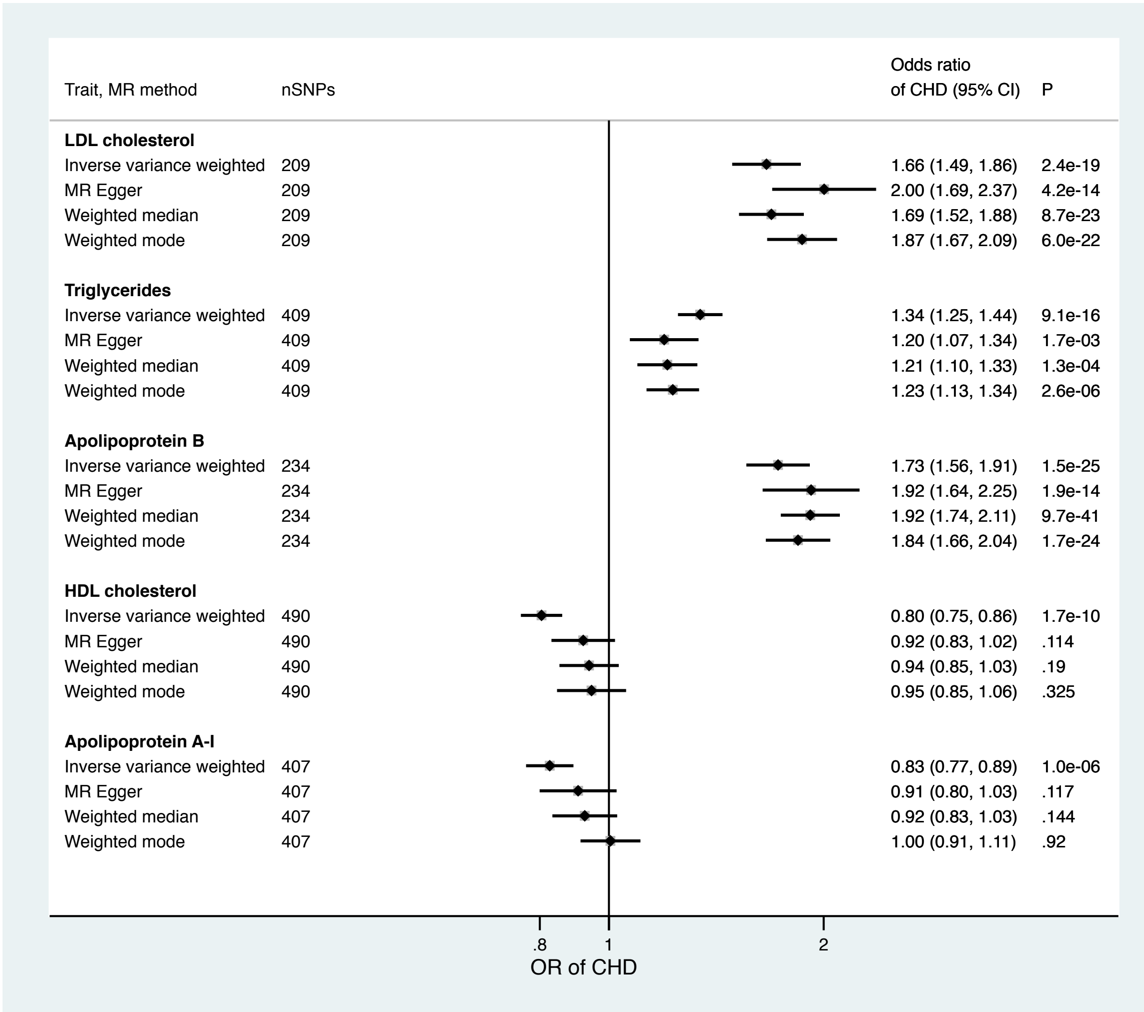
S2 Fig: Univariable Mendelian randomization estimates for individual lipid and apolipoprotein traits



Legend: Effect estimates are odds ratios of coronary heart disease (CHD) per 1 standard deviation higher genetically instrumented trait, using a range of univariable Mendelian randomization approaches (see Methods for further details). Plot generated using Stata SE 13.1 (StataCorp). CI = confidence interval, HDL = high-density lipoprotein, LDL = low-density lipoprotein, MR = Mendelian randomization, OR = odds ratio, nSNPs = number of single nucleotide polymorphisms.