

**Supplementary Material for manuscript CIRCULATIONAHA/2008/834986**

Genome-wide Association Scan Identifies Variants near *Matrix Metalloproteinase (MMP)* Genes on Chromosome 11q21-22 Strongly Associated with Serum MMP-1 Levels

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**Supplementary Figure Legends**

**Figure S1.** Linkage disequilibrium structure of the 179 genome-wide significant SNPs on chromosome 11q: 95,569,593-107,024,176bp region. (above:  $|D'|$ ; bottom:  $r^2$ )

**Figure S2.** Results of SNP association with MMP-1 levels on chromosome 11q: 95,569,593-107,024,176 bp region in the forward regression model building. *P*-values of SNPs after including (A) rs495366, (B) rs495366 and rs12289128, and (C) rs495366, rs12289128 and rs11226373, in the model.

**Table S1.** Information of the 179 SNPs significantly associated with MMP-1 levels, ordered by physical position on chromosome 11

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs523519	11	95569593	q21	A/C	0.391	0.815	99.9	0.23	0.062	3.93E-10	4.57E-07
rs10501846	11	95592312	q21	G/T	0.266	0.344	99.5	-0.21	0.044	5.28E-08	1.10E-05
rs12417347	11	95596852	q21	G/A	0.267	0.309	99.9	-0.21	0.043	8.88E-08	1.55E-05
rs11212360	11	95972541	q21	T/C	0.216	0.988	98.6	0.26	0.036	4.07E-09	1.95E-06
rs4320978	11	95977664	q21	G/A	0.218	0.672	95.1	0.26	0.037	3.27E-09	1.68E-06
rs3019723	11	96086712	q21	C/T	0.195	0.916	99.9	-0.26	0.063	3.04E-09	1.93E-06
rs3019692	11	96106466	q21	A/C	0.195	0.895	99.7	-0.26	0.063	3.33E-09	2.06E-06
rs1439528	11	96115783	q21	A/G	0.357	0.157	95.9	-0.22	0.058	5.82E-09	2.79E-06
rs11226865	11	96888090	q22.1	A/G	0.155	0.197	99.7	0.31	0.039	4.64E-10	4.67E-07
rs1815913	11	97357708	q22.1	C/T	0.471	0.271	100.0	0.20	0.044	6.14E-09	2.56E-06
rs11213924	11	97450907	q22.1	A/G	0.175	0.084	99.5	-0.33	0.070	1.71E-12	1.19E-08
rs3018249	11	97540643	q22.1	T/G	0.255	0.098	100.0	-0.27	0.057	2.61E-11	6.88E-08
rs7939072	11	97635266	q22.1	T/C	0.177	0.101	100.0	-0.33	0.073	6.31E-13	6.19E-09
rs2155912	11	97684699	q22.1	A/G	0.298	0.756	100.0	-0.20	0.035	9.34E-08	1.55E-05
rs10790140	11	97937406	q22.1	G/A	0.429	0.988	99.7	0.20	0.039	7.35E-08	1.33E-05
rs4342998	11	97953696	q22.1	A/C	0.377	0.121	97.7	0.22	0.042	1.89E-08	5.43E-06
rs11217332	11	98261448	q22.1	T/C	0.299	0.488	99.4	0.21	0.036	8.09E-08	1.41E-05
rs1601690	11	98266953	q22.1	C/T	0.260	0.035	96.9	0.22	0.038	8.84E-08	0.000015
rs11217456	11	98277793	q22.1	T/C	0.257	0.110	100.0	0.23	0.042	2.80E-08	7.05E-06
rs7944622	11	98279344	q22.1	A/G	0.257	0.092	98.7	0.22	0.040	6.59E-08	1.25E-05
rs7947532	11	98279373	q22.1	C/G	0.257	0.110	100.0	0.23	0.042	2.80E-08	7.05E-06
rs11607090	11	98620980	q22.1	A/T	0.233	0.513	99.2	-0.22	0.056	8.09E-08	1.71E-05

**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs2466912	11	98892027	q22.1	A/G	0.477	0.896	98.2	-0.26	0.067	1.06E-12	8.37E-09
rs10750313	11	98903530	q22.1	C/T	0.224	0.215	100.0	0.24	0.042	1.64E-08	4.92E-06
rs11220658	11	98994224	q22.1	A/G	0.240	0.394	99.6	0.25	0.047	2.37E-09	1.36E-06
rs666825	11	99079899	q22.1	C/T	0.424	0.478	99.4	-0.28	0.082	2.40E-15	1.51E-10
rs605521	11	99092323	q22.1	A/G	0.492	0.374	99.9	0.21	0.036	6.60E-09	2.68E-06
rs17094347	11	99472494	q22.1	T/C	0.188	0.561	99.6	-0.26	0.047	3.28E-08	8.09E-06
rs1301784	11	99748688	q22.1	G/A	0.460	0.289	98.2	0.21	0.032	1.87E-09	1.20E-06
rs1301783	11	99750118	q22.1	G/A	0.496	0.084	99.2	0.22	0.034	6.58E-11	1.38E-07
rs7930146	11	99835818	q22.1	C/T	0.223	0.187	98.8	-0.29	0.035	2.39E-11	7.13E-08
rs12289202	11	99891485	q22.1	C/T	0.281	0.009	99.9	-0.23	0.017	5.25E-09	2.75E-06
rs7125960	11	99973945	q22.1	C/T	0.422	0.510	98.6	-0.19	0.040	6.09E-08	1.18E-05
rs17710616	11	100001885	q22.1	T/C	0.128	0.674	99.4	-0.37	0.073	5.29E-12	2.70E-08
rs7946913	11	100108524	q22.1	A/G	0.488	0.931	99.5	-0.22	0.040	9.66E-10	7.50E-07
rs7947761	11	100129809	q22.1	G/A	0.409	0.186	98.2	-0.21	0.043	2.65E-08	6.81E-06
rs17095426	11	100143813	q22.1	A/G	0.425	0.568	99.0	-0.21	0.047	1.03E-08	3.68E-06
rs17095429	11	100144512	q22.1	A/C	0.421	0.674	100.0	-0.21	0.050	5.04E-09	2.31E-06
rs626596	11	100282500	q22.1	A/G	0.478	0.458	98.6	-0.20	0.049	1.37E-08	4.57E-06
rs10791432	11	100307731	q22.1	T/C	0.388	0.353	100.0	-0.23	0.067	1.29E-10	2.28E-07
rs543146	11	100319780	q22.1	G/A	0.299	0.110	99.5	0.23	0.058	3.91E-09	2.13E-06
rs7939782	11	100327525	q22.1	C/T	0.481	0.447	99.7	-0.21	0.053	7.41E-09	3.10E-06
rs10895033	11	100329024	q22.1	C/T	0.388	0.353	100.0	-0.23	0.067	1.29E-10	2.28E-07
rs1944432	11	100334730	q22.1	T/C	0.415	0.839	99.6	0.30	0.101	4.87E-17	1.32E-11

**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs10895036	11	100342796	q22.1	C/T	0.387	0.316	99.7	-0.23	0.068	1.18E-10	2.14E-07
rs1893069	11	100352553	q22.1	A/T	0.379	0.110	96.3	-0.22	0.064	5.33E-10	5.80E-07
rs523332	11	100379529	q22.1	G/T	0.359	0.224	99.9	-0.23	0.073	1.25E-10	2.51E-07
rs1145465	11	100488204	q22.1	C/A	0.262	0.708	99.5	-0.22	0.060	1.65E-08	6.07E-06
rs565186	11	100488839	q22.1	C/T	0.260	0.510	99.5	-0.22	0.061	2.44E-08	8.17E-06
rs562894	11	100496895	q22.1	C/T	0.260	0.479	99.5	-0.21	0.057	7.36E-08	1.65E-05
rs538343	11	100561549	q22.1	A/G	0.260	0.541	100.0	-0.22	0.059	3.09E-08	9.32E-06
rs11224733	11	100740407	q22.1	A/T	0.172	0.993	99.7	-0.28	0.053	3.50E-09	1.86E-06
rs1938988	11	100767635	q22.1	C/G	0.177	0.526	96.0	-0.28	0.055	4.85E-09	2.36E-06
rs1938859	11	101052933	q22.1	C/T	0.176	0.843	98.5	0.30	0.053	8.75E-11	1.52E-07
rs17744964	11	101093883	q22.1	A/G	0.343	0.392	97.3	0.21	0.047	6.09E-08	1.25E-05
rs4754019	11	101096133	q22.1	A/G	0.464	0.345	97.4	0.26	0.082	2.95E-13	4.14E-09
rs1939052	11	101131785	q22.1	C/T	0.404	0.127	100.0	0.27	0.094	1.14E-14	5.38E-10
rs10895193	11	101137143	q22.1	A/G	0.174	0.812	96.9	0.31	0.074	6.36E-11	1.55E-07
rs10501990	11	101172368	q22.1	C/T	0.465	0.181	99.9	0.19	0.056	6.42E-08	1.46E-05
rs4754800	11	101172540	q22.1	G/A	0.460	0.122	100.0	0.19	0.057	4.45E-08	1.16E-05
rs10791523	11	101174030	q22.1	G/A	0.465	0.193	100.0	0.19	0.056	6.15E-08	1.42E-05
rs10791524	11	101174095	q22.1	T/C	0.465	0.204	99.9	0.19	0.056	6.25E-08	1.43E-05
rs7101850	11	101176555	q22.1	T/C	0.463	0.222	99.7	0.19	0.056	6.38E-08	1.45E-05
rs10791539	11	101247149	q22.1	A/G	0.451	0.762	100.0	0.20	0.064	9.52E-09	4.42E-06
rs7930416	11	101432254	q22.1	A/G	0.307	0.635	99.5	0.23	0.065	1.52E-09	1.24E-06
rs10791555	11	101433435	q22.1	C/T	0.308	0.742	100.0	0.22	0.065	2.43E-09	1.71E-06

**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs10895257	11	101491854	q22.1	A/G	0.203	0.847	99.9	0.31	0.059	1.19E-12	8.80E-09
rs11602707	11	101550853	q22.1	T/C	0.195	0.413	99.7	0.35	0.076	6.52E-15	2.85E-10
rs10791569	11	101593545	q22.1	C/A	0.398	0.501	99.2	0.22	0.053	4.92E-09	2.34E-06
rs2846836	11	101610883	q22.2	A/G	0.386	0.360	98.5	0.22	0.058	2.05E-09	1.35E-06
rs480846	11	101850444	q22.2	A/G	0.093	0.178	100.0	0.34	0.047	1.19E-08	4.05E-06
rs480950	11	101850484	q22.2	A/C	0.443	0.851	98.6	0.24	0.058	2.69E-11	7.04E-08
rs651853	11	101871180	q22.2	A/G	0.093	0.178	100.0	0.34	0.047	1.19E-08	4.05E-06
rs520100	11	101882479	q22.2	A/G	0.233	0.444	99.9	-0.25	0.035	1.62E-09	1.07E-06
rs2510488	11	101882638	q22.2	A/T	0.232	0.376	99.6	-0.25	0.036	6.21E-10	5.72E-07
rs9651711	11	101933923	q22.2	A/G	0.227	0.481	99.0	0.28	0.057	1.36E-11	4.44E-08
rs1940054	11	101955161	q22.2	C/A	0.378	0.988	100.0	0.26	0.058	1.24E-12	9.06E-09
rs1939008	11	102161633	q22.2	A/G	0.286	0.382	98.7	0.25	0.067	3.04E-11	8.26E-08
rs603050	11	102185439	q22.2	T/C	0.361	0.626	100.0	-0.44	0.170	1.15E-33	1.28E-22
rs11225434	11	102196692	q22.2	C/T	0.384	0.158	98.5	0.39	0.135	9.03E-29	2.07E-19
rs495366	11	102200318	q22.2	A/G	0.361	0.750	98.6	-0.44	0.175	5.73E-34	8.39E-23
rs7926920	11	102203934	q22.2	A/G	0.397	0.074	97.6	0.38	0.122	1.03E-26	4.75E-18
rs650108	11	102213997	q22.2	A/G	0.353	0.823	95.5	-0.42	0.156	9.44E-31	1.06E-20
rs610950	11	102224940	q22.2	C/T	0.119	0.035	95.5	-0.37	0.062	1.08E-10	1.87E-07
rs613804	11	102225631	q22.2	A/G	0.123	0.889	97.4	-0.39	0.055	1.91E-12	1.21E-08
rs11225458	11	102270618	q22.2	T/C	0.206	0.779	98.2	0.38	0.096	8.98E-19	8.09E-13
rs948399	11	102276350	q22.2	C/T	0.203	0.858	99.6	0.38	0.093	4.78E-19	5.27E-13
rs7115014	11	102310143	q22.2	A/G	0.352	0.534	99.7	0.32	0.095	3.99E-19	4.70E-13

**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs10502008	11	102310812	q22.2	T/C	0.161	0.784	98.7	0.33	0.063	3.63E-12	1.87E-08
rs3819089	11	102327943	q22.2	T/C	0.257	0.404	100.0	-0.30	0.081	1.07E-13	2.00E-09
rs671188	11	102334665	q22.2	A/G	0.484	0.359	97.4	0.20	0.044	2.00E-08	5.68E-06
rs659383	11	102336301	q22.2	A/G	0.484	0.263	100.0	0.20	0.043	5.38E-09	2.34E-06
rs2513998	11	102488778	q22.3	C/G	0.347	0.279	99.9	-0.31	0.085	1.88E-16	2.76E-11
rs685395	11	102572670	q22.3	T/C	0.260	0.225	100.0	-0.33	0.100	3.22E-17	9.78E-12
rs664310	11	102590048	q22.3	T/C	0.233	0.097	100.0	0.25	0.040	3.78E-09	1.84E-06
rs11225649	11	102656726	q22.3	A/C	0.205	0.543	99.9	0.30	0.054	5.30E-12	2.37E-08
rs11225721	11	102710521	q22.3	C/T	0.284	0.593	99.0	-0.31	0.085	3.20E-16	3.96E-11
rs10895399	11	102715325	q22.3	A/G	0.283	0.294	99.6	-0.30	0.080	3.91E-15	2.08E-10
rs10895400	11	102715424	q22.3	T/C	0.283	0.628	99.0	-0.31	0.081	1.33E-15	1.01E-10
rs7118092	11	102720958	q22.3	T/C	0.288	0.366	99.2	-0.31	0.086	4.78E-16	5.21E-11
rs7941666	11	102726747	q22.3	A/G	0.230	0.289	100.0	-0.33	0.086	4.07E-15	2.27E-10
rs3910095	11	102754839	q22.3	G/A	0.236	0.188	98.1	-0.33	0.088	3.65E-15	2.16E-10
rs11225755	11	102755298	q22.3	G/A	0.228	0.427	97.2	-0.30	0.074	9.17E-14	1.67E-09
rs7129349	11	102787153	q22.3	A/G	0.230	0.289	100.0	-0.33	0.086	4.07E-15	2.27E-10
rs11225822	11	102850240	q22.3	C/A	0.249	0.166	100.0	-0.33	0.084	2.55E-15	1.60E-10
rs4754974	11	103015011	q22.3	A/C	0.204	0.315	100.0	0.28	0.065	3.96E-10	4.78E-07
rs10791634	11	103029222	q22.3	G/A	0.204	0.315	100.0	0.28	0.065	3.96E-10	4.78E-07
rs11225952	11	103029324	q22.3	T/G	0.204	0.315	100.0	0.28	0.065	3.96E-10	4.78E-07
rs2060752	11	103032699	q22.3	T/C	0.221	0.250	98.7	0.26	0.056	1.33E-09	9.87E-07
rs10488753	11	103035917	q22.3	T/C	0.221	0.426	99.5	0.25	0.053	6.73E-09	2.91E-06

**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs7120812	11	103036338	q22.3	T/C	0.201	0.097	99.5	0.28	0.065	3.02E-10	4.00E-07
rs10488749	11	103045991	q22.3	G/C	0.221	0.397	100.0	0.25	0.054	6.64E-09	2.90E-06
rs10791643	11	103179549	q22.3	A/G	0.221	0.124	95.2	0.28	0.064	9.32E-11	1.74E-07
rs10502019	11	103218742	q22.3	C/T	0.106	0.357	97.8	-0.31	0.039	8.23E-08	1.44E-05
rs1052313	11	103413945	q22.3	A/G	0.395	0.326	100.0	-0.20	0.028	3.35E-08	8.03E-06
rs2515081	11	103473686	q22.3	T/A	0.138	0.612	98.6	-0.36	0.077	8.48E-12	4.04E-08
rs168636	11	103487043	q22.3	G/A	0.237	0.249	100.0	0.26	0.047	2.99E-10	3.42E-07
rs668285	11	103508755	q22.3	T/C	0.239	0.194	99.7	0.23	0.048	8.76E-09	3.31E-06
rs12226700	11	103518473	q22.3	T/A	0.350	0.022	100.0	-0.23	0.062	8.32E-11	1.57E-07
rs12274835	11	103518670	q22.3	A/G	0.350	0.022	100.0	-0.23	0.062	8.32E-11	1.57E-07
rs10895597	11	103542270	q22.3	A/G	0.396	0.293	97.8	-0.28	0.097	8.73E-16	9.21E-11
rs11226367	11	103826844	q22.3	C/T	0.153	0.393	99.4	0.43	0.112	5.02E-18	3.44E-12
rs11226373	11	103839449	q22.3	G/A	0.152	0.423	99.6	0.44	0.116	1.38E-18	1.50E-12
rs1487694	11	103861379	q22.3	A/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs2046652	11	103865864	q22.3	G/A	0.130	0.490	99.9	0.41	0.085	1.11E-14	4.43E-10
rs7114728	11	103874971	q22.3	G/T	0.135	0.773	97.9	0.41	0.085	4.67E-15	2.46E-10
rs4558140	11	103877366	q22.3	A/T	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs2408942	11	103888924	q22.3	G/C	0.133	0.619	98.6	0.40	0.083	1.72E-14	5.87E-10
rs7930608	11	103889136	q22.3	A/T	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs11226402	11	103890581	q22.3	A/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs11226403	11	103890838	q22.3	A/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs1565130	11	103893230	q22.3	T/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10

**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs1565131	11	103893472	q22.3	A/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs1565132	11	103893539	q22.3	A/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs1487683	11	103893924	q22.3	T/G	0.130	0.469	100.0	0.41	0.086	9.05E-15	3.92E-10
rs11226407	11	103893969	q22.3	A/T	0.129	0.528	99.4	0.41	0.083	1.87E-14	6.23E-10
rs10502035	11	103908419	q22.3	G/A	0.132	0.451	98.3	0.41	0.087	6.84E-15	3.28E-10
rs2220349	11	103917498	q22.3	A/G	0.116	0.123	96.7	0.39	0.081	5.52E-12	3.20E-08
rs17102636	11	103922584	q22.3	T/C	0.131	0.658	99.9	0.41	0.085	8.64E-15	3.74E-10
rs1942518	11	104045499	q22.3	C/A	0.371	0.998	100.0	0.35	0.128	4.03E-21	3.16E-14
rs1942517	11	104047073	q22.3	A/G	0.400	0.967	100.0	-0.29	0.070	1.96E-15	1.28E-10
rs1893462	11	104064008	q22.3	A/G	0.399	0.885	99.5	-0.29	0.068	2.08E-15	1.34E-10
rs6591093	11	104068778	q22.3	T/A	0.400	0.967	100.0	-0.29	0.070	1.96E-15	1.28E-10
rs883505	11	104069736	q22.3	T/A	0.371	0.957	100.0	0.35	0.126	1.49E-20	7.77E-14
rs17102902	11	104078814	q22.3	C/T	0.078	0.877	98.7	-0.35	0.032	9.05E-08	1.52E-05
rs2155161	11	104079038	q22.3	C/T	0.400	0.881	99.6	-0.28	0.068	4.29E-15	2.15E-10
rs7122441	11	104103584	q22.3	T/A	0.413	0.073	100.0	-0.26	0.066	4.26E-14	9.75E-10
rs1147027	11	104109472	q22.3	C/A	0.402	0.694	99.5	-0.29	0.069	2.23E-15	1.40E-10
rs1147049	11	104164746	q22.3	C/T	0.397	0.962	99.2	0.29	0.100	2.01E-15	1.82E-10
rs1529337	11	104186900	q22.3	G/A	0.445	0.650	100.0	0.22	0.061	2.06E-09	1.42E-06
rs6591099	11	104196203	q22.3	G/A	0.464	0.224	95.2	0.21	0.057	2.84E-08	8.30E-06
rs1030395	11	104201267	q22.3	C/T	0.445	0.650	100.0	0.22	0.061	2.06E-09	1.42E-06
rs10736643	11	104201414	q22.3	A/T	0.445	0.650	100.0	0.22	0.061	2.06E-09	1.42E-06
rs1559839	11	104201936	q22.3	G/A	0.445	0.677	99.6	0.22	0.062	1.04E-09	9.00E-07



**Table S1** (continued)

RS ID	Chr	Position	Cytoband	Minor/ major allele	MAF	HWE <i>P</i>	Call Rate (%)	Effect Size*	Proportion. of Variation	<i>P</i> <sup>†</sup>	GC <i>P</i> <sup>‡</sup>
rs573894	11	104276696	q22.3	A/G	0.346	0.001	99.9	-0.23	0.079	3.78E-10	6.55E-07
rs488928	11	104294431	q22.3	G/A	0.478	0.334	97.4	0.19	0.063	5.43E-08	1.51E-05
rs3181174	11	104381934	q22.3	A/T	0.162	0.735	99.9	-0.29	0.049	1.38E-09	9.55E-07
rs2510177	11	104946270	q22.3	A/G	0.130	0.038	100.0	0.27	0.030	8.65E-08	1.48E-05
rs11226791	11	104965252	q22.3	C/T	0.084	0.833	99.7	0.34	0.042	3.31E-08	7.89E-06
rs10502062	11	105126467	q22.3	G/T	0.435	0.288	100.0	0.20	0.045	1.83E-08	5.35E-06
rs10502063	11	105126491	q22.3	C/T	0.435	0.256	99.0	0.20	0.044	2.06E-08	5.79E-06
rs10895950	11	105770571	q22.3	G/A	0.265	0.147	100.0	0.21	0.042	8.04E-08	1.44E-05
rs10895951	11	105770740	q22.3	G/A	0.266	0.143	99.9	0.21	0.042	9.57E-08	1.62E-05
rs11227059	11	105842332	q22.3	T/G	0.281	0.066	99.0	0.23	0.056	2.34E-09	1.45E-06
rs10502070	11	105844419	q22.3	A/G	0.282	0.022	100.0	0.24	0.061	4.00E-10	4.52E-07
rs10502072	11	105855084	q22.3	C/T	0.243	0.027	99.4	0.24	0.050	2.70E-09	1.51E-06
rs12290638	11	105869193	q22.3	G/T	0.269	0.011	95.9	0.21	0.049	7.14E-08	1.41E-05
rs12805072	11	105874003	q22.3	T/C	0.267	0.059	98.3	0.26	0.068	2.94E-11	8.20E-08
rs12274945	11	105880509	q22.3	C/A	0.431	0.220	98.7	0.19	0.044	3.02E-08	7.50E-06
rs879929	11	106159569	q22.3	A/T	0.128	0.052	99.6	-0.36	0.063	1.88E-10	2.78E-07
rs7125424	11	106284519	q22.3	T/G	0.134	0.527	99.9	-0.35	0.068	1.31E-11	4.68E-08
rs10502081	11	106376316	q22.3	G/T	0.135	0.506	97.7	-0.35	0.065	2.09E-11	6.29E-08
rs11212024	11	106452810	q22.3	A/G	0.129	0.984	99.4	-0.34	0.057	2.00E-10	2.72E-07
rs17106456	11	106504670	q22.3	C/A	0.136	0.953	95.9	-0.30	0.049	7.99E-09	3.14E-06
rs10890667	11	106619432	q22.3	C/T	0.075	0.179	99.4	0.38	0.043	3.78E-08	8.69E-06
rs7946787	11	106645757	q22.3	C/A	0.359	0.634	100.0	-0.21	0.047	4.19E-08	9.57E-06
rs661889	11	106762599	q22.3	T/C	0.365	0.973	98.6	-0.20	0.045	9.20E-08	1.61E-05
rs502318	11	106922204	q22.3	C/T	0.305	0.158	99.9	-0.23	0.046	6.66E-09	2.72E-06
rs1531751	11	107024176	q22.3	C/G	0.246	0.067	98.3	-0.24	0.054	6.09E-10	5.65E-07

Abbreviations: Chr, chromosome; MAF, minor allele frequency; HWE, Hardy-Weinberg equilibrium

\* Change in  $\ln$ -MMP1 per copy of minor allele

†  $P$ -value from primary association analysis

‡ Genomic control-corrected  $P$ -value

**Table S2.** Associations between MMP-1 levels, MMP-1 associated SNPs and baseline characteristics\*

Baseline characteristics	Correlation coefficients		Change in trait by SNP genotype			
	with <i>ln</i> -MMP-1 levels		$(\beta \pm \text{S.E.})$			
	<i>r</i>	<i>P</i> -value	rs495366 <sup>†</sup>	rs12289128 <sup>†</sup>	rs11226373 <sup>†</sup>	rs12289128- rs495366 <sup>‡</sup>
Body mass index (kg/m <sup>2</sup> )	0.04	0.50	-0.11 ± 0.23	0.30 ± 0.30	-0.08 ± 0.31	-0.01 ± 0.23
Fasting triglyceride (mg/dL)	0.14	0.0006	0.01 ± 2.14	2.54 ± 2.80	1.79 ± 2.88	-0.64 ± 2.11
Fasting total cholesterol (mg/dL)	0	0.73	1.54 ± 2.41	-2.74 ± 3.14	2.57 ± 3.23	-0.02 ± 2.42
HDL/LDL cholesterol ratio	-0.06	0.05	-0.004 ± 0.01	-0.01 ± 0.02	-0.002 ± 0.02	0.01 ± 0.01
Systolic blood pressure	0.06	0.09	-0.58 ± 0.70	1.23 ± 0.91	-0.39 ± 0.94	-0.21 ± 0.68
Diastolic blood pressure	0.01	0.83	0.51 ± 0.44	0.62 ± 0.58	-0.22 ± 0.61	-0.87 ± 0.45
Pulse Pressure	0.08	0.04	-1.05 ± 0.53 <sup>§</sup>	0.66 ± 0.69	-0.22 ± 0.71	0.61 ± 0.52

\* Adjusted for age, age<sup>2</sup>, sex, age-by-sex and age<sup>2</sup>-by-sex interactions.

<sup>†</sup> Change in trait per copy of minor allele.

<sup>‡</sup> Change in trait per copy of G<sub>rs12289128</sub>-C<sub>rs495366</sub> haplotype

§  $P < 0.05$

**Table S3.** SNPs in *MMP-1* promoter region reported previously in Caucasians\*

<b>SNP</b>	<b>Location</b>	<b>MAF<sup>†</sup></b>	<b>Function</b>	<b>Traits studied</b>	<b>Ref</b>
rs494379	102174420	N.A.	Unknown	No associations with CAD found	<sup>1</sup>
rs514921	102174440	0.333	Promoter activity	MMP-1 expression in atherosclerotic plaques; CAD	<sup>1, 2</sup>
rs475007	102174522	0.458	Unknown	No associations with CAD found	<sup>1</sup>
rs1144393	102174619	0.353	Promoter activity	MMP-1 expression in atherosclerotic plaques; CAD, BMI	<sup>1-3</sup>
rs498186	102174855	0.475	Unknown	No associations with CAD found	<sup>1</sup>
rs1799750	102175706	N.A.	Promoter activity	CAD; internal carotid artery	<sup>1, 3-9</sup>

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stenosis; BMI; left ventricular

remodeling

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Abbreviations: N.A. Not available in Hapmap; CAD, coronary artery disease; BMI, body mass index.

\* Data source: SeattleSNPs Program for Genomic Applications Genome Variation Server (<http://gvs.gs.washington.edu/GVS/>); populations included are HapMap-CEU, EGP-CEU, Perlegen European panel and Affy Caucasian populations; rs1799750, which was not genotyped in above-mentioned populations but has been cited from previous literature, is also included in the table.

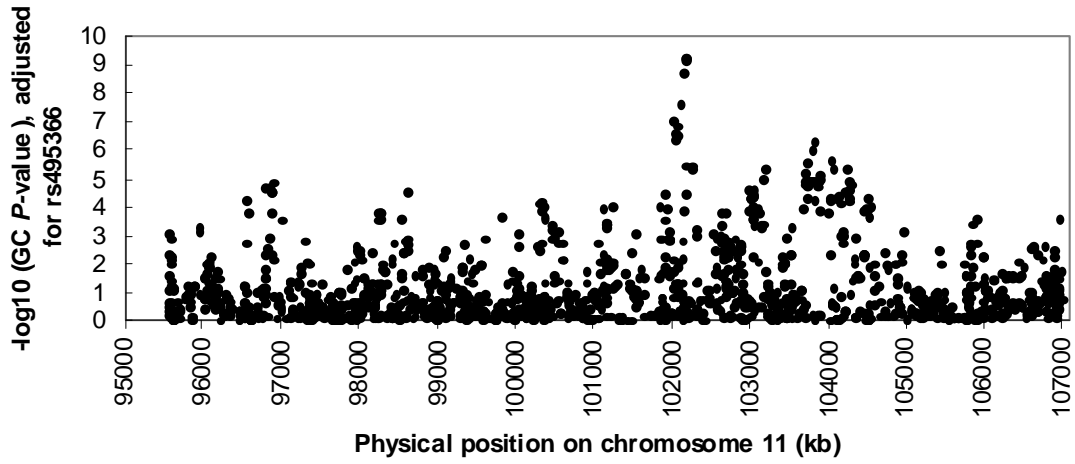
† Based on Hapmap CEU population

Figure S1.

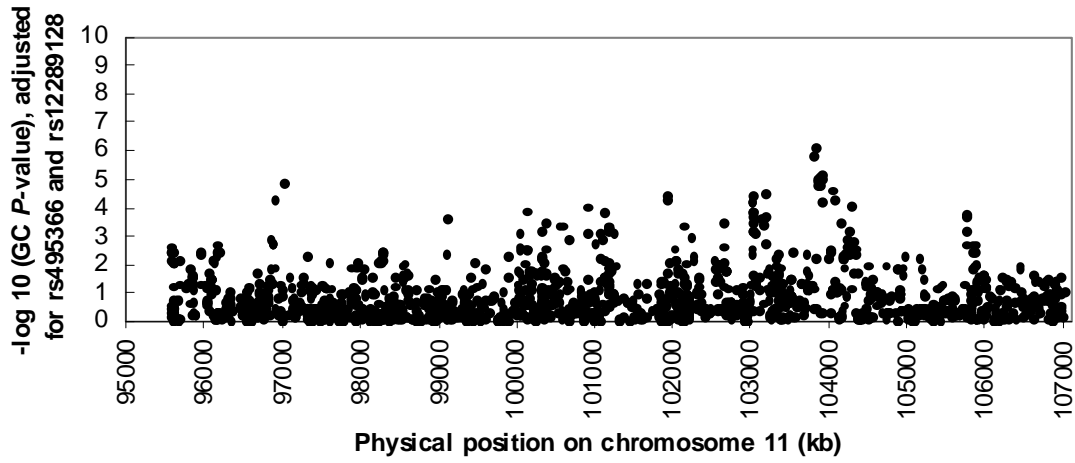


Figure S2.

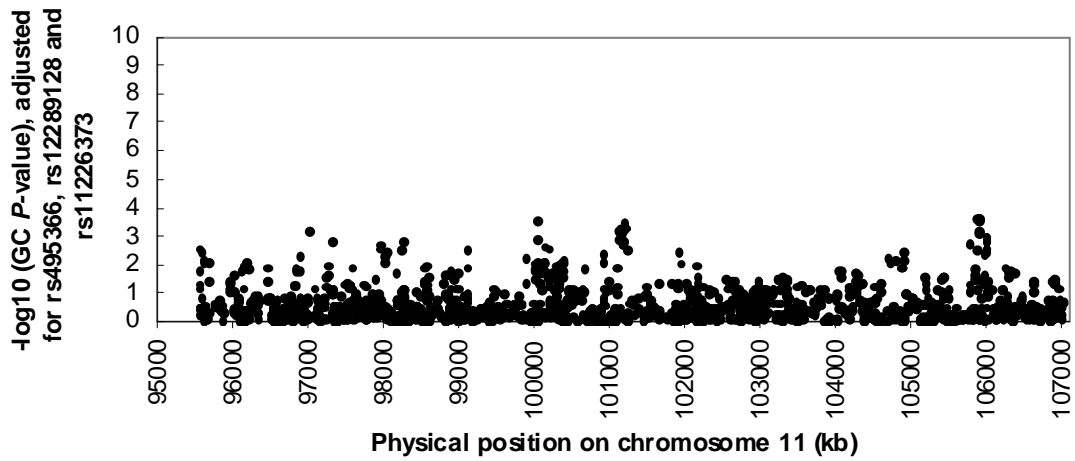
A



B



C





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