Table 5: Influence of genotype and inferred haplotypes on age diagnosed with type 2 diabetes.

	Age diagnosed			
	Beta	95% CI	Р	
V162*	2.6	0.2–5.1	0.034	
C2528†	-1.1	-2.0-0.2	0.022	
Haplotype				
L162-G2582	Ref			
L162-C2528	-0.40	-1.25 — 0.45	0.36	
V162-G2528	3.89	1.26 – 6.51	0.004	
V162-C2528	-0.28	-1.65 – 1.10	0.69	

^{*}Co-dominant model

associated with the C2528 was not linked to raised cholesterol levels. When a combined endpoint of death from all cause, and non-fatal myocardial infarction was considered in the same model it was found that the V162 continued to demonstrate a reduced risk of an event although the association was attenuated (HR 0.52, 95%CI 0.28–0.98, p = 0.044). C2528 again demonstrated an increased risk although this was now weak and borderline non-significant (HR 1.52, 95% CI 0.99–2.31, p = 0.052).

Discussion

It has been previously demonstrated that two common variants at the *PPARA* locus are associated with opposing risks of development of atherosclerotic vascular disease and myocardial infarction in two separate populations of non-diabetic male subjects taking part in the LOCAT and NPHS2 studies [11]. Individuals with type 2 diabetes are

however particularly susceptible to atherosclerotic macrovascular disease, and PPARα activators such as the fibrate group of drugs appear to be particularly beneficial in reducing cardiovascular events in this group of patients [13]. In this study we have confirmed the observation that V162 is associated with a decreased risk and the C2528 variant is associated with an increased risk of cardiovascular disease and that this observation can be extended to individuals with type 2 diabetes. We also found that the association is similar in both male and female individuals. Finally we confirm a recent finding that these variants are associated with opposing influences on age of diagnosis with type 2 diabetes [12], and that the C2528 variant is also associated with significantly higher total cholesterol and calculated LDL cholesterol levels.

Table 6: Prospective model of PPARA variants and non-fatal myocardial infarction risk in the Go-DARTs cohort. A full set of data was available on 1806 individuals, 108 recorded non fatal myocardial infarctions during the period of observation, with a total of 94497.6 months of observation. Both PPARA variants were analysed using a co-dominant model.

	Hazard Ratio	95% CI	P
V162	0.31	0.10 0.93	0.037
C2528	2.77	1.34 5.75	0.006
Smoking	1.39	0.93 2.10	0.112
Gender	0.72	0.48 1.08	0.107
Age at recruitment	1.05	1.02 1.07	<0.001
Insulin treatment	2.56	1.69 3.89	<0.001
Prevalent angina	5.64	3.80 8.40	<0.001
Prevalent cerebrovascular disease	1.29	0.67 2.51	0.445
Prevalent myocardial infarction	3.90	2.60 5.81	<0.001
Haplotypes			
L162-G2582	Ref		
L162-C2528	1.68	1.16-2.43	0.006
V162-G2528	0.54	0.20-1.48	0.23
V162-C2528	0.96	0.48-1.94	0.91

[†] Dominant model

Both variants included in the model