

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

Phenotype	pQTL (Chr)	LRS (max)	SNP (max)	1.5 LOD support interval (Mb)	Additive allele effect (-) C57BL/6J / (+) 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/ 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	rs13482547 - 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

pQTL (Chr)	Phenotype	LRS (max)	SNP (max)	1.5 LOD support interval (Mb)	Additive allele effect (-) C57BL/6J (+) 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
	F-score	20.3	rs3703247-rs8255275	48.2 - 53.7	0.562	male/both
7	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.



**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 ( $p < 0.05$ ); **Selection criteria:** (●) 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.