Supplementary Table 1: Lipid-related genetic variants associated with CAD risk at a Bonferroni-corrected level of significance

SNP	Nearest gene	Association of variant with… [beta coefficient (standard error)]			
		LDL-c	HDL-c	Triglycerides	CAD risk
rs646776	*CELSR2*	**0.160 (0.004)**	**-0.034 (0.004)**	0.003 (0.004)	**0.101 (0.011)**
rs1367117	*APOB*	**0.119 (0.004)**	**-0.022 (0.004)**	**0.025 (0.004)**	*0.041 (0.011)*
rs515135	*APOB*	**0.139 (0.005)**	-0.011 (0.004)	*0.019 (0.004)*	**0.068 (0.012)**
rs6544713	*ABCG8*	**0.081 (0.004)**	-0.003 (0.004)	0.013 (0.004)	*0.051 (0.010)*
rs4148218	*ABCG8*	**0.044 (0.005)**	-0.003 (0.004)	0.004 (0.004)	*0.050 (0.012)*
rs4530754	*CSNK1G3*	**-0.028 (0.004)**	-0.001 (0.003)	-0.002 (0.003)	*0.035 (0.009)*
rs998584	*VEGFA*	0.000 (0.004)	**-0.026 (0.004)**	**0.029 (0.004)**	*0.042 (0.010)*
rs2297374	*SLC22A1*	**0.032 (0.004)**	-0.006 (0.004)	0.009 (0.003)	*0.038 (0.010)*
rs2954022	*TRIB1*	**0.055 (0.004)**	**-0.040 (0.003)**	**0.078 (0.003)**	*0.043 (0.009)*
rs579459	*ABO*	**0.066 (0.004)**	0.014 (0.004)	-0.014 (0.004)	**0.073 (0.011)**
rs2068888	*CYP26A1*	*0.017 (0.004)*	**-0.019 (0.004)**	**0.024 (0.003)**	*0.039 (0.010)*
rs12801636	*PCNX3/ PCNXL3*	-0.008 (0.004)	**-0.024 (0.004)**	*0.018 (0.004)*	*0.050 (0.011)*
rs653178	*ATXN2*	**-0.023 (0.004)**	**-0.026 (0.004)**	0.010 (0.003)	**0.064 (0.010)**
rs1169288	*HNF1A*	**0.038 (0.004)**	0.010 (0.004)	0.002 (0.004)	*0.047 (0.010)*
rs952044	*Intergenic*	-0.003 (0.004)	**-0.023 (0.004)**	0.010 (0.004)	*0.043 (0.010)*
rs6511720	*LDLR*	**0.221 (0.006)**	*-0.025 (0.006)*	0.008 (0.006)	**0.125 (0.017)**
rs688	*LDLR*	**0.054 (0.004)**	-0.011 (0.003)	0.004 (0.003)	*0.037 (0.010)*

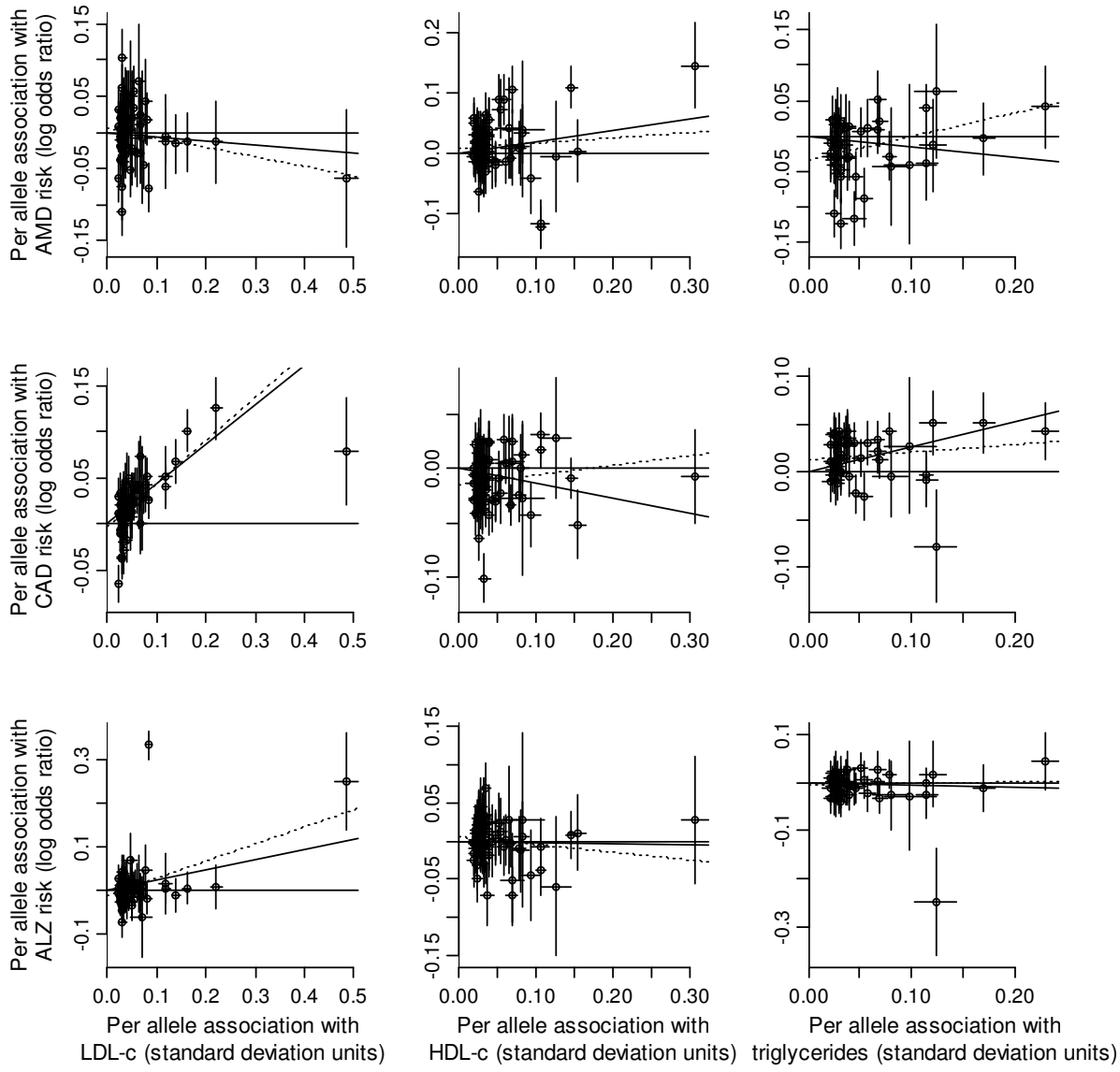
SNPs are those associated with coronary artery disease (CAD) risk at a Bonferroni-corrected level of significance ($p < 0.05/182 = 0.0003$). Associations with lipid fractions (low-density lipoprotein cholesterol [LDL-c], high-density lipoprotein cholesterol [HDL-c] and triglycerides) are in standard deviation units. Associations with age-related macular degeneration are log odds ratios from logistic regression analyses. Bold face indicates association at a genome-wide level of significance ($p < 5 \times 10^{-8}$); italics indicates association at a Bonferroni-corrected level of significance. All variants are orientated to the CAD risk-increasing allele.

Supplementary Table 2: Lipid-related genetic variants associated with ALZ risk at a Bonferroni-corrected level of significance

SNP	Nearest gene	Association of variant with… [beta coefficient (standard error)]			
		LDL-c	HDL-c	Triglycerides	ALZ risk
rs1883025	*ABCA1*	**-0.030 (0.004)**	**-0.070 (0.004)**	**-0.022 (0.004)**	*0.070 (0.018)*
rs17788930	*FNBP4*	0.005 (0.004)	**0.036 (0.004)**	-0.011 (0.004)	*0.070 (0.016)*
rs6859	*APOC*	**0.084 (0.004)**	**-0.018 (0.004)**	*0.014 (0.004)*	**0.334 (0.016)**
rs7254892	*APOC*	**0.485 (0.012)**	*-0.053 (0.011)*	**-0.124 (0.011)**	*0.250 (0.057)*

SNPs are those associated with Alzheimer's disease (ALZ) risk at a Bonferroni-corrected level of significance ($p < 0.05/182 = 0.0003$). Associations with lipid fractions (low-density lipoprotein cholesterol [LDL-c], high-density lipoprotein cholesterol [HDL-c] and triglycerides) are in standard deviation units. Associations with age-related macular degeneration are log odds ratios from logistic regression analyses. Bold face indicates association at a genome-wide level of significance ($p < 5 \times 10^{-8}$); italics indicates association at a Bonferroni-corrected level of significance. All variants are orientated to the Alzheimer's disease risk-increasing allele.

Supplementary Figure 1: Genetic associations with lipid fractions and disease outcomes



Genetic associations for all variants associated with the lipid fraction at a genome-wide level of significance ($p < 5 \times 10^{-8}$). Each point represents a single genetic variant, lines are 95% confidence intervals for the associations. The solid line is the inverse-variance weighted estimate, the dotted line is the MR-Egger estimate. This figure is also available as an interactive graph online at http://mendelianrandomization.com/amd_lipids_motionchart.htm.

Supplementary Figure 2: Distribution of causal estimates from univariable Mendelian randomization analysis of HDL-cholesterol on AMD risk on omission of 30% of the variants from the analysis at random based on 1 million iterations