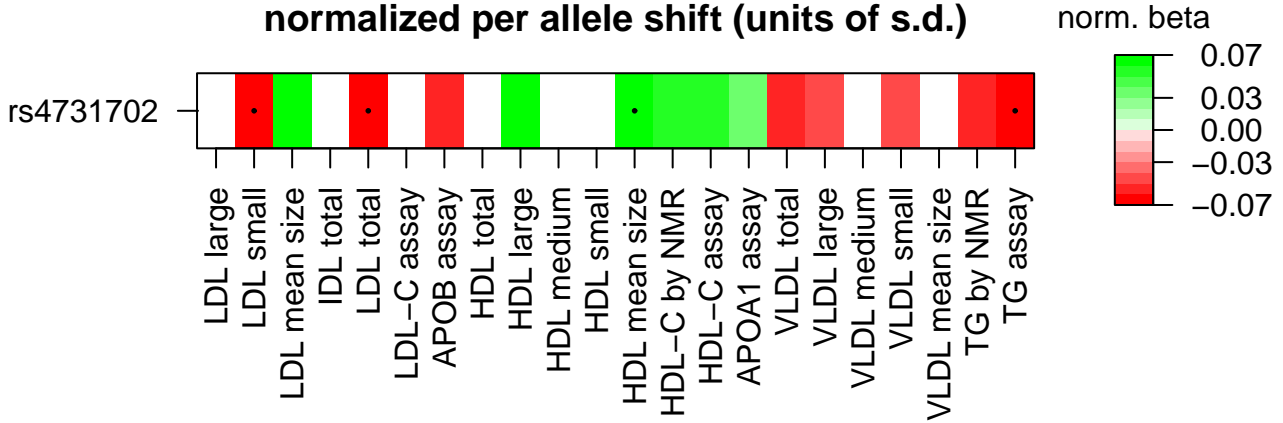
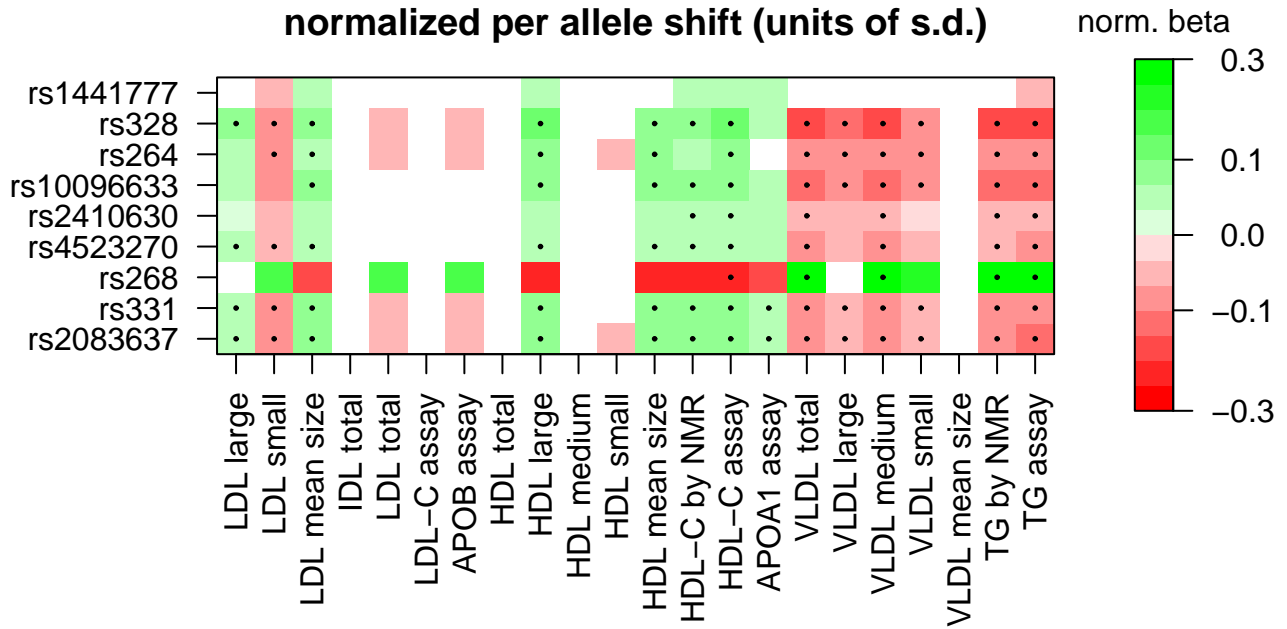


Figure S4. Normalized SNP effects (beta coefficients) from univariate regression models. All plots correspond to analysis in the whole sample except for locus 8p23.1, for which genomewide association was detected only in the fasting subsample as shown. Locus SNPs are shown if they were retained in the model selection procedure for at least one lipoprotein fraction. Absence of shading indicates the univariate beta coefficient was not significant ($p > 0.05$). A small black dot for some combinations of SNPs and lipoprotein fractions indicates genomewide significance for the univariate beta coefficient.

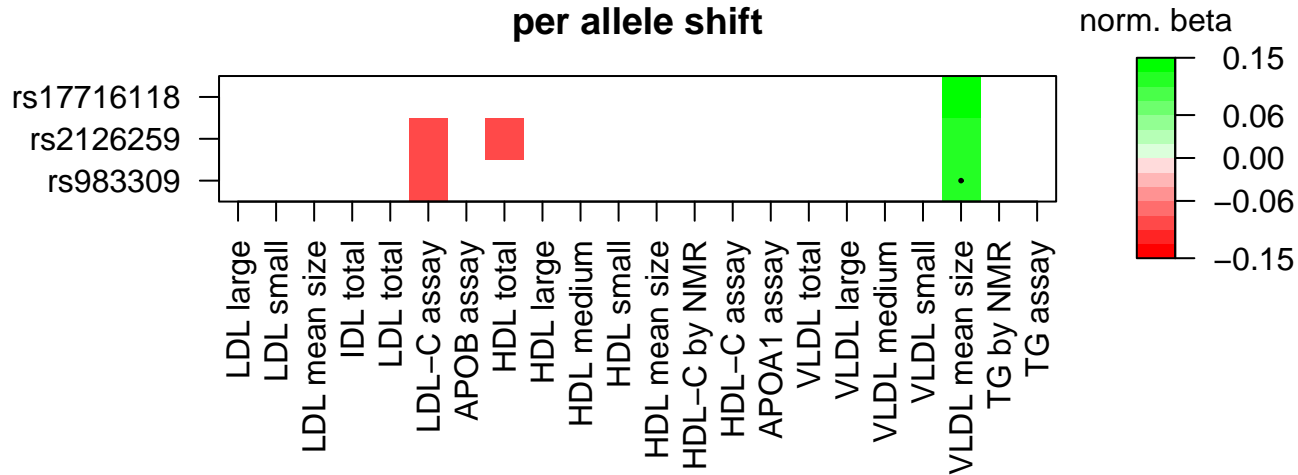
7q32.2 (COPG2, KLF14, TSGA13)
normalized per allele shift (units of s.d.)



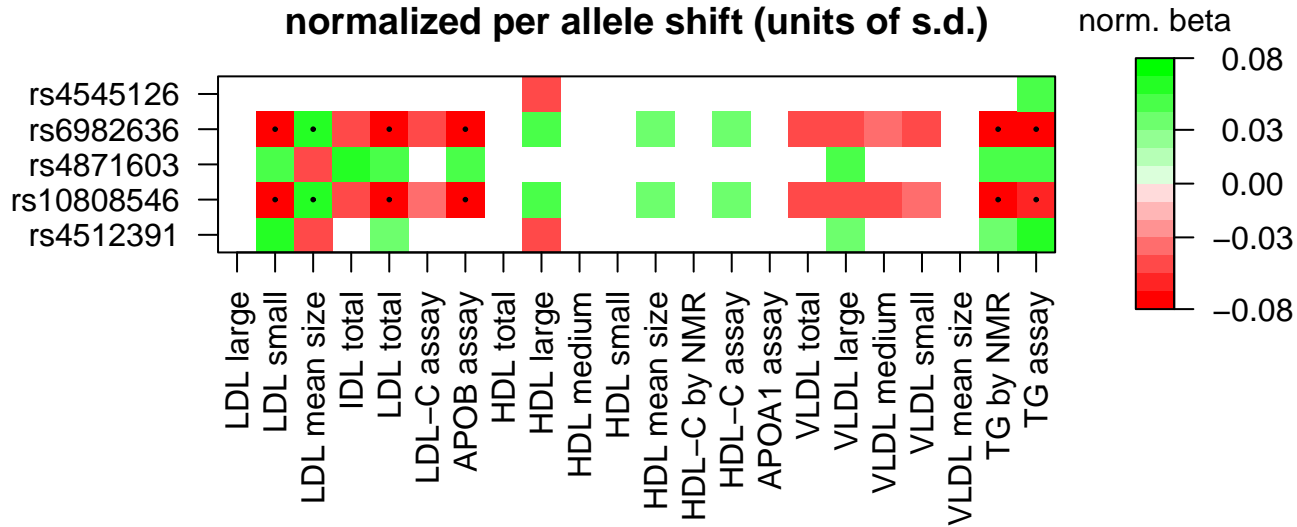
8p21.3 (LPL)
normalized per allele shift (units of s.d.)



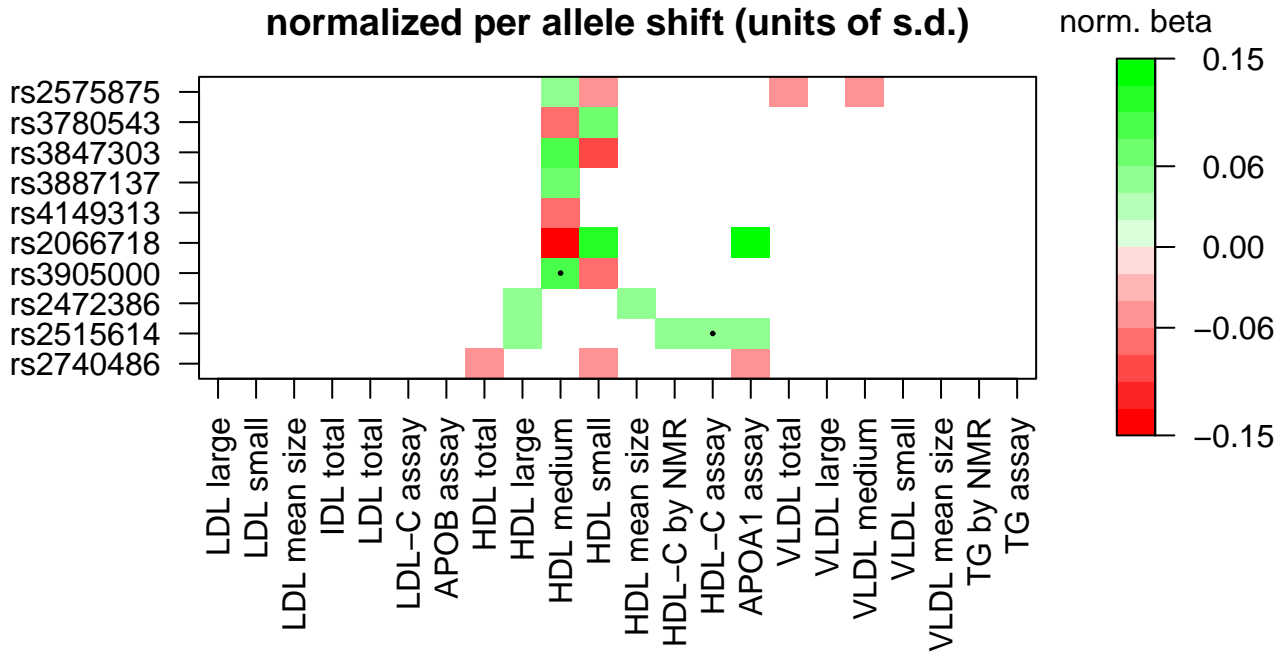
8p23.1 per allele shift



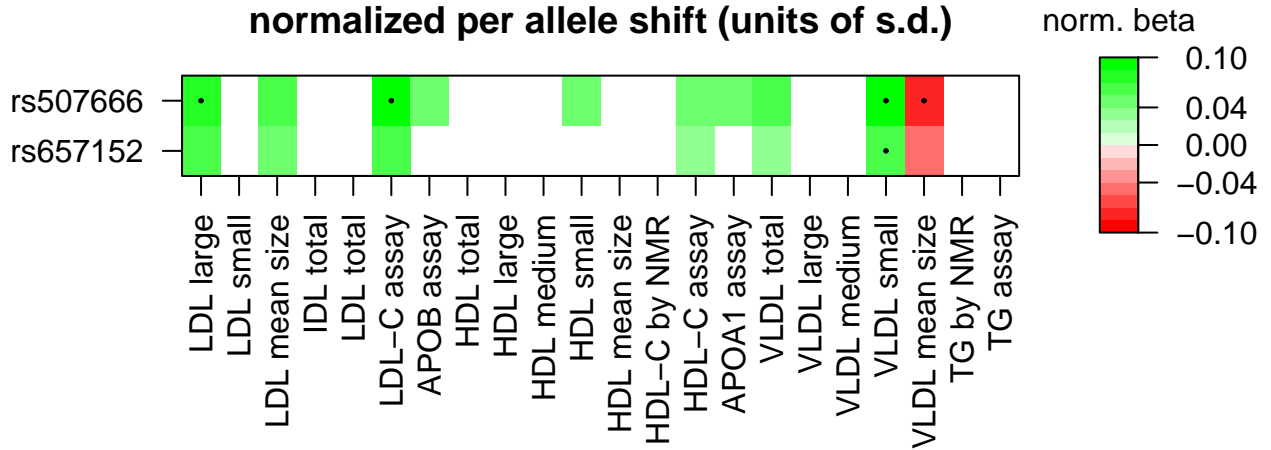
8q24.13 (TRIB1)
normalized per allele shift (units of s.d.)



9q31.1 (ABCA1)
normalized per allele shift (units of s.d.)



9q34.2 (ABO)
normalized per allele shift (units of s.d.)



20q13.12.B (PLTP)
normalized per allele shift (units of s.d.)

