



Figure S1 Construction and verification of the MMP9 rs9509 mutant plasmid. (A) Information of the vector of the mutant plasmid. (B) Results of the verification of the MMP9 rs9509 mutant plasmid by polymerase chain reaction. Lane 1: blank control (ddH₂O). Lane 2: blank control (vector). Lane 3: positive control (glyceraldehyde-3-phosphate dehydrogenase). Lane 4: Marker. Lane 5-12: converter 1#-8#. MMP, matrix metalloproteinase.

Table S1 Demographic information of the included participants in our study

Characteristics	Graft fibrosis group (n=69)	Control group (n=131)	P value
Age, years, mean ± SD	40.67±2.96	41.29±1.92	NS
Sex (male/female)	42/27	82/49	NS
PRA before transplantation (%)	0.00	0.00	NS
HLA matching, mean ± SD	1.05±1.26	0.98±1.17	NS
Type of donor (living-related/DCD)	6/63	18/113	NS

SD, standard deviation; NS, not significant; PRA, panel reactive antibody; HLA, human leukocyte antigen; DCD, donation after cardiac death.

Table S2 The genetic information of the SNPs detected in this study

Chromosome	Location	Wild-type allele	Mutation allele	Gene	Function	Serial number
chr11	102666316	T	C	<i>MMP1</i>	Exonic	rs470558
chr11	102649856	T	C	<i>MMP10</i>	Intronic	rs470263
chr11	102650246	G	A	<i>MMP10</i>	Exonic	rs17860949
chr16	55516767	G	A	<i>MMP2</i>	Intronic	rs1030868
chr16	55517162	A	G	<i>MMP2</i>	Intronic	rs1477017
chr16	55519535	G	C	<i>MMP2</i>	Exonic	rs1132896
chr16	55519607	C	T	<i>MMP2</i>	Exonic	rs1053605
chr16	55519701	C	T	<i>MMP2</i>	Intronic	rs17859889
chr16	55519832	T	G	<i>MMP2</i>	Intronic	rs111278338
chr16	55523705	T	C	<i>MMP2</i>	Exonic	rs243849
chr16	55523782	G	C	<i>MMP2</i>	Intronic	rs12599775
chr16	55523902	G	T	<i>MMP2</i>	Intronic	rs17859922
chr16	55525913	G	C	<i>MMP2</i>	Intronic	rs243846
chr16	55527026	A	T	<i>MMP2</i>	Intronic	rs11640428
chr16	55527113	G	A	<i>MMP2</i>	Exonic	rs2287074
chr16	55527298	G	A	<i>MMP2</i>	Intronic	rs243843
chr16	55530762	G	T	<i>MMP2</i>	Intronic	rs171498
chr16	55530772	T	G	<i>MMP2</i>	Intronic	rs243838
chr16	55531030	C	T	<i>MMP2</i>	Intronic	rs17859975
chr16	55532120	G	A	<i>MMP2</i>	Intronic	rs2287075
chr16	55532458	T	C	<i>MMP2</i>	Intronic	rs2287076
chr16	55536622	C	T	<i>MMP2</i>	Intronic	rs243835
chr16	55536687	A	G	<i>MMP2</i>	Splicing	rs243834
chr16	55536727	C	T	<i>MMP2</i>	Exonic	rs14070
chr16	55539191	C	G	<i>MMP2</i>	Intronic	rs243832
chr11	102709425	A	G	<i>MMP3</i>	Exonic	Chr11:102709425
chr11	102709522	T	A	<i>MMP3</i>	Intronic	Chr11:102709522
chr11	102711338	T	C	<i>MMP3</i>	Intronic	Chr11:102711338
chr11	102713046	C	T	<i>MMP3</i>	Intronic	Chr11:102713046
chr11	102713465	A	G	<i>MMP3</i>	Exonic	Chr11:102713465
chr11	102713620	T	C	<i>MMP3</i>	Exonic	Chr11:102713620
chr20	44638781	A	G	<i>MMP9</i>	Intronic	rs3918251
chr20	44639692	G	T	<i>MMP9</i>	Splicing	rs2274755
chr20	44640225	A	G	<i>MMP9</i>	Exonic	rs17576
chr20	44640391	C	T	<i>MMP9</i>	Splicing	rs3918254
chr20	44640575	A	G	<i>MMP9</i>	Intronic	rs2236416
chr20	44642406	G	C	<i>MMP9</i>	Exonic	rs2250889
chr20	44642833	A	C	<i>MMP9</i>	Exonic	rs13969
chr20	44643111	G	A	<i>MMP9</i>	Exonic	rs17577
chr20	44644965	G	A	<i>MMP9</i>	Exonic	rs13925
chr20	44645153	T	C	<i>MMP9</i>	Utr3	rs9509

SNPs, single-nucleotide polymorphisms; MMP, matrix metalloproteinase.

Table S3 Results of the multiple inheritance model analysis using general linear models adjusted by confounding factors

SNPs	Codominant	Dominant	Recessive	Overdominant	Log-additive
rs243849	0.220393	0.087684	0.417312	0.170904	0.088015
rs243838	0.255049	0.106782	0.417312	0.203766	0.102959
rs3918254	0.25433	0.243541	0.165771	0.432447	0.152375
rs12599775	0.357842	0.222657	0.309334	0.351358	0.169048
rs2287075	0.357842	0.222657	0.309334	0.351358	0.169048
rs470263	0.175916	0.12944	0.412819	0.090871	0.200515
rs243835	0.411849	0.190254	0.503278	0.389942	0.200606
rs243834	0.411849	0.190254	0.503278	0.389942	0.200606
rs243832	0.411849	0.190254	0.503278	0.389942	0.200606
Chr11.102709425	0.333776	0.885557	0.148333	0.452751	0.431614
Chr11.102713620	0.333776	0.885557	0.148333	0.452751	0.431614
rs171498	0.788821	0.498979	0.740657	0.612026	0.501166
Chr11.102713465	0.298527	0.932643	0.148333	0.326251	0.54053
rs1030868	0.521779	0.898947	0.268753	0.579418	0.550946
Chr11.102709522	0.490034	0.459217	0.412819	0.375489	0.566727
Chr11.102713046	0.490034	0.459217	0.412819	0.375489	0.566727
rs2274755	0.877018	0.614495	0.811599	0.674247	0.612582
rs2236416	0.877018	0.614495	0.811599	0.674247	0.612582
rs1132896	0.115272	0.25304	0.209927	0.074817	0.615429
Chr11.102711338	0.367137	0.860899	0.20295	0.326251	0.637736
rs1477017	0.486985	0.956649	0.268753	0.460553	0.645083
rs470558	0.358902	0.88675	0.154649	0.832029	0.660505
rs17577	0.913405	0.683513	0.811599	0.748531	0.670709
rs13925	0.913405	0.683513	0.811599	0.748531	0.670709
rs3918251	0.946079	0.744491	0.958126	0.777409	0.800454
rs17576	0.963295	0.873979	0.792019	0.997059	0.810855
rs17859922	0.805175	0.970225	0.517929	0.87908	0.839698
rs17859889	0.787249	0.933456	0.517929	0.783833	0.927627
rs111278338	0.787249	0.933456	0.517929	0.783833	0.927627
rs14070	0.890442	0.825938	0.740657	0.67904	0.975255
rs17859975	0.759119	0.840024	0.517929	0.693669	0.984919
rs2250889	0.78695	0.763555	0.633295	0.548008	0.986081
rs17860949	0.79562	NA	NA	NA	NA
rs13969	0.143072	0.124977	0.104802	0.371857	0.061997

SNPs, single-nucleotide polymorphisms.

Table S4 Association between SNPs and the severity of IFTA

SNPs	Likelihood ratio	P value
rs243846	0.37	0.99
rs1053605	7.94	0.094
rs11640428	2.74	0.60

SNPs, single-nucleotide polymorphisms; IFTA, interstitial fibrosis and tubular atrophy.