Table 3: Estimated Haplotype frequencies in Go-DARTS. Frequencies in NPHS2 are given for comparison

Haplotype	Go-DARTS	NPHS2
L162-G2528	0.802	0.804
L162-C2528	0.130	0.132
V162-G2528	0.016	0.021
V162-C2528	0.052	0.041

found an association of genotype with age diagnosed with type 2 diabetes, with the V162 allele being associated with a significantly later age of diagnosis and the C2528 allele with a significantly earlier age of diagnosis (Table 5). When we considered haplotypes we found that V162-G2528 was associated with almost a 4 year delay in diagnosis with diabetes compared to the common L162-G2582 haplotype (p = 0.004). This association was completely abrogated when C2528 occurred together with V162 as a haplotype.

During a median follow up time 49.6 months there were 108 non-fatal myocardial infarction events and 355 deaths from all causes. In a fully adjusted Cox's proportional hazards model (table 6) we found that V162 was significantly protective against non-fatal myocardial infarction (HR 0.31, 95%CI 0.10–0.93, p = 0.037), while the C2528 variant was associated with a significantly higher risk of non-fatal myocardial infarction (HR 2.77, 95%CI 1.34–5.75, p = 0.006). This association was found to be similar in both sexes. Neither variant demonstrated any evidence of an association with risk of myocardial infarction when considered in isolation. Again, when we considered haplotypes, we found that compared to the haplotype with both common alleles, the haplotype L162-C2528 was associated with a significantly increased cardiovascular risk (HR 1.68 95%CI 1.16–2.43 p = 0.006) and the V162-G2528 a decreased risk although in this case this was not significant (HR 0.54, 95%CI 0.20–1.48, p = 0.23). Again the relative associations of each variant were completely abrogated when they occurred together on the same haplotype. The inclusion of total cholesterol in the model did not attenuate these observed associations but rather further strengthened them (V162: HR 0.28, 95% CI 0.09–0.89, p = 0.031 and C2528: HR 2.87, 95%CI 1.38–5.95, p = 0.005) demonstrating that the increased risk

Table 4: Biochemical parameters at genotyping. Mean and 95% confidence intervals of all readings taken within 2 years prior to enrolment in study

			L162V			
	L/L		**L/V**		**V/V**	
BMI	30.5	30.2–30.7	30.7	30.0–31.4	28.9	26.0–31.9
SBP mmHg	142.5	141.7-141.3	141.3	139.3–143.3	134.9	126.7–143.1
DBP mmHg	79.5	79.1–79.8	79.7	78.6–80.7	77.3	73.1–81.5
Cholrat† mmol/L	4.5	4.4–4.6	4.8	4.5–5.0	4.3	3.3–5.3
Chol mmol/L	5.2	5.2–5.3	5.3	5.1–5.4	5.3	4.8–5.8
Trigs mmol/L	2.7	2.6–2.8	2.8	2.6–3.1	2.4	1.3–3.5
HDL mmol/L	1.22	1.20–1.24	1.23	1.20–1.28	1.31	1.13–1.50
LDL mmol/L	2.89	2.84–2.92	2.89	2.78–3.00	2.92	2.42–3.41
			G2528C			
	G/G		**G/C**		**C/C**	
BMI	30.5	30.2–30.8	30.4	29.9–30.8	31.40	30.1–32.7
SBP mmHg	142.5	141.7–143.4	142	140.7–143.3	140.2	135.5–143.9
DBP mmHg	79.5	79.0–79.9	79.7	79.0–80.3	78.2	76.3–80.1
Cholrat† mmol/L	4.49	4.37–4.60	4.74	4.57–4.91	4.51	4.03–4.98
Chol mmol/L	5.20	5.15–5.25	5.26	5.18–5.34	5.56	5.33–5.79*
Trigs mmol/L	2.73	2.62–2.83	2.75	2.59–2.91	2.65	2.18–3.12
HDL mmol/L	1.22	1.20–1.24	1.23	1.20–1.25	1.25	1.17–1.34
LDL mmol/L	2.88	2.83–2.92	2.88	2.81–2.95	3.22	3.01–3.44*

*P < 0.05 ANOVA co-dominant model
† Cholrat = Total cholesterol/HDL Ratio