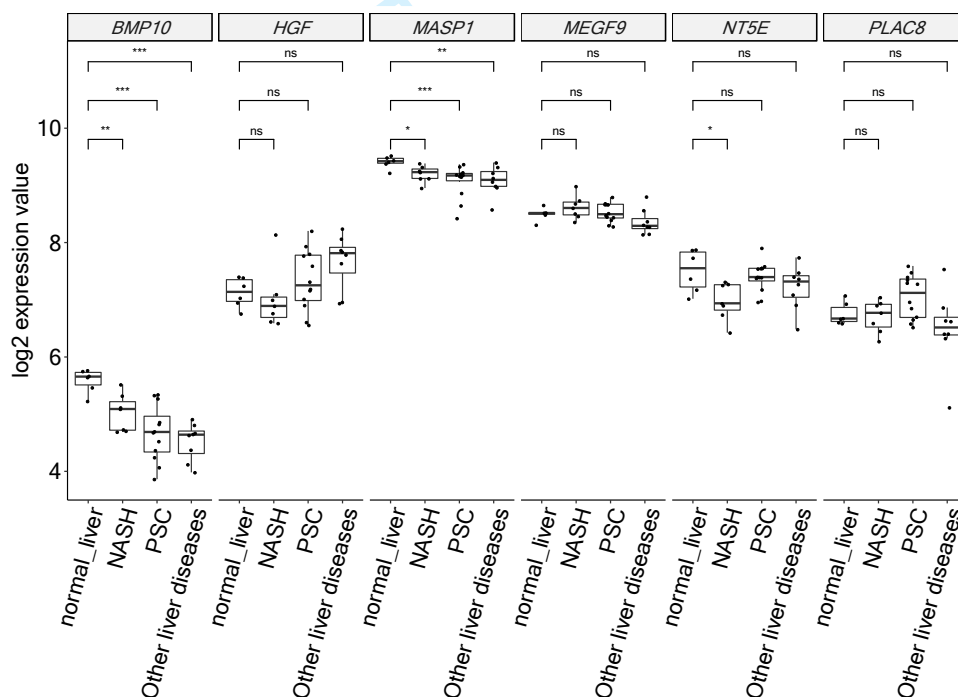
**Fig. S13: Expression of SLIT2 and PMSC 7-gene signature in the *Abcb4*<sup>-/-</sup> and CCl<sub>4</sub> mouse models of liver fibrosis.**

Hepatic expression of *Slit2*, *Acta2*, *Col1a1*, *vWF* and of PMSC 7-gene signature was measured by RT-qPCR in liver tissue from (A) *Abcb4*<sup>+/+</sup> (n=9) and *Abcb4*<sup>-/-</sup> (n=5) mice at the age of 8 weeks, (B) vehicle- or CCl<sub>4</sub>-i.p.-injected mice for 6 weeks (n=5/group). Data represent individual values and means  $\pm$  SEM. \**p*<0.05; \*\**p*<0.01; \*\*\**p*<0.001 (Wilcoxon test).

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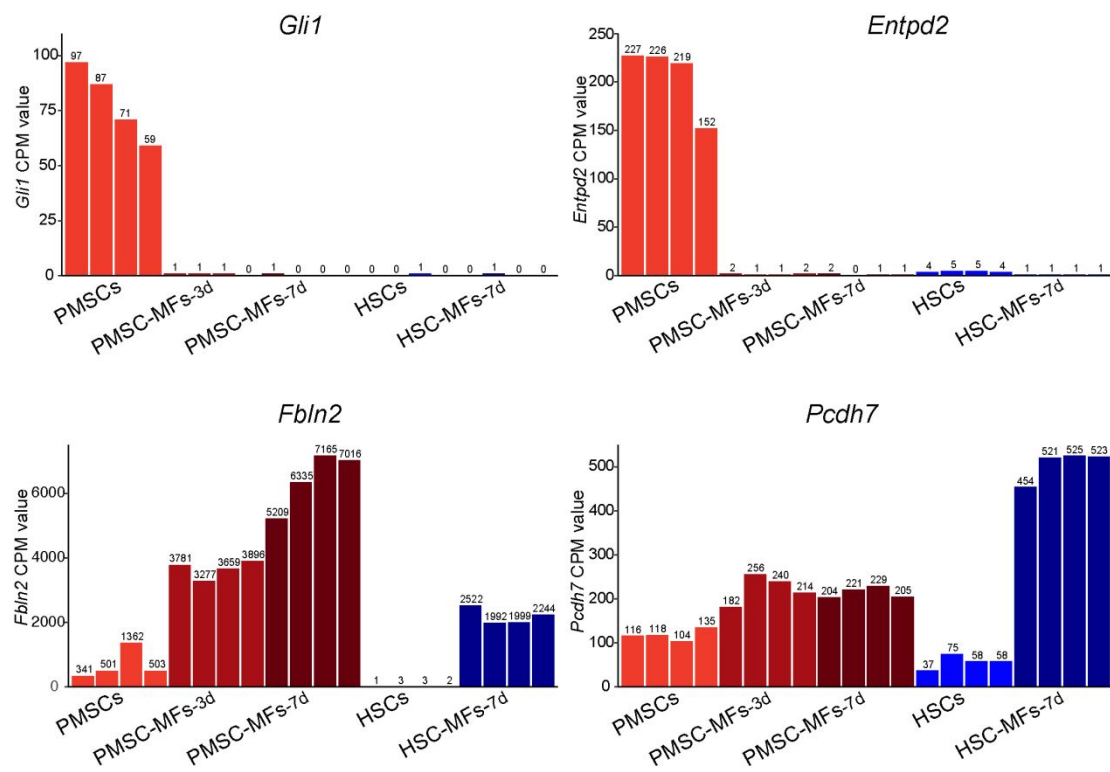
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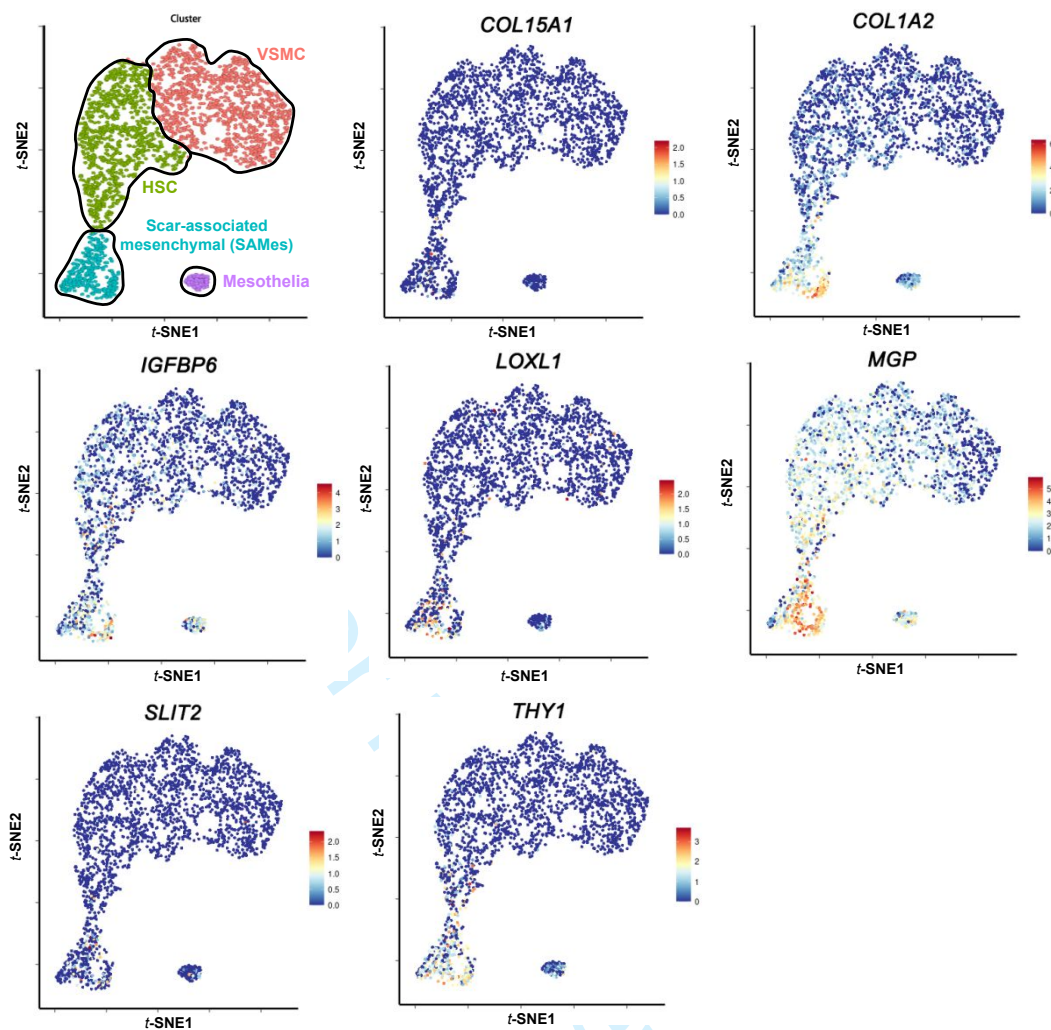
**Fig. S14: Individual expression of the PMSC and HSC signature genes in human liver fibrosis.**

Hepatic expression of the genes of (A) PMSC/PMSC-MF, and (B) HSC/HSC-MF signatures, was assessed by Affymetrix microarray analysis of normal human liver (n=5 patients) and of liver tissue samples from patients with NASH (n=7 patients), PSC (n=6 patients, 2 biopsies/patient) or other liver diseases (n=8 patients). Data represent individual values and means  $\pm$  SEM. \* $p < 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p < 0.001$ ; ns, non-significant; statistical significance was evaluated using non-parametric Wilcoxon test.

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**Fig. S15: *Gli1*, *Entpd2*, *Fbln2* and *Pcdh7* expression in the bulk RNAseq analysis of PMSCs and HSCs, in resting or myofibroblastic states after 3 days (-MFs-3d) or 7 days (-MFs-7d) in primary culture. CPM, counts per million.**



**Fig. S16: Comparison of PMSCs/PMSC-MFs with the previously annotated scar-associated mesenchymal cells.**

*t*-SNE plot of PMSC/PMSC-MF signature genes in human mesenchymal cells from Ramachandran et al. (<https://www.livercellatlas.ed.ac.uk/>).

**Table S1: Antibodies used for cell sorting, flow cytometry and immunofluorescence.**

Antibody	Company	Cat no.	Clone no.
Cell sorting & Flow cytometry			
rat anti-mouse CD9-BV421	BD Biosciences	564235	KMC8
rat anti-mouse CD11b-FITC	BioLegend	101245	M1/70
hamster anti-mouse CD29-PE/Cy7	BioLegend	102222	HM $\beta$ 1-1
rat anti-mouse CD31-FITC	BD Biosciences	561813	MEC 13.3
rat anti-mouse CD34-APC	BioLegend	119310	MEC14.7
rat anti-mouse CD45-FITC	BioLegend	103137	30-F11
rat anti-mouse CD105-BV510	BD Biosciences	740188	MJ7/18
rat anti-mouse CD200-APC-R700	BD Biosciences	565546	OX-90
rat anti-mouse Epcam-FITC	BioLegend	118207	G8.8
rat anti-mouse PDGFRa-PE	eBioscience	12-1401-81	APA5
rat anti-mouse Sca1-BV510	BD Biosciences	565507	D7
rat anti-mouse Thy1-PE-Cy7	eBioscience	25-0902-81	53-2.1
Immunofluorescence			
mouse anti-human $\alpha$ -SMA	Agilent	M085129-2	1A4
rabbit anti-human Col15a1	Abcam	ab58717	N/A

**Table S2: Primers used for qPCR.**

Gene	GenBank	Forward primer	Reverse primer
<b>Mouse</b>			
<i>Acta2</i>	NM_007392.3	CTGTCAGGAACCCTGA	TACTCCCTGATGTCT
<i>Bmp10</i>	NM_009756.3	CGGAGCTTCAAGAACG	TGGTGAGGGATAGAC
<i>Col1a1</i>	NM_007742.4	GCTCCTCTTAGGGGCC	CCACGTCTCACCATT
<i>Col1a2</i>	NM_007743.3	CAAGCATGTCTGGTTA	AGGACACCCCTTCTA
<i>Col15a1</i>	NM_009928.3	AGATTTACGGGTTCCA	CAACGTGTGATTCTTT
<i>Hgf</i>	NM_001289458.1	CACCCCTTGGGAGTAT	GGGACATCAGTCTCA
<i>Hprt</i>	NM_013556.2	TCAAATCCCTGAAGTA	AGGACCTCTCGAAGT
<i>Igfbp6</i>	NM_008344.3	GGGCTCTATGTGCCAA	CCTGCGAGGAACGAC
<i>Loxl1</i>	NM_010729.3	TATGCCTGCACCTCTC	TGTCCGCATTGTATG
<i>Masp1</i>	NM_001359083.1	CCTACAGAGCGGCAG	GGCTCGATTTTCCCG
<i>Megf9</i>	NM_172694.2	ACAACCGGTCTGATAG	TTTGCATTCTTCACAG
<i>Mgp</i>	NM_008597.4	TCACGAAAGCATGGAG	GCTGAGGGGACATAA
<i>Nt5e</i>	NM_001204813	CCATTGATGAGAAGAA	GTCAAATGTCCCTCC
<i>Plac8</i>	NM_139198.3	TGTGTGCCAACTCAAG	GTTGAGCTTCTTCAG
<i>Slit2</i>	NM_178804.5	ATCTGCCTGAGACCAT	CGTCTAAGCTTTTTGT
<i>Thy1</i>	NM_009382.3	GAAAACTGCGGGCTTC	CCAAGAGTTCCGACT
<i>vWf</i>	NM_011708.4	CTACCTAGAACGCGAG	CATCGATTCTGGCCG
<i>18S</i>	NR_003278.3	GAGCGAAAGCATTTC	GGCATCGTTTATGGT
<b>Human</b>			
<i>ACTA2</i>	NM_001613.4	GACAATGGCTCTGGGC	CTGTGCTTCGTCACC
<i>COL1A</i>	NM_000088.4	GTGCGATGACGTGATC	CGGTGGTTTCTTGGT
<i>HPRT</i>	NM_000194.3	TAATTGGTGGAGATGA	TGCCTGACCAAGGAA
<i>SLIT2</i>	NM_004787.4	GTGTTTCGTGCCAGCTA	TTCCATCATTGATTGT
<i>vWF</i>	NM_000552.5	CTCCCACGCCTACATC	GCGGTGATCTTGCT

**Table S3: Probes used for FISH.**

Probe name	Sequence
Scrambled	5' TAGCGAATCTCAGGCAAG – AT 633 3'
SLIT2-1	5' GGACCACGTCTCGCAGCGGTTCTGCGGC – 6 Fam 3'
SLIT2-2	5' CACGGGTCCTTATAGGGGGCGTTGTGGC – 6 Fam 3'
SLIT2-3	5' CTTACGGTTGTTCTATTTGACGGAAGC – 6 Fam 3'
SLIT2-4	5' CACCTGCTCCAACCTCTTTCACCACTTCACGC – 6 Fam 3'

For Peer Review



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**Table S4: Differentially expressed genes in each scRNAseq cluster compared to all others.**

Tab 1: All differentially expressed genes classified according to Seurat R toolkit;  
Tab 2: Top 10 differentially expressed genes classified according to average log Fold-Change (avg\_logFC).  
(Provided separately).

**Table S5: GO enrichment of differentially expressed genes in the scRNAseq clusters of Fibroblasts (Fib), Hepatic stellate cells (HSCs), and Vascular smooth muscle cells (VSMCs).**

(Provided separately).

**Table S6: Differential gene expressions in bulk RNAseq analyses, between PMSCs or HSCs and their myofibroblastic progenies after 3 days (-MFs-3d) or 7 days (-MFs-7d) in primary culture.**

Genes (ID) are classified according to average log Fold-Change (logFC) from 4 replicates per condition.  
(Provided separately)

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3 **Portal fibroblasts with mesenchymal stem cell features form a reservoir of**  
4 **proliferative myofibroblasts in liver fibrosis**  
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34 Laboratoire de Biologie du Développement, Paris, France.  
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49 \*These authors share senior authorship  
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56 **Keywords:** Angiogenesis; Cirrhosis; Hepatic stellate cell; Single-cell RNA-  
57 sequencing; SLIT2.  
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**Abbreviations:** ABCB4, ATP-binding cassette B4;  $\alpha$ -SMA, alpha-smooth muscle actin; CK19, cytokeratin 19; CCl<sub>4</sub>, carbon tetrachloride; CDAA, choline-deficient, L-amino acid-defined; CFU-F, colony forming unit-fibroblast; CSAA, choline-sufficient, L-amino acid-defined; DDC, 3,5-diethoxycarbonyl-1,4-dihydrocollidine; DEG, differentially expressed gene; EC, endothelial cell; ECM, extracellular matrix; FISH, fluorescent *in situ* hybridization; GO, gene ontology; HSC, hepatic stellate cell; HUVEC, human umbilical vein endothelial cell; LSEC, liver sinusoidal endothelial cell; MSC, mesenchymal stem cell; NAFLD, non-alcoholic fatty liver disease; NASH, non-alcoholic steatohepatitis; NCD, normal chow diet; PCA, principal component analysis; PMSC, portal fibroblast with mesenchymal stem cell features; PSC, primary sclerosing cholangitis; ROBO, Roundabout; RT-qPCR, Reverse transcription-quantitative PCR; scRNAseq, single-cell RNA-sequencing; *t*-SNE, *t*-distributed stochastic neighbor embedding; VSMC, vascular smooth muscle cell.

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4  
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6  
7 fellowship from the China Scholarship Council (CSC).  
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12 **Authors contributions:** L.L., T.J., A.C., C.H. designed the study; L.L., A.B., H.E.M.,  
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14 J.Gu., T.F., T.H.K., B.H., R.M., E.G-S., C.G., V.R., J.Ga., T.J. acquired experimental  
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16 and clinical data; L.L., A.B., H.E.M., J.Gu., S.L., P.C., F.T., T.J., C.H., A.C. analyzed  
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18 and interpreted the data; L.L., S.L., A.C., C.H. drafted the manuscript, with critical  
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20 revision from all authors.  
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## Abstract

**Background & Aims:** In liver fibrosis, myofibroblasts derive from hepatic stellate cells (HSCs) and as yet undefined mesenchymal cells. We aimed to identify portal mesenchymal progenitors of myofibroblasts. **Approach & Results:** Portal mesenchymal cells were isolated from mouse bilio-vascular tree and analyzed by scRNAseq. Thereby, we uncovered the landscape of portal mesenchymal cells in homeostatic mouse liver. Trajectory analysis enabled inferring a small cell population further defined by surface markers used to isolate it. This population consisted of portal fibroblasts with mesenchymal stem cell features (PMSCs), *i.e.*, high clonogenicity and tri-lineage differentiation potential, that generated proliferative myofibroblasts, contrasting with non-proliferative HSC-derived myofibroblasts (-MFs). Using bulk RNAseq, we built oligogene signatures of the two cell populations, that remained discriminant across myofibroblastic differentiation. *SLIT2*, a prototypical gene of PMSC/PMSC-MF signature, mediated pro-fibrotic and angiogenic effects of these cells, whose conditioned medium promoted HSC survival and endothelial cell tubulogenesis. Using PMSC/PMSC-MF 7-gene signature and *SLIT2* FISH, we showed that PMSCs display a perivascular portal distribution in homeostatic liver and largely expand with fibrosis progression, contributing to the myofibroblast populations that form fibrotic septa, preferentially along neo-vessels, in murine and human liver disorders, irrespective of aetiology. We also unraveled a 6-gene expression signature of HSCs/HSC-MFs that did not vary in these disorders, consistent with their low proliferation rate. **Conclusions:** PMSCs form a small reservoir of expansive myofibroblasts, which in interaction with neo-vessels and HSC-MFs that mainly arise *via* differentiation from a preexisting pool, underlie the formation of fibrotic septa in all types of liver diseases.

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5 Mesenchymal cells are key players in tissue homeostasis and wound healing. In the  
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7 liver, mesenchymal cells comprise hepatic stellate cells (HSCs), that reside in  
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9 sinusoids, and perivascular cells including vascular smooth muscle cells (VSMCs) and  
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11 fibroblasts, that reside in the portal tracts and around central veins. Genetic-based  
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13 lineage-tracing analyses have demonstrated that HSCs and perivascular  
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15 mesenchymal cells as well as mesothelial cells all derive from the septum transversum  
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17 during liver development (1). Over the past 30 years, HSCs have been extensively  
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19 investigated for their capacity to undergo myofibroblastic differentiation, and have been  
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21 identified as a major source of myofibroblasts in liver fibrosis (2). However, the other  
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23 liver mesenchymal cells, particularly portal mesenchymal cells have gained increasing  
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25 interest as evidence has accumulated that indicates they could also generate  
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27 myofibroblasts (3-6). The portal tracts contain three main structures referred to as the  
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29 portal triad, *i.e.*, the portal vein, hepatic artery and bile duct, surrounded by a  
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31 mesenchyme, which has remained poorly defined so far. Little is known regarding the  
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33 identity, spatial distribution or functions of portal mesenchymal cells and how they  
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35 contribute to fibrosis. A major limitation has been the lack of markers, especially  
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37 surface markers that would allow to isolate portal mesenchymal cells or track them *in*  
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39 *vivo*. Using a model of outgrowth from fragments of the bilio-vascular tree isolated from  
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41 rat liver, we previously showed that portal cells distinct from HSCs could generate  
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43 myofibroblasts, that we referred to as portal myofibroblasts, characterized by  
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45 COL15A1 expression, a high proliferation rate and pro-angiogenic properties (4, 7, 8).  
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47 However, the precursors of portal myofibroblasts have not been truly identified in these  
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49 studies. In the present study, we isolated portal mesenchymal cells from mouse liver  
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51 as a single-cell preparation and analyzed their diversity using single-cell RNA-  
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3 sequencing (scRNAseq). A minimal set of surface markers enabled us to isolate a  
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5 subset of portal fibroblasts with mesenchymal stem cell features (PMSCs) and the  
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7 ability to generate myofibroblasts. Markers of PMSCs were discovered and used to  
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9 examine the expansion potential of these cells in murine and human liver fibrosis.  
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## 14 **Experimental procedures**

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16 Details are provided in Supplementary material.  
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19 **Animals.** Male mice of C57BL/6J or FVB.129 genetic background, were used at the  
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21 age of 8-12 weeks for cell isolation and liver fibrosis models, in compliance with  
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23 ARRIVE guidelines.  
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26 **Cell isolation and culture.** The bilio-vascular tree was isolated from mouse liver, by  
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28 adapting a procedure we previously described in rat (7), and further processed using  
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30 cell sorting and flow cytometry analysis to collect and analyze mesenchymal cells.  
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32 Ultrapure HSCs and other liver cell types were isolated using established methods.  
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34 Cell clonogenicity, trilineage and myofibroblastic differentiation were examined in cell  
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36 culture.  
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40 **RNAseq.** ScRNAseq of the bilio-vascular tree Lin-negative cells (gated as Epcam-  
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42 CD31-CD45-CD11b- cells), was performed using the 10X Genomics 3' v3 kit (10x  
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44 Genomics). NextSeq500 (Illumina) device was used for single-cell and bulk RNAseq.  
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46 ScRNAseq analyses were performed using CellRanger, Seurat and Monocle, and bulk  
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48 RNAseq analyses, using STAR, RSEM and edgeR R package.  
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51 **Human liver samples.** Fresh and frozen samples of normal and pathological liver  
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53 tissue were collected with the approval of ethical committees, from patients who gave  
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55 written informed consent.  
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3 **Reverse transcription-quantitative PCR (RT-qPCR), Immunofluorescence and**  
4 **fluorescent *in situ* hybridization (FISH).** Primers, antibodies and probes are listed in  
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6 Table S1-3.  
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10 **Microarray analyses.** Pangenomic analysis of frozen liver tissue samples, was  
11 performed using the Affymetrix human gene 1.0 st microarray.  
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14 **SLIT2-mediated functions analyses.** The conditioned medium of PMSC-derived  
15 myofibroblasts (PMSC-MFs) was tested for potential effects on the viability of the LX-  
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17 2 HSC cells, and the tubulogenesis of human umbilical vein endothelial cells  
18 (HUVECs). In these experiments, SLIT2 signaling was blocked using siRNA,  
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20 CRISPR/Cas9, anti-ROBO1 antibody or a recombinant ROBO1/Fc chimera.  
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24 **Statistical analyses.** Unless otherwise stated, statistical analyses were performed  
25 using Graphpad Prism v6.0 and R. Unpaired two-sided Wilcoxon test and ANOVA with  
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27 a Scheffe post-hoc test were used to compare differences between two groups, and  
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29 more than two groups, respectively. A significant difference was defined as  $p < 0.05$ .  
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## 38 **Results**

### 39 **Landscape of the portal mesenchyme revealed by scRNAseq**

40 Portal mesenchymal cells represent a small cell population. They are tightly bound to  
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42 the portal triad, relying on basement membranes. This makes them more difficult to  
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44 isolate than hepatocytes or sinusoidal cells, which reside in a loose, basement  
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46 membrane-free, extracellular matrix (ECM). In the present study, we set up a specific  
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48 procedure to isolate portal mesenchymal cells, for scRNAseq analysis. We adapted a  
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50 method we previously established for the culture of rat portal myofibroblasts (7), to  
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52 isolate fragments of the bilio-vascular tree from mouse liver. The bilio-vascular tree  
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54 fragments were submitted to enzymatic digestion, resulting in a single-cell suspension,  
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3 which was depleted in cells expressing the lineage (Lin) markers of cholangiocytes  
4 (EpCAM), endothelial cells (CD31), and hematopoietic cells (CD45 and CD11b) using  
5 cell sorting. Lin-negative single-cell suspension was then processed to generate a  
6 scRNAseq cDNA library (Fig. 1A). We captured 4,976 sequenced cells that met quality  
7 control metrics (Fig. S1A) from healthy mouse liver. Unsupervised clustering identified  
8 16 distinct clusters that were assigned to fibroblast (5 clusters), VSMC (5 clusters),  
9 endothelial (4 clusters), HSC (1 cluster) and mesothelial (1 cluster) identities (Fig. 1B).  
10 The hierarchical clustering of gene expression profiles supported this classification  
11 except for the very small cluster of VSMC-5 (Fig. 1C). The most selective expressed  
12 genes that allowed to segregate cell clusters are shown in Fig. 1D, Fig. S2 and Table  
13 S4. In all clusters, the expression of cell cycle-related genes, e.g., *Mki67*, was at the  
14 limit of detection, as expected from resting cells in homeostatic liver (Fig. S3).

### 32 ***The non-mesenchymal components: mesothelial and endothelial cells***

33 Mesothelial cells display an intermediate phenotype between epithelial and  
34 mesenchymal cells and form a single layer that covers the liver surface (9). The liver  
35 capsule also covers the intrahepatic parenchyma surrounding the Glissonian pedicles  
36 including bile ducts (10), which can explain the presence of mesothelial cells in our cell  
37 suspension. Genes expressed in these cells included previously reported mesothelial  
38 markers, among which the most specific were *Msln* and *Upk1b* as well as epithelial  
39 markers, such as *Krt8* and *Krt19*, and mesenchymal markers, such as *Vim* but almost  
40 no *Pdgfrb*. Additional putative markers restricted to this cluster included *Fxyd3*, *Myl7*  
41 and *Slpi* (Fig. S4A).

42 We identified four clusters of endothelial cells (ECs), enriched in markers such as  
43 *Pecam1*, *Cdh5*, *Kdr* and *Egfl7* (Fig. S4B). The PECAM1 protein (alias CD31) has been  
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3 shown to be intracellular in liver sinusoidal endothelial cells (LSECs) (11), which  
4 explains, at least partly, why ECs escaped our negative selection according to the  
5 membrane antigen CD31. Moreover, even though cells from the bilio-vascular tree  
6 were preferentially retrieved by our method, basement membrane-free LSECs adhere  
7 to other cell types and are prone to be collected during isolation procedures, as  
8 previously reported (12). As shown in Fig. S5, we found markers of EC zonation in the  
9 liver, *i.e.*, of peri-central LSECs in EC-1, of peri-portal LSECs and/or portal vascular  
10 ECs in EC-2, of lymphatic ECs in EC-3, and of hepatic arterial ECs in EC-4 (12, 13).  
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### 24 ***The mesenchymal components: fibroblasts, HSCs and VSMCs***

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26 Our single-cell analysis revealed five clusters of fibroblasts (Fig. 1B-D), which  
27 predominantly expressed genes involved in vascular ECM such as *Mmp19*, *Col6a5*,  
28 *Col6a6* or *Col15a1*, and also expressed genes of interstitial collagens such as *Col1a1*,  
29 *Col1a2*, *Col3a1* at higher levels than other clusters. Both fibroblasts and HSCs  
30 expressed *Pdgfra*, whereas *Eln* previously reported as a marker of portal fibroblasts  
31 (5), was expressed in many other clusters (Fig. S4C). Fib-3 highly expressed *Ptn* (Fig.  
32 1D), a pericyte-derived trophic factor for ECs (14), suggesting a particular interaction  
33 of this cluster with portal vessels, whereas Fib-5 was enriched in HSC markers, such  
34 as *Lrat* (2) and *Reln* (5) (Fig. S4D), which was not driven by doublets (Fig. S1B), and  
35 may thus represent an intermediate population between fibroblasts and HSCs. All five  
36 fibroblast clusters were enriched in the gene ontology (GO) terms “ECM organization”  
37 and “Wound healing” (Fig. S6, Table S5). Individual clusters were also enriched in  
38 terms related to cell (including leucocyte) chemotaxis (Fib-1), epithelial cell proliferation  
39 and migration (Fib-2), tissue development or morphogenesis (Fib-3, Fib-4, Fib-5).  
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Cells of cluster 8 were recognized as HSCs. They were enriched in GO terms related to immunity and cell differentiation (Fig. S6). Among classical markers of HSCs, *Lrat* and *Reln* (2, 5) appeared to be not fully specific, being expressed notably in Fib-2 and Fib-5 (Fig. S4D). Like others (2, 15), we found virtually no expression of *Gfap*, whereas *Des* and *Cygb* (2, 3), were expressed at variable levels in virtually all clusters. Among HSC markers newly identified by scRNAseq (15-18) or bulk RNAseq (19), our analysis confirmed that some of them were restricted to HSCs, such as *Tmem56*, *Colec10*, *Mapt* or *Bco1*. Others such as *Fcna* or *Angptl6*, although not fully specific, were largely overexpressed in HSCs, whereas yet others such as *Rgs5*, *Pcdh7*, *Adamtsl2*, *Gucy1a1/b1* or *Colec11* were expressed at relatively high levels in several other mesenchymal cells, in addition to HSCs. Both *Ngfr* and *I134* on one hand, *Vipr1* and *Pth1r* on the other one, previously reported to preferentially mark peri-portal and peri-central HSCs, respectively (15), were expressed in the HSC cluster, indicating that this cluster was representative of all HSCs (Fig. S4D).

We identified 5 clusters of VSMCs that expressed at highest levels markers such as *Myh11*, *Cnn1*, *Acta2* or *Tagln* (13, 15) (Fig. S4E). VSMC clusters were enriched in GO terms related to muscle functions but also to “Inflammatory response” (Fig. S6).

### Identification of PMSCs

As a first approach to assess differentiation potency of the different clusters, we computed single-cell entropy, an approximation of single-cell differentiation potency based on predicted signalling promiscuity (20). Of all clusters, Fib-3 displayed the highest differentiation potency as suggested by the highest entropy value (Fig. 2A). We also examined the differentiation dynamics among mesenchymal cells, and analyzed all cells except mesothelial and endothelial cells, using Monocle 2 (21). This

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3 analysis showed a common trajectory of mesenchymal cells with one bifurcation and  
4 three branches defining states (Fig. 2B). On the basis of entropy analysis, the branch  
5 containing Fib-3 was defined as the root state. As shown in Fig. 2B, the root state was  
6 mainly populated by Fib-3 and Fib-4 cells, which were consequently assumed to be  
7 progenitor cells, contrasting with the two other states populated by VSMCs, notably  
8 VSMC-1, and HSCs, both well-differentiated cell types with high pseudotime values.  
9 Consistent with this assumption, GO terms related to development were concentrated  
10 in Fib-3 and Fib-4, suggesting multilineage potential of these two clusters (Fig. 2C).  
11 Genes previously reported to demarcate universal fibroblasts in mouse tissues, *i.e.*  
12 *Pi16* and *Col15a1* (22), or portal fibroblasts/myofibroblasts, *i.e.*, *Col15a1* (4), *Cd34* (6,  
13 15), *Thy1* alias CD90 (6, 23, 24), *Gli1* (19, 25), *Clec3b* (15), *Fbln2* (26) and *Entpd2*  
14 (27), were mainly expressed in these two clusters (Fig. 2D). *Pi16*<sup>+</sup> cells, were recently  
15 shown to serve as resource fibroblasts that would pass through *Col15a1*<sup>+</sup> fibroblasts  
16 able to secrete basement membrane proteins, before developing into specialized  
17 fibroblasts, in all steady-state mouse tissues (22). In addition, CD34, Thy1 and Gli1  
18 are all considered as stem cell markers. To further analyze Fib-3 and Fib-4 clusters,  
19 we defined a minimal set of surface markers enabling to isolate them together. As  
20 shown in Fig. 2E, a high expression of *Pdgfra*, *Cd34* and *Cd9* combined with a low  
21 expression of *Cd200* appeared to discriminate Fib-3 and Fib-4 from other Lin-negative  
22 cells. We FACS-sorted Lin (Epcam/CD31/CD45/CD11b)-negative,  
23 PDGFR $\alpha$ /CD34/CD9-positive, and CD200-low cells (Gate 4 in Fig. 2F) and examined  
24 this population for stem cell features. The percentage of cells recovered was  
25 approximately 0.03 % of total liver cells. The cells of this population were highly  
26 clonogenic (80 colony forming unit-fibroblast (CFU-F) per 2,000 cells) (Fig. 2G)  
27 irrespective of whether they were Thy1-positive or negative (Fig. S7). They also  
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3 displayed the expression of classical mesenchymal stem cell (MSC) markers, *i.e.*,  
4 CD105, Sca-1, CD29 (Fig. 2H), and the ability to undergo trilineage (adipogenic,  
5 osteogenic and chondrogenic) differentiation, in culture (Fig. 2I). Taken together, the  
6 cells isolated by our gating strategy displayed MSC attributes and were designated  
7 PMSCs. When cultured on a stiff substratum (Fig. 2J, bottom panels), PMSCs  
8 proliferated and gave rise to cells phenotypically similar to portal myofibroblasts  
9 expressing COL15A1 (4), here referred to as PMSC-MFs. This phenotypic change was  
10 accompanied by the expected up-regulation of *Acta2*, the gene encoding alpha-  
11 smooth muscle actin ( $\alpha$ -SMA), no change in *Col1a1* expression, and a down-regulation  
12 of *Col15a1* (Fig. 2K). Despite such down-regulation, *Col15a1* demarcates both PMSCs  
13 and portal myofibroblasts (4). It was possible to maintain PMSCs in a resting state by  
14 cultivating them in spheroids, on ultra-low attachment plates, in which case the  
15 expression of  $\alpha$ -SMA was not induced and that of Col15a1, less reduced (Fig. 2J-K).  
16 Overall, these data indicate that our screening strategy and isolation procedure  
17 enabled identifying portal fibroblasts with MSC properties and high collagen expression  
18 as precursors of portal myofibroblasts.

### Specific phenotypes and molecular profiles of PMSCs, HSCs and derived myofibroblasts

19 The isolation of PMSCs provided a unique opportunity to compare them with HSCs,  
20 and uncover specific markers of the two cell populations and of their myofibroblastic  
21 progenies. We performed transcriptomic analyses using bulk RNAseq, to compare  
22 PMSCs with ultrapure HSCs (28), as ascertained by vitamin A fluorescence (Fig. S8A).  
23 We identified 3,273 genes expressed at higher levels in PMSCs, and 3,122, in HSCs  
24 (Fig. 3A, upper panel). Projections onto *t*-SNE plot (Fig. 3A, lower panel), showed that  
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3 the top 10 differentially expressed genes in PMSCs included common markers of portal  
4 fibroblasts, as expected from a comparison with HSCs, but were expressed at highest  
5 levels in Fib-3/Fib-4, indicating that PMSCs comprised mainly if not exclusively Fib-  
6 3/Fib-4 fibroblasts. The top 10 differentially expressed genes of HSCs included  
7 common markers with ECs, but none with the other mesenchymal cells. Consistent  
8 with the GO analyses of scRNAseq (Fig. S6, Table S5), bulk RNAseq analysis showed  
9 enrichment in pathways related to “Extracellular matrix organization” in PMSCs and  
10 “Immunity” in HSCs, and further highlighted pathways related to “Angiogenesis” in  
11 PMSCs and to “Metabolism of fat-soluble vitamins” in HSCs (Fig. 3B).

12 Both PMSCs (Fig. 2J-K), and HSCs (3, 4), undergo phenotypic changes into  
13 myofibroblasts in primary culture. Phenotypically, the major difference we observed  
14 between the two cell populations, was an intense proliferation in PMSCs as they  
15 became myofibroblastic, whereas HSCs differentiated into myofibroblasts without  
16 dividing (Fig. S8A, D-E including videomicroscopy). We extended bulk RNAseq  
17 analyses to the myofibroblasts derived from both cell populations in culture, including  
18 an early and late stage of differentiation for PMSC-MFs (Table S6). Principal  
19 component analysis (PCA) showed a clear discrimination of PMSCs and HSCs from  
20 their myofibroblastic progenies according to PC1, while PMSC-MFs were  
21 discriminated from HSC-derived myofibroblasts (HSC-MFs) according to PC2 (Fig.  
22 3C). The molecular profiles of PMSCs and HSCs became more similar as they  
23 differentiated into myofibroblasts. Yet, they retained specificities at the stage of  
24 myofibroblasts as confirmed by GO analysis (Fig. 3D). When fully differentiated into  
25 myofibroblasts, *i.e.*, after 7 days of culture, both cell populations were enriched in  
26 themes related to muscle differentiation, whereas additionally, PMSC-MFs were  
27 enriched in themes related to axonogenesis and ECM organization. To a large extent,  
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3 PMSCs/PMSC-MFs overexpressed genes encoding fibrillar collagens (*Col1a1*,  
4 *Col1a2*, *Col3a1*), *Timp1* and *Acta2*, the hallmarks of liver fibrosis, whereas *Col4a1*, a  
5 major component of sinusoidal ECM was overexpressed in HSC-MFs (Fig. S9). At an  
6 early stage of myofibroblastic differentiation, *i.e.*, after 3 days of culture, PMSC  
7 transcriptome was highly enriched in pathways related to cell proliferation (Fig. 3D). At  
8 a later stage of myofibroblastic differentiation, *i.e.*, after 7 days of culture, PMSC-MFs  
9 compared to HSC-MFs still markedly overexpressed genes involved in cell  
10 proliferation, consistent with videomicroscopy and CFU-F assays, showing that only  
11 PMSCs as opposed to HSCs were clonogenic and divided in culture (Fig. S8B-E).

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24 Next, we looked for gene expressions that would demarcate the two cell populations  
25 both in their resting and myofibroblastic states, and that could thus be used in fibrotic  
26 liver tissue analyses to assess if PMSCs/PMSC-MFs were more expansive than  
27 HSCs/HSC-MFs, also *in vivo*. Altogether, comparative analyses of gene expressions  
28 indicated that 100 genes in PMSCs (or Fib-3/Fib-4) and 112 genes in HSCs, i) were  
29 overexpressed according to both scRNAseq and bulk RNAseq analyses, and ii)  
30 remained differentially expressed in these cells throughout myofibroblastic  
31 differentiation (Fig. 3E). Among such genes, we selected those that combined the  
32 highest differential expression (>3.5-fold), a relatively high expression (CPM>40) in the  
33 demarcated cell population, limited variation with myofibroblastic differentiation, and  
34 no or little expression in the other liver cell types, to build an oligogene expression  
35 signature of PMSCs/PMSC-MFs (7 genes) and HSCs/HSC-MFs (6 genes) (Fig. 3F-  
36 G). Projection of the two signatures onto current (Fig. 1B) and previous scRNAseq  
37 datasets (15, 18) showed that the PMSC/PMSC-MF signature demarcated liver  
38 fibroblasts, with highest intensity in Fib-3/Fib-4 (Fig. S10A) and in liver fibroblasts  
39 accumulating in liver fibrosis induced either by carbon tetrachloride (CCl<sub>4</sub>) or bile duct  
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3 ligation (BDL) (Fig. S10B-C), with little or no signal in other liver cell types. The  
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5 HSC/HSC-MF signature demarcated the HSC cluster (Fig. S10A), as well as the vast  
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7 majority of HSCs in mouse liver, including in CCl<sub>4</sub>- and BDL-induced liver fibrosis, and  
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9 virtually no other liver cell populations except a small portion of ECs (Fig. S10B-C).  
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### 14 **Implication of PMSCs and PMSC-MFs in liver fibrosis**

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16 Our transcriptome analyses highlighted *Slit2* as a prototypical gene of PMSC/PMSC-  
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18 MF signature. Its expression was particularly stable in PMSCs throughout their  
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20 myofibroblastic differentiation and virtually absent from all other liver cell types  
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22 including HSCs/HSC-MFs (Fig. 4A, left panel). Using FISH, we confirmed that PMSC-  
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24 MFs in culture were distinguishable from HSC-MFs by *Slit2* expression (Fig. 4A, right  
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26 panel). SLIT2 is an axon guidance molecule, which was previously shown to trigger  
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28 HSC activation and fibrosis (29-31) as well as angiogenesis, in the liver (32). However,  
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30 so far, the endogenous source of SLIT2 in the liver, had not been accurately identified.  
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32 Our scRNAseq data showed that *Slit2* expression was concentrated in Fib-3/Fib-4,  
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34 whereas its roundabout (ROBO) receptors were mainly expressed in the HSC and EC  
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36 clusters, and to a lesser extent in the fibroblast clusters (Fig. 4B). Therefore, previous  
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38 and current findings suggested that PMSCs had the potential to signal towards HSCs  
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40 and ECs via *Slit2*, to promote their pro-fibrotic and pro-angiogenic activity, respectively.  
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42 Supporting such mechanisms, PMSC-MF conditioned medium prevented the  
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44 decrease in cell viability induced by an oxidative stress in the LX-2 HSC cell line and  
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46 this effect was abolished by silencing *Slit2* via SiRNA in PMSC-MFs (Fig. 4C). PMSC-  
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48 MF conditioned medium also increased tubulogenesis in HUVECs and this effect was  
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50 largely SLIT2-dependent. It was prevented in the presence of anti-ROBO1 antibody or  
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52 recombinant ROBO1/Fc chimera that entraps soluble SLIT2 and it was reduced by  
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3 *Slit2* depletion *via* CRISPR/Cas9 in PMSC-MFs (Fig. 4D). We used *SLIT2* FISH to  
4 demarcate PMSCs/PMSC-MFs and address their connections with other cell types in  
5 normal and cirrhotic human liver. In normal liver, *SLIT2*<sup>+</sup> cells were scarce, although  
6 more abundant in large portal tracts than in the small ones. They were virtually  
7 restricted to portal tracts and displayed a perivascular distribution (Fig. 4E, left panel,  
8 Fig. S11, upper panel). In cirrhotic liver, irrespective of aetiology (*i.e.*, alcoholic liver  
9 disease, non-alcoholic steatohepatitis (NASH) or chronic hepatitis C), *SLIT2*<sup>+</sup> cells  
10 were much more abundant than in normal liver (Fig. 4E, middle and right panels). They  
11 were mainly located in the fibrotic septa, displayed  $\alpha$ -SMA expression and were thus  
12 identified as PMSC-MFs. Within fibrotic septa, *SLIT2*<sup>+</sup>/ $\alpha$ -SMA<sup>+</sup> PMSC-MFs were  
13 intermingled with, and outnumbered by *SLIT2*<sup>-</sup>/ $\alpha$ -SMA<sup>+</sup> myofibroblasts, and were  
14 frequently located in the surrounding of vascular lumens (Fig. 4E, middle panel).  
15 Consistent with PMSC/PMSC-MF interacting with HSCs/HSC-MFs and ECs, we found  
16 that in cirrhosis, *SLIT2*<sup>+</sup> PMSC-MFs often lined up along CD31<sup>+</sup> neo-vessels, and thus  
17 appeared as a scaffold for the accumulation of abundant *SLIT2*<sup>-</sup>/ $\alpha$ -SMA<sup>+</sup>  
18 myofibroblasts, most likely largely derived from HSCs (Fig. 4F). Both in normal and  
19 cirrhotic human livers, *SLIT2*<sup>+</sup> cells were clearly distinct from cytokeratin 19 (CK19)-  
20 labeled cholangiocytes (Fig. S11).

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22 To further ascertain that PMSCs/PMSC-MFs accumulated in liver fibrosis, we  
23 measured *SLIT2* mRNA levels in mouse and human injured livers. We found that the  
24 hepatic expression of *Slit2* increased in mouse models of either cholestatic diseases,  
25 *i.e.*, 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC), *Abcb4*<sup>-/-</sup>, or NASH, *i.e.*, choline-  
26 deficient, L-amino acid-defined (CDAA) and cytotoxic injury, *i.e.*, CCl<sub>4</sub> (Fig. S12), along  
27 with those of fibrosis markers (*Acta2*, *Col1a1*) in all models, and of an angiogenesis  
28 marker (*vWF*) in the cholestatic models (Fig. 5A and S13). The complete  
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3 PMSC/PMSC-MF 7-gene signature was increased in the DDC, *Abcb4*<sup>-/-</sup> and CDAA  
4 models, whereas the HSC/HSC-MF 6-gene signature that was tested in the DDC and  
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7 CDAA models, was not (Fig. 5A and S13). The analysis of a cohort of patients with  
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10 non-alcoholic fatty liver disease (NAFLD) showed that the expression of *SLIT2* was  
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12 increased in the group with advanced fibrosis, *i.e.* F3-F4 according to the SAF score  
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14 (33) (Fig. 5B). We also examined the microarray data of liver tissue samples from  
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16 patients with NASH, primary sclerosing cholangitis (PSC) and other chronic liver  
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18 diseases (alcoholic liver disease, haemochromatosis, primary biliary cholangitis,  
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20 autoimmune hepatitis), for *SLIT2* expression and the oligogene expression signatures  
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22 of PMSCs/PMSC-MFs and of HSCs/HSC-MFs. This analysis showed that *SLIT2*  
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24 expression and the 7-gene expression signature of PMSCs/PMSC-MFs were both  
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26 significantly increased in the liver of patients with all types of chronic liver diseases, as  
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28 compared to normal liver (Fig. 5C-D, left panels and S14A). *SLIT2* expression and the  
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30 7-gene expression signature were both similarly correlated with *ACTA2*, *COL1A1* and  
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32 *vWF* expression in these samples (Fig. 5C-D). The analysis of the microarray data also  
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34 indicated that in contrast to the PMSC/PMSC-MF 7-gene signature, the 6-gene  
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36 expression signature of HSCs/HSC-MFs was not significantly different between any  
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38 group of diseased livers and normal livers (Fig. 5E and S14B). This finding is consistent  
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40 with a low proliferation rate of HSCs and further supports the assumption that HSC-  
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42 MFs would primarily derive from myofibroblastic differentiation of the HSC preexisting  
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44 pool. We concluded from these results that PMSCs give rise to a highly expansive  
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46 population of myofibroblasts in liver fibrosis irrespective of the cause.  
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## 56 Discussion

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3 In the present study, we provide a detailed atlas of portal mesenchymal cells, that were  
4 obtained *via* dissociation of the bilio-vascular tree. While being consistent with previous  
5 scRNAseq studies of the liver, notably from a *Pdgfrb*-GFP reporter mouse (15), our  
6 analysis revealed the existence of several clusters of fibroblasts. Among them, the Fib-  
7 3 and Fib-4 clusters, displayed relatively low levels of *Pdgfrb* expression compared to  
8 the other clusters of liver mesenchymal cells (Fig. S4A), and thus may have been  
9 underestimated in the study of PDGFR $\beta$ <sup>+</sup> cells (15). Fib-3 and Fib-4 were highlighted  
10 as potential progenitor cells on the basis of entropy, GO and trajectory analyses as  
11 well as the expression of stem cell markers. Thus, Fib-3 and Fib-4 appeared as the  
12 most primitive of liver mesenchymal cells, which form a continuum of cells with  
13 overlapping markers, along a gradient of differentiation that bifurcates towards mature  
14 VSMCs on one hand and HSCs on the other one. In this context, PMSCs were isolated  
15 as a cell population, that primarily comprised Fib-3 and Fib-4. MSCs were first  
16 identified in the bone marrow as clonogenic, multipotent cells, able to differentiate into  
17 lineages of mesenchymal tissues including osteoblasts, chondrocytes and adipocytes  
18 in culture (34). Subsequently, cells with similar properties were identified in multiple  
19 organs and also referred to as MSCs (35), although a controversy over the MSC  
20 terminology has been fueled by studies showing that MSCs from different tissues  
21 exhibited different differentiation capacities (36). Yet, MSCs from different tissues  
22 share common features including a small cell population, clonogenicity, the ability to  
23 differentiate into the afore-mentioned mesenchymal cell lineages *in vitro* and a frequent  
24 perivascular distribution (35, 36). PMSCs displayed all these characteristics. Thy1 and  
25 Gli1, two stem cell markers predominantly expressed in Fib-3, as well as fibulin-2 and  
26 ENTPD2, predominantly expressed in Fib-4, were previously immunolocalized in the  
27 portal tracts of homeostatic liver, with a perivascular or periductal distribution (19, 23-  
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3 25, 27, 37-39). We found that the sub-populations of Thy1<sup>+</sup> and Thy1<sup>-</sup> PMSCs were  
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equally clonogenic (Fig. S7), implying that both Fib-3 and Fib-4 are resource fibroblasts in the liver. COL15A1 (4) and SLIT2, that we identified as PMSC markers, are expressed in both clusters, and also display a perivascular or periductal distribution in the homeostatic liver. As formerly proposed for other MSCs, e.g., in the skeletal muscle (36), we suggest that Fib3 and Fib4 represent subsets of the same original population, recruited to the surface of nascent portal blood vessels or later, of developing bile ducts.

The lack of markers that would enable to differentiate HSC-derived from non-HSC-derived myofibroblasts has been a major hurdle so far, to gain insight into the specificities of the different types of liver myofibroblasts and their contributions to liver fibrosis. The isolation of PMSCs allowed us to gain such insight and seek invaluable markers of the two populations. The comparison of transcriptional profiles indicated that in their resting state, PMSCs primarily ensure ECM organization and vasculature integrity whereas HSCs are mainly involved in immunity and the metabolism of vitamin A. A striking difference between the two cell populations as they transform into myofibroblasts *in vitro*, is that PMSCs intensely proliferate whereas HSCs do not divide. In addition, whereas the expression of  $\alpha$ -SMA is induced in both cell types, that of ECM genes such as *Col1a1*, is up-regulated in HSCs but not in PMSCs, so that they both converge towards more similar phenotypes. As a result, most of gene expressions that could demarcate the two cell populations in their resting state are lost or no longer discriminant between their myofibroblastic progenies. Thus, among markers of PMSCs, the expression of *Gli1* or *Entpd2* is totally suppressed in PMSC-MFs, whereas that of *Fbln2* expression is induced in HSC-MFs (Fig. S15). Our strategy was to build

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3 oligogene expression signatures, which included only markers of the two cell  
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5 populations that maintained high differential expression, with limited variation (average  
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7 fold-change of approximately one), throughout their myofibroblastic differentiation.  
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9 Specificity of the cell signatures for liver fibroblasts and HSCs *in vivo*, was attested by  
10  
11 their projection onto previous scRNAseq datasets of mouse liver fibrosis (15, 18).  
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13 PMSC gene signature was predominantly expressed in Fib-3/Fib-4, but also to a lesser  
14  
15 extent in other fibroblast clusters (Fig. S10A), which therefore could also proliferate in  
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17 liver injury.  
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24 *Slit2*, known as a profibrotic and proangiogenic factor in the liver (29-32), is a  
25  
26 prototypical gene of PMSC/PMSC-MF signature. From the present data, we may  
27  
28 postulate that following liver injury, SLIT2, produced by proliferating PMSCs/PMSC-  
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30 MFs, promotes the formation of new vessels and the survival of HSC-MFs. Supporting  
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32 this view, FISH analyses showed that *SLIT2*<sup>+</sup> PMSCs/PMSC-MFs accumulated along  
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34 neo-vessels in the fibrotic septa of cirrhotic livers, surrounded by *SLIT2*<sup>+</sup>  
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36 myofibroblasts, likely mostly HSC-derived. As we previously showed for *COL15A1* (4),  
37  
38 the hepatic expression of *SLIT2* increased in injured liver in correlation with that of  
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40 *COL1A1* and *vWF*, in all types of liver fibrosis. Akin to *SLIT2*, the complete  
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42 PMSC/PMSC-MF 7-gene signature increased, indicating that this cell population  
43  
44 expanded in mouse and human liver fibrosis of multiple causes. As they expand,  
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46 PMSCs/PMSC-MFs may promote liver fibrosis *via* several mechanisms including the  
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48 SLIT2/ROBO axis, but also the production of COL15A1, a multiplexin that anchors  
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50 interstitial collagen to basement membranes forming a scaffold for fibrosis progression  
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52 (4, 40), the overproduction of COL1A1 and COL1A2, that form the major interstitial  
53  
54 collagen in liver fibrosis, and of LOXL1, which promotes elastin cross-linking, among  
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3 others. ScRNAseq analysis of human liver mesenchymal cells in cirrhosis (13),  
4  
5 previously identified a cluster distinguished by PDGFRA expression that expanded in  
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7 cirrhotic livers and was annotated scar-associated mesenchymal cells. We found that  
8  
9 the expression of all PMSC/PMSC-MF signature genes is largely predominant in this  
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11 population (Fig. S16), supporting the clinical relevance of our findings and our  
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13 conclusion regarding the expansion of PMSC-MFs in liver fibrosis. In a previous study,  
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15 a 122-gene HSC signature was shown to be increased in experimental and human  
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17 liver fibrosis (41). However, this latter signature was designed in comparison with other  
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19 liver cell types that did not include other liver mesenchymal cells, and highlighted  
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21 genes such as *Pcdh7* that were herein found to be expressed not only in HSCs/HSC-  
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23 MFs but also in PMSCs/PMSC-MFs (Fig. S4D and S15). Our HSC/HSC-MF 6-gene  
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25 expression signature did not increase in human fibrosis, which is consistent with a low  
26  
27 proliferation rate of HSCs/HSC-MFs *in vitro*, as shown here and *in vivo*, in recent  
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29 scRNAseq analysis of HSCs/HSC-MFs in mouse models of liver fibrosis (17, 18).  
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31 Despite little or no proliferation, HSC-MFs that derive from the large preexisting pool  
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33 of HSCs, likely form the major part of liver myofibroblasts. However, as they proliferate  
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35 and expand within the lobule, PMSC-MFs may develop interactions with ECs and  
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37 HSCs anticipated to play crucial roles in fibrosis progression.  
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52  
53 Pierre-Emmanuel Rautou (CRI, Université de Paris) for their contributions.  
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3 Data availability: All sequencing data are deposited in the Gene Expression Omnibus  
4 (GEO) with the accession numbers GSE163777 (scRNAseq), GSE164037 (bulk  
5 RNAseq) and GSE159676 (microarrays).  
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8 Author names in bold designate shared co-first authorship  
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### 11 12 13 **Figure legends**

#### 14 15 **Fig. 1. ScRNAseq profiling of mesenchymal cells from the bilio-vascular tree.** (A)

16 Outline of the experimental procedure for preparation of Lin  
17 (EpCam,CD31,CD45,CD11b)-negative cells from the mouse bilio-vascular tree for  
18 scRNAseq analysis. (B) *t*-SNE projection of 4,976 single cells from one healthy liver,  
19 revealing 16 clusters (color-coded), identified by their expression profiles and ordered  
20 according to the number of cells they comprise. (C) Dendrogram showing the  
21 relationships of clusters. (D) Dot plot of two selective differentially expressed genes in  
22 each cluster.  
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#### 36 **Fig. 2. Characterization of PMSCs.** (A) Single-cell entropy of all clusters. (B)

37 Inference of sequenced mesenchymal cells by Monocle 2 reverse graph embedding  
38 (pseudotime along differentiation trajectory in inset). (C) Heatmap of GO enrichment  
39 related to development. (D) Dot plot of genes previously reported to demarcate  
40 progenitor fibroblasts (red frame) or portal (myo)fibroblasts (black frame). (E) Dot plot  
41 of genes encoding surface markers *Pdgfra/Cd34/Cd9* and *Cd200*. (F) FACS plot  
42 showing the gating strategy for Fib-3/Fib-4 cell sorting (Gate 4). (G) CFU-F formed by  
43 sorted cells from gates as defined in F (n=3-9). (H) Flow cytometry analysis of MSC  
44 surface markers in cells from gate 4 (n=4-10). (I) Trilineage differentiation of cells from  
45 gate 4 (PMSCs), towards adipocytes (Oil red O), osteoblasts (Alizarin red S) and  
46 chondrocytes (Alcian blue). (J) Immunofluorescence of Col15A1 and  $\alpha$ -SMA in PMSC  
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spheroids (upper panel) or grown into PMSC-MFs on stiff substratum (lower panel). (K) *Col15a1*, *Acta2* and *Col1a1* expression in PMSCs (freshly isolated or cultured as in J) (n=3). Means  $\pm$  SEM; \*\* $p$ <0.01; \*\*\* $p$ <0.001; \*\*\*\* $p$ <0.0001 (Wilcoxon test); Scale bars=50  $\mu$ m.

**Fig. 3. Transcriptomic features of PMSCs/PMSC-MFs compared to HSCs/HSC-MFs.** (A,B) Bulk RNAseq analysis of PMSCs and HSCs, A) Volcano plot (upper panel) showing 3,273 and 3,122 DEGs (FDR  $\leq$  0.05, fold-difference  $\geq$  2) in PMSCs and HSCs, respectively. Top 10 DEGs are labeled and their average expression, projected on  $t$ -SNE plot of scRNAseq (lower panel); (B) Gene Set Enrichment Analysis (GSEA) of all genes overexpressed in PMSCs or HSCs. (C) Overview of cell preparations (n=4 per condition), analyzed by bulk RNAseq and PCA of variance of read counts (ellipses: 95% CI). (D) K-means clustering of 5,000 genes with highest variance showing enriched GO terms. (E) Venn diagram showing DEGs in PMSCs (or Fib-3/Fib-4) and in HSCs, both in bulk RNAseq and scRNAseq and maintaining high differential expression after myofibroblastic differentiation (-MFs-7d). (F-G) Heatmaps of PMSC and HSC oligogene expression signatures assessed by F) bulk RNAseq or G) RT-qPCR analyses of PMSCs, HSCs, derived myofibroblasts (-MFs-7d), and other liver cell types. KCs, Kupffer cells.

**Fig. 4. *Slit2* marker in PMSCs/PMSC-MFs and its functional analysis.** (A) *Slit2* RT-qPCR in PMSCs, HSCs, their derived myofibroblasts (-MFs-d7), and other liver cell types (n=3) (left panel); *Slit2* FISH and  $\alpha$ -SMA immunofluorescence in PMSC-MFs-d7 and HSC-MFs-d7 (right panel). (B)  $t$ -SNE plot of *Slit2* and its *Robo* receptors in scRNAseq clusters. (C) PMSC-MFs that were transfected with *Slit2* or scramble (Scr)

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2  
3 siRNA, were examined for *Slit2* and *Acta2* expression by RT-qPCR, and their  
4 conditioned medium (CM) tested towards the cell viability, assessed by MTT, of LX-2  
5 cells exposed to H<sub>2</sub>O<sub>2</sub> (n=5-8). (D) Tube formation was evaluated in HUVECs  
6 incubated with PMSC-MF CM in the absence (n=6) or presence of ROBO1/Fc (n=5)  
7 or anti-ROBO1 antibody (n=5), or with control (CTL) serum-free medium (n=9); and in  
8 HUVECs incubated with the CM of PMSC-MFs infected with a lentivirus expressing  
9 Cas9 and a gRNA targeting the first exon of *Slit2* (LV*Slit2*, n=8) or a control lentivirus  
10 expressing Cas9 and a scramble gRNA (LV, n=8), or with CTL serum-free medium  
11 (n=3). After 6 hours, pictures were taken and the number of junctions, counted, using  
12 the Angiogenesis Analyzer tool Fiji. (E, F) *SLIT2* FISH and  $\alpha$ -SMA or CD31  
13 immunofluorescence in normal and cirrhotic human liver; E) In normal liver (left panel),  
14 a small number of *SLIT2*<sup>+</sup> PMSCs (arrowheads) are visible in portal tracts (perivascular  
15 *SLIT2*<sup>+</sup> PMSCs, distinct from  $\alpha$ -SMA<sup>+</sup> VSMCs, shown in insets), representative of n=2  
16 (CV, central vein; PV, portal vein). In cirrhosis (middle panel), *SLIT2*<sup>+</sup> are intermingled  
17 with *SLIT2*<sup>-</sup> myofibroblasts in fibrotic septa (FS) (*SLIT2*<sup>+</sup>,  $\alpha$ -SMA<sup>+</sup> PMSC-MF, shown in  
18 inset); right panel: quantification of labeled areas; F) *SLIT2*<sup>+</sup> PMSC-MFs (red  
19 arrowheads) line up along CD31<sup>+</sup> neo-vessels (white arrowheads), surrounded by  
20 several layers of  $\alpha$ -SMA<sup>+</sup> myofibroblasts that populate the entire fibrotic septa (dashed  
21 green line) (merge shown in inset), representative of cirrhosis of alcoholic (n=3), NASH  
22 (n=1) or hepatitis C (n=1) origins (Scale bars=50  $\mu$ m). Means  $\pm$  SEM; \**p*<0.05;  
23 \*\**p*<0.01; \*\*\*\**p*<0.0001 (One-way ANOVA in A, Wilcoxon test in C and D).  
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54 **Fig. 5. Expression of *SLIT2*, PMSC/PMSC-MF and HSC/PMSC-MF oligogene**  
55 **signatures in liver fibrosis.** Hepatic expression of *SLIT2*, *ACTA2*, *COL1A1*, *vWF*,  
56 PMSC/PMSC-MF or HSC/HSC-MF oligogene signatures assessed by (A,B) RT-qPCR,  
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3 A) in liver tissue from mice fed normal chow diet (NCD, n=12) or DDC (n= 8) for 4  
4 weeks (upper panels), or fed CSAA (n=5) or CDAA (n=17) for 8 weeks (lower panels),  
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7 B) in liver biopsy from patients with NAFLD, at stages of fibrosis F0 (n=26), F1 (n=15),  
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10 F2 (n=12), F3-F4 (n=7). (C) by Affymetrix microarray analysis of normal human liver  
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12 (n=5 patients) and of liver tissue samples from patients with NASH (n=7 patients), PSC  
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14 (n=6 patients, 2 biopsies/patient) or other liver diseases (n=8 patients) (left panel); (D)  
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16 PMSC/PMSC-MF and (E) HSC/HSC-MF oligogene signatures assessed by Affymetrix  
17  
18 microarray analysis of human liver tissue samples as in C. Correlations between *SLIT2*  
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20 or PMSC 7-gene signature and *ACTA2*, *COL1A1*, or *vWF* expression are shown in C  
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22 and D right panels. Individual values and means  $\pm$  SEM are shown; \* $p < 0.05$ ; \*\* $p < 0.01$ ;  
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24 \*\*\* $p < 0.001$ ; \*\*\*\* $p < 0.0001$ ; ns, non-significant (Wilcoxon test in A, C-E; one-way  
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26 ANOVA in B); r values are Pearson correlation coefficients.  
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**Portal fibroblasts with mesenchymal stem cell features form a reservoir  
of proliferative myofibroblasts in liver fibrosis**

Lin Lei, Alix Bruneau, Haquima El Mourabit, Justine Guégan, Trine Folseraas, Sara Lemoine, Tom Hemming Karlsen, Bénédicte Hoareau, Romain Morichon, Ester Gonzalez-Sanchez, Claire Goumard, Vlad Ratziu, Pierre Charbord, Jérémie Gautheron, Frank Tacke, Thierry Jaffredo, Axelle Cadoret\*, Chantal Housset\* (\*co-senior authorship).

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## Supplementary Experimental procedures

### **Animal experiments.**

Animal experiments were conducted in the CRSA animal facility (DDPP agreement No. C 75-12-01) and were approved under Nos. 2018060418401070v2, 2018102211507258, 2019090307246392v3 and 2018072719352187v1 by the Ethics Committee of Animal Experiments, Charles Darwin No. 5, Paris. Animals, all males, were housed in a temperature-controlled, specific pathogen-free environment, on a 12-hour light-dark cycle, with free access to chow and water. *Abcb4*<sup>-/-</sup> mice and their wildtype *Abcb4*<sup>+/+</sup> littermates were bred, using *Abcb4*<sup>+/-</sup> heterozygous mice on an FVB/N genetic background (FVB.129P2-*Abcb4*tm1Bor/J) provided by Sanofi R&D (Chilly-Mazarin, France). Liver fibrosis was also induced in C57BL/6J male mice, by 3 methods: 1) 10-week-old mice were fed a diet containing 0.1% DDC (Sigma, 137030) or a normal control diet (NCD), for 4 weeks; 2) 8-week-old mice were fed a CDAA or CSAA diet (Ssniff spezialdiäten GmbH, Soest, Germany), for 8 weeks; 3) 8-week-old mice received i.p. injections of CCl<sub>4</sub> (1 μL/g body weight) diluted at 50% (V/V) in mineral oil or mineral oil (vehicle), twice a week for 6 weeks.

### **Cell isolation.**

*Cell collection from the bilio-vascular tree.* *In situ* retrograde perfusion of the liver was performed through the inferior vena cava with Ca<sup>2+</sup>,Mg<sup>2+</sup>-free HBSS (Gibco, 14170-088)/1% EDTA (Sigma, 03690) for 5 minutes at 37°C, and then with HBSS containing Ca<sup>2+</sup>,Mg<sup>2+</sup> (Gibco, 24020117)/0.15 mg/mL collagenase P (Sigma, 11213873001) for 20 minutes at 37°C. Next, the liver was collected and placed in L15 Leibovitz medium (Sigma, L5520) at 4°C. The liver parenchyma was mechanically detached and discarded. The remaining bilio-vascular tree was minced and incubated in MEM (Gibco, 21090-022) containing 0.075 mg/mL collagenase P, 0.02 mg/mL DNase (Sigma, DN25), 3% FBS (FBS; Gibco, 10270-098), 1 mg/mL BSA (Sigma, A7030), 1% HEPES (Gibco, 15630) and 1% Penicillin-Streptomycin (Gibco, 15140-122), under agitation for 15 minutes at 37°C. The bilio-vascular fragments were collected on top of a 40-μm cell strainer and centrifuged at 1,500 rpm, for 5 minutes at 4°C. The cell pellet was resuspended in 0.05% Trypsin-EDTA (Invitrogen, 25300-054) with 0.02 mg/mL DNase and incubated under agitation for 15 minutes at 37°C, and the dissociated cells were filtered three times through a 20-μm cell strainer. Following red blood cell lysis with ACK lysis buffer, the cell suspension was centrifuged at 1,500 rpm, for 5 minutes at 4°C, and the cell pellet was resuspended in a FACS buffer composed of PBS with 2% FBS, 1% HEPES and 1% Penicillin-Streptomycin, at a concentration of 1 × 10<sup>7</sup> cells/mL for cell sorting. For cholangiocyte isolation, cells were incubated with an anti-Epcam-FITC antibody (BioLegend, Clone: G8.8) for 30 minutes at 4°C and cells were sorted using a FACSAria II cell sorter (BD Biosciences).

*Hepatocyte, Kupffer cell, LSEC and HSC collection.* Hepatocytes, LSECs and Kupffer cells were isolated as previously described (1), with modifications. For



hepatocyte isolation, the liver was perfused *in situ* with HBSS containing 0.15 mg/mL collagenase P for 20 minutes at 37°C. The cell suspension was filtered through a 70- $\mu$ m strainer and centrifuged twice at 400 rpm, for 5 minutes at 4°C, to eliminate non-parenchymal cells. LSEC and Kupffer cell isolation was performed by *ex situ* dissociation of the liver using a gentleMACs dissociator (Miltenyi) and magnetic selection using CD146 microbeads (Miltenyi, 130-092-007) and anti-F4/80 microbeads (Miltenyi, 130-110-443), respectively. For HSC isolation, the liver was perfused *in situ*, with HBSS containing 0.4 mg/mL pronase (Sigma, 10165921001) for 5 minutes at 37°C, and then with 0.05 mg/mL collagenase P for 15 min at 37°C. The liver was collected, minced and further digested in HBSS containing 0.044 mg/mL collagenase P, 0.5 mg/mL pronase and 0.02 mg/mL DNase, under agitation for 15 minutes at 37°C. The resulting cell suspension was submitted to density gradient-centrifugation at 1,380 g for 17 minutes, in GBSS (Gibco)/Histodenz (Sigma, D2158) at 4°C. HSCs were collected from the interface and resuspended in FACS buffer for further purification by cell sorting based on retinoid autofluorescence, as previously described (2).

### **Cell sorting and flow cytometry analysis**

Cells isolated from the bilio-vascular tree were incubated with 1% anti-mouse CD16/CD32 antibody (BD Pharmingen, 553141) for 10 minutes on ice, to block Fc receptors before incubation with anti-Epcam-FITC, anti-CD31-FITC, anti-CD45-FITC and anti-CD11b-FITC antibodies, all at concentrations of 1:100, for 30 minutes at 4°C. Dead cells were stained with 7-aminoactinomycin D (7-AAD; BD Biosciences, 559925) immediately before cell sorting was performed, using a FACSAria II cell sorter (BD Biosciences). Lin-negative cells, gated as Epcam<sup>+</sup>CD31<sup>+</sup>CD45<sup>+</sup>CD11b<sup>-</sup> cells, were collected and subjected to scRNAseq analysis. To isolate PMSCs from the bilio-vascular tree, cells were labeled with anti-Epcam-, anti-CD31-, anti-CD45- and anti-CD11b-FITC antibodies as above, and anti-PDGFR $\alpha$ -PE, anti-CD34-APC, anti-CD9-BV421 and anti-CD200-APC-R700, all at concentrations of 1:100 except for anti-PDGFR $\alpha$ -PE (1:50). PMSCs were gated as Lin<sup>-</sup>PDGFR $\alpha$ <sup>+</sup>CD34<sup>+</sup>CD9<sup>+</sup>CD200<sup>low</sup> cells. To sort Thy1<sup>-</sup>, Thy1<sup>low</sup> and Thy1<sup>high</sup> PMSCs, cells from the bilio-vascular tree were labeled with anti-Epcam-FITC, anti-CD31-FITC, anti-CD45-FITC, anti-CD11b-FITC, anti-PDGFR $\alpha$ -PE, anti-CD34-APC, anti-CD9-BV421, anti-CD200-APC-R700 antibodies as above, and anti-Thy1-PE-Cy7 antibody at a concentration of 1:100. For flow cytometry analysis, freshly isolated PMSCs were labeled either with anti-CD105-BV510, anti-Sca1-BV510 or anti-CD29-PE/Cy7, all at concentrations of 1:100. Analyses were performed using BD FACSDiva™ and FlowJo (Tree Star) software. All antibodies are listed in Table S1.

### **Cell culture.**

PMSCs and HSCs were seeded in 6-well plates at a density of 20,000 cells/cm<sup>2</sup> and cultured in DMEM containing 20% FBS, 1% HEPES and 1% Penicillin-Streptomycin to obtain PMSC-MFs and HSC-MFs, respectively. To maintain PMSCs in a resting state, cells were seeded in 96-well ultra-low attachment

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(ULA) round-bottomed plates. The LX-2 human HSC cell line (provided by Human HepCell, IHU-ICAN) was cultured in DMEM containing 10% FBS, 1% HEPES and 1% Penicillin-Streptomycin. HUVECs were grown in EndoGRO™-VEGF complete medium (Millipore).

### **Cell clonogenicity and differentiation assays.**

Cell clonogenicity was examined by CFU-F assay, as follows: 2,000 sorted cells were plated onto a 10-cm plastic dish and maintained in DMEM/20% FBS. The presence of more than 50 cells in a cluster after 14 days in culture, was counted as a colony. The capacity of PMSCs to differentiate towards adipogenic, osteogenic or chondrogenic lineages was analyzed using specific protocols. For adipogenic and osteogenic differentiation, sorted PMSCs were plated in 48-well plates coated with matrigel (Corning, 356231) at a density of 5,000 cells/cm<sup>2</sup> in DMEM/20% FBS until subconfluence. Then, the culture medium was changed for adipogenic (R&D Systems, CCM011) or osteogenic (R&D Systems, CCM009) differentiation medium. After 21 days, cells were fixed with 4% paraformaldehyde and stained using Oil Red O (Sigma) or Alizarin Red solution (Sigma), respectively. For chondrogenic differentiation, 50,000 sorted PMSCs were plated in ULA plate in chondrogenic differentiation medium (R&D Systems, CCM006) to form spheroids. After 21 days, the spheroids were fixed in 4% paraformaldehyde, embedded in OCT (Sakura Finetek) and cryosections (8 μm) were stained with Alcian blue (Santa Cruz Biotechnology) and counterstained with nuclear fast red (Vector).

### **Videomicroscopy.**

PMSCs and HSCs were seeded in 24-well plates at densities of 5,000 and 50,000 per well, respectively, and cultured in standard conditions. Twenty-four hours after seeding, the cells were placed in the CellVivo Incubation System (Pecon GmbH, Ernah, Germany) driven by a high-end inverted microscope IX83 (Olympus Corporation, Tokyo, Japan). One picture has been taken every hour, using a 10X UPLFN 0.3NA PH1 objective lens and ORCA-Flash 4 LT digital (Hamamatsu Photonics KK, Tokyo, Japan) driven by Cellsens dimension 1.16 (Olympus). The movies have been built using the open source software Fiji (3).

### **ScRNAseq.**

Cells were loaded onto a GemCode instrument (10x Genomics) to generate single-cell barcoded droplets, *i.e.*, gel beads in emulsion (GEMs). Sequencing libraries were constructed using the Chromium Single-cell 3' Library Kit (10x Genomics) according to the manufacturer's protocol and sequenced on a NextSeq 500 device (Illumina). Average read depth of the sample was 79,199 reads/cell. Reads were then aligned to the mouse genome mm10/Grcm38 using the Cell Ranger 3.0.2 software. Subsequent analysis was performed in R using the filtered barcode and count matrices produced by Cell Ranger. The data were analyzed using Seurat 3.6.1 (4). Genes expressed in less than 6 cells, as well as cells with less than 500 or more than 25,000 unique molecular identifiers (UMIs), were filtered out. Any single-cell with more than 10% UMIs

mapped to mitochondrial genes was also removed. Seurat SCTransform function (5) was used to normalize and scale the data (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE163777>).

Dimensionality reduction was performed through PCA on the gene expression matrix and using the first 30 PCs for clustering and visualization. Unsupervised shared nearest neighbor clustering was performed using Seurat FindClusters function at the resolution of 0.6 and visualization was achieved using spectral *t*-SNE of the principal components as implemented in Seurat. Cluster dendrogram was constructed using BuildClusterTree built-in function of the R package Seurat which used cluster averaged PCs for calculating a PC distance matrix. The cell clusters identified were evaluated for differential genes expression (DGE), using Seurat FindAllMarkers function. All genes considered for cell-type classification were determined with *p* value < 0.01 and log (fold-change) > 0.25 as cutoff by performing DGE analysis between the clusters using Wilcoxon rank sum test and Benjamini and Hochberg procedure for *p*-values adjustment. Single-cell entropy was calculated using LandSCENT v. 0.99.3, as previously described. Doublet analysis was performed, using two methods, *i.e.*, DoubletFinder, R package v 2.0 and Scrublet, python library v0.1. Thereby, we identified 334 and 103 potential doublets, respectively. They included 66 doublets in common, that were plotted on *t*-SNE projection (Fig. S1B). The Monocle version 2.14.0 R package (6) was used to organize cells in pseudotime and infer cell trajectories from the Seurat dataset. We ran reduceDimension with *t*-SNE as the reduction method, num\_dim=12, norm\_method="log" and max\_components = 2. Cells were clustered with the density peak clustering algorithm by setting P to 2 and Δ to 4 (and skip\_rho\_sigma = T to facilitate the computation). The top 1000 significantly differentially expressed genes between clusters were selected as the ordering genes and used in Monocle for clustering and ordering cells using the DDRTree method and reverse graph embedding.

### **Bulk RNAseq.**

RNA was extracted using Rneasy Micro Kit (Qiagen). Libraries were generated from total RNA and paired-end sequencing was performed on a NextSeq 500 device (Illumina). Raw sequencing data were quality-controlled with the FastQC program. Paired reads were aligned to the mouse reference genome (mm10 build) with the STAR software v2.5.3a (option for no multihits). Mapping results were quality-checked using RNASEQC. Gene counts were obtained by using RSEM tools v1.2.28 (rsem-calculate-expression, option for paired-end and stranded). Expected gene counts were first normalized using TMM method in the edgeR R package and genes with a count per million (CPM) < 1 in 20% of samples, were removed

(<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164037>).

Differential gene expression analysis was performed using DEseq2. A log<sub>2</sub> of fold change of 1 and a Benjamini-Hochberg adjusted *p* value cutoff < 0.05 (FDR) was set to determine significant differentially expressed genes.

## GO enrichment and Gene Set Enrichment Analysis.

Symbol gene IDs were first converted to Entrez gene IDs using the clusterProfiler R package (7). Functional enrichment in GO biological processes of differentially expressed genes was performed using EnrichGO built-in function of the clusterProfiler version 3.14 with default parameters. The comparison of enriched functional enrichment among mesenchymal cell populations was performed using clusterProfiler CompareCluster function (7). Heatmap of enriched term was generated in R. GSEA was implemented using the R package ReactomePA with default parameters (8).

### ***Import of previously published data sets.***

We downloaded the raw scRNAseq data of i) 23,291 Pdgfrb-GFP+ mesenchymal cells from uninjured and fibrotic (6 weeks CCl<sub>4</sub>) mouse livers published and deposited in the GEO by Dobie *et al.* (GSE137720), ii) 47,752 liver cells of all types from uninjured oil-treated (10,636) and fibrotic (CCl<sub>4</sub> 3 weeks, 18,185; BDL 10 days, 18,931) mouse livers published and deposited in the GEO by Yang *et al.* (GSE171904).

### ***Slit2 silencing by siRNA and LX-2 survival.***

*Slit2* and scramble siRNA (SMARTpool: ON-TARGETplus *Slit2* siRNA L-058235-00-0005, ON-TARGETplus Non-targeting Pool D-001810-10-05) were purchased from Dharmacon. PMSC-MFs at passage 1 in 6-well plates were transfected with siRNA (50 nmol/L) using Dharmafect1. Forty-eight hours after transfection, the cells were incubated with serum-free DMEM for 24 hours to generate conditioned medium. LX-2 cells were seeded in 96-well plates (7,000/well) and 24 hours later, were incubated in serum-free DMEM containing H<sub>2</sub>O<sub>2</sub> (200 μmol/L) for 30 min. Thereafter, the medium was replaced by serum-free DMEM or conditioned medium from transfected PMSC-MFs and 24 hours later, cell viability was assessed using MMT assay. Absorbance was quantified at 540 nm (TECAN).

### ***Slit2 deletion by CRISPR/Cas9.***

The lentiviral plasmid plentiCRISPRv2, a gift from Zhang lab (Addgene, MA, USA; plasmid #52961), contains hSpCas9, a guide RNA (gRNA), and a puromycin resistance sequence. The gRNA targeting exon 1 of *Slit2* was designed using <http://cistrome.org/SSC>, that ensures specificity and high cleavage efficiency.

Its sequence was sense, 5' CTTGAACAAGGTGGCGCCGC 3', antisense, 5' GCGGCGCCACCTTGTTCAAG 3'. The web-based tool, CRISPOR (<http://crispor.tefor.net>) that predicts the risk of off-target sequences by providing a cutting frequency determination (CFD) specificity score ranging from 1 to 100, was used to avoid off-target sequences. Guides with a CFD specificity score > 50 are recommended by Doench JG *et al.* (9). The gRNA we used to target *Slit2* exon 1 has a CFD score of 98. This gRNA did not perfectly match any other genomic region. One off-target with three mismatches was found in an intronic region of *Mapk4* and 40 off-targets were found with four

mismatches, making unlikely that these off-targets were involved in the effect caused by *Slit2* ablation. Lentiviruses dedicated to *Slit2* knockout (LV*Slit2*) and a control lentivirus (LV) expressing Cas9 and a scramble gRNA were produced by the VVTG platform (Federative Research Institute, Necker, France). Sub-confluent PMSC-MFs at day 7 of primary culture, were infected with viral particles at a minimal titer of  $10^8$  units per mL. Forty-eight hours post-infection, the culture medium was discarded and conditioned medium was prepared by incubating the cells with serum-free medium for 24 hours.

### **Tube assay.**

HUVECs (15,000 cells/well) were plated in 15-well  $\mu$ -slide angiogenesis Ibidi plates (Clinisciences) previously coated with 50  $\mu$ l of growth factor-reduced Matrigel (BD Biosciences) and incubated in the presence of PMSC-MF conditioned medium (harvested from cells incubated with serum-free medium for 24 hours) or serum-free medium as a control. To assess the contribution of SLIT2 secreted by PMSC-MFs in angiogenesis, HUVECs were incubated with PMSC-MF conditioned medium a) in the presence of 100 ng/mL of recombinant rat ROBO1/Fc chimera protein (R&D Systems, #1749B) (10), b) after they had been preincubated for 1 hour with 10  $\mu$ g/mL of anti-human ROBO1 antibody (R&D Systems, #AF7118), or c) with the conditioned medium from PMSC-MFs infected with a lentivirus expressing Cas9 and a gRNA targeting the first exon of *Slit2*, dedicated to *Slit2* knockout (LV*Slit2*) or a control lentivirus (LV) expressing Cas9 and a scramble gRNA. HUVECs were placed in the CellVivo Incubation System as for videomicroscopy (described above) and tube formation was evaluated after 6 hours of incubation using the Angiogenesis Analyzer tool (Fiji software).

### **Human liver tissue samples.**

Samples of normal liver from patients undergoing liver resections for focal lesions (n=2 patients), and of cirrhotic livers from patients with NASH (n=1), chronic hepatitis C (n=1) or alcoholic liver disease (n=3) undergoing liver resection or transplantation, were provided by Human HepCell platform (IHU-ICAN, Declaration No. AC-2020-3861) for FISH. Frozen samples of liver biopsy from subjects with a suspicion of non-alcoholic fatty liver disease at stages of fibrosis F0 (n=26), F1 (n=15), F2 (n=12), F3-F4 (n=7), were provided by the Biological Resource Center, BIO-ICAN, Paris, France, with ethical approval from the Persons Protection Committee (CPP Ile de France VI) for RT-qPCR analyses. The RNA used for microarray experiments was extracted from frozen tissue obtained from explanted livers or diagnostic liver biopsies from i) normal human liver tissue (tumor-free tissue from livers with colorectal cancer metastasis) (n=5 patients) and ii) liver tissue from patients with chronic liver diseases, including PSC (n=6 patients, 2 biopsies/patient), NASH (n=7 patients) and other liver diseases including autoimmune hepatitis (n=3), primary biliary cholangitis (n=2), alcoholic liver disease (n=1), haemochromatosis (n=1) and sarcoidosis (n=1). The liver specimens were provided by the Norwegian biobank for primary sclerosing cholangitis, Oslo, Norway with ethical approval

1 from the Regional Committee for Medical and Health Research ethics of South  
2 East Norway. All subjects gave written informed consent before to allow the use  
3 of the samples.  
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### 6 **RT-qPCR.**

7 Total RNA was extracted from frozen liver tissue samples or harvested cells  
8 using the RNeasy Mini Kit or Micro Kit (Qiagen), respectively. The cDNA was  
9 synthesized using the MMLV-RT (Invitrogen, 28025013) or SuperScript™ II  
10 (Invitrogen, 18064014) and real-time PCR was performed using the LightCycler  
11 480 SYBR Green I Master Kit on an LC480 device (Roche Diagnostics). Target  
12 gene mRNA levels were normalized using HPRT or 18S as a reference gene  
13 and expressed as relative levels ( $2^{-\Delta\Delta Ct}$  method). Normalized values ( $\Delta Ct$ )  
14 were used for oligogene signature analysis and presented as  $0-\Delta Ct$ , so that  
15 higher values indicate higher expression levels. The primers (Table S2) were  
16 designed using the primer software from Roche Diagnostics.  
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### 22 **Immunofluorescence and FISH.**

23 For immunofluorescence, cell preparations were fixed in 4% paraformaldehyde  
24 at 4°C for 15 minutes, and incubated with primary antibodies against COL15A1  
25 (Abcam, ab58717, 1:200) or  $\alpha$ -SMA (Agilent, M085129-2, 1:100) at 4°C  
26 overnight. Nuclear staining was performed using Draq5 (Abcam). Cells were  
27 examined with a SP2 confocal microscope (Leica, Bannockburn, IL, USA).  
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29 For co-labeling by FISH and immunofluorescence, cell preparations and tissue  
30 samples were fixed in 4% paraformaldehyde at 4°C for 20 minutes and 4 hours,  
31 respectively. Tissue samples were then transferred to 30% sucrose in PBS at  
32 4°C until sinking and then placed in a plastic mold filled with O.C.T. that was  
33 immersed in 2 methyl-butane maintained at -70°C, and stored at -80°C. Tissue  
34 sectioning was performed at -25°C and 10- $\mu$ m cryosections were mounted on  
35 SuperFrostPlus™ slides that were kept on dry ice. Before processing, tissue  
36 sections were thawed in 100% ethanol for 5 minutes, followed by 1 minute in  
37 TBS buffer. Cell preparations or tissue sections were then transferred to pre-  
38 warmed hybridization buffer (5X SSC / 1% BSA / 10% Formamid / 0,1% (w/v)  
39 SDS) at 75°C for 20 minutes. The probes, directed at *SLIT2* or Scramble (Table  
40 S3), conjugated to Fam-6 or Atto-633, respectively, were diluted at 50 ng/ $\mu$ L  
41 and denatured at 85°C for 5 minutes while the samples were dried and  
42 denatured on a preheated plate at 85°C for 2 minutes. The probes (100 $\mu$ L) were  
43 added to tissue sections then covered with a coverslip and sealed with glue. In  
44 the following steps the samples were kept in the dark. They were incubated at  
45 75°C overnight in a dark wet chamber. After removal of the coverslip, the slides  
46 were transferred to freshly prepared hybridization buffer at 75°C for 15 minutes.  
47 The slides were washed with TBS for 5 minutes, and then with TBS-Triton x100  
48 0.3% for 15 minutes, at room temperature. After a 5-minute TBS wash at room  
49 temperature, the slides were blocked for 60 minutes with 2% Normal Goat  
50 Serum (Thermo Fisher) in TBS-T (0.1%). Tissue sections were incubated with  
51 anti- $\alpha$ -SMA (1:100, M085129-2, Agilent) in blocking buffer, overnight at 4°C.  
52 Slides were washed with TBS 3 times for 5 minutes at room temperature and  
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1 incubated with secondary antibody (Goat anti-mouse IgG Alexa Fluor 555  
2 Conjugate, CellSignaling #4409, 1:500) and DAPI 2 $\mu$ g/mL (Sigma-Aldrich).  
3 Large field imaging acquisition was performed on a Zeiss Axio Observer 7. For  
4 image processing, the large field images were stitched and background was  
5 subtracted, using the default settings of ZEISS software ZEN 3.1 (blue edition).  
6 Exported single channel grayscale in .tiff were later processed in Fiji. The  
7 background due to FISH staining was assessed using the scramble probe and  
8 this autofluorescence was subtracted from the *SLIT2* channel using image  
9 calculator module. For quantification, binary masks of at least two independent  
10 experiments were generated using the trainable classification software Ilastik  
11 (v 1.3.3). Marked areas were then measured using Fiji. The plugin Color pixel  
12 counter was used to count the number of pixels on the image of a specific color.  
13 Results are expressed as a percentage of pixels in the Region of Interest.  
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### 19 **Microarray analyses.**

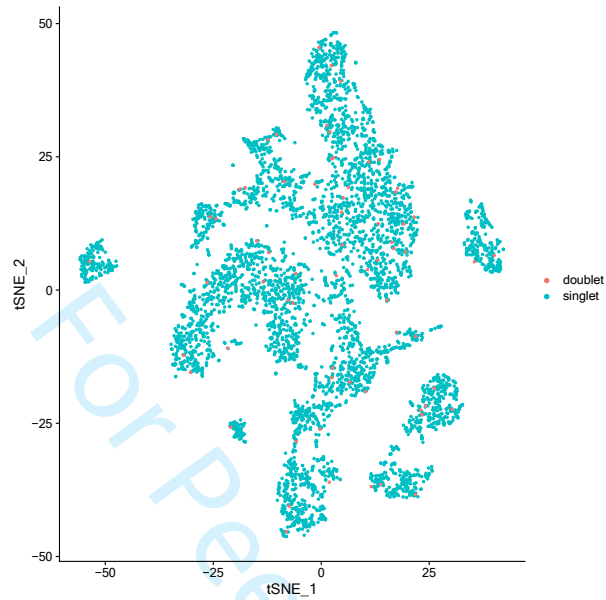
20 Pangenomic analysis of frozen liver tissue samples, was performed using the  
21 Affymetrix human gene 1.0 st microarray. Analysis was conducted using  
22 R. *oligo* bioconductor package to import raw data CEL files in an ExpressionSet  
23 object and *rma* function to normalize the data. After normalization,  
24 summarization was performed because transcripts are represented by multiple  
25 probes, on the Affymetrix platform. For each gene, the background-adjusted  
26 and normalized intensities of all probes were summarized into one estimated  
27 amount proportional to the amount of RNA transcripts. Summarized data have  
28 been annotated with hugene10sttranscriptcluster.db bioconductor package  
29 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE159676>).  
30 Statistical analysis was performed using non-parametric Wilcoxon test.  
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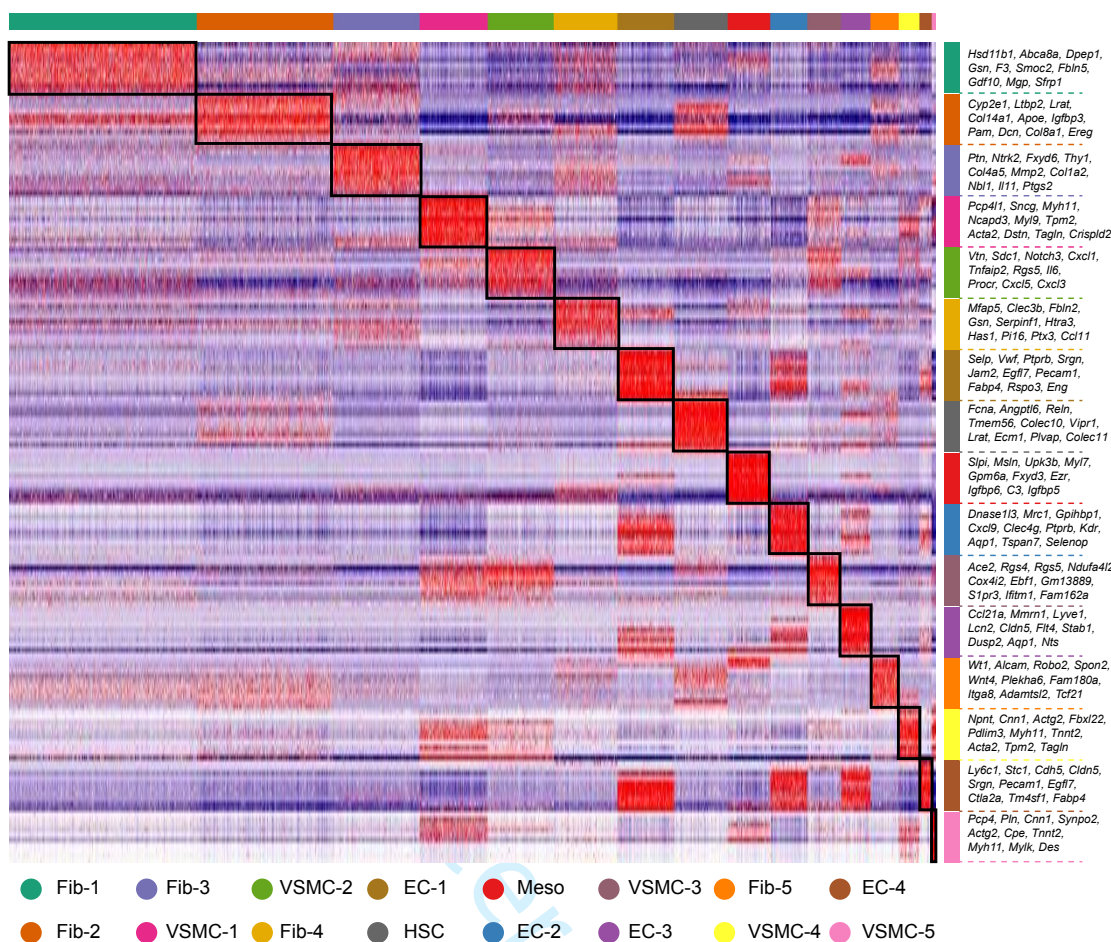
	nCounts (transcripts)	nFeatures (genes)	% mitochondrial genes
Mean per cell	10539	2951	3.14 %

B

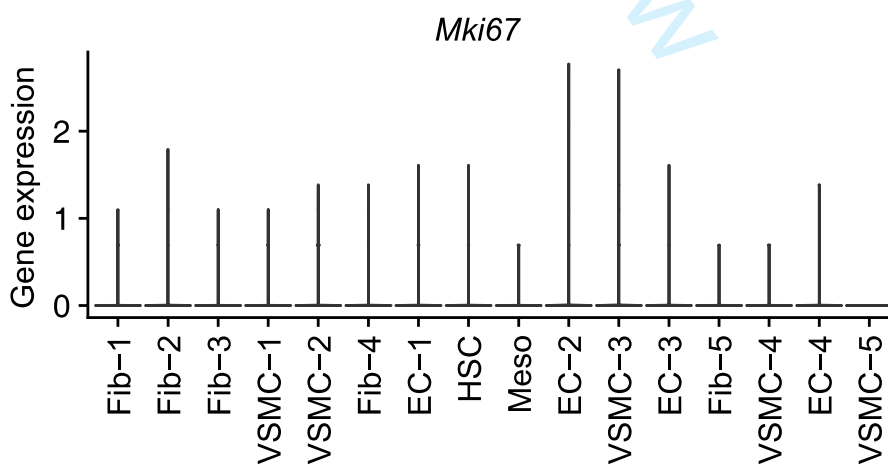


**Fig. S1: scRNAseq (A) Quality control metrics; (B) Analysis of doublets (plotted on *t*-SNE).**



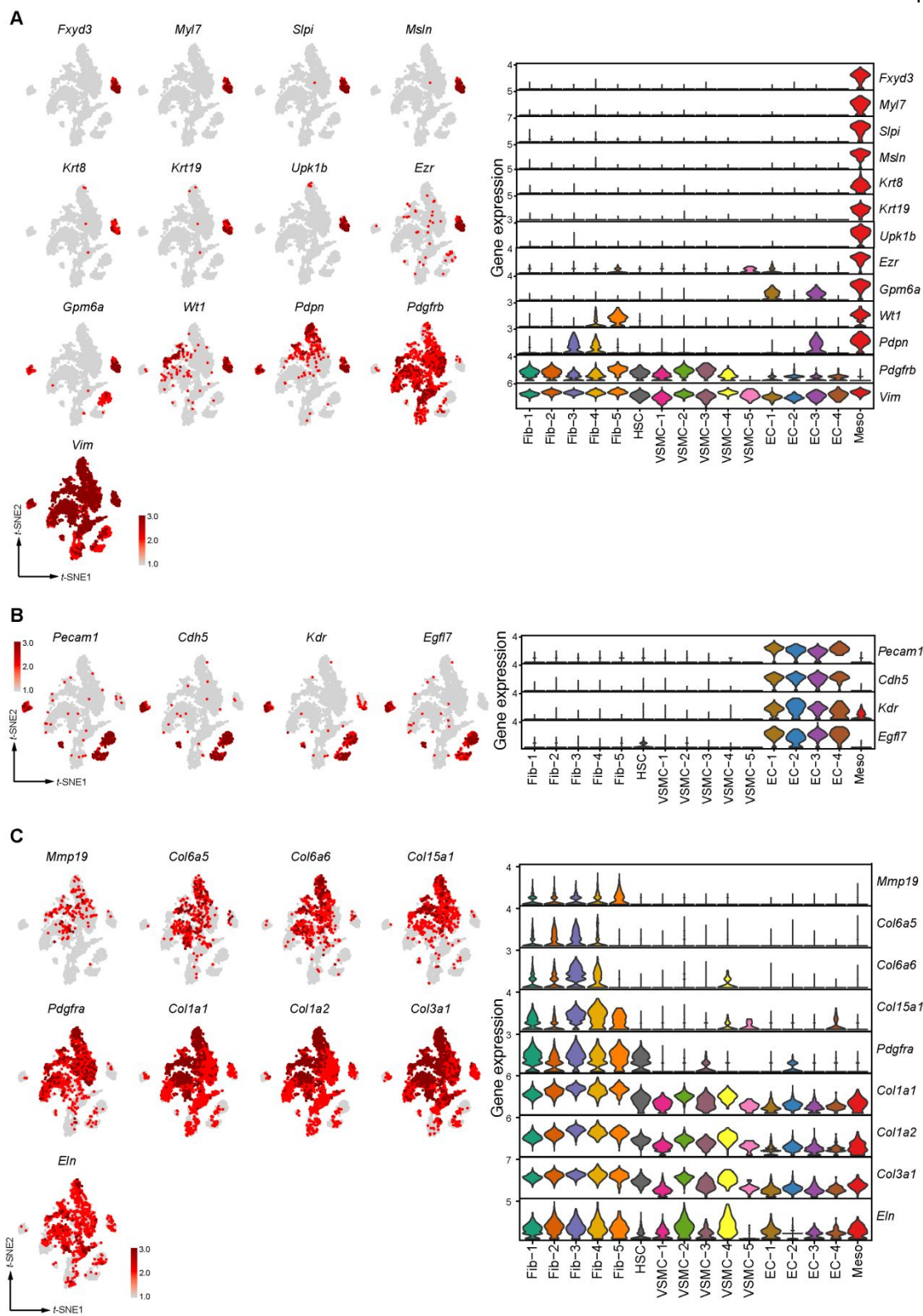


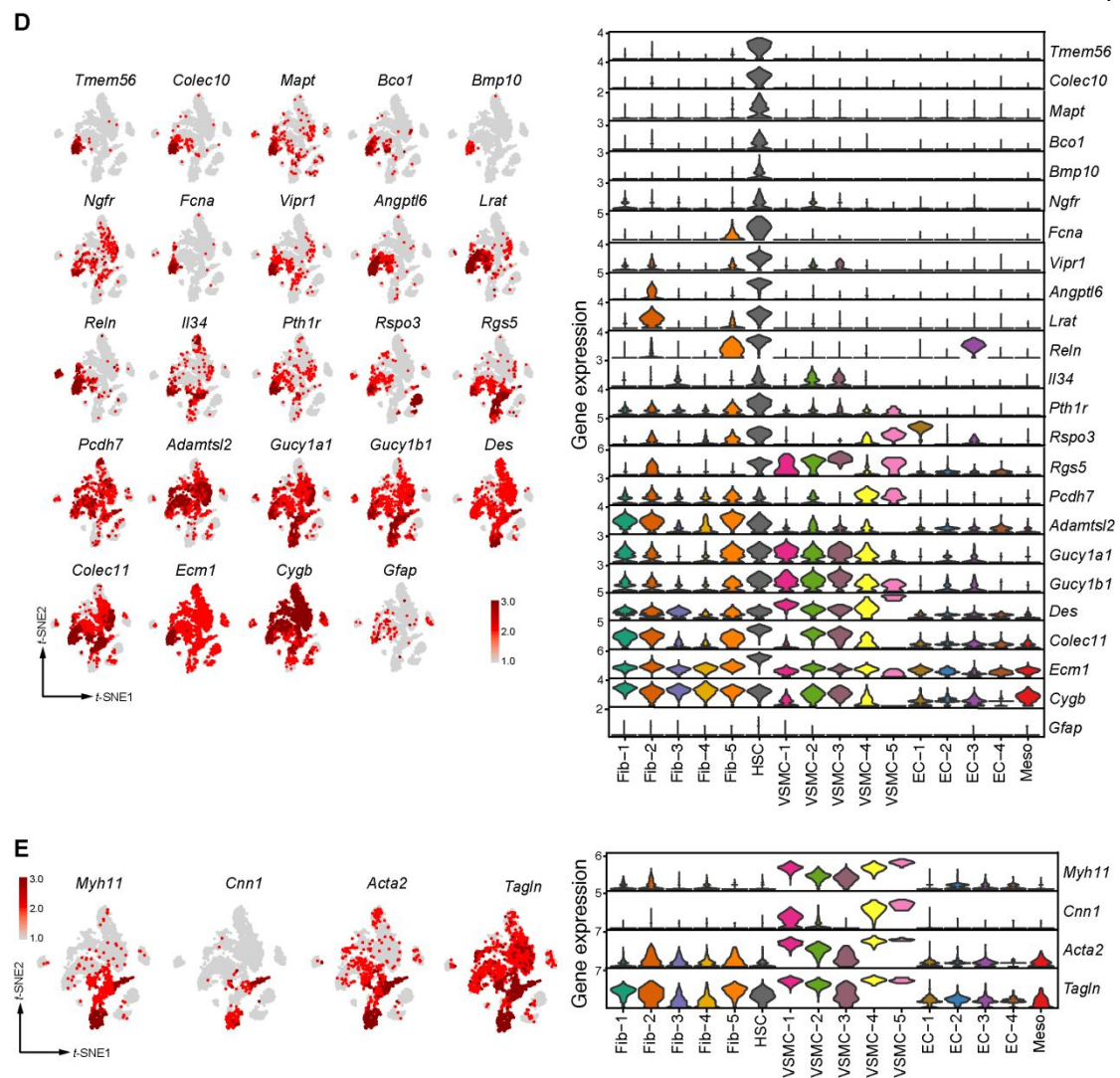
**Fig. S2: Heatmap of the top 10 differentially expressed genes in scRNAseq clusters.** (see also Table S4).



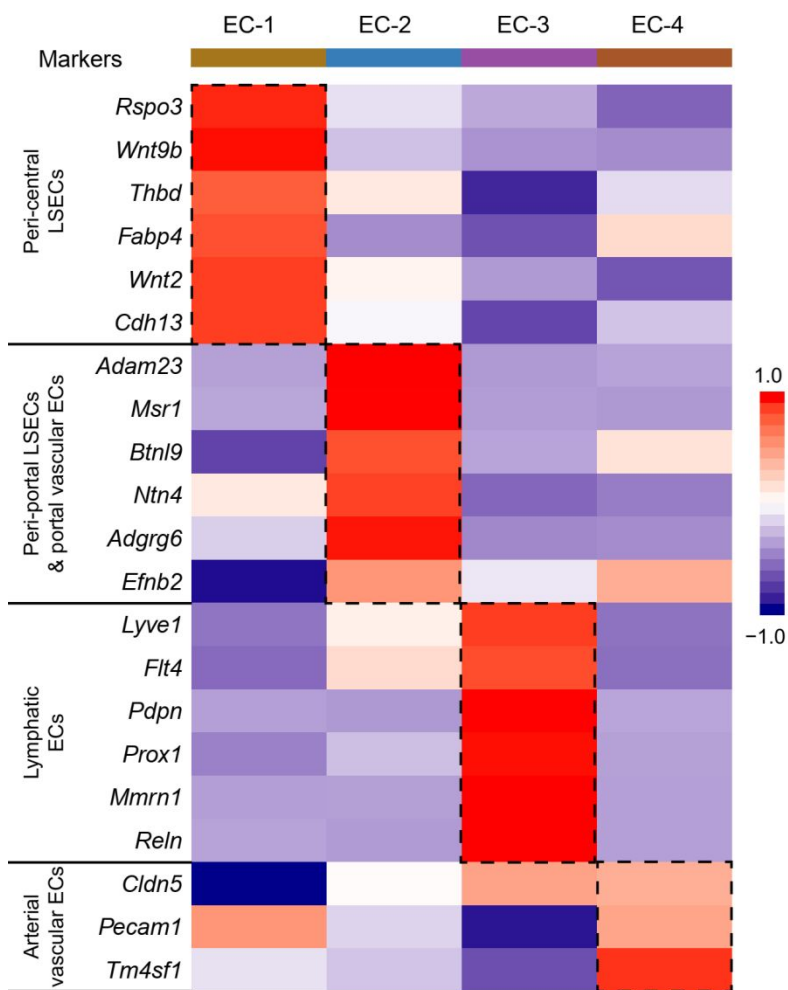
**Fig. S3: Violin plots showing the expression of the proliferation marker Mki67 across all scRNAseq clusters.**

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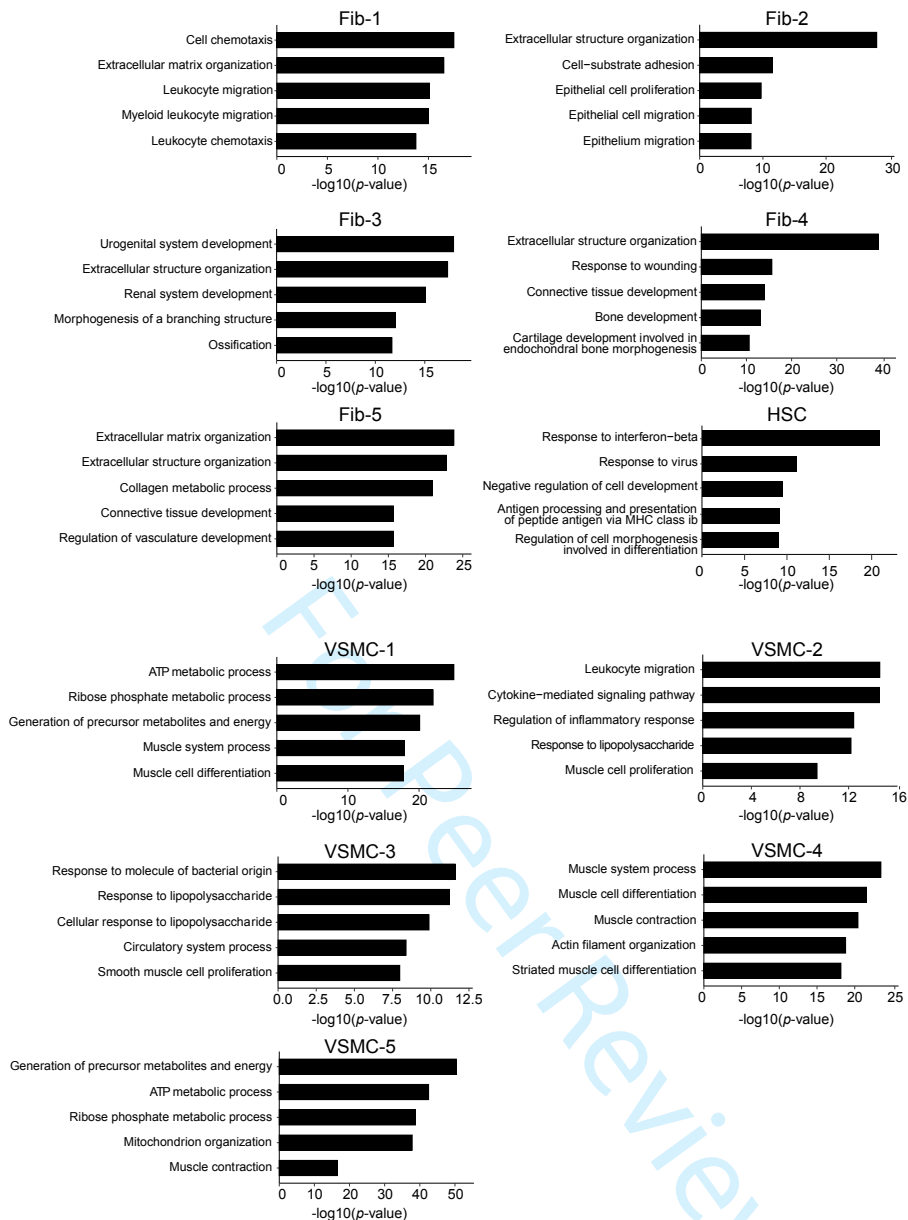


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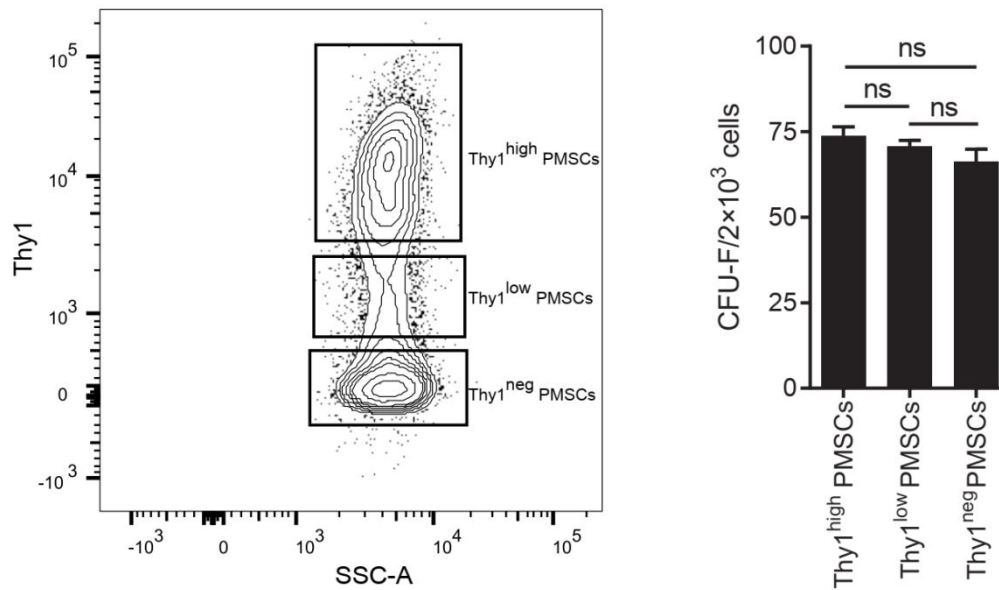


**Fig. S5: Heatmap depicting representative genes expressed in the endothelial cell (EC) clusters of the scRNAseq.**

Color scale represents the average expression level across all cells within each cluster. LSECs, liver sinusoidal endothelial cells.

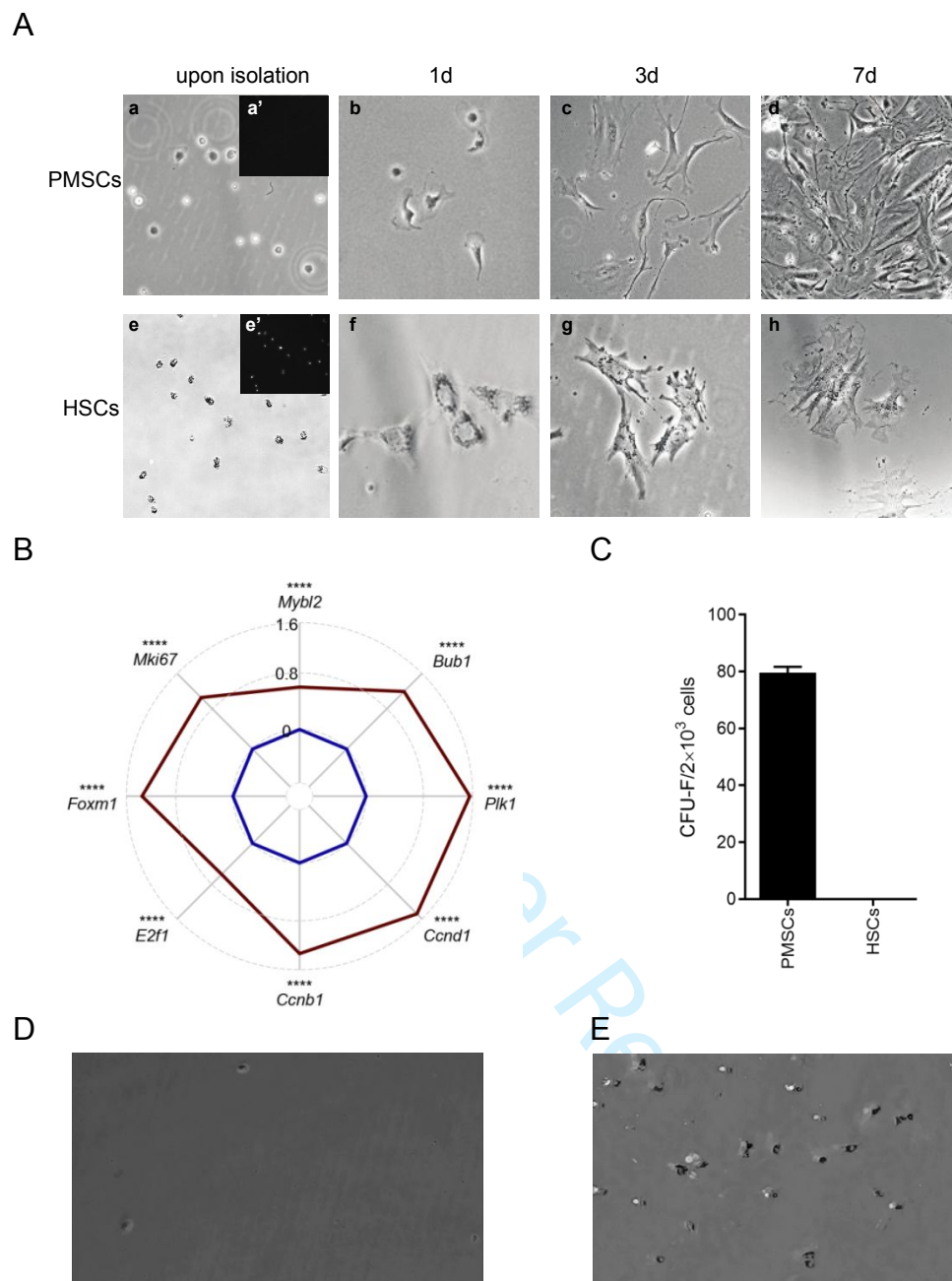


**Fig. S6: GO enrichment of genes significantly overexpressed in the different mesenchymal cell clusters of the scRNAseq. (see also Table S5).**



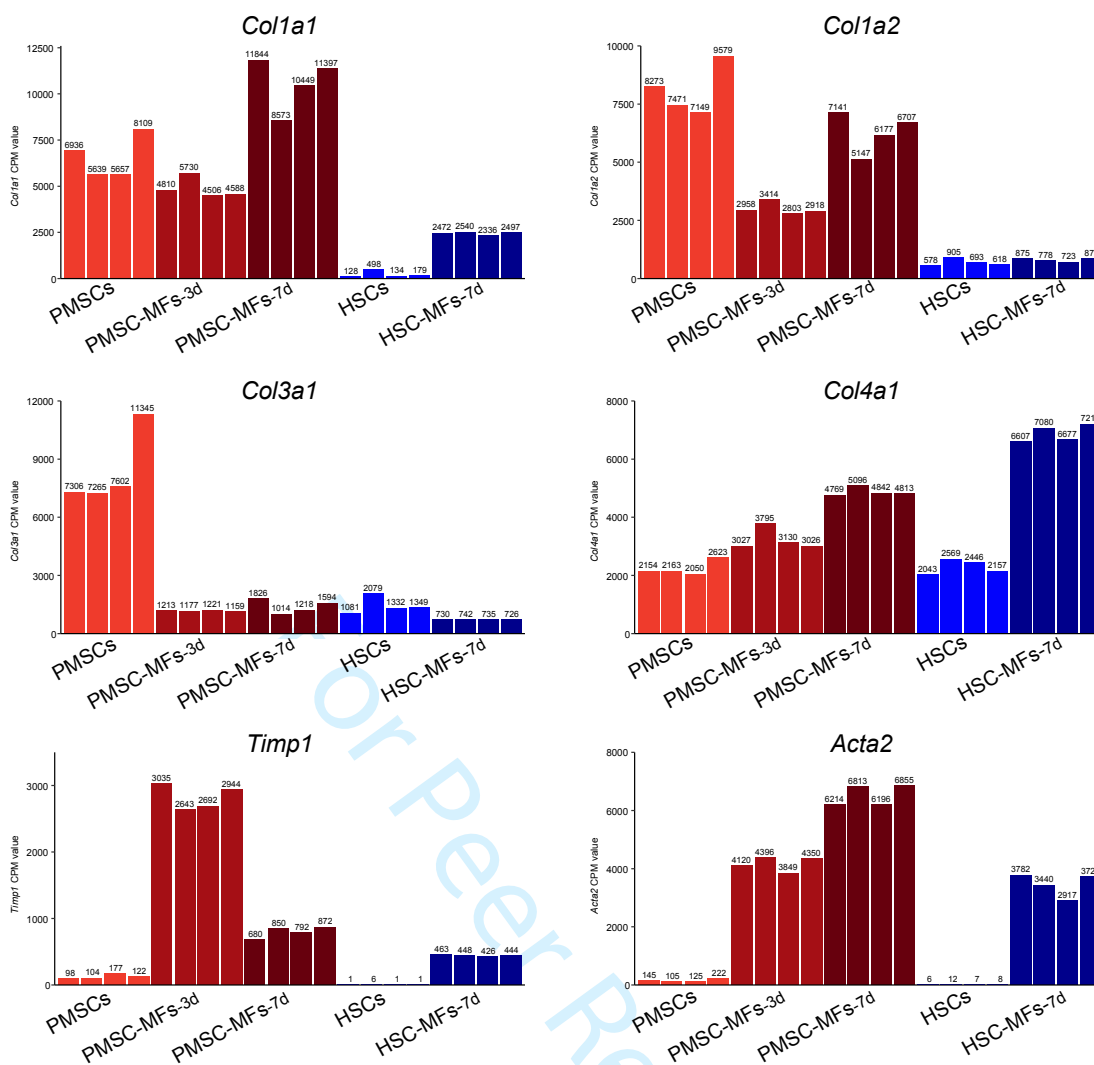
**Fig. S7: Clonogenicity of PMSCs according to Thy1 expression.**

Left panel: Representative flow cytogram of Thy1 expression on PMSCs. Right panel: CFU-F formed by Thy1<sup>neg</sup>, Thy1<sup>low</sup> and Thy1<sup>high</sup> PMSCs. Data represent means  $\pm$  SEM (n=3). Statistical significance was evaluated using one-way ANOVA; ns, non-significant.



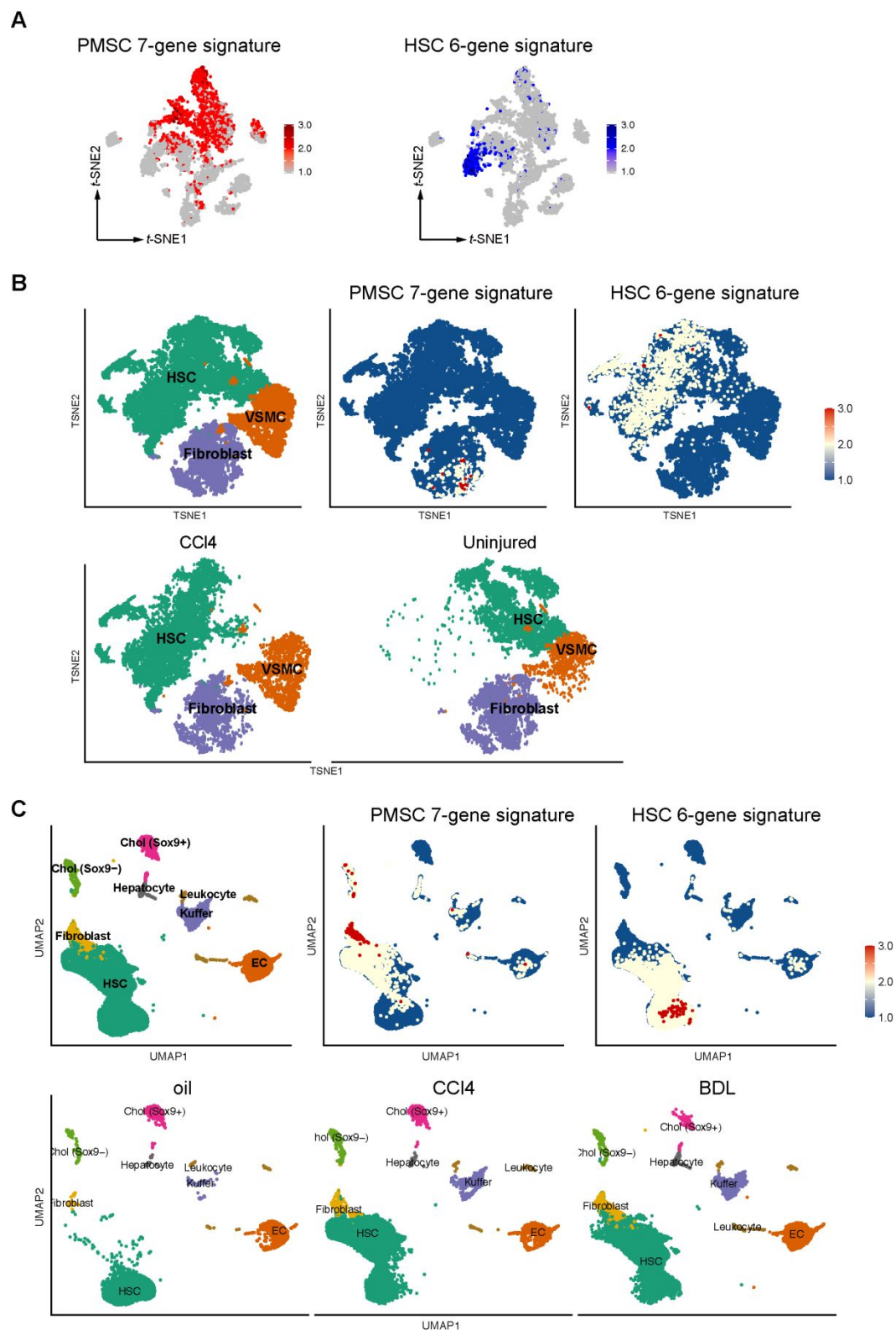
**Fig. S8: Phenotypic comparison of PMSCs/PMSC-MFs and HSCs/HSC-MFs.**

(A) Microscopic appearance: Cells were observed under phase-contrast microscopy (fluorescence microscopy under 328-nm ultraviolet excitation in insets) (a,e) immediately after cell sorting, (b-d, f-h) at the indicated days (d) of primary culture. (B-E) Proliferative properties: B) Proliferation-related gene expressions in PMSC-MFs vs. HSC-MFs. Radar plot showing the log<sub>2</sub> fold-difference in the expression of cell proliferation-related genes in bulk RNAseq analysis of PMSC-MFs (red line) and HSC-MFs (blue line) after 7 days in culture. Statistical significance was evaluated using Wilcoxon test; \*\*\*\**p*<0.0001; C) CFU-F formed by sorted PMSCs and HSCs (Means ± SEM, *n*=8); Videomicroscopy (provided separately) of D) PMSCs and E) HSCs between day 1 and day 5 of primary culture (representative of 2 random fields).



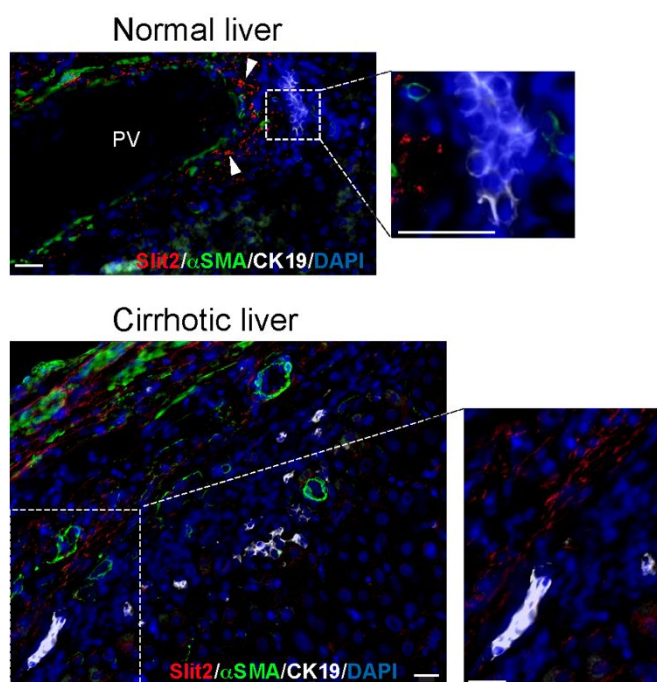
**Fig. S9: Expression of pro-fibrotic genes in PMSCs and HSCs, in resting or myofibroblastic states after 3 days (-MFs-3d) or 7 days (-MFs-7d) in primary culture. CPM, counts per million.**





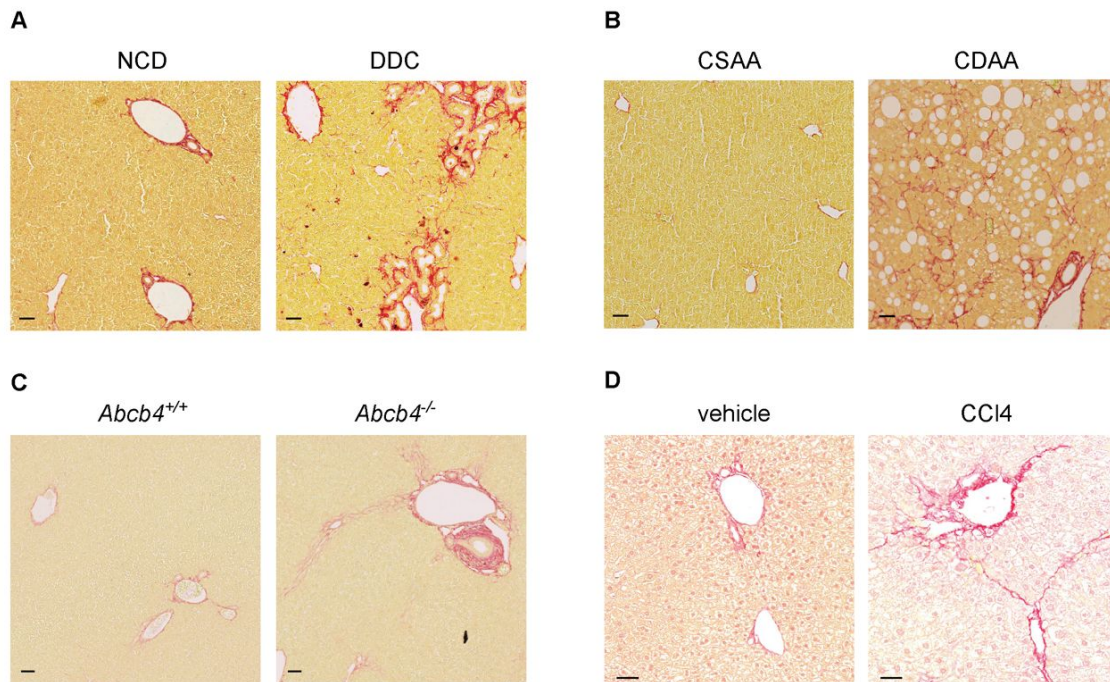
**Fig. S10: PMSC/PMSC-MF and HSC/HSC-MF oligogene signatures projected onto (A) current and (B, C) previous scRNAseq data sets.**

A) Clustering of portal mesenchymal cells from uninjured mouse liver as in Fig. 1B; B) Clustering of *Pdgfrb*-GFP<sup>+</sup> mesenchymal cells from uninjured and fibrotic (6 weeks CCI4) mouse livers from Dobie *et al.* (GSE137720); C) Clustering of all liver cells from uninjured (oil) and fibrotic (3 weeks CCI4, 10 days BDL) mouse livers from Yang *et al.* (GSE171904). Chol, cholangiocytes.



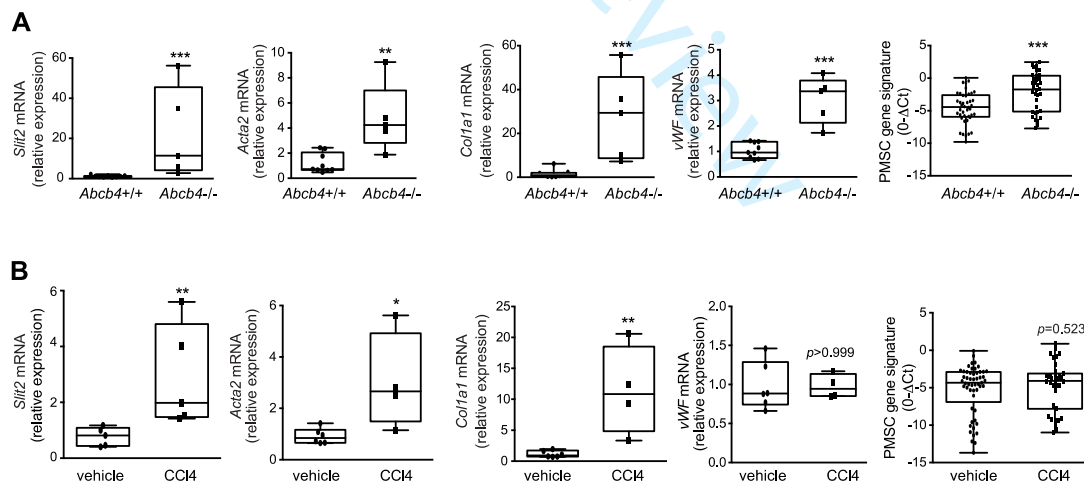
**Fig. S11: Distinct localization of *SLIT2*<sup>+</sup> cells and cholangiocytes.**

*SLIT2* FISH and  $\alpha$ -SMA or CK19 immunofluorescence were performed on normal and cirrhotic human liver tissue sections. In normal liver (upper panel), perivascular *SLIT2*<sup>+</sup> cells (arrowheads) in a large portal tract are distinct from  $\alpha$ -SMA<sup>+</sup> VSMCs and from CK19<sup>+</sup> cholangiocytes (higher magnification in inset), representative of n=2 (PV, portal vein). In cirrhotic liver (lower panel), *SLIT2*<sup>+</sup> intermingled with *SLIT2*<sup>-</sup> myofibroblasts in fibrotic septa, are distinct from CK19<sup>+</sup> cholangiocytes (higher magnification in inset), representative of cirrhosis of alcoholic (n=3), NASH (n=1) or hepatitis C (n=1) origins (Scale bars=50  $\mu$ m).



**Fig. S12: Mouse models of liver fibrosis.**

Sirius red staining of the liver from (A) mice fed NCD or DDC diet for 4 weeks; (B) mice fed CSAA or CDAA diet for 8 weeks; (C) *Abcb4*<sup>+/+</sup> and *Abcb4*<sup>-/-</sup> mice at the age of 8 weeks; (D) vehicle- or CCl<sub>4</sub>-i.p.-injected mice for 6 weeks. NCD, normal chow diet; DDC, 3,5-diethoxycarbonyl-1,4-dihydrocollidine; CSAA, choline-sufficient L-amino acid-defined; CDAA, choline-deficient L-amino acid-defined diet. Representative of 5 to 17 animals per group. Scale bars=50  $\mu$ m.

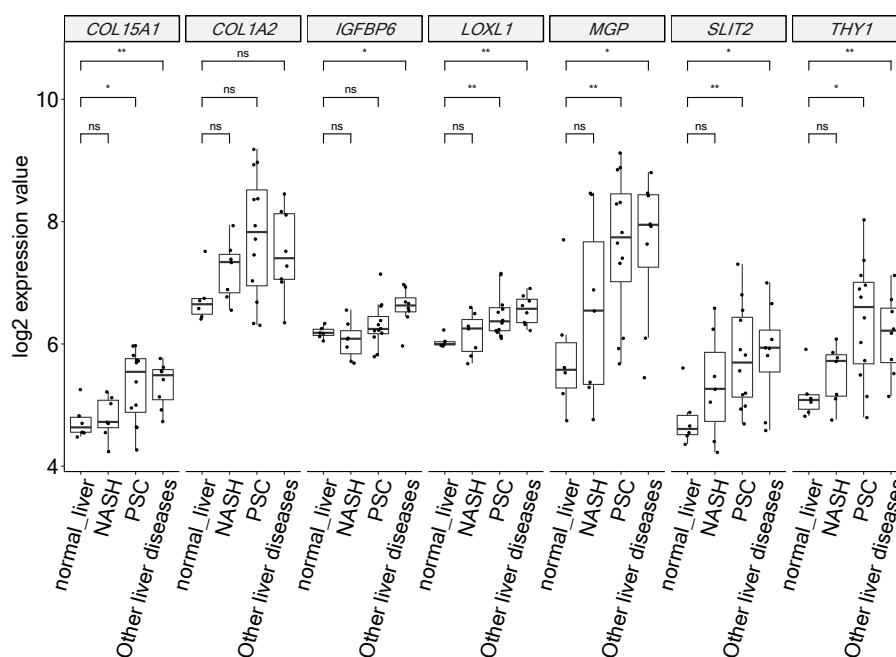


**Fig. S13: Expression of SLIT2 and PMSC 7-gene signature in the *Abcb4*<sup>-/-</sup> and CCl<sub>4</sub> mouse models of liver fibrosis.**

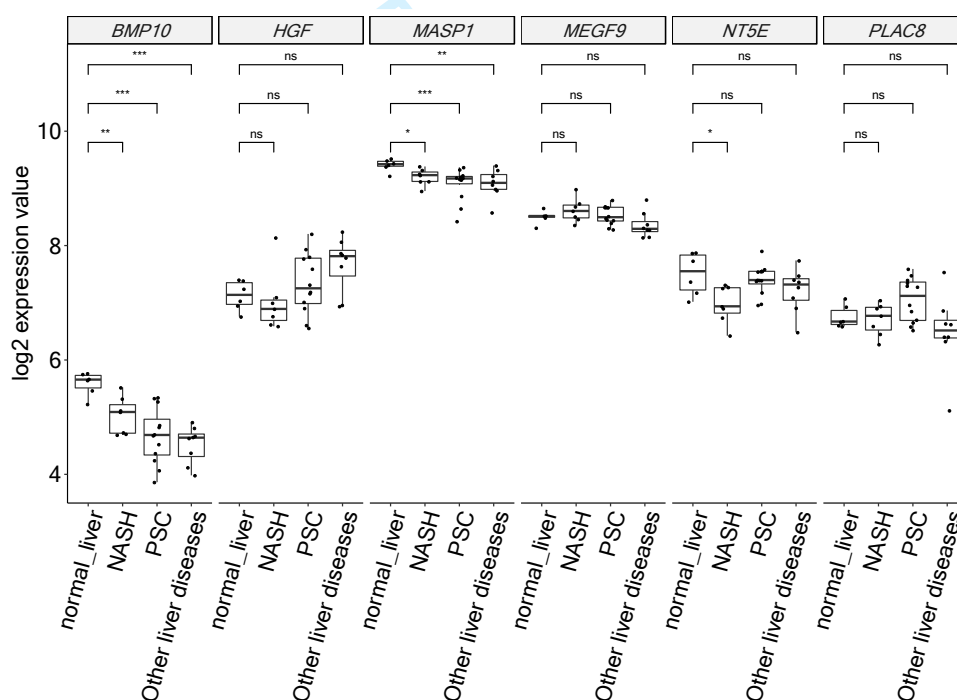
Hepatic expression of *Slit2*, *Acta2*, *Col1a1*, *vWF* and of PMSC 7-gene signature was measured by RT-qPCR in liver tissue from (A) *Abcb4*<sup>+/+</sup> (n=9) and *Abcb4*<sup>-/-</sup> (n=5) mice at the age of 8 weeks, (B) vehicle- or CCl<sub>4</sub>-i.p.-injected mice for 6 weeks (n=5/group). Data represent individual values and means  $\pm$  SEM. \**p*<0.05; \*\**p*<0.01; \*\*\**p*<0.001 (Wilcoxon test).

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A

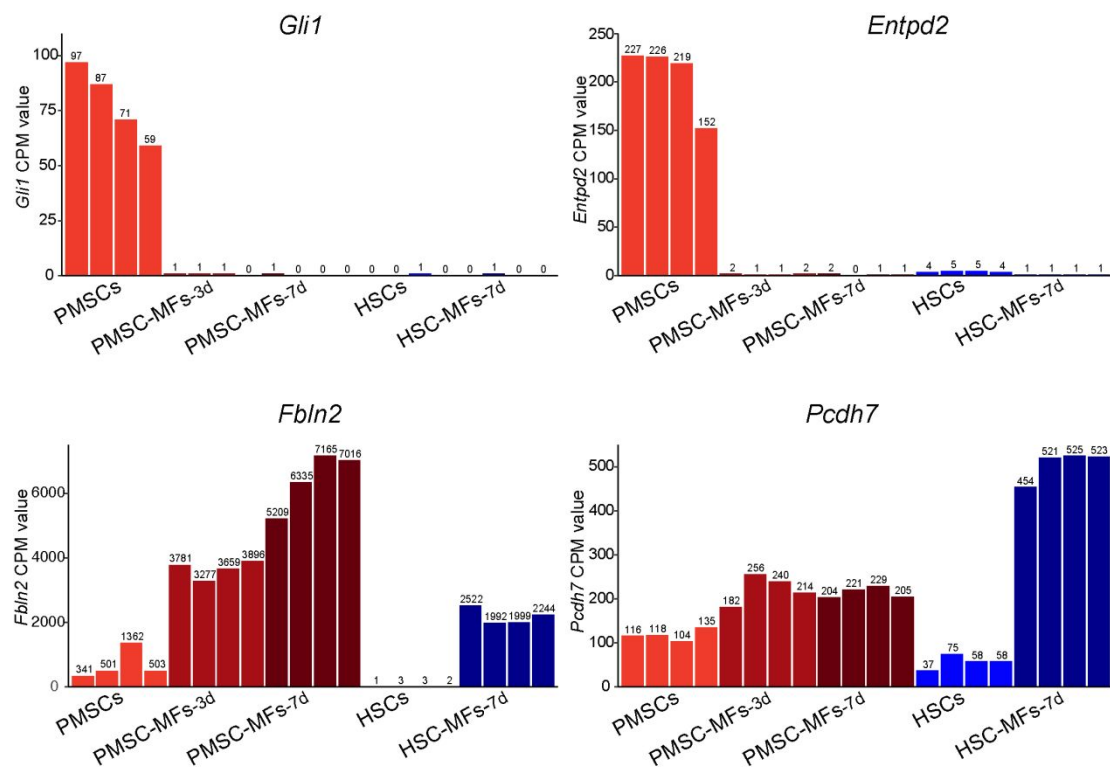


B



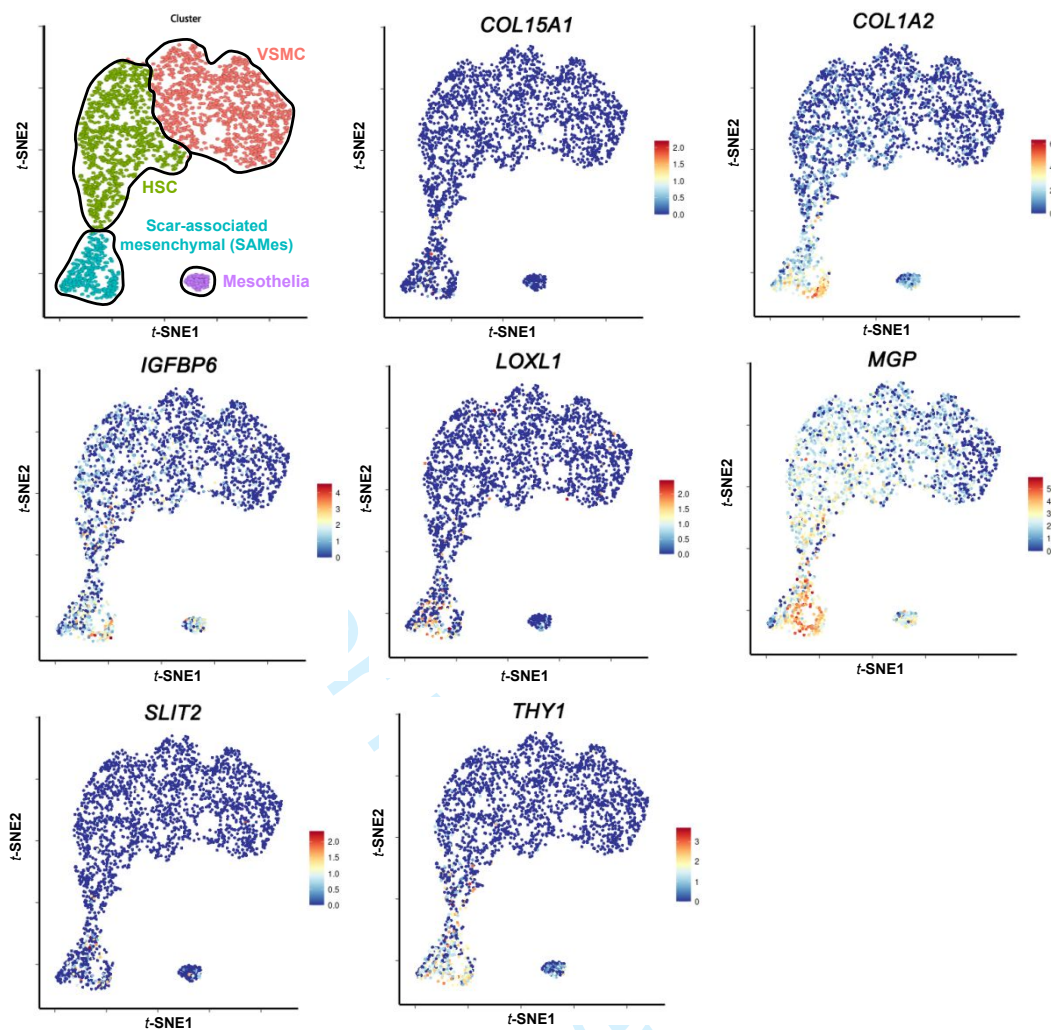
**Fig. S14: Individual expression of the PMSC and HSC signature genes in human liver fibrosis.**

Hepatic expression of the genes of (A) PMSC/PMSC-MF, and (B) HSC/HSC-MF signatures, was assessed by Affymetrix microarray analysis of normal human liver (n=5 patients) and of liver tissue samples from patients with NASH (n=7 patients), PSC (n=6 patients, 2 biopsies/patient) or other liver diseases (n=8 patients). Data represent individual values and means  $\pm$  SEM. \* $p < 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p < 0.001$ ; ns, non-significant; statistical significance was evaluated using non-parametric Wilcoxon test.



**Fig. S15: *Gli1*, *Entpd2*, *Fbln2* and *Pcdh7* expression in the bulk RNAseq analysis of PMSCs and HSCs, in resting or myofibroblastic states after 3 days (-MFs-3d) or 7 days (-MFs-7d) in primary culture. CPM, counts per million.**

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**Fig. S16: Comparison of PMSCs/PMSC-MFs with the previously annotated scar-associated mesenchymal cells.**

*t*-SNE plot of PMSC/PMSC-MF signature genes in human mesenchymal cells from Ramachandran et al. (<https://www.livercellatlas.ed.ac.uk/>).

**Table S1: Antibodies used for cell sorting, flow cytometry and immunofluorescence.**

Antibody	Company	Cat no.	Clone no.
Cell sorting & Flow cytometry			
rat anti-mouse CD9-BV421	BD Biosciences	564235	KMC8
rat anti-mouse CD11b-FITC	BioLegend	101245	M1/70
hamster anti-mouse CD29-PE/Cy7	BioLegend	102222	HM $\beta$ 1-1
rat anti-mouse CD31-FITC	BD Biosciences	561813	MEC 13.3
rat anti-mouse CD34-APC	BioLegend	119310	MEC14.7
rat anti-mouse CD45-FITC	BioLegend	103137	30-F11
rat anti-mouse CD105-BV510	BD Biosciences	740188	MJ7/18
rat anti-mouse CD200-APC-R700	BD Biosciences	565546	OX-90
rat anti-mouse Epcam-FITC	BioLegend	118207	G8.8
rat anti-mouse PDGFRa-PE	eBioscience	12-1401-81	APA5
rat anti-mouse Sca1-BV510	BD Biosciences	565507	D7
rat anti-mouse Thy1-PE-Cy7	eBioscience	25-0902-81	53-2.1
Immunofluorescence			
mouse anti-human $\alpha$ -SMA	Agilent	M085129-2	1A4
rabbit anti-human Col15a1	Abcam	ab58717	N/A

**Table S2: Primers used for qPCR.**

Gene	GenBank	Forward primer	Reverse primer
<b>Mouse</b>			
<i>Acta2</i>	NM_007392.3	CTGTCAGGAACCCTGA	TACTCCCTGATGTCT
<i>Bmp10</i>	NM_009756.3	CGGAGCTTCAAGAACG	TGGTGAGGGATAGAC
<i>Col1a1</i>	NM_007742.4	GCTCCTCTTAGGGGCC	CCACGTCTCACCATT
<i>Col1a2</i>	NM_007743.3	CAAGCATGTCTGGTTA	AGGACACCCCTTCTA
<i>Col15a1</i>	NM_009928.3	AGATTTACGGGTTCCA	CAACGTGTGATTCTTT
<i>Hgf</i>	NM_001289458.1	CACCCCTTGGGAGTAT	GGGACATCAGTCTCA
<i>Hprt</i>	NM_013556.2	TCAAATCCCTGAAGTA	AGGACCTCTCGAAGT
<i>Igfbp6</i>	NM_008344.3	GGGCTCTATGTGCCAA	CCTGCGAGGAACGAC
<i>Loxl1</i>	NM_010729.3	TATGCCTGCACCTCTC	TGTCCGCATTGTATG
<i>Masp1</i>	NM_001359083.1	CCTACAGAGCGGCAG	GGCTCGATTTTCCCG
<i>Megf9</i>	NM_172694.2	ACAACCGGTCTGATAG	TTTGCATTCTTCACAG
<i>Mgp</i>	NM_008597.4	TCACGAAAGCATGGAG	GCTGAGGGGACATAA
<i>Nt5e</i>	NM_001204813	CCATTGATGAGAAGAA	GTCAAATGTCCCTCC
<i>Plac8</i>	NM_139198.3	TGTGTGCCAACTCAAG	GTTGAGCTTCTTCAG
<i>Slit2</i>	NM_178804.5	ATCTGCCTGAGACCAT	CGTCTAAGCTTTTTGT
<i>Thy1</i>	NM_009382.3	GAAAACTGCGGGCTTC	CCAAGAGTTCCGACT
<i>vWf</i>	NM_011708.4	CTACCTAGAACGCGAG	CATCGATTCTGGCCG
<i>18S</i>	NR_003278.3	GAGCGAAAGCATTTC	GGCATCGTTTATGGT
<b>Human</b>			
<i>ACTA2</i>	NM_001613.4	GACAATGGCTCTGGGC	CTGTGCTTCGTCACC
<i>COL1A</i>	NM_000088.4	GTGCGATGACGTGATC	CGGTGGTTTCTTGGT
<i>HPRT</i>	NM_000194.3	TAATTGGTGGAGATGA	TGCCTGACCAAGGAA
<i>SLIT2</i>	NM_004787.4	GTGTTTCGTGCCAGCTA	TTCCATCATTGATTGT
<i>vWF</i>	NM_000552.5	CTCCCACGCCTACATC	GCGGTGATCTTGCT



**Table S3: Probes used for FISH.**

Probe name	Sequence
Scrambled	5' TAGCGAATCTCAGGCAAG – AT 633 3'
SLIT2-1	5' GGACCACGTCTCGCAGCGGTTCTGCGGC – 6 Fam 3'
SLIT2-2	5' CACGGGTCCTTATAGGGGGCGTTGTGGC – 6 Fam 3'
SLIT2-3	5' CTTACGGTTGTTCTATTTGACGGAAGC – 6 Fam 3'
SLIT2-4	5' CACCTGCTCCAACCTCTTTCACCACTTCACGC – 6 Fam 3'

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**Table S4: Differentially expressed genes in each scRNAseq cluster compared to all others.**

Tab 1: All differentially expressed genes classified according to Seurat R toolkit;

Tab 2: Top 10 differentially expressed genes classified according to average log Fold-Change (avg\_logFC).

(Provided separately).

**Table S5: GO enrichment of differentially expressed genes in the scRNAseq clusters of Fibroblasts (Fib), Hepatic stellate cells (HSCs), and Vascular smooth muscle cells (VSMCs).**

(Provided separately).

**Table S6: Differential gene expressions in bulk RNAseq analyses, between PMSCs or HSCs and their myofibroblastic progenies after 3 days (-MFs-3d) or 7 days (-MFs-7d) in primary culture.**

Genes (ID) are classified according to average log Fold-Change (logFC) from 4 replicates per condition.

(Provided separately)

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