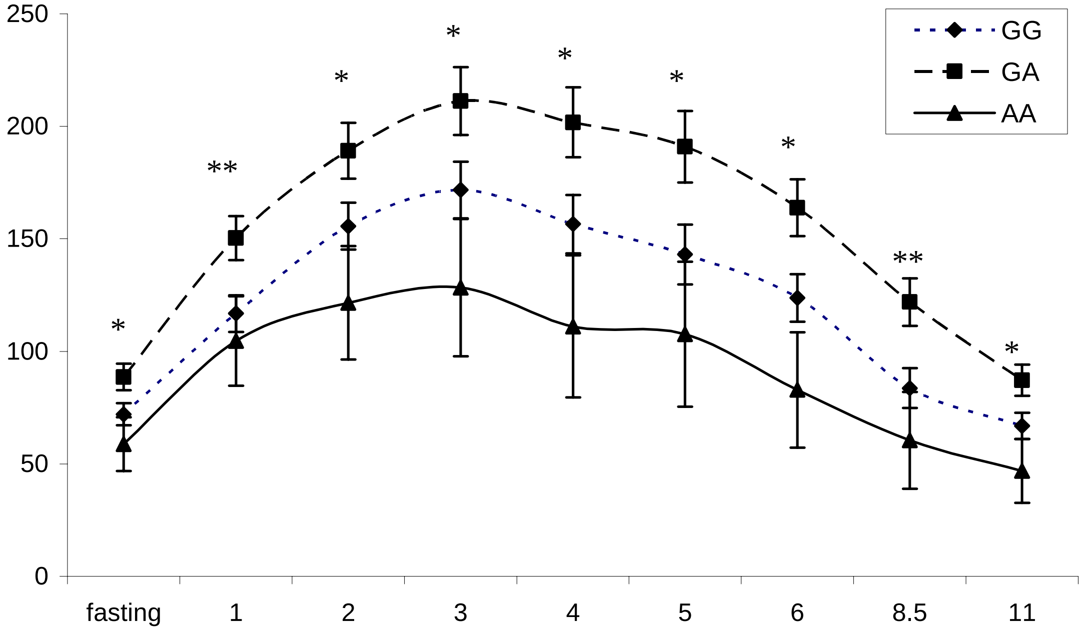
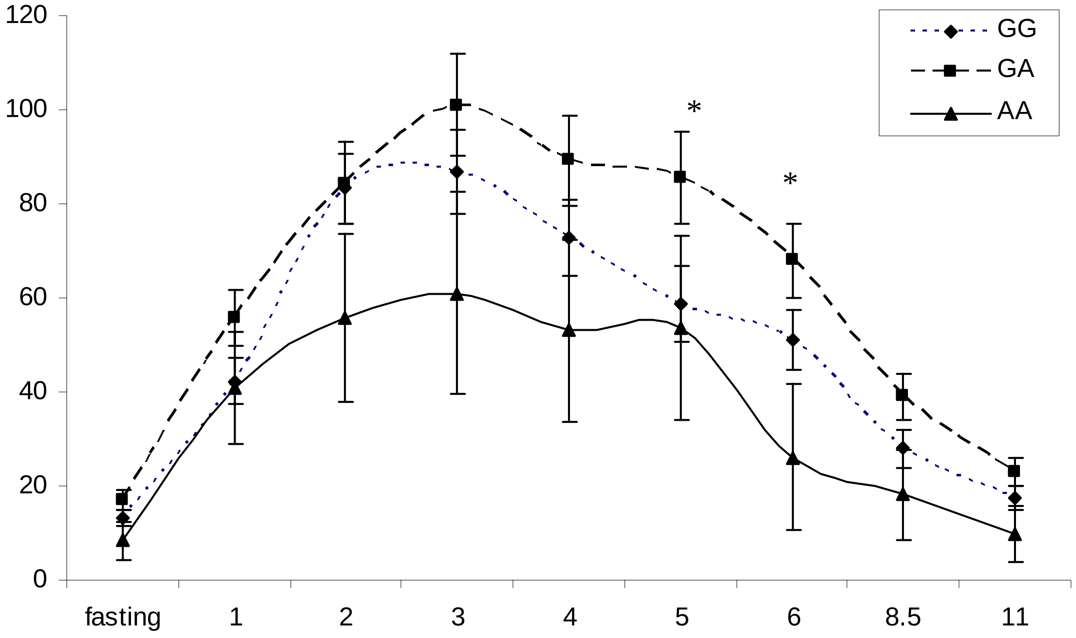
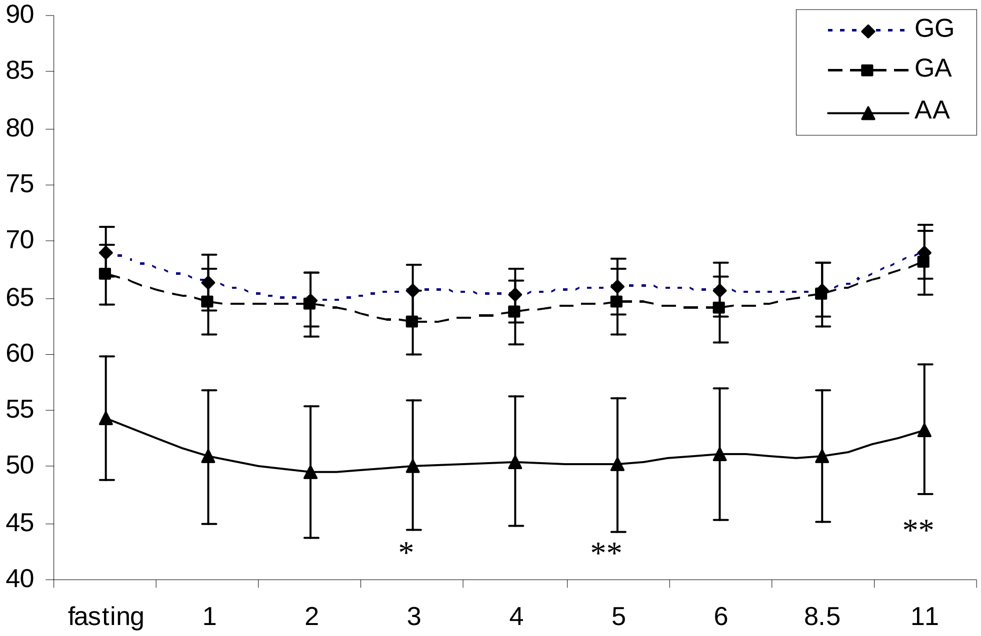
Supplemental Fig 1: Postprandial evolution lines of Total TG depending on *APOA1* -2803 genotype. * p<0,05 GA VS AA; **p<0,05 GA VS GG and AA.



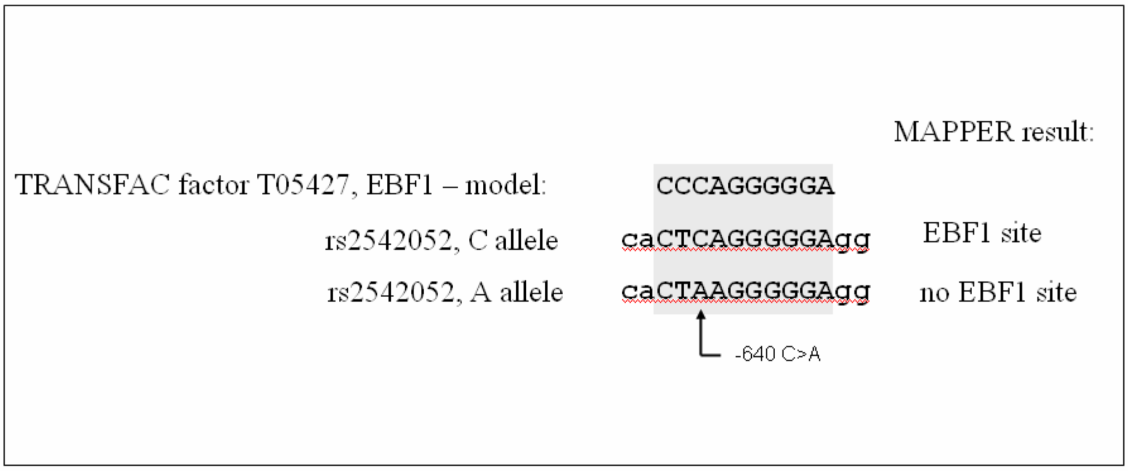
Supplemental Fig 2: Postprandial evolution lines of Large TRL-TG (mg/dl) depending on *APOA1* -2803 genotype. * p<0,05 GA VS AA.



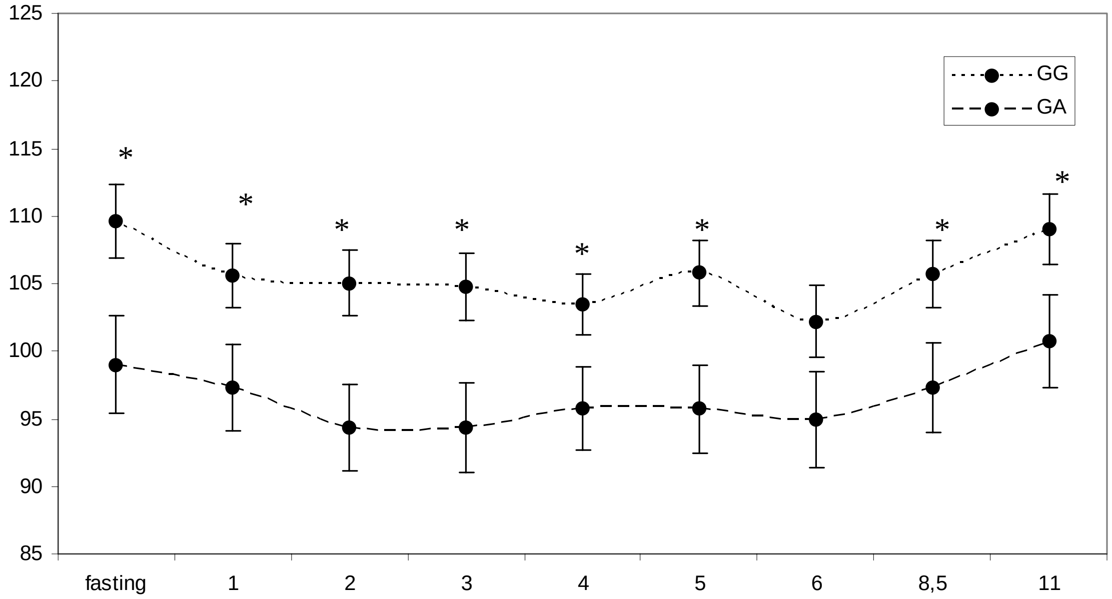
Supplemental Fig 3: Postprandial evolution lines of APOB (mg/dl) depending on *APOA1* -2803 genotype. * p<0,05 AA VS GG; **p<0,05 AA VS GG and GA.



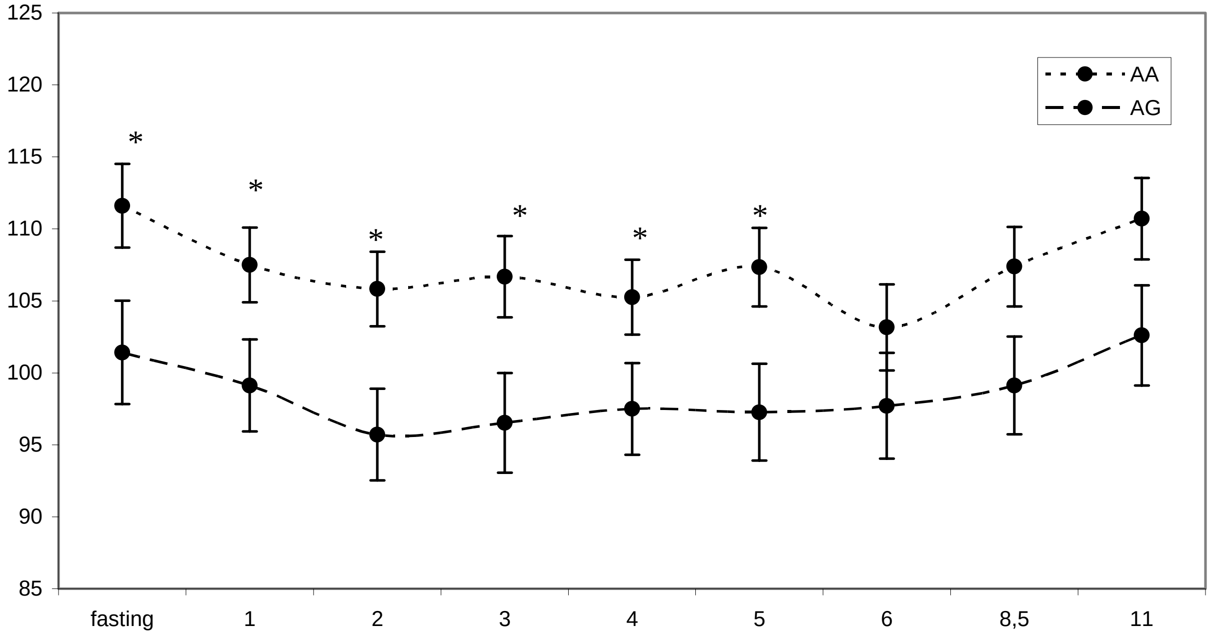
Supplemental Fig 4: Allele-specific binding of transcription factor EBF1 at APOC3 -640C>A. TRANSFAC factor T05427 for EBF1 as applied by MAPPER is predicted to bind to a region of the APOC3 promoter from position -633 to -642 only when the allele is C at position -640 (SNP rs2542052). The minor A allele at -640 is not predicted to support binding of EBF1.



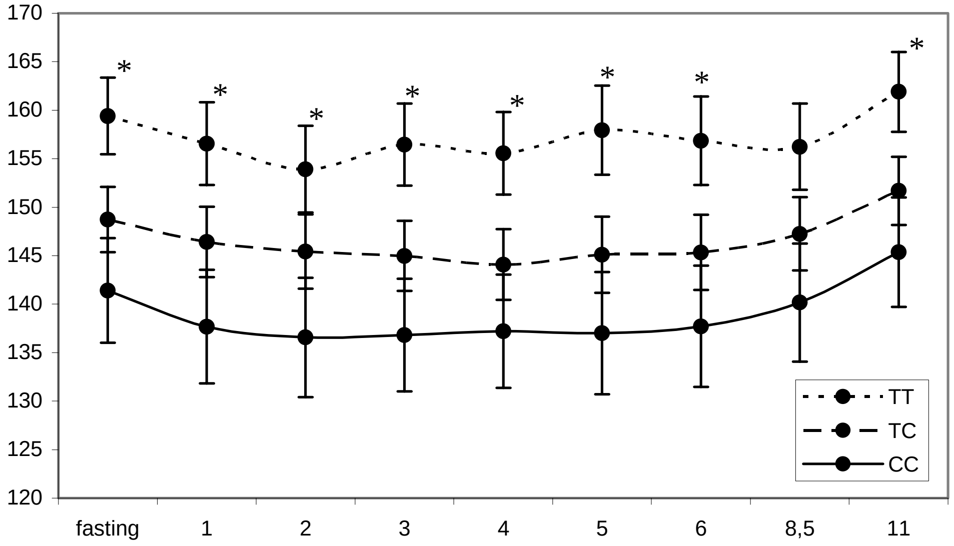
Suplemmental Fig 5: Postprandial evolution lines of APOA1 (mg/dl) depending on *APOA4* N147S. * p<0,05 GG VS GA.



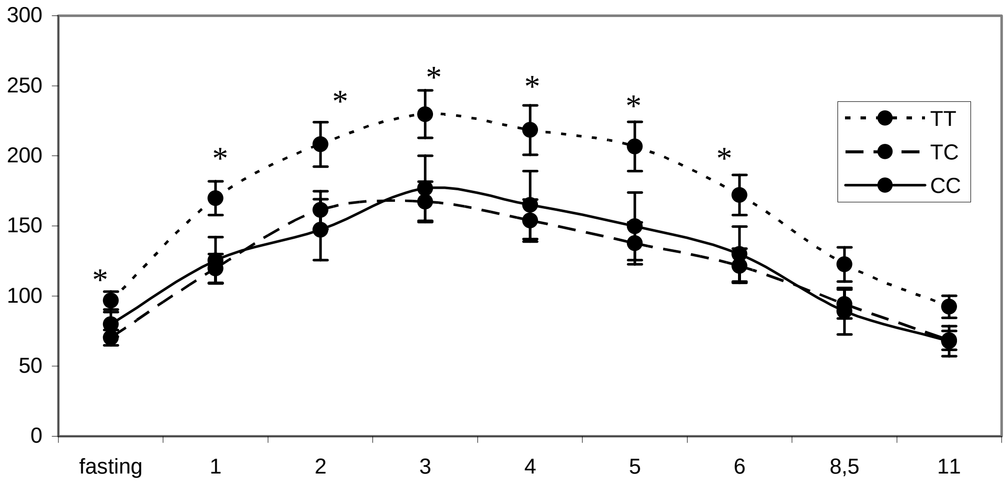
Supplemental Fig 6: Postprandial evolution lines of APOA1 (mg/dl) depending on *APOA4* T29T. * p<0,05 AA VS AG.



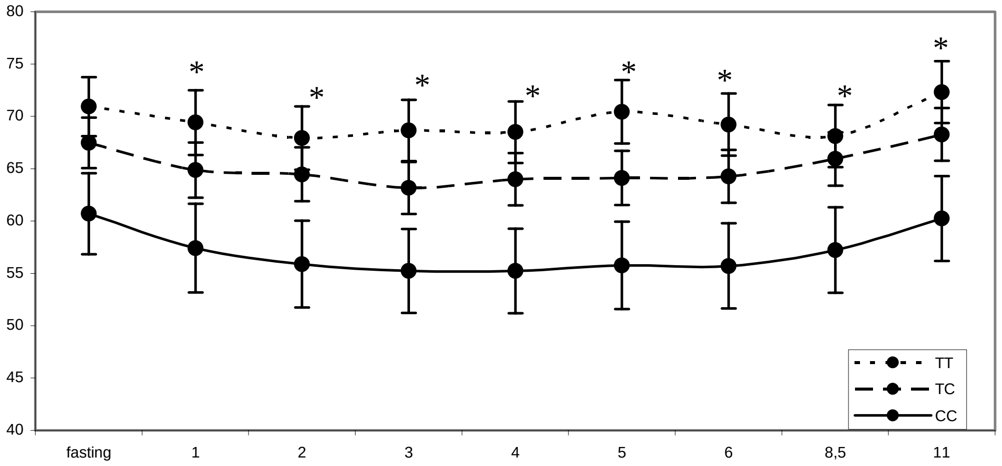
Supplemental Fig 7: Postprandial evolution lines of total cholesterol (mg/dl) depending on *A4A5_inter*. *p<0,05 TT VS CC.



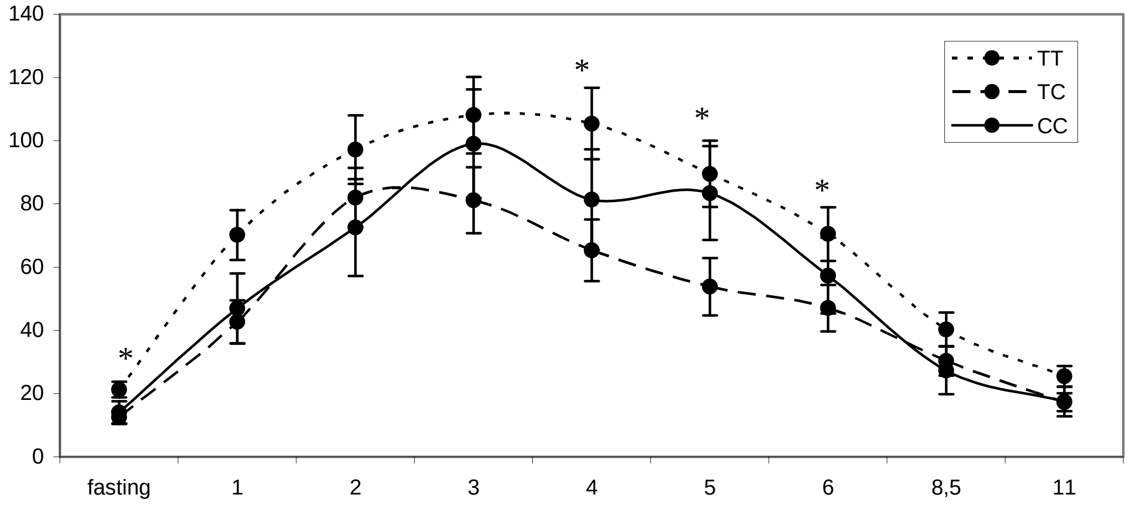
Supplemental Fig 8: Postprandial evolution lines of TG (mg/dl) depending on *A4A5_inter*. *p<0,05 TT VS TC.



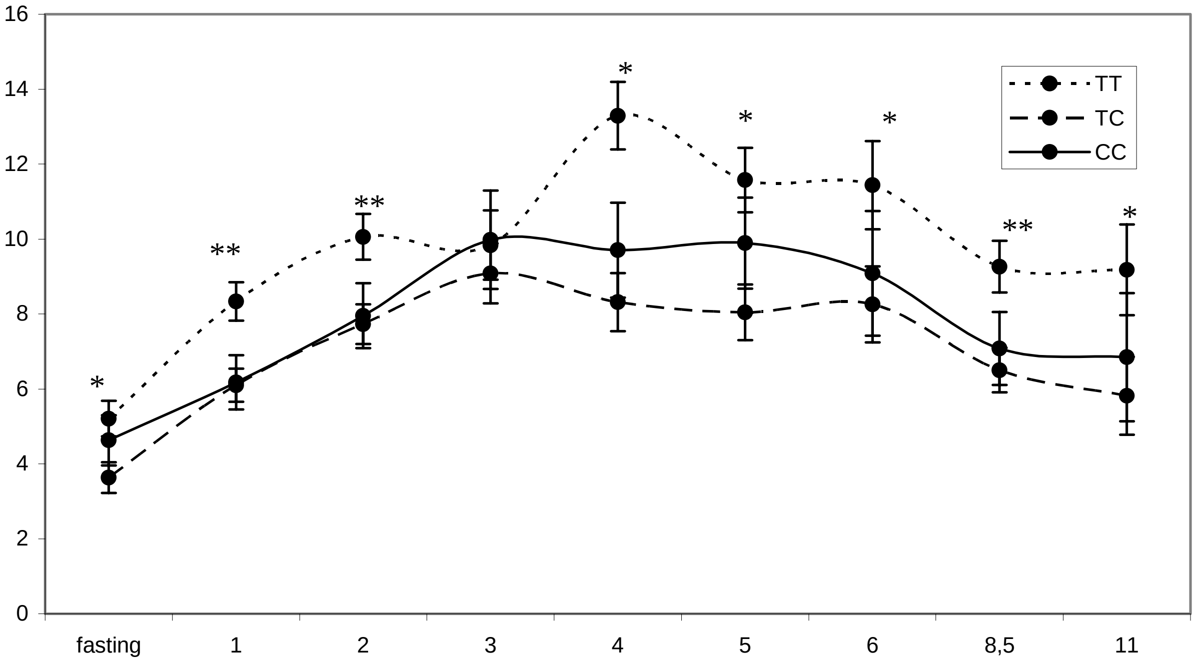
Supplemental Fig 9: Postprandial evolution lines of APOB (mg/dl) depending on *A4A5_inter*. *p<0,05 TT VS TC.



Supplemental Fig 10: Postprandial evolution lines of large TRL-TG (mg/dl) depending on *A4A5_inter*. *p<0,05 TT VS TC.



Supplemental Fig 11: Postprandial evolution lines of large TRL-CHOL (mg/dl) depending on *A4A5_inter*. *p<0,05 TT VS TC; **p<0,05 TT VS TC and CC.



Supplemental Table1: Common names, rs accession numbers and primer sequences of the SNPs assayed in this study.

SNP (rs number)	PRIMERS
APOA1 -2630 (rs613808)	5´-CACAGGCAAAAATCACAAGGGTAAA 3´-GTGGCCAAAGCACTTTCACAA
APOA1 -2803 (rs2727784)	5´-CAGCACCCCCTATCCTGATG 3´-TTTGAGGGTGGCCTTGCA
APOA1 -3012 (rs11216158)	5´-TGTATTTTTCCATCAGCTCTGTCCAG 3´-TTGCAAGGTATTTGGCTTAAACTAGTCTAA
APOC3 -2886 (rs2542051)	5´-GGTCAGTCCAGAGGTCAGAGT 3´-GAGGCACATGTCCGTGTGA
APOC3 -640 (rs2542052)	5´-CGGCCTTGGCCCTTCTC 3´-GCCCCCACCCTGTGT
APOC3 G34G (rs4520)	5´-GAGCTTCAGAGGCCGAGGAT 3´-CTCCTGCACGCTGCTCAGT
APOA4 N147S (rs5104)	5´-CCGCAGCACTCTCTCCAT 3´- ACAACCTGCGAGAGCTTCAG
APOA4 T29T (rs5092)	5´-GGCCTCCTTGGCATTGTTG 3´-CCTCATGAATTGCTCTCTGTTACCA
APOA4A5_inter (rs1263177)	5´-GTGGCCTGCCAGTTTGG 3´-CTGGCTGTGCTGATGAGACT

Supplemental Table 2. Results of codon usage and transcription factor binding site analysis.

SNP	dbSNP ID	Allele	Major/Minor	Codon preference[a]	MAPPER values: Transcription factor	Model ID	Score[b]	E-value[b]
APOA1 -2630	rs613808	G	major	TNP	no prediction			
		A	minor	TNP	SRF	M00922	6.0	6.2
					SRF	MA0083	5.2	2.4
APOA1 -2803	rs2727784	G	major	TNP	no prediction			
		A	minor	TNP	no prediction			
APOA1 -3012	rs11216158	A	major	TNP	no prediction			
		G	minor	TNP	no prediction			
APOC3 -2886	rs2542051	A	major	TNP	AR	MA0007	2.8	8.1
		C	minor	TNP	no prediction			
APOC3 -640	rs2542052	C	major	TNP	EBF1	T05427	5.4	5.8
		A	minor	TNP	MZF1	MA0057	2.0	9.2
APOC3 G34G	rs4520	C	major	22.2	TNP			
		T	minor	10.8	TNP			
APOA4 N147S	rs5104	G	major	TNP	TNP			
		A	minor	TNP	TNP			
APOA4 T29T	rs5092	A	major	15.1	TNP			
		G	minor	6.1	TNP			
APOA4A5_inter	rs1263177	T	major	TNP	PITX2	T02413	4.0	8.9
					CRX	M00623	4.9	9.4
		C	minor	TNP	MZF1	M00084	4.3	8.9
					SPZ1	MA0111	1.6	10.0

TNP = test not performed

[a] Values are given as frequency per thousand codons, based on ref. 47

[b] Values from analysis by MAPPER for putative transcription factor binding sites are reported only for score > 0 and E-value < 12