Supplementary Table 1. Power to detect association between genetic variants and CAAD.

Homozygote (Heterozygote) Relative Risk	Risk Allele Frequency	Linkage Disequilibrium (r^2)	Power (p<0.05)
2.0 (1.5)	0.05	1	0.72
2.0 (1.5)	0.1	1	0.91
2.0 (1.5)	0.2	1	0.99
2.0 (1.5)	0.3	1	0.99
2.0 (1.5)	0.05	0.8	0.63
2.0 (1.5)	0.1	0.8	0.85
2.0 (1.5)	0.2	0.8	0.96
2.0 (1.5)	0.3	0.8	0.98
2.0 (1.5)	0.05	0.64	0.55
2.0 (1.5)	0.1	0.64	0.74
2.0 (1.5)	0.2	0.64	0.92
2.0 (1.5)	0.3	0.64	0.94

Power estimates are based on 1000 simulations per parameter set for a sample size of 530 CAAD cases and 770 controls, assuming a population prevalence of 0.04. Association tests were performed using logistic regression as described in Methods.

Supplementary Table 2. Minor allele frequencies in the sub-sample typed for KIV2 repeat and the complete sample.

SNP	Complete sample minor allele freq	Sub-sample minor allele freq	Fisher's exact p-value
rs3123629	0.30	0.30	1.00
rs7754014	0.23	0.27	0.20
rs7449650	0.33	0.34	0.68
rs6919346	0.15	0.18	0.29
rs3798220	0.02	0.01	0.37
rs11751605	0.16	0.13	0.40
rs4708871	0.03	0.02	0.48
rs7761293	0.47	0.42	0.25
rs6415084	0.47	0.48	0.94
rs3798221	0.20	0.18	0.63
rs10455872	0.08	0.07	1.00
rs1367209	0.28	0.29	0.73
rs1321195	0.15	0.11	0.23
rs783149	0.17	0.13	0.26
rs1358753	0.13	0.18	0.12
rs9458005	**0.22**	**0.31**	**0.01**
rs1950562	**0.42**	**0.51**	**0.03**
rs9458011	0.06	0.07	0.62
rs1853017	0.30	0.27	0.50
rs2295368	0.40	0.41	0.94
rs9456577	0.03	0.01	0.32
rs4252129	0.01	0.02	0.35
rs813641	**0.16**	**0.24**	**0.0046**
rs1317026	0.02	0.02	1.00
rs2859879	**0.34**	**0.48**	**0.00018**
rs4252170	**0.07**	**0.13**	**0.0090**
rs783182	0.49	0.53	0.32
rs783176	**0.17**	**0.25**	**0.011**

Bold indicates 6 SNPs which show significantly different minor allele frequencies in the sub-sample of 90 individuals typed for the KIV2 repeat compared with the complete sample at p < 0.05 (FDR = 0.14).