Table S1: Chromosomal regions of pQTLs determined by single QTL scans and CIM

| Phenotype | $\begin{aligned} & \hline \text { pQTL } \\ & \text { (Chr) } \end{aligned}$ | $\begin{gathered} \hline \text { LRS } \\ (\text { max }) \end{gathered}$ | $\begin{gathered} \hline \text { SNP } \\ (\max ) \end{gathered}$ | 1.5 LOD support interval (Mb) | Additive allele effect <br> (-) C57BL/6J / <br> (+) DBA/2J | Dataset |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Collagen area | 2 | 14.0 | rs638488-rs3664044 | 167.7-179.3 | 0.303 | male |
| Collagen area | 3 | 12.5 | rs13476999 - mCV24211562 | 12.0-20.6 | 0.331 | female |
| Collagen area | 3 | 15.0 | rs13477485-rs13477494 | 146.1-157.0 | 0.320 | female |
| Collagen area | 5* | 18.1 | mCV23582150 - rs6392739 | 3.1-20.1 | 0.323 | male/both |
| Collagen area | 5* | 23.1 | rs3678577-rs6167407 | 85.1-97.9 | 0.451 | female/both |
| Collagen area | 7 | 12.5 | gnf07.050.858 - rs6166250 | 55.3-74.2 | 0.340 | female |
| Collagen area | 7 | 12.5 | rs13479559-rs3659292 | 141.7-149.0 | 0.302 | male |
| Collagen area | 9 | 14.4 | D9Mit227-rs13480169 | 41.1-46.6 | -0.350 | female |
| Collagen area | 13 | 16.7 | rs6411274-rs3682400 | 45.5-51.7 | 0.251 | male/both |
| Collagen area | 15 | 13.9 | rs3710055-rs13482702 | 82.3-95.8 | 0.265 | male |
| Collagen area | 19 | 13.3 | rs13483649-rs8257607 | 36.2-52.2 | 0.288 | male |
| Collagen area | X | 17.1 | gnfX.023.534 - gnfX.026.801 | 25.2-41.9 | 0.357 | male |
| Hyp | 4* | 17.4 | rs6254381-rs13477745 | 55.1-73.9 | 58.957 | female/both |
| Hyp | 7* | 16.3 | rs3703247-rs8255275 | 52.8-56.7 | 56.761 | female/both |
| Hyp | 5 | 14.4 | rs13478413-rs6228198 | 82.8-103.9 | 49.673 | female/both |
| Hyp | 12* | 25.0 | rs3716547-rs13481511 | 60.5-73.3 | -77.257 | female/both |
| Hyp | X | 12.9 | CEL-X_154048891 | 145.8-162.6 | 53.563 | female |
| F-score | 2 | 13.3 | rs3719468 | 74.9-76.8 | 0.365 | male/both |
| F-score | 2 | 15.2 | rs6305540-rs6402916 | 174.5-181.5 | 0.395 | male/female/ <br> both |
| F-score | 4 | 13.7 | rs4224919 - rs3669806 | 139.1-152.7 | 0.442 | female |
| F-score | 7* | 20.3 | rs3703247-rs8255275 | 48.2-53.7 | 0.562 | male/both |
| F-score | 8 | 12.8 | rs3699325-rs13479628 | 9.13-18.42 | 0.415 | male |
| F-score | 11 | 12.1 | rs13481150-rs3688955 | 79.8-93.5 | 0.372 | male/both |
| F-score | 13 | 16.7 | rs3688207-rs429721 | 44.2-52.7 | 0.430 | male/both |
| F-score | 15 | 12.9 | rs13482436-rs4139555 | 9.4-15.3 | 0.396 | female |
| F-score | 15 | 16.7 | rs 13482547-rs3692040 | 44.2-51.7 | 0.406 | female |
| F-score | 15 | 13.8 | rs13482723-3664692 | 92.8-95.9 | 0.395 | male |
| F-score | 17* | 22.0 | rs13483077-rs13483081 | 64.9-71.1 | 0.516 | female |

## Abbreviations and definitions:

pQTL (chr): chromosomal position of phenotype linked quantitative trait locus; (*): indicates a QTL significantly associated with the respective phenotype; LRS (max): likelihood ratio statistic, maximum association between genotype and phenotype variation; SNP (max): single nucleotide polymorphism with maximum LRS in QTL region; 1.5 LOD support interval (Mb): chromosomal region in Megabases spanning QTL position; Additive allele effect: estimate of a change in the average phenotype by substitution of one parental allele by another at a given marker position; $(-)$ values indicate an increase of phenotype by C57BL/6J allele, (+) values indicate an increase of phenotype by DBA/2J allele. Dataset: dataset in which the QTL was identified; Hyp: hydroxyproline; CIM: composite interval mapping.

Table S2: Overlapping pQTL regions for different fibrosis phenotypes determined by single QTL scans and CIM

| $\begin{aligned} & \text { pQTL } \\ & \text { (Chr) } \end{aligned}$ | Phenotype | $\begin{gathered} \hline \text { LRS } \\ (\max ) \end{gathered}$ | $\begin{gathered} \hline \text { SNP } \\ (\max ) \end{gathered}$ | $\begin{gathered} \hline 1.5 \mathrm{LOD} \\ \text { support interval } \\ (\mathrm{Mb}) \\ \hline \end{gathered}$ | Additive allele effect <br> (-) C57BL/6J <br> (+) DBA/2J | Dataset |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 2 | Collagen area | 14.0 | rs638488-rs3664044 | 167.7-179.3 | 0.303 | male |
|  | F-score | 15.2 | rs6305540-rs6402916 | 174.5-181.5 | 0.395 | male/female/both |
| 5 | Hyp | 14.4 | rs13478413-rs6228198 | 82.8-103.9 | 49.673 | female/both |
|  | Collagen area | 23.1 | rs3678577-rs6167407 | 85.1-97.9 | 0.451 | female/both |
| 7 | F-score | 20.3 | rs3703247-rs8255275 | 48.2-53.7 | 0.562 | male/both |
|  | Hyp | 16.3 | rs3703247-rs8255275 | 52.8-56.7 | 56.761 | female/both |
|  | Collagen area | 12.5 | gnf07.050.858-rs6166250 | 55.3-74.2 | 0.34 | female |
| 13 | F-score | 16.7 | rs3688207-rs429721 | 44.2-52.7 | 0.43 | male/both |
|  | Collagen area | 16.7 | rs6411274-rs3682400 | 45.5-51.7 | 0.251 | male/both |
| 15 | Collagen area | 13.9 | rs3710055-rs13482702 | 82.3-95.8 | 0.265 | male |
|  | F-score | 13.8 | rs13482723-3664692 | 92.8-95.9 | 0.395 | male |

## Abbreviations and definitions:

pQTL (chr): chromosomal position of quantitative trait locus; LRS (max): likelihood ratio statistic, maximum association between genotype and phenotype variation; SNP (max): single nucleotide polymorphism with maximum LRS in QTL region; 1.5 LOD support interval (Mb): chromosomal region in Megabases spanning QTL position; Additive allele effect: estimate of a change in the average phenotype by substitution of one parental allele by another at a given marker position; $(-)$ values indicate an increase of phenotype by C57BL/6J allele, $(+)$ values an increase of phenotype by DBA/2J allele; Dataset: dataset in which the QTL was identified; Hyp: hydroxyproline; CIM: composite interval mapping.

Table S3: Candidate genes of hepatic fibrogenesis

|  |  |  | cisQTL | Gene regulation |  |  |  | Gene to phenotype correlation |  |  | Selection criteria |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Chr) | $\begin{aligned} & \text { Gene } \\ & \text { symbol } \end{aligned}$ | Description | $\begin{gathered} \text { Location } \\ \text { (Chr @ Mb) } \end{gathered}$ | $\begin{gathered} \text { Mean } \\ \text { expression } \end{gathered}$ | $\begin{aligned} & \hline \text { Max } \\ & \text { LRS } \end{aligned}$ | $\begin{gathered} \hline \text { Max LRS } \\ \text { location } \\ \text { (Chr @ Mb) } \\ \hline \end{gathered}$ | $\begin{gathered} \text { Collagen } \\ \text { area } \end{gathered}$ | Hyp | F-score | $\begin{gathered} \hline \text { 1.Correlated } \\ \text { with } \\ \text { phenotype } \\ \hline \end{gathered}$ | 2. Fibrosis specific regulation | 3.nsSNP |
| 1 | 2 | Ogfr | opioid growth factor receptor | Chr 2 @ 180.3 | 10.1 | 23.6 | Chr2: 180.8 | -0.027 | -0.222 | -0.158 |  |  | - |
| 2 |  | Arfipl | ADP-ribosylation factor related protein 1 | Chr 2 @ 181.1 | 9.1 | 29.8 | Chr2: 180.8 | 0.116 | 0.216 | 0.416* | - |  |  |
| 3 | 4 | BC026590 | cDNA sequence BC026590 | Chr 4 @ 56.8 | 9.3 | 15.5 | Chr4: 56.5 | -0.007 | -0.383* | -0.181 | - | - |  |
| 4 |  | Susdl | sushi domain containing 1 | Chr 4 @ 59.3 | 8.6 | 17.4 | Chr4: 58.4 | 0.002 | -0.503* | 0.051 | - | - | - |
| 5 |  | Mup20 | major urinary protein 20 | Chr 4 @ 61.7 | 13.0 | 16.8 | Chr4: 58.4 | -0.075 | -0.242 | -0.001 |  | - |  |
| 6 |  | Zfp37 | zinc finger protein 37 | Chr 4 @ 61.9 | 7.3 | 15.7 | Chr4: 62.4 | -0.059 | -0.188 | -0.122 |  | - | - |
| 7 |  | Slc31a2 | solute carrier family 31, meer 2 | Chr 4 @ 61.9 | 10.8 | 20.3 | Chr4: 63.3 | -0.005 | -0.391* | -0.311 | - | - |  |
| 8 |  | Tnc | tenascin C | Chr 4 @ 63.6 | 8.0 | 13.2 | Chr4: 65.6 | 0.120 | -0.332 | -0.291 |  | - |  |
| 9 |  | Rasef | RAS and EF hand domain containing | Chr 4 @ 73.4 | 6.4 | 13.7 | Chr4: 69.8 | -0.180 | -0.414* | 0.039 | - | - |  |
| 10 | 5 | Mtch2 | mitochondrial carrier homolog 2 (C.elegans) | Chr 5 @ 81.3 | 12.0 | 16.5 | Chr5: 82.8 | -0.482* | -0.317 | -0.234 | - | - |  |
| 11 |  | MobklIa | MOB1, Mps One Binder kinase activator-like 1A (yeast) | Chr 5 @ 89.1 | 10.4 | 12.1 | Chr5: 90.5 | -0.079 | -0.176 | 0.334 |  | - |  |
| 12 |  | Cox18 | COX18 cytochrome c oxidase assely homolog (complex iV assely) | Chr 5 @ 90.6 | 11.8 | 59.7 | Chr5: 94.2 | 0.402* | 0.397 | 0.127 | $\bullet$ |  | - |
| 13 |  | Afm | afamin | Chr 5 @ 90.9 | 11.3 | 15.8 | Chr5: 90.5 | 0.257 | 0.429* | 0.336 | - | - | - |
| 14 |  | Ereg | epiregulin | Chr 5 @ 91.5 | 7.2 | 13.0 | Chr5: 82.8 | -0.278 | -0.405* | -0.087 | - | - |  |
| 15 |  | Thap6 | THAP domain containing 6 | Chr 5 @ 92.4 | 8.6 | 54.3 | Chr5: 90.5 | -0.356 | -0.424* | -0.105 | - | - |  |
| 16 |  | Naaa | N -acylethanolamine acid amidase | Chr 5 @ 92.7 | 9.5 | 13.8 | Chr5: 94.2 | -0.075 | -0.425* | -0.389 | - |  | - |
| 17 |  | Sdad1 | SDA1 domain containing 1 | Chr 5 @ 92.7 | 7.6 | 13.3 | Chr5: 94.2 | 0.369* | 0.247 | 0.249 | - |  | - |
| 18 |  | Cxcllo | chemokine (C-X-C motif) ligand 10 | Chr 5 @ 92.8 | 9.7 | 13.7 | Chr5: 98.2 | -0.115 | -0.070 | 0.045 |  | - |  |
| 19 |  | Sept11 | septin 11 | Chr 5 @ 93.5 | 10.2 | 21.5 | Chr5: 85.1 | 0.199 | 0.068 | -0.222 |  | - |  |
| 20 |  | Antxr 2 | anthrax toxin receptor 2 | Chr 5 @ 98.3 | 10.4 | 24.7 | Chr5: 98.2 | -0.056 | -0.527* | -0.165 | - |  |  |
| 21 | 7 | Klkl | kallikrein 1 | Chr 7 @ 51.2 | 8.6 | 42.2 | Chr7: 48.2 | -0.047 | -0.438* | -0.169 | - | - |  |
| 22 |  | Klklb26 | kallikrein 1-related petidase b26 | Chr 7 @ 51.3 | 8.0 | 15.2 | Chr7: 53.3 | -0.233 | -0.413* | -0.086 | - | - | - |
| 23 |  | Klklb21 | kallikrein 1-related peptidase b21 | Chr 7 @ 51.4 | 7.8 | 39.6 | Chr7: 48.2 | -0.017 | -0.449* | -0.111 | - | - | - |
| 24 |  | Klklb22 | kallikrein 1-related peptidase b22 | Chr 7 @ 51.4 | 6.3 | 38.4 | Chr7: 48.2 | -0.027 | -0.361* | -0.032 | - | - | - |
| 25 |  | Klklb4 | kallikrein 1-related pepidase b4 | Chr 7 @ 51.5 | 9.5 | 39.0 | Chr7: 48.2 | -0.085 | -0.473* | -0.181 | - |  |  |
| 26 |  | Klklb5 | kallikrein 1-related peptidase b5 | Chr 7 @ 51.5 | 6.8 | 18.4 | Chr7: 48.2 | -0.109 | -0.370* | -0.305 | - | - | - |
| 27 |  | Josd2 | Josephin domain containing 2 | Chr 7 @ 51.7 | 9.6 | 16.1 | Chr7: 48.2 | -0.183 | -0.165* | -0.141 |  | - |  |
| 28 |  | NrIh2 | nuclear receptor subfamily 1 , group H , meer 2 | Chr 7 @ 51.8 | 10.6 | 23.4 | Chr7: 52.8 | 0.031 | -0.207 | 0.066 |  | - |  |
| 29 |  | Napsa | napsin A aspartic peptidase | Chr 7 @ 51.8 | 8.0 | 19.7 | Chr7: 48.2 | 0.069 | -0.489* | -0.271 | - | $\bullet$ | - |
| 30 |  | Hsdl7bl4 | hydroxysteroid (17-beta) dehydrogenase 14 | Chr 7 @ 52.8 | 7.4 | 17.9 | Chr7: 47.6 | 0.114 | 0.424* | 0.265 | $\bullet$ | - | - |
| 31 |  | Abcc6 | ATP-binding cassette, sub-family C (CFTR/MRP), meer 6 | Chr 7 @ 53.2 | 10.0 | 26.3 | Chr7: 53.3 | -0.226 | $-0.316$ | -0.276 | $\bullet$ |  | - |
| 32 |  | Nomol | nodal modulator 1 | Chr 7 @ 53.3 | 10.5 | 23.0 | Chr7: 48.2 | -0.110 | -0.483* | -0.219 | - | - | - |
| 33 |  | Gm9860 | predicted gene 9860 | Chr7 @ 53.5 | 7.2 | 18.2 | Chr7: 52.8 | -0.177 | -0.360* | -0.204 | - | - |  |
| 34 |  | Tubgcp 5 | tubulin, gamma complex associated protein 5 | Chr 7 @ 63.0 | 8.1 | 32.3 | Chr7: 56.7 | 0.209 | 0.321 | 0.041 |  | - | $\bullet$ |
| 35 |  | Fanl | FANCD2/FANCI-associated nuclease 1 | Chr 7 @ 71.5 | 8.0 | 48.9 | Chr7: 63.8 | -0.363* | -0.245 | -0.204 | - | - | - |
| 36 |  | Mphosph10 | M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) | Chr 7 @ 71.5 | 8.3 | 22.7 | Chr7: 63.8 | 0.249 | 0.184 | 0.351 |  |  | - |
| 37 |  | Mcee | methylmalonyl CoA epimerase | Chr 7 @ 71.5 | 12.5 | 15.1 | Chr7: 63.8 | -0.492* | 0.010 | -0.047 | - | - |  |
| 38 |  | Ndnl2 | necdin-like 2 | Chr 7 @ 72.0 | 9.1 | 20.0 | Chr7: 63.8 | 0.396* | 0.258 | 0.315 | - |  |  |
| 39 |  | Snrpal | small nuclear ribonucleoprotein polypeptide $\mathrm{A}^{\prime}$ | Chr 7 @ 73.2 | 9.3 | 25.0 | Chr7: 73.3 | 0.263 | 0.192 | 0.030 |  | - |  |
| 40 |  | Asb7 | ankyrin repeat and SOCS boxcontaining 7 | Chr 7 @ 73.8 | 8.3 | 27.2 | Chr7: 73.3 | -0.136 | -0.268 | -0.053 |  | $\bullet$ | - |
| 41 |  | Adamts 17 | a disintegrin-like and metallopeptidase (reprolysin type) with throospondin type 1 motif, 17 | Chr 7 @ 74.2 | 7.2 | 17.8 | Chr7: 73.3 | 0.171 | 0.132 | 0.116 |  | - | - |
| 42 | 12 | Gm71 | predicted gene 71 | Chr 12 @ 70.7 | 8.5 | 34.5 | Chr 12: 70.7 | -0.217 | -0.360 | -0.025 | - | - |  |
| 43 |  | Atp5s | ATP synthase, $\mathrm{H}+$ transporting, mitochondrial F0 complex, subunit s | Chr 12 @ 70.8 | 7.9 | 20.3 | Chr 12: 70.7 | 0.090 | 0.220 | 0.227 |  | - |  |
| 44 |  | Nin | ninein | Chr 12 @ 71.1 | 8.5 | 18.2 | Chr 12: 70.7 | -0.180 | -0.498* | -0.290 | - | $\bullet$ | - |
| 45 |  | Dactl | dapper homolog 1, antagonist of betacatenin (xenopus) | Chr 12 @ 72.4 | 8.0 | 15.2 | Chr 12: 70.7 | 0.249 | 0.244 | 0.186 |  | - | - |
| 46 | 13 | Gm10786 | predicted gene 10786 | Chr 13 @ 45.6 | 9.4 | 16.0 | Chr 13: 45.5 | 0.146 | 0.009 | -0.038 |  | $\bullet$ |  |
| 47 | 15 | Rrp7a | ribosomal RNA processing 7 homolog A (S. cerevisiae) | Chr 15 @ 82.9 | 9.7 | 12.8 | Chr 15: 82.9 | -0.119 | -0.015 | 0.270 |  | $\bullet$ |  |
| 48 |  | Rnu12 | RNA U12, small nuclear | Chr 15 @ 83.0 | 7.5 | 16.6 | Chr 15: 91.7 | -0.222 | 0.128 | 0.035 |  | - |  |
| 49 |  | Cyb5r3 | NADH-cytochrome b5 reductase 3 (diaphorase-1, methemoglobinemia) | Chr 15 @ 83.0 | 13.5 | 60.8 | Chr 15: 82.9 | 0.102 | -0.112 | -0.221 |  | - |  |
| 50 |  | Tspo | translocator protein | Chr 15 @ 83.4 | 10.8 | 18.2 | Chr 15: 82.9 | -0.263 | -0.019 | 0.056 |  | - |  |
| 51 |  | Ttc38 | tetratricopeptide repeat domain 38 | Chr 15 @ 85.7 | 10.4 | 56.6 | Chr 15: 82.9 | 0.289 | 0.128 | -0.011 |  | - |  |
| 52 |  | Fam19a5 | family with sequence similarity 19 , meer A5 | Chr 15 @ 87.4 | 8.3 | 23.5 | Chr 15: 87.8 | -0.329 | -0.139 | 0.144 |  | - |  |
| 53 |  | Rabl2 | RAB, meer of RAS oncogene familylike 2 | Chr 15 @ 89.4 | 8.2 | 52.8 | Chr15: 87.8 | 0.167 | -0.060 | -0.201 |  | $\bullet$ |  |
| 54 |  | Cpne8 | copine VIII | Chr 15 @ 90.3 | 7.8 | 21.4 | Chr 15: 90.6 | -0.024 | -0.191 | -0.048 |  | - |  |
| 55 |  | Lrrk2 | leucine-rich repeat kinase 2 | Chr 15 @ 91.5 | 7.9 | 17.2 | Chr15: 90.8 | 0.295 | 0.208 | -0.402* | - | - |  |

## Abbreviations and definitions:

cisQTG: genes located in the pQTL region (regulated by markers within a 10 Mb distance) with LRS $\geq 12.0$; Location ( Chr @ Mb): Chromosomal position in Megabases of candidate gene; Mean expression: mean expression value determined across all BXD lines; LRS (max): likelihood ratio statistic, maximum association detected in pQTL analysis; Max LRS location (Chr @ Mb): Chromosomal position of regulatory genetic marker with maximum association to cisQTG; Gene to phenotype correlation: Pearson correlation coefficient r with a (-) negative or ( + ) positive correlation of the cisQTG to fibrosis phenotypes; $(*)$ : indicate a significant correlation ( $\mathrm{p}<0.05$ ); Selection criteria: $(\bullet)$ indicates that the gene fulfills the following selection criteria for candidate genes: 1) significant correlation to phenotype, 2) differentially regulated during fibrosis as compared with healthy animals, or 3) non-synonymous single nucleotide polymorphism (nsSNP) in coding region of the gene.

