Table S2. Results of the association analysis from the largest CAD GWAS study [49] for single nucleotide polymorphisms included in the current work.

Gene	SNP	Effect allele	EAF	β	SE	OR (95% CI)	*P*
CYBA	rs7195830	A	0.3960	-0.0063	0.0052	0.99 (0.98-1.00)	0.220
	rs1049255	T	0.5004	0.0066	0.0051	1.01 (1.00-1.02)	0.196
	rs1049254	A	0.3995	-0.0062	0.0056	0.99 (0.98-1.00)	0.264
	rs4673	A	0.3371	0.0083	0.0053	1.01 (1.00-1.02)	0.118
	rs13306296	A	0.3635	-0.0044	0.0054	1.00 (0.99-1.01)	0.412
	rs72811418	A	0.9181	0.0037	0.0095	1.00 (0.99-1.02)	0.698
	rs16966671	C	0.5487	-0.0055	0.0053	0.99 (0.98-1.00)	0.298
	rs9932581	T	0.3811	-0.0018	0.0056	1.00 (0.99-1.01)	0.741
XDH	rs206860	A	0.7187	-0.0020	0.0056	1.00 (0.99-1.01)	0.717
	rs207454	T	0.9045	-0.0099	0.0091	0.99 (0.97-1.01)	0.280
	rs1042039	T	0.5235	0.0023	0.0049	1.00 (0.99-1.01)	0.635
	rs1054889	A	0.4732	-0.0015	0.0049	1.00 (0.99-1.01)	0.755
	rs2043013	A	0.5908	0.0084	0.0050	1.01 (1.00-1.02)	0.090
	rs2073316	A	0.4651	0.0004	0.0049	1.00 (0.99-1.01)	0.931
	rs2295475	A	0.2977	-0.0089	0.0053	0.99 (0.98-1.00)	0.095
	rs11904439	A	0.9496	-0.0112	0.0116	0.99 (0.97-1.01)	0.337
	rs45547640	Lack of data					
	rs148756340	A	0.9838	-0.0227	0.0211	0.98 (0.94-1.02)	0.282
MPO	rs2333227	T	0.2033	0.0220	0.0063	1.02 (1.01-1.03)	4.53×10^{-4}
	rs34097845	T	0.0560	-0.0189	0.0122	0.98 (0.96-1.01)	0.122
SOD1	rs202449	A	0.8113	-0.0068	0.0065	0.99 (0.98-1.01)	0.293
	rs1041740	T	0.2980	0.0039	0.0054	1.00 (0.99-1.01)	0.463
	rs2070424	A	0.9139	0.0138	0.0090	1.01 (1.00-1.03)	0.125
	rs2173962	T	0.9494	-0.0177	0.0117	0.98 (0.96-1.01)	0.133
	rs4817420	T	0.2979	0.0044	0.0054	1.00 (0.99-1.02)	0.410
	rs4998557	A	0.1342	-0.0023	0.0073	1.00 (0.98-1.01)	0.752
	rs9974610	A	0.8262	0.0014	0.0066	1.00 (0.99-1.01)	0.836
	rs10432782	T	0.8685	0.0021	0.0073	1.00 (0.99-1.02)	0.775
	rs17880135	T	0.9378	-0.0008	0.0108	1.00 (0.98-1.02)	0.940

Gene	SNP	Effect allele	EAF	β	SE	OR (95% CI)	*P*
	rs17880487	T	0.0011	0.0929	0.1480	1.10 (0.82-1.47)	0.530
	rs36232792	Lack of data					
SOD2	rs4880	A	0.5058	-0.0030	0.0049	1.00 (0.99-1.01)	0.540
SOD3	rs1799895	C	0.9806	-0.0542	0.0254	0.95 (0.90-1.00)	0.033
	rs2159757	A	0.7634	-0.0196	0.0058	0.98 (0.97-0.99)	7.24×10^{-4}
	rs2284659	T	0.3606	0.0142	0.0053	1.01 (1.00-1.02)	0.008
	rs2536512	A	0.6374	-0.0104	0.0055	0.99 (0.98-1.00)	0.057
	rs2855262	T	0.3697	0.0090	0.0053	1.01 (1.00-1.02)	0.094
	rs13435617	A	0.0974	-0.0131	0.0083	0.99 (0.97-1.00)	0.118
CAT	rs769214	A	0.6558	0.0072	0.0052	1.01 (1.00-1.02)	0.161
	rs1001179	T	0.2294	-0.0019	0.0061	1.00 (0.99-1.01)	0.748
	rs1049982	T	0.3445	-0.0069	0.0052	0.99 (0.98-1.00)	0.181
	rs7943316	A	0.3473	-0.0059	0.0052	0.99 (0.98-1.00)	0.249
GPX1	rs3448	T	0.2516	0.0026	0.0057	1.00 (0.99-1.01)	0.646
	rs1050450	A	0.3054	-0.0336	0.0053	0.97 (0.96-0.98)	3.27×10^{-10}
	rs1800668	A	0.3047	-0.0337	0.0054	0.97 (0.96-0.98)	3.08×10^{-10}
	rs3811699	T	0.6943	0.0337	0.0053	1.03 (1.02-1.05)	3.05×10^{-10}
	rs8179164	A	0.0316	-0.0237	0.0159	0.98 (0.95-1.01)	0.137
GCLC	rs17883901	A	0.0865	-0.0140	0.0095	0.99 (0.97-1.00)	0.140
GCLM	rs41303970	A	0.1733	-0.0009	0.0065	1.00 (0.99-1.01)	0.894
GSTP1	rs1695	A	0.6626	-0.0098	0.0052	0.99 (0.98-1.00)	0.060
NOS3	rs1799983	T	0.3181	0.0193	0.0055	1.02 (1.01-1.03)	4.27×10^{-4}
	rs2070744	T	0.6288	-0.0240	0.0052	0.98 (0.97-0.99)	4.44×10^{-6}
	rs3918226	T	0.0807	0.1119	0.0095	1.12 (1.10-1.14)	4.60×10^{-32}
	rs61722009	Lack of data					

Legend: CAD - coronary artery disease; CI - confidence interval; EAF - effect allele frequency; GWAS - genome-wide association study; OR - odds ratio; SE - standard error of β. Data were obtained from the full GWAS summary statistics of Aragam et. al. (2022) [49]. The 95% CIs were calculated from β and SE as exp[β ± 1.96 × SE]. "Lack of data" denotes variants not available in the summary statistics.