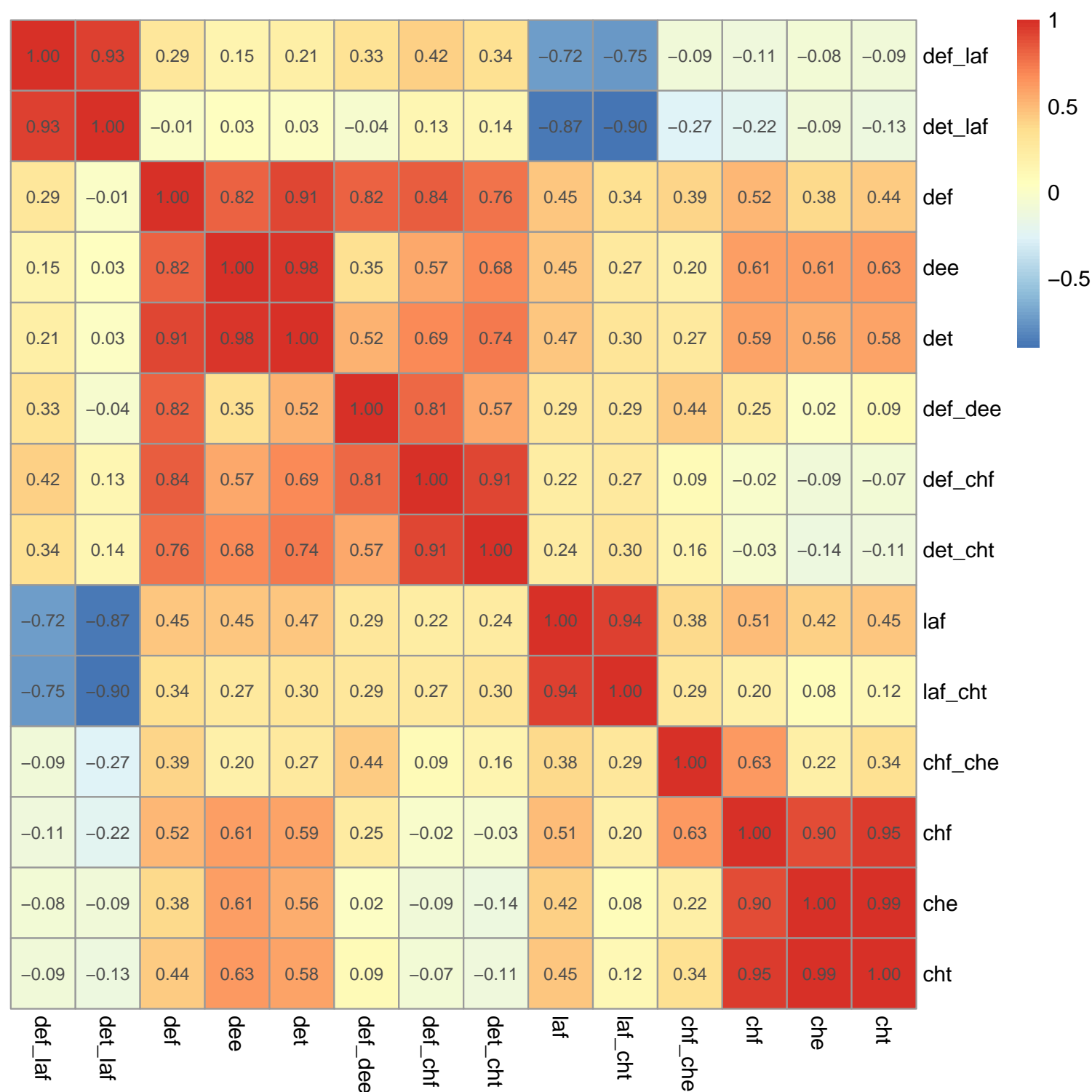
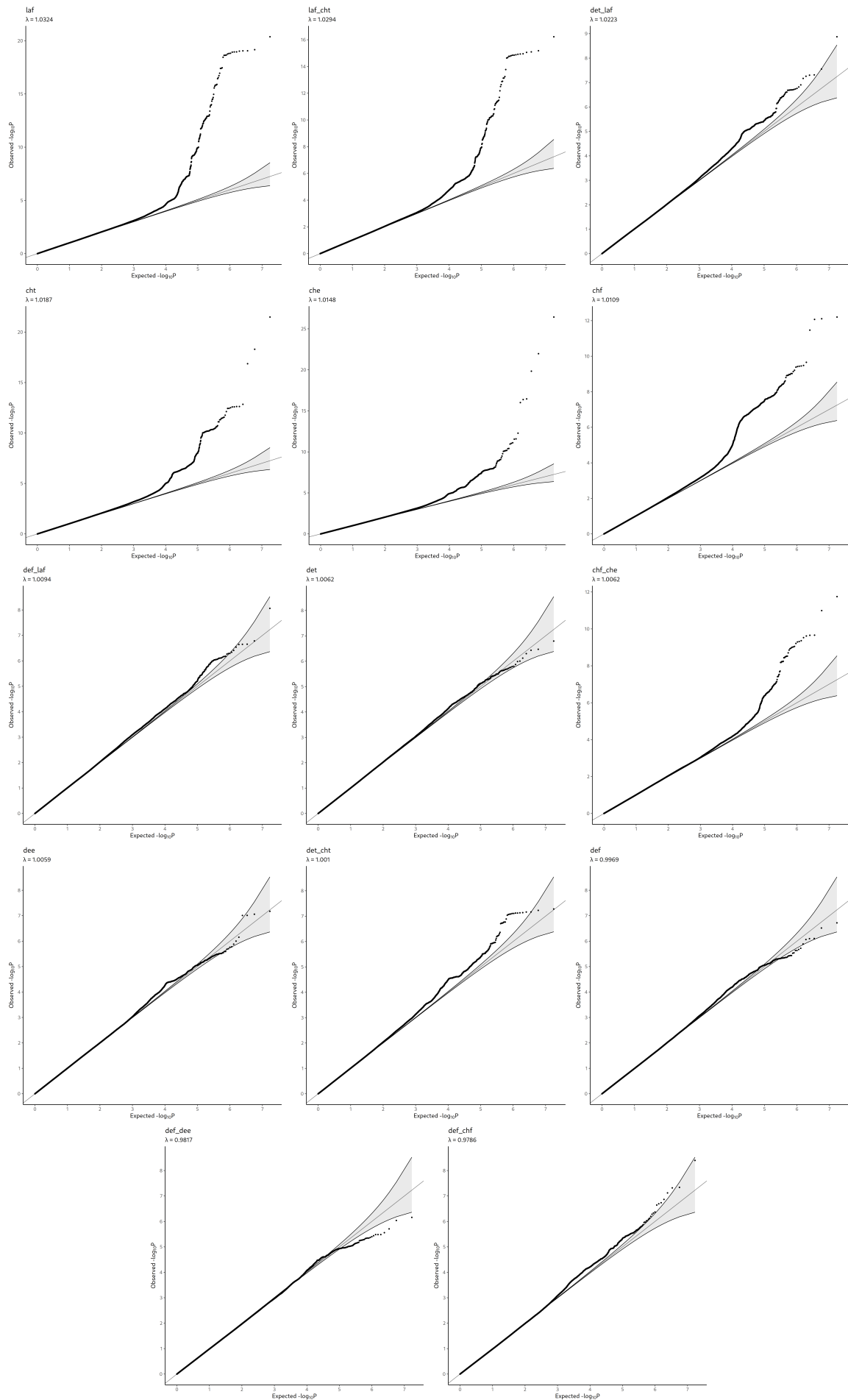


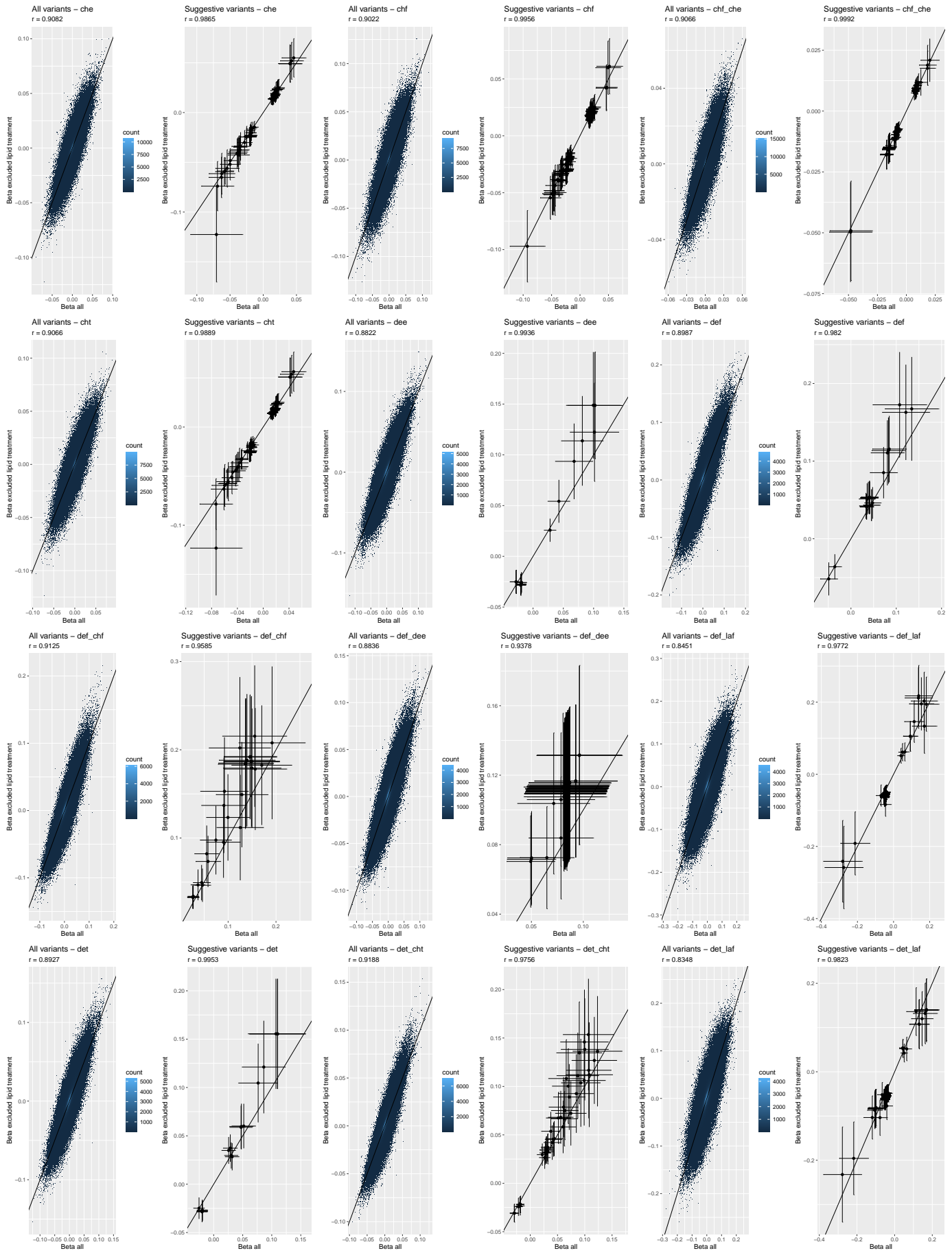
## Supplementary Figures



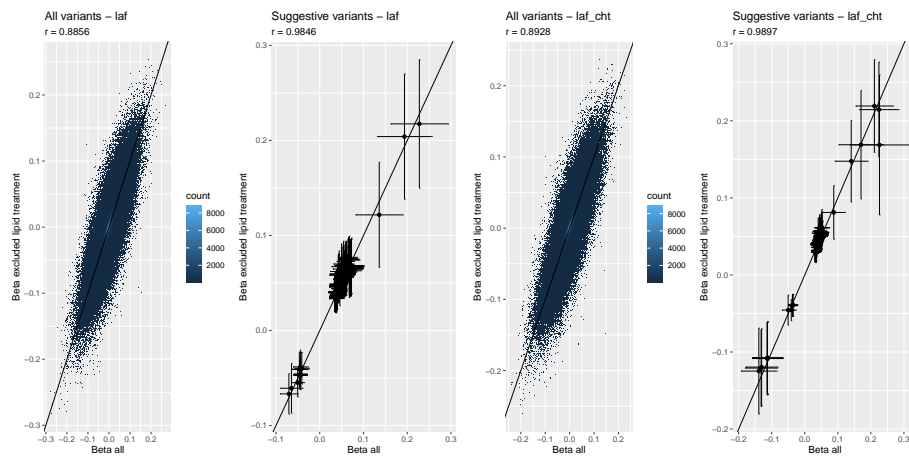
Sup. Fig. S1: Pearson correlation coefficients obtained from pairwise partial correlation of zoosterol traits. Phenotype abbreviations: laf - free lanosterol, def - free desmosterol, dee - esterified desmosterol, det - total desmosterol, chf - free cholesterol, che - esterified cholesterol, cht - total cholesterol. Ratio traits are indicated with an underscore.



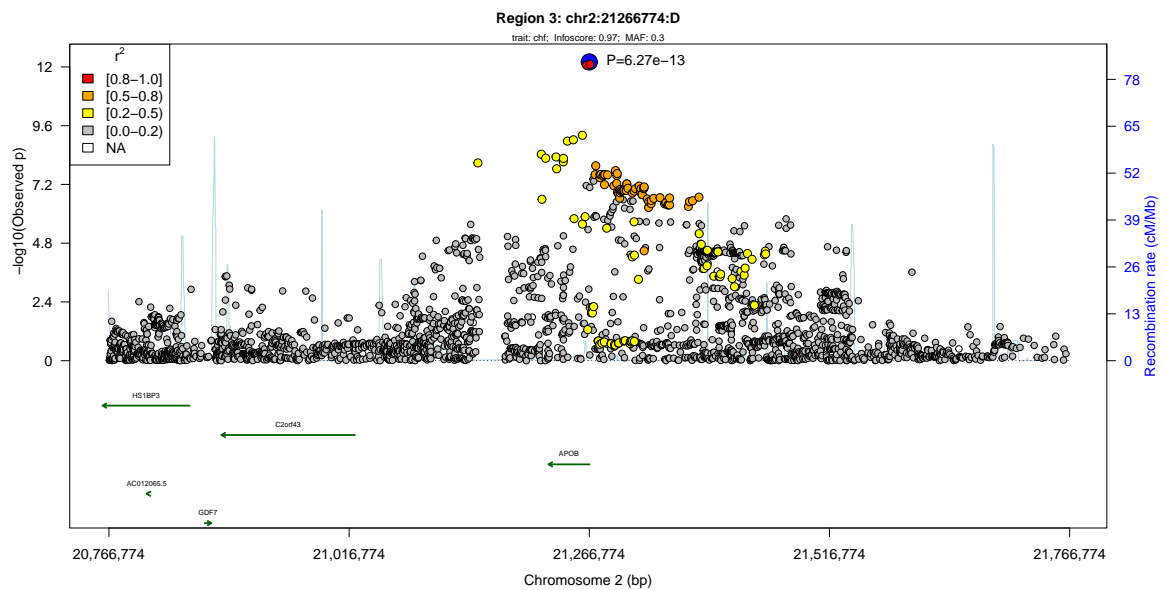
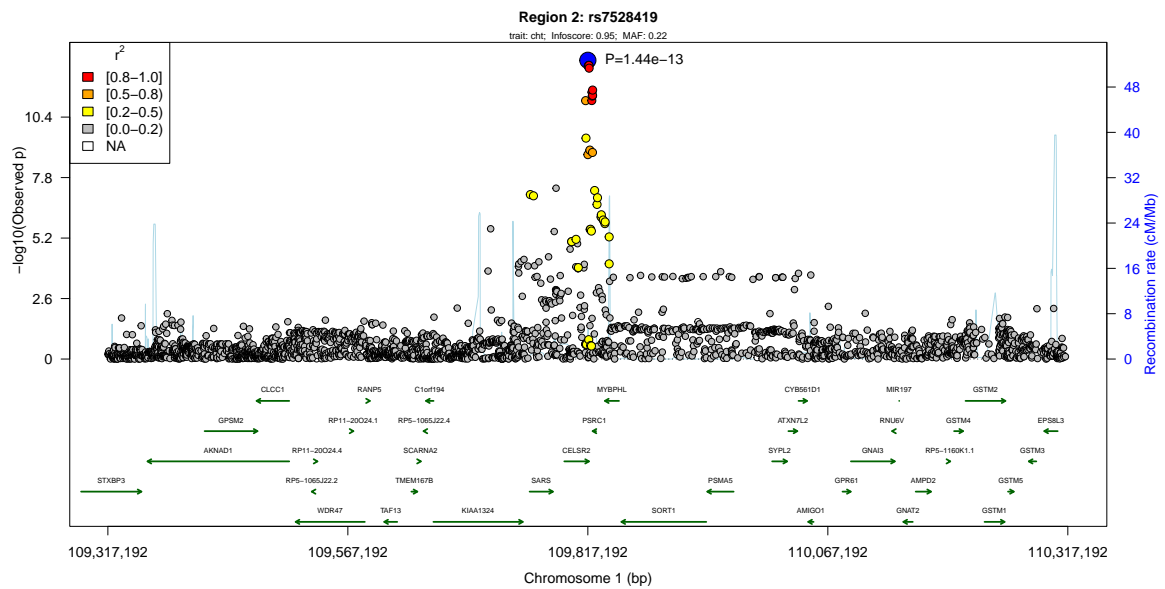
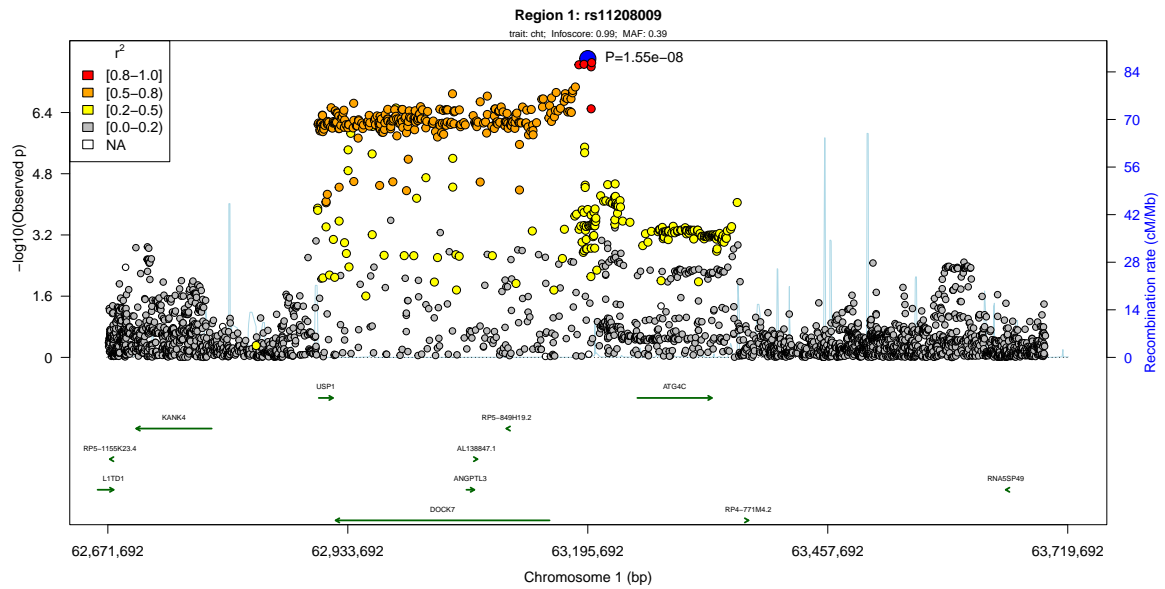
Sup. Fig. S2: Quantile-Quantile-plots and genomic-inflation factors  $\lambda$  for investigated traits. Only variants passing quality-control criteria were included in the calculation of  $\lambda$ . Traits are ordered from left to right in order of decreasing  $\lambda$ . Phenotype abbreviations: laf - free lanosterol, def - free desmosterol, dee - esterified desmosterol, det - total desmosterol, chf - free cholesterol, che - esterified cholesterol, cht - total cholesterol. Ratio traits are indicated with an underscore.

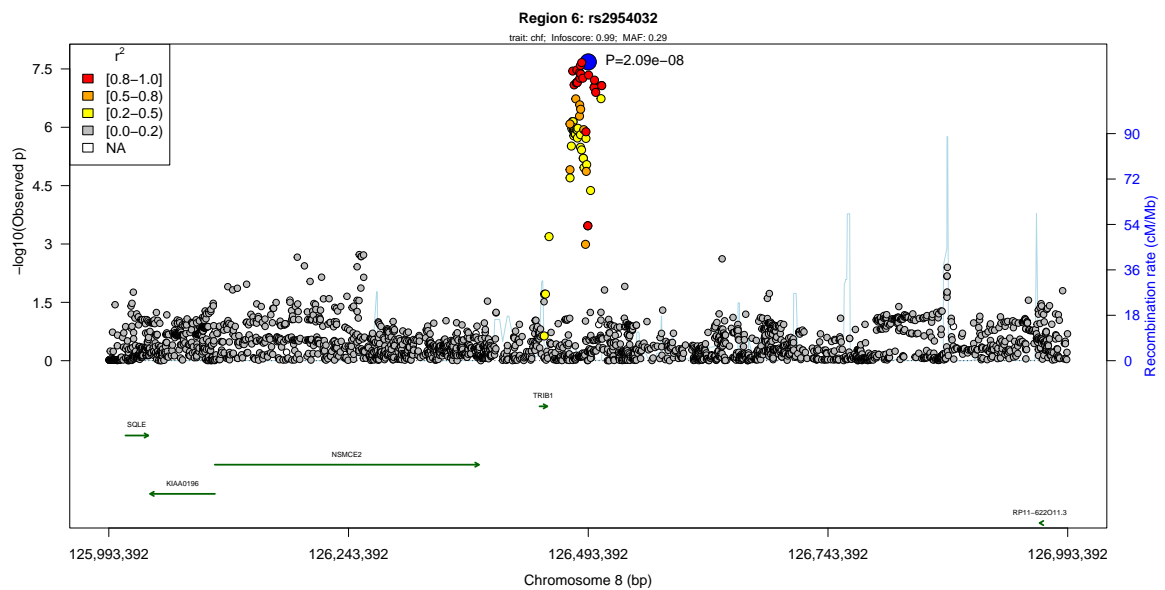
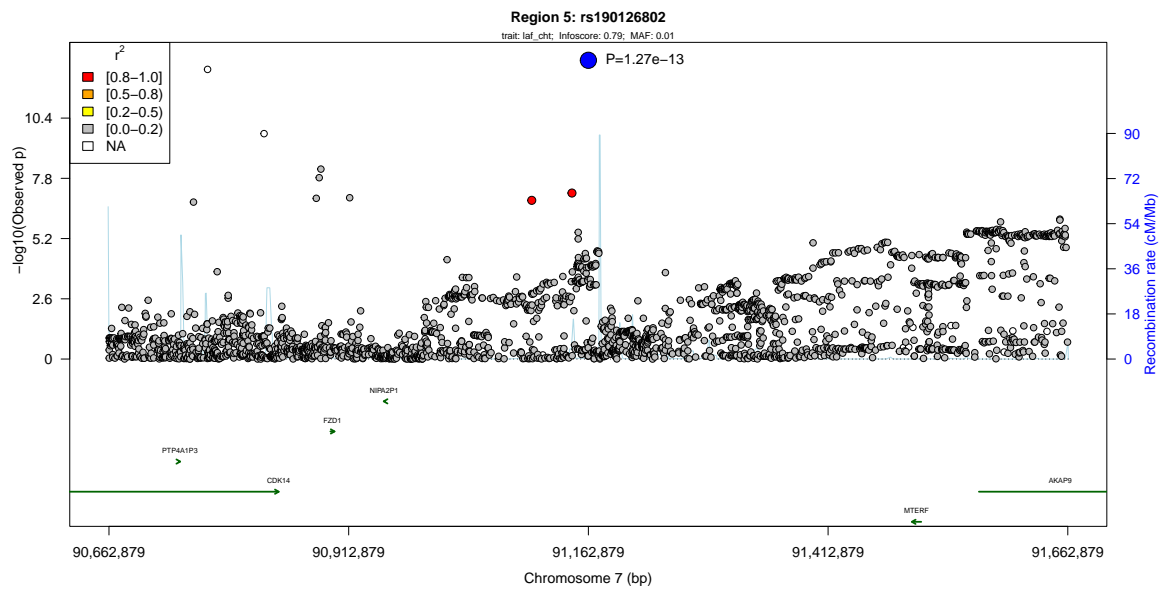
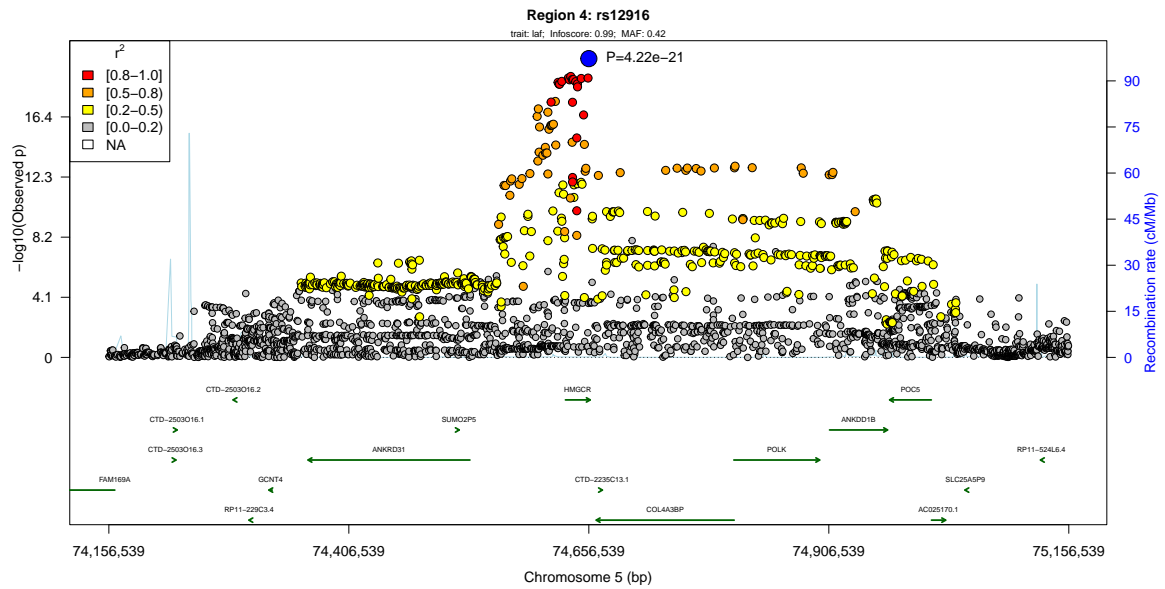


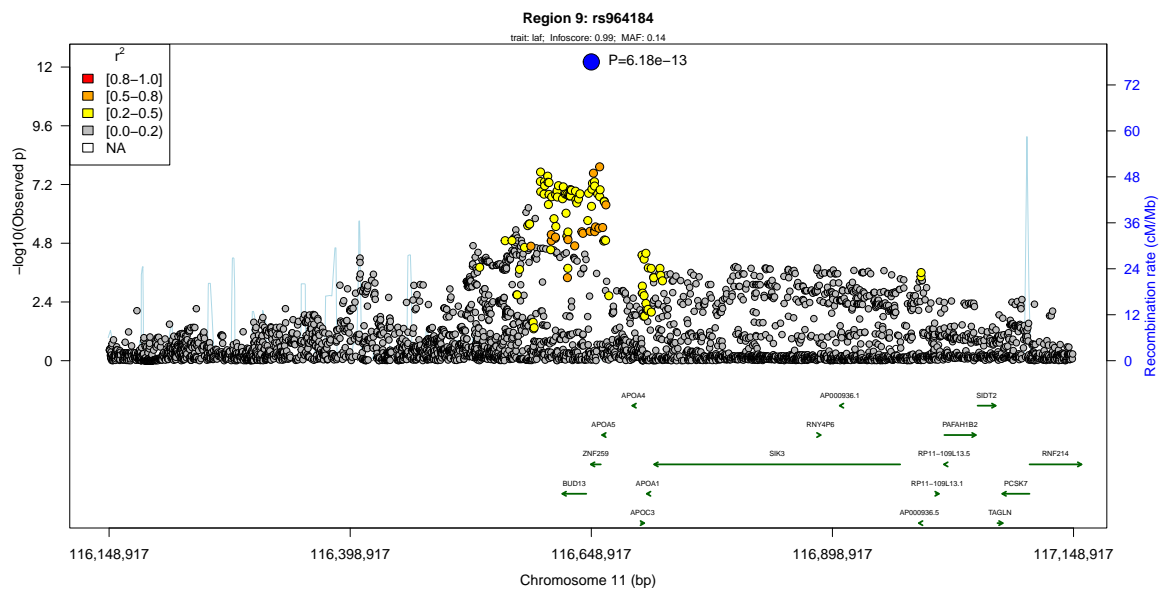
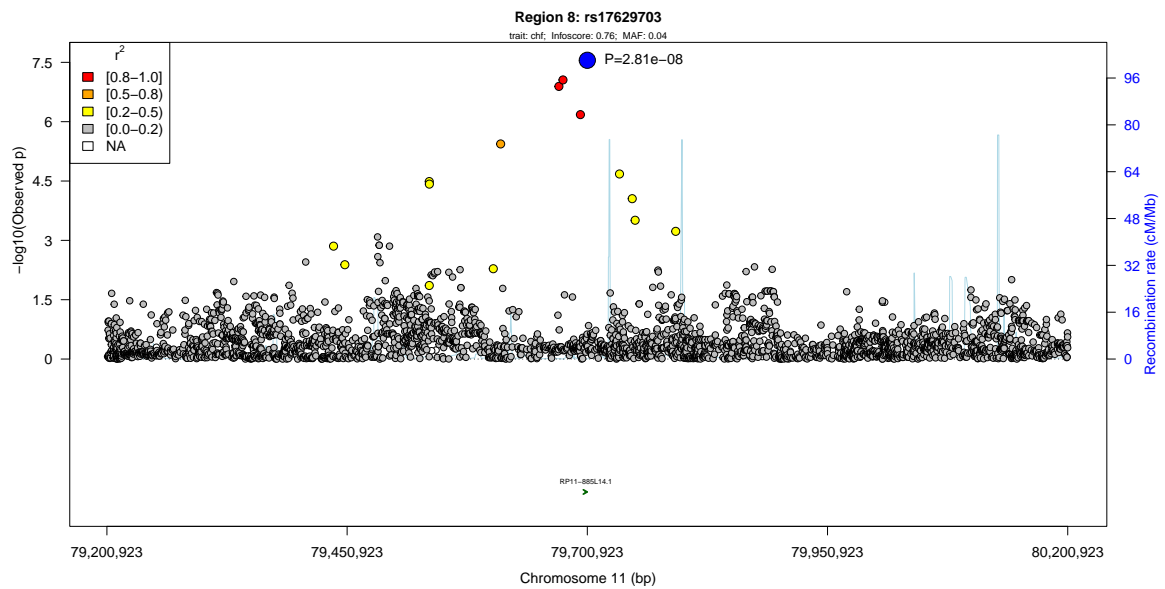
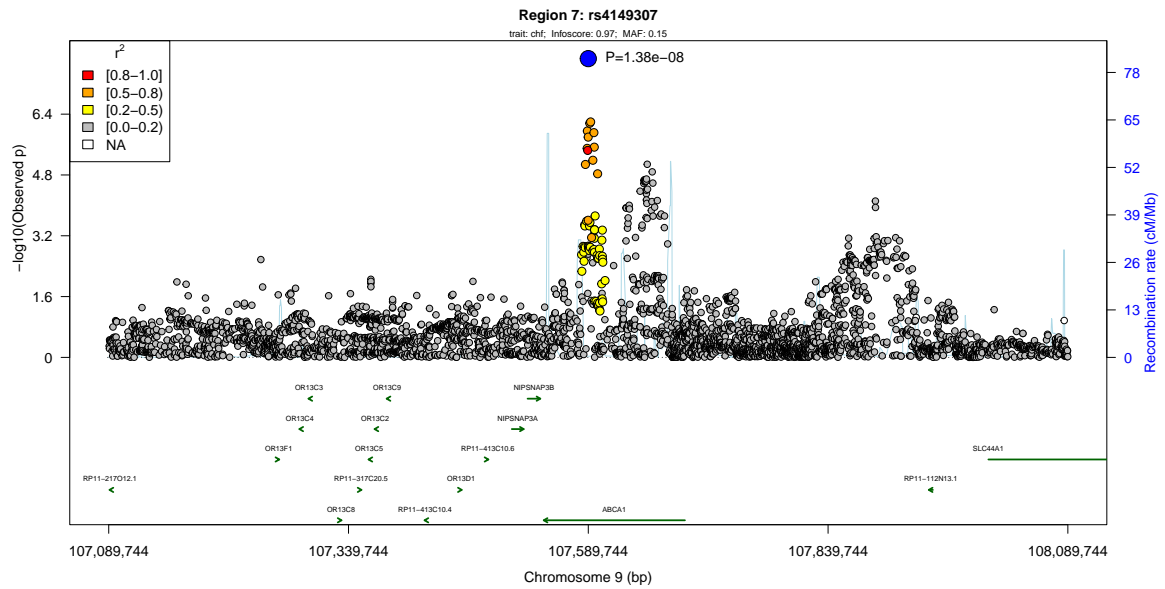


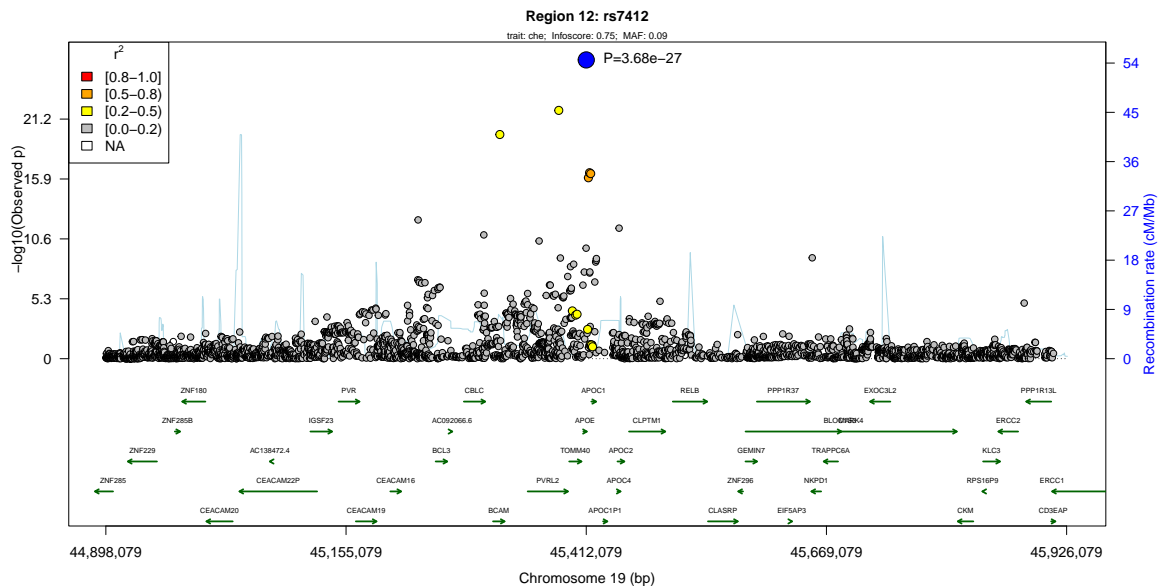
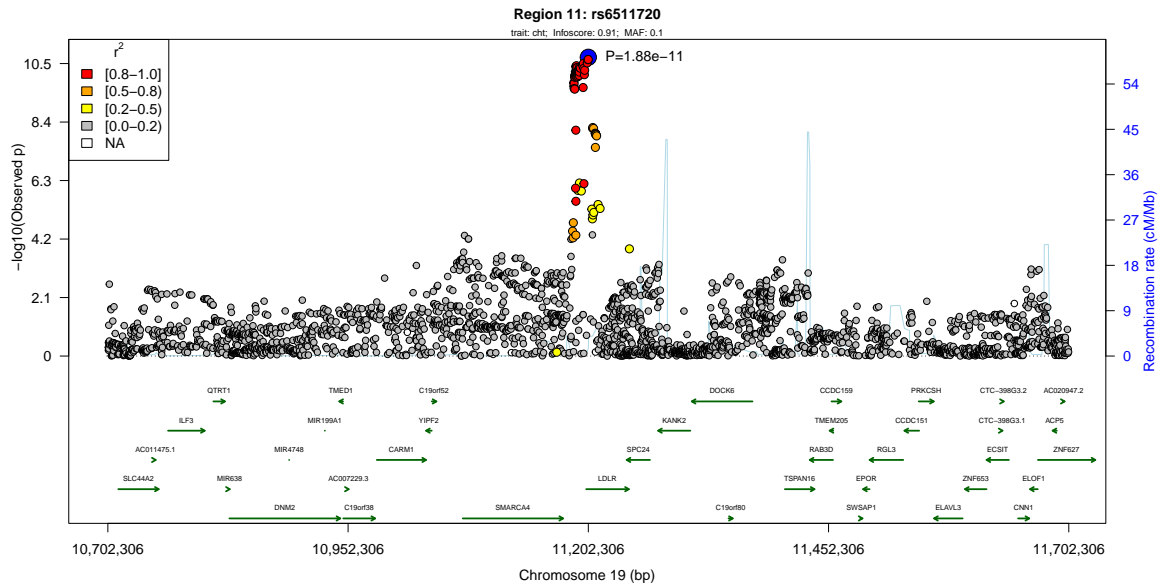
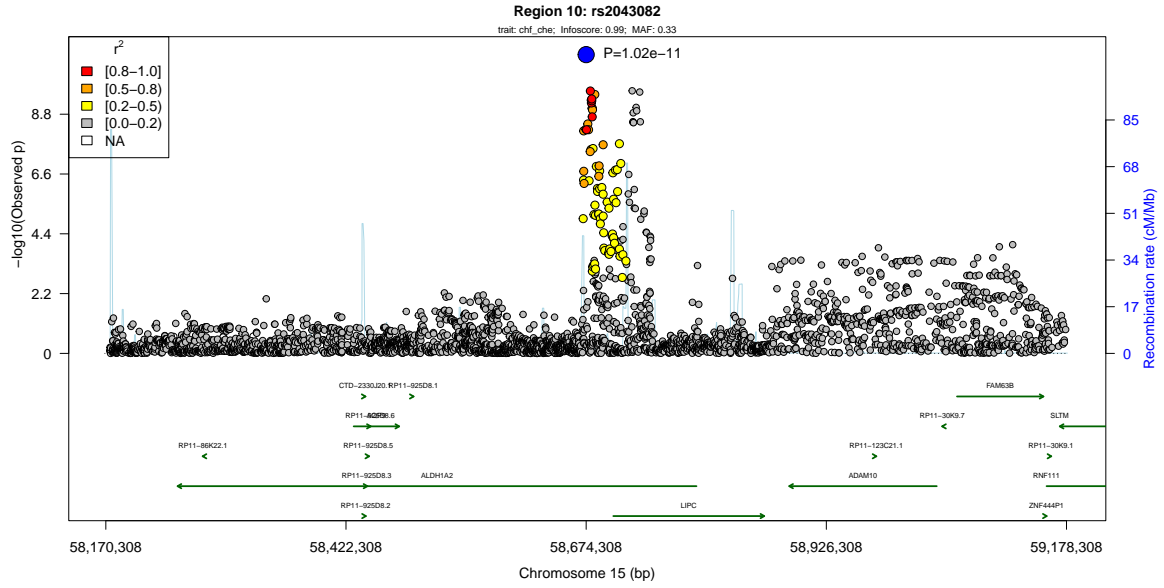


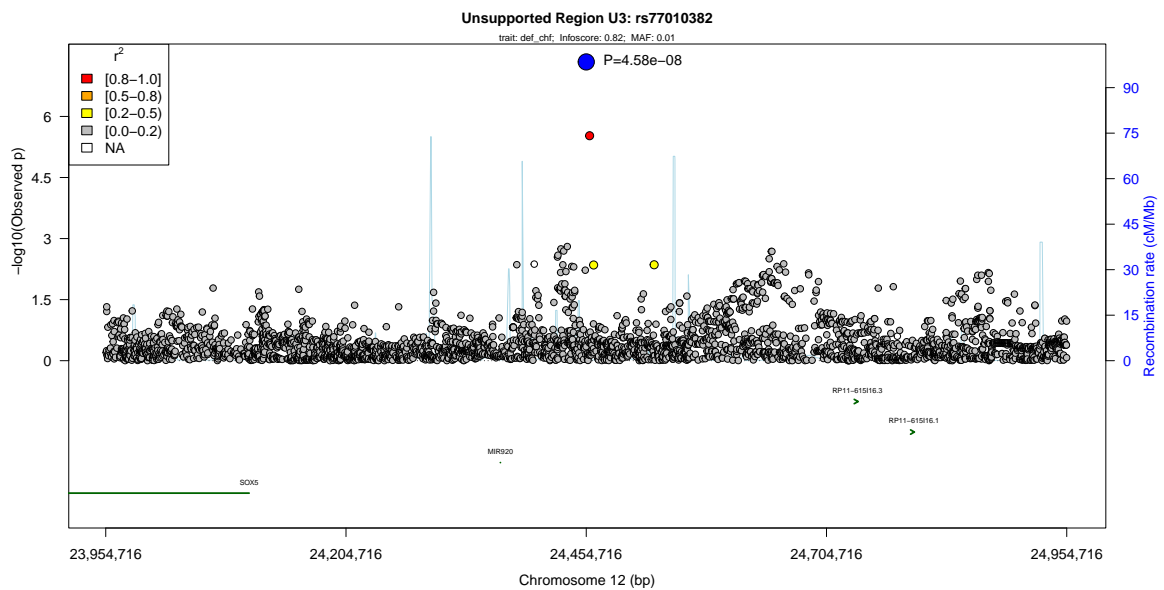
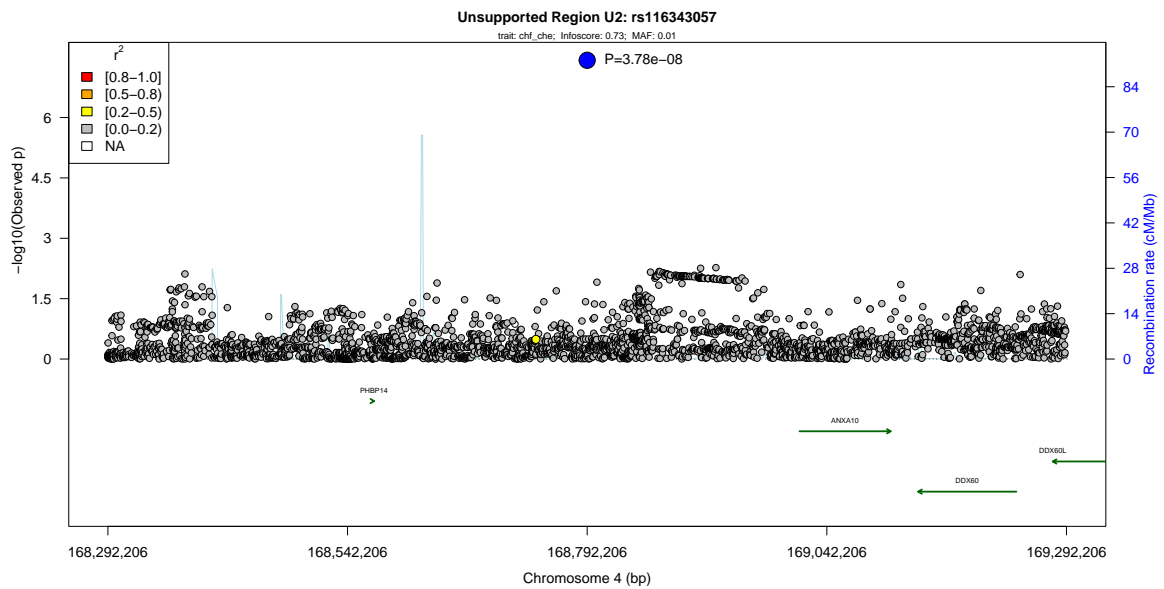
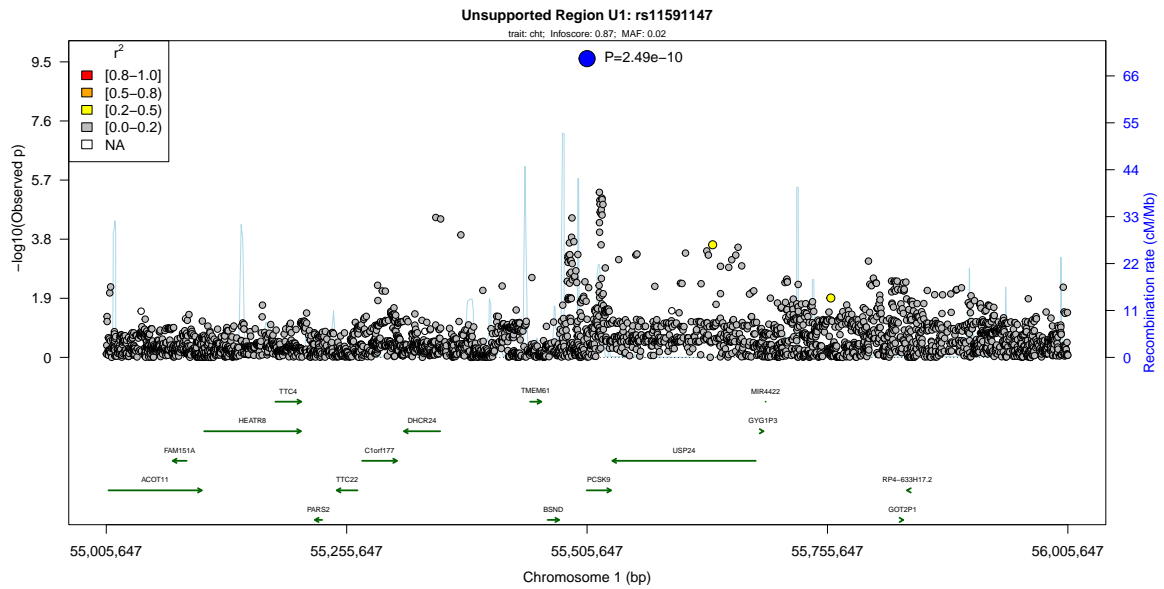
Sup. Fig. S3: Sensitivity analysis for the impact of lipid-lowering medication. Effect estimates of a meta-regression of all individuals including lipid-lowering medication as a covariate (Beta all) and a meta-regression excluding treated individuals (Beta excluded lipid treatment) are compared. Comparison and calculation of Pearson regression coefficients ( $r$ ) was done for all quality-filtered variants and the subset of variants that reached suggestive significance ( $p < 10^{-6}$ ) in either of the analysis settings. For suggestive variants, the 95% confidence interval is shown.

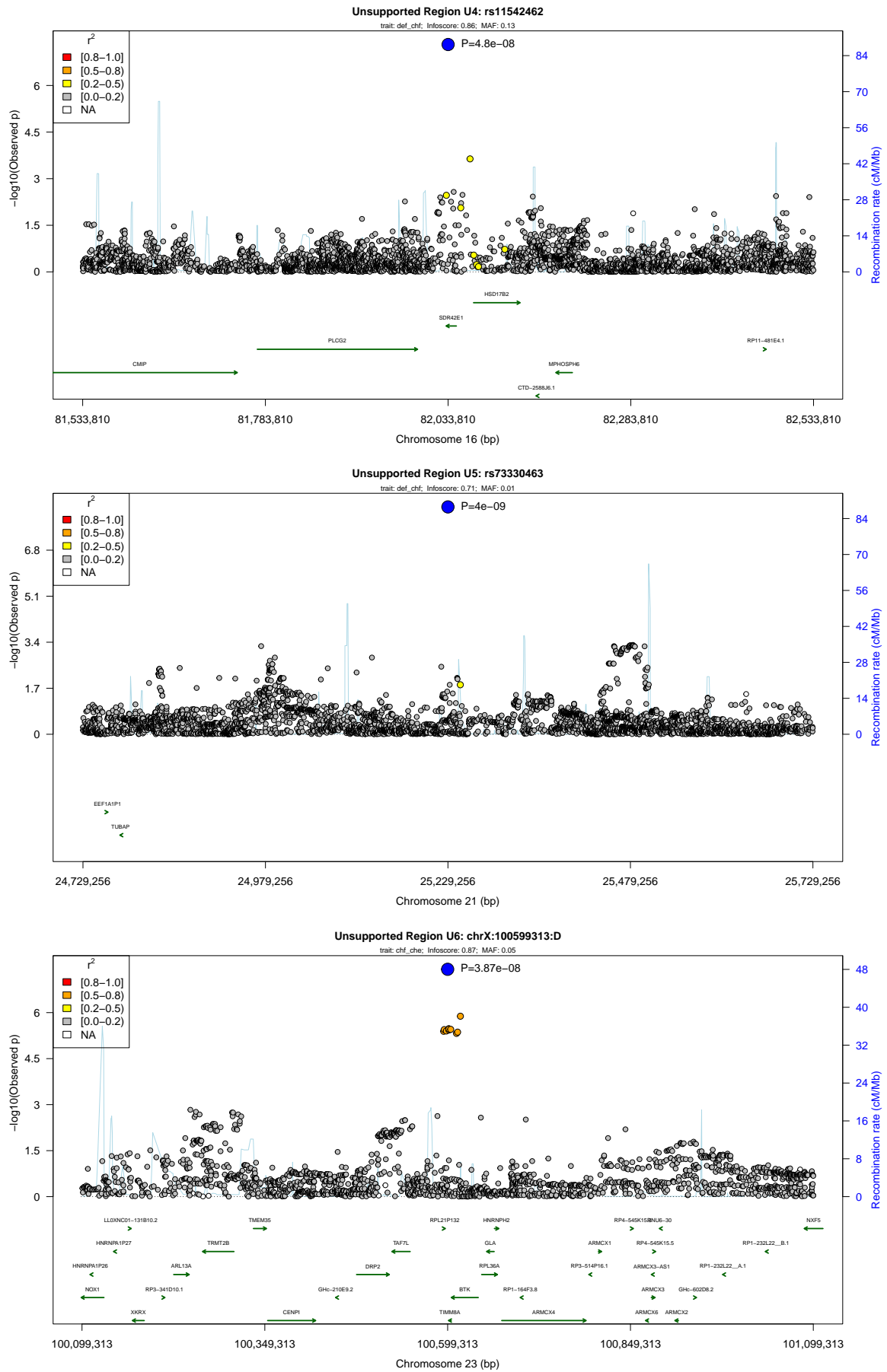




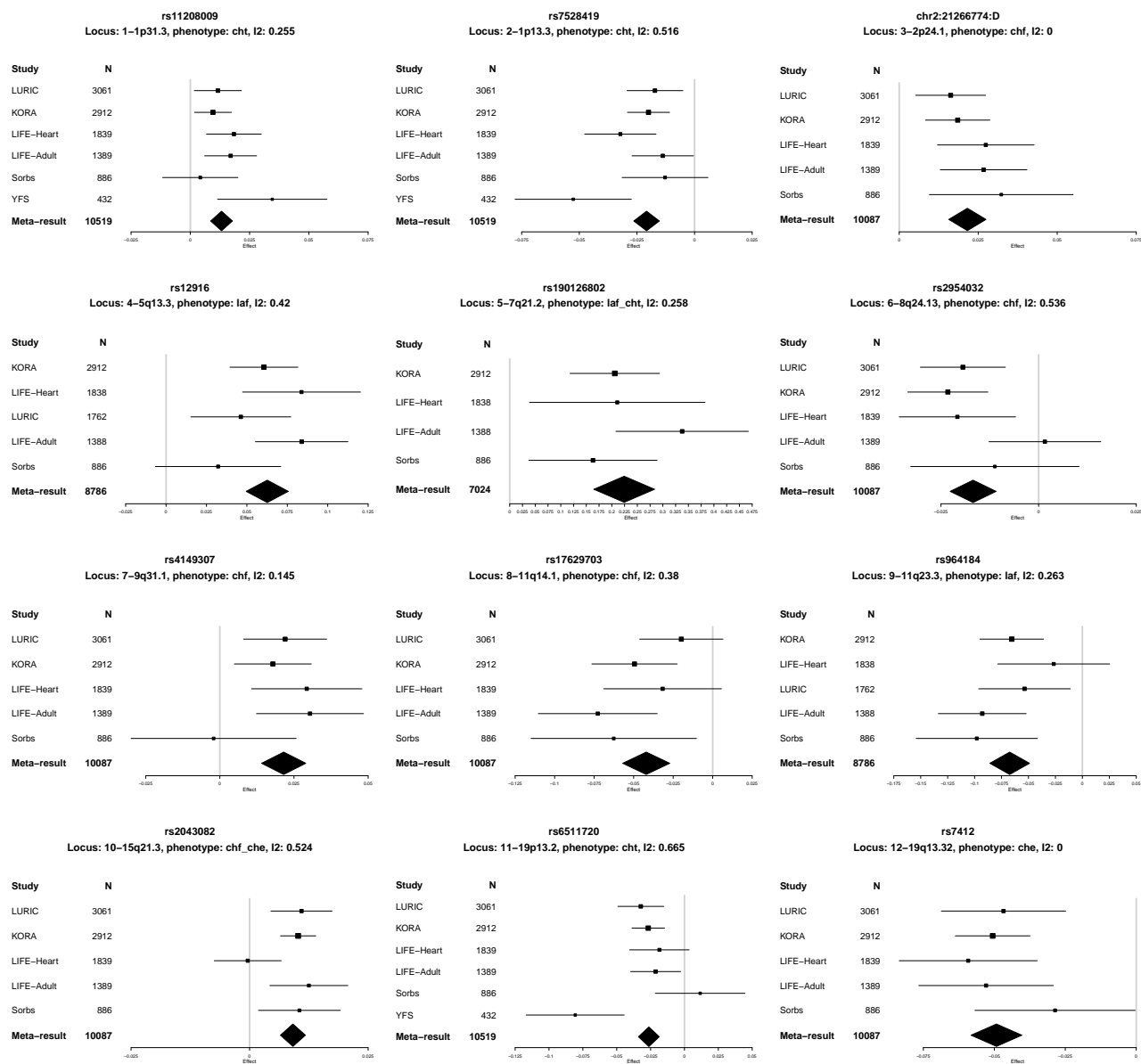






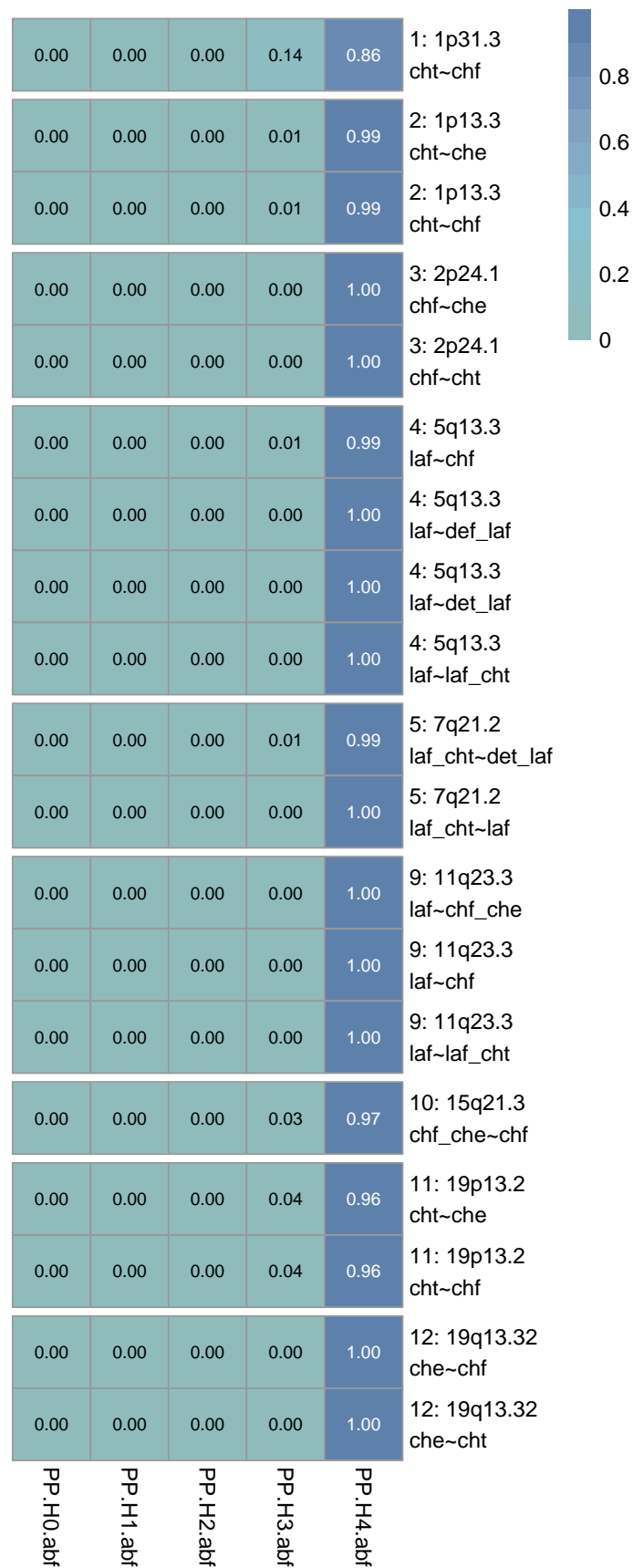


Sup. Fig. S4: Regional association plots of loci with genome-wide significant association with zoosterol traits. Only the best-associated trait is shown for each locus. Loci, where no variant besides the index variant reached at least suggestive significance ( $p < 10^{-6}$ ) were classified as unsupported.



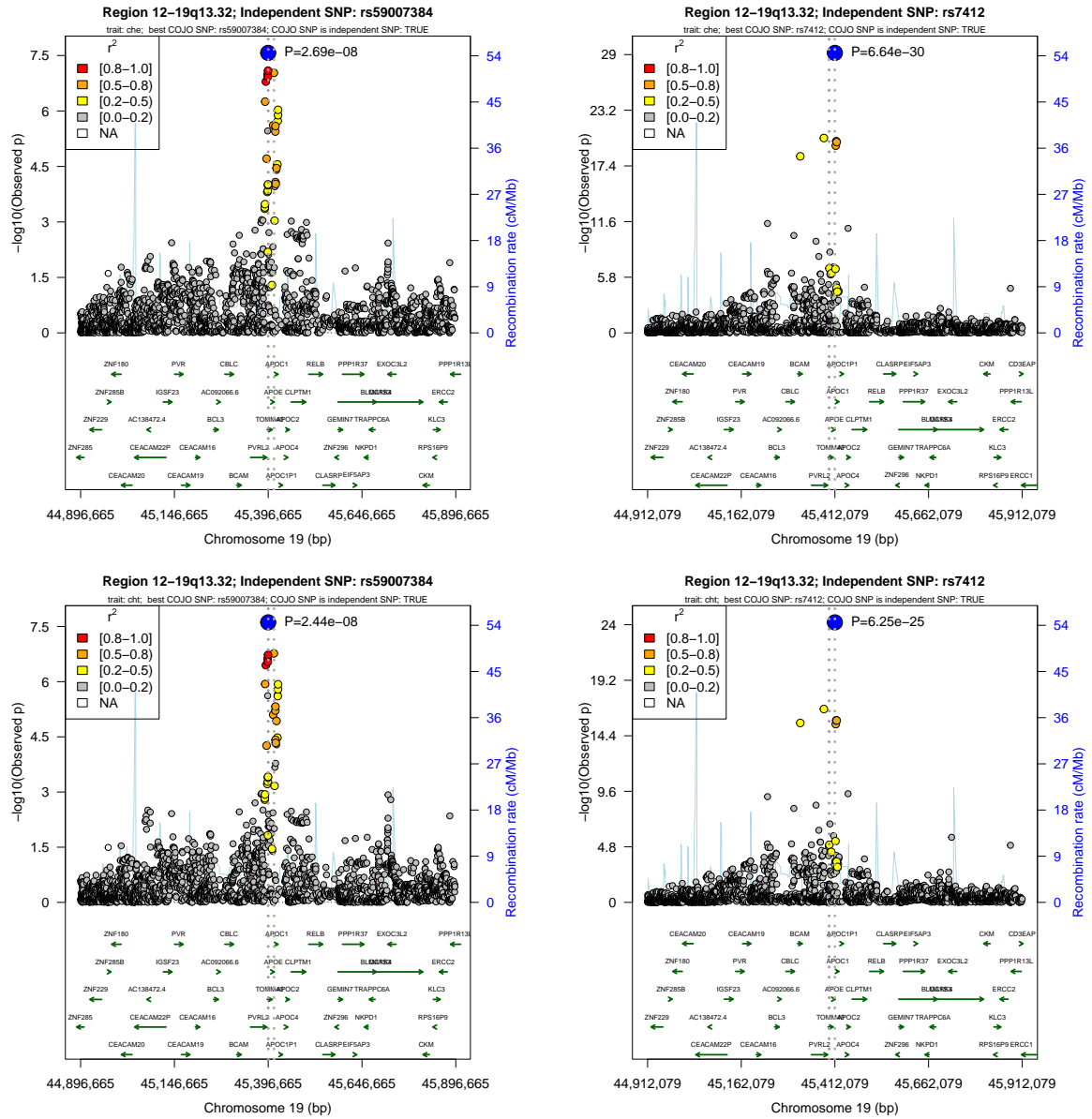
Sup. Fig. S5: Forest plots of supported genome-wide significant loci. Shown are single study effect estimates and corresponding 95% confidence intervals. Meta-results were calculated under a fixed-effect model, weighting studies according to their inverse variance. For each locus, data is shown for the best-associated phenotype. Phenotype abbreviations: laf - free lanosterol, def - free desmosterol, dee - esterified desmosterol, det - total desmosterol, chf - free cholesterol, che - esterified cholesterol, cht - total cholesterol. Ratio traits are indicated with an underscore.



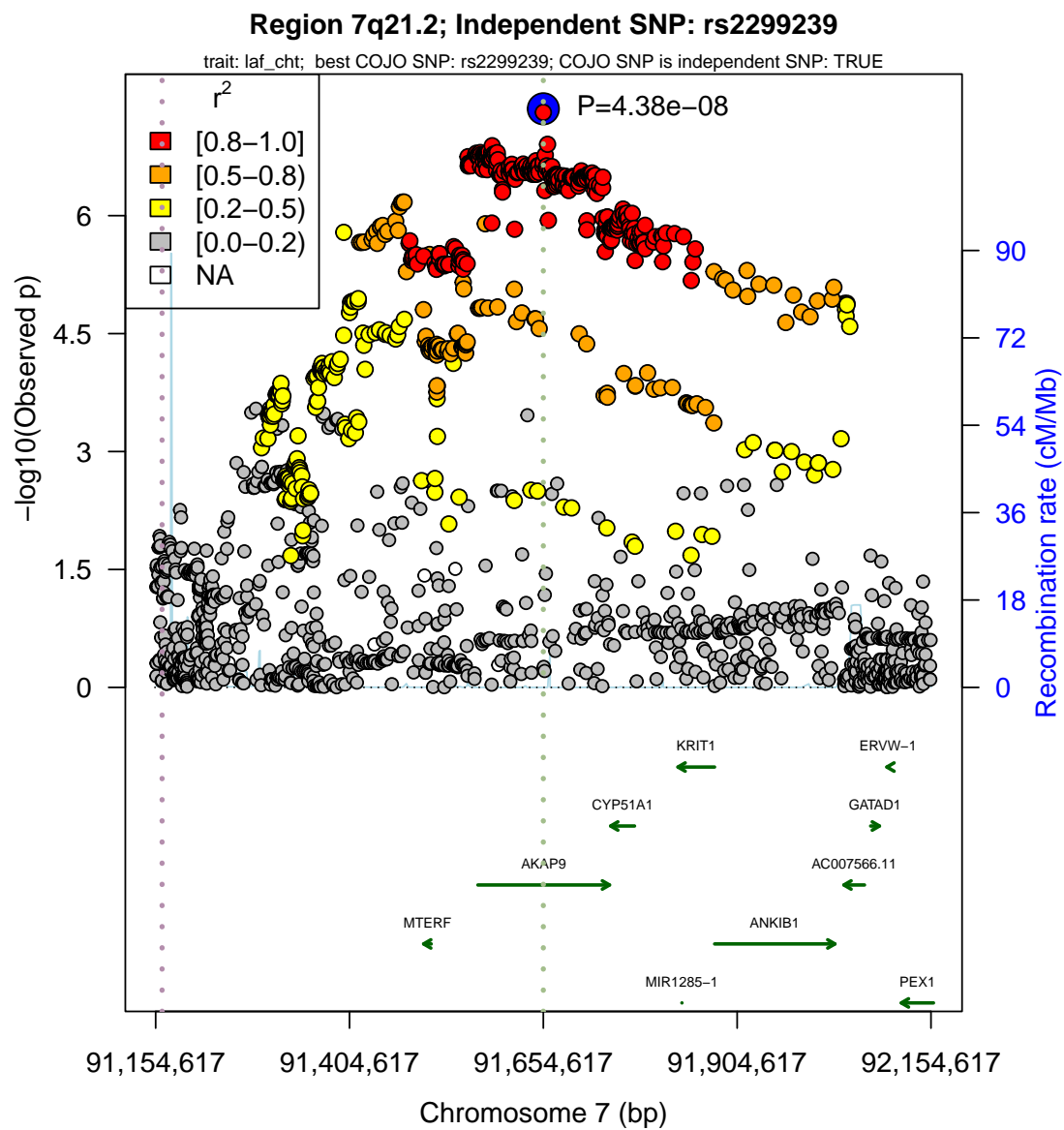


Sup. Fig. S6: Colocalization of traits with genome-wide significant association for loci with multiple associated traits. The analysed pair of traits is separated by a tilde. Phenotype abbreviations: laf - free lanosterol, def - free desmosterol, dee - esterified desmosterol, det - total desmosterol, chf - free cholesterol, che - esterified cholesterol, cht - total cholesterol. Ratio traits are indicated with an underscore.

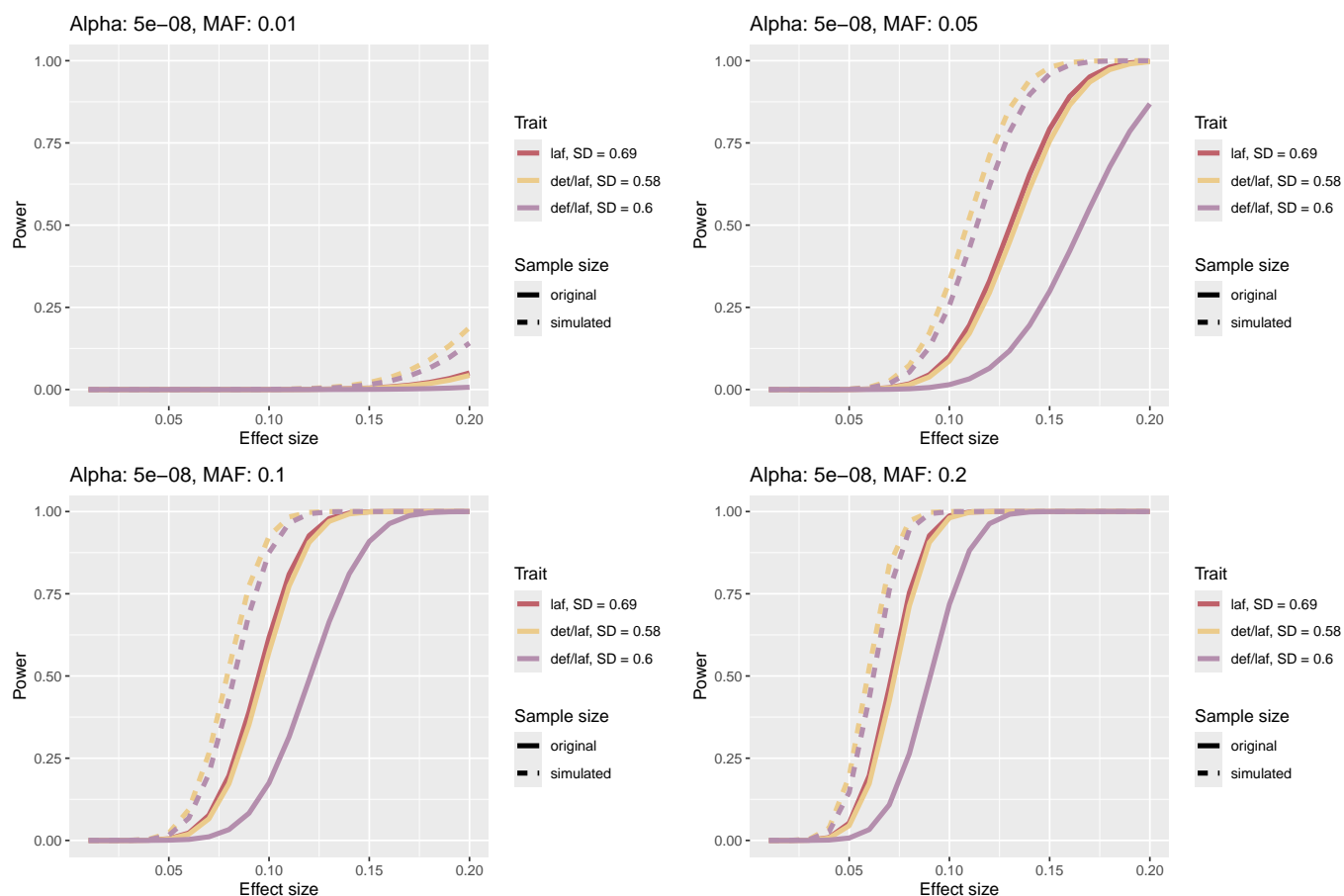




Sup. Fig. S7: Regional-association plots based on conditional statistics for loci with multiple independent variants. Conditional statistics for the best associated trait were obtained for the specified SNP by conditioning on all other independent variants at the respective locus. This procedure was iterated for each phenotype where multiple independent variants were found. Positions of independent variants are indicated by dotted lines. The variant with the strongest association after conditioning is shown as 'best COJO SNP'. If this variant is identical to the independent variant, the entry 'COJO SNP is independent SNP' is set to TRUE.



Sup. Fig. S8: Regional-association plot based on conditional statistics for the secondary independent variant rs2299239 found at locus 7q21.2. The original locus was extended 500 kb downstream before conditioning on the index variant rs190126802.



Sup. Fig. S9: Power analysis for lanosterol and desmosterol to lanosterol ratios for a range of minor allele frequencies. Power was calculated for free lanosterol (laf), total desmosterol to lanosterol ratio (det/laf), and free desmosterol to lanosterol ratio (def/laf). Original sample sizes (laf: 8786, det/laf: 5873, def/laf: 4111) were used. We also simulated power for desmosterol ratios, when sample size increased to that of free lanosterol. The x-axis shows the effect size and the y-axis the power. We assumed an additive genetic model. Standard deviation (SD) of traits was calculated in LIFE-Heart.