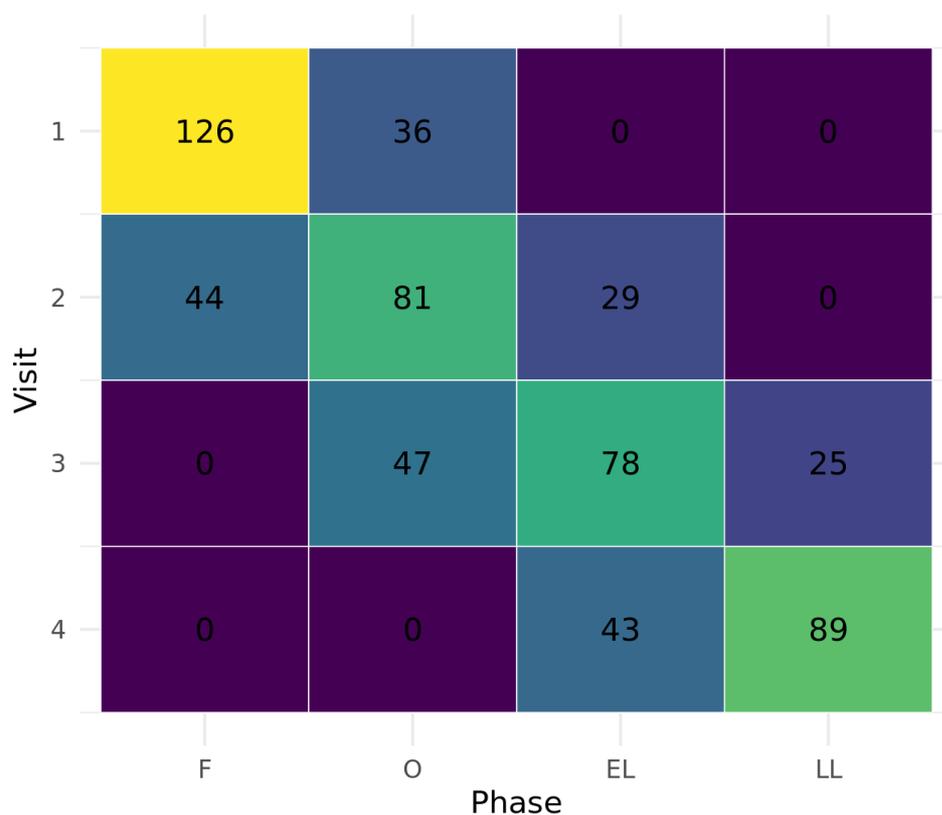# Supplementary Figures

Figure S1. Confusion matrix of the visit number vs predicted menstrual phase.
The matrix provides the number of samples for each visit (Y axis) and for each newly attributed phase (X axis). Off the diagonal it shows for how many samples the re-classified phase did not correspond to the original visit.
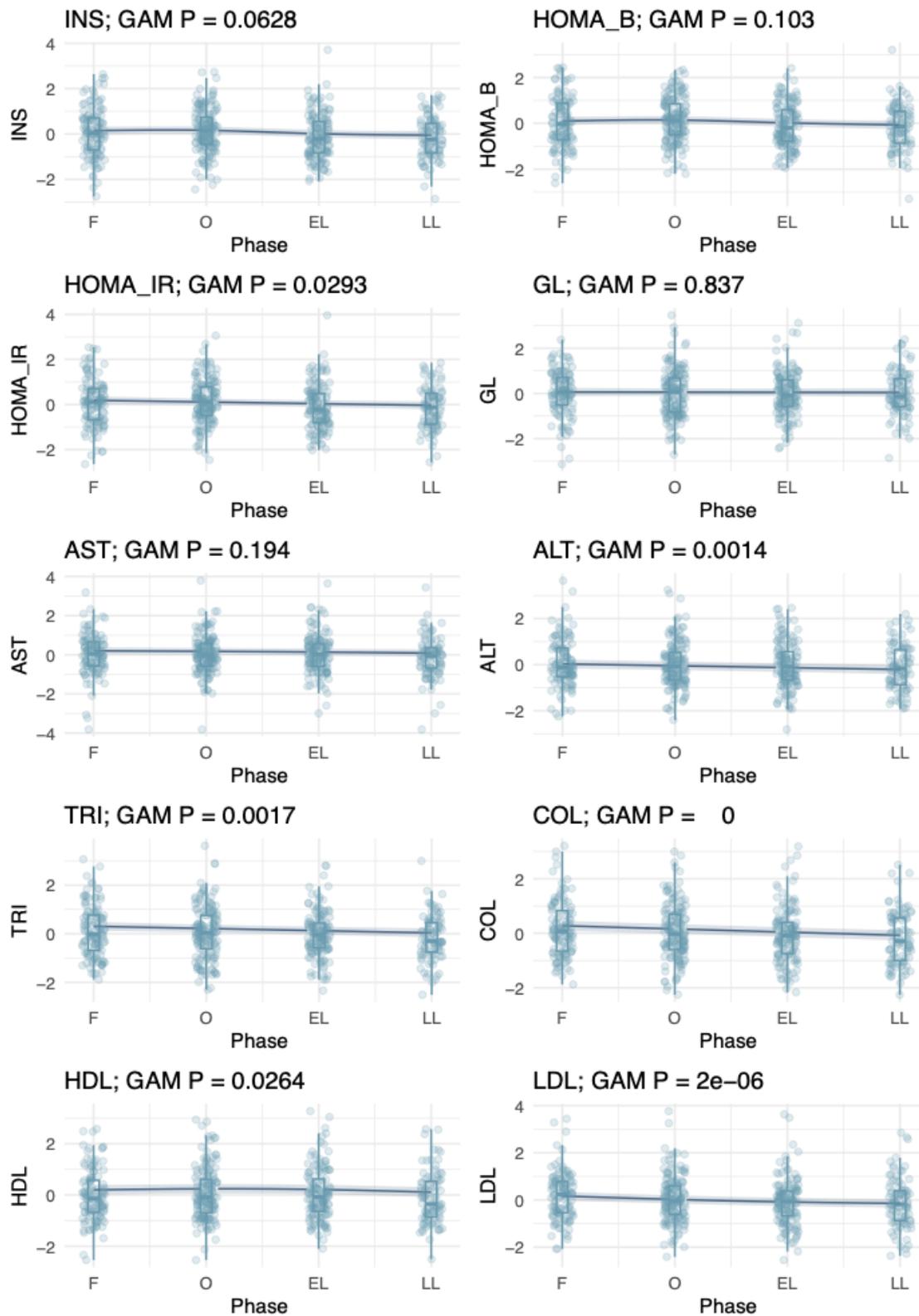
Figure S2. Changes in CMD-related phenotype levels during the menstrual cycle.
Phases are given on the X axis, while phenotype values adjusted for covariates are shown on the Y axis. Lines correspond to predicted values based on GAM fits.INS - insulin, HOMA_B - homeostasis model assessment of β-cell function, HOMA_IR - homeostasis model assessment of insulin resistance, GL - glucose, AST - aspartate aminotransferase, ALT - alanine aminotransferase, TRI - triglycerides, COL - total cholesterol, HDL - high-density lipoprotein cholesterol, LDL - low-density lipoprotein cholesterol.
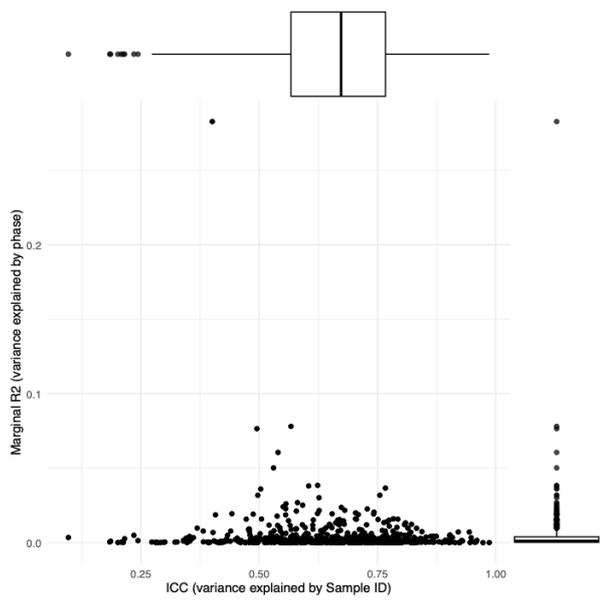
Figure S3. Heatmap of associations between covariate and protein PCs.
Association with continuous covariates was estimated using linear regression; association with categorical covariates was estimated using Kruskall-Wallis test. Colours represent significance of the association. Bonferroni-significant associations are marked with an asterisk.

Figure S4. Contribution of intra- and inter- individual variance to variation in protein abundance. For each protein the scatter plot shows on the X axis the ICC value (the amount of protein variance explained by inter-individual variation) and on the Y axis - the contribution of phase number to the total protein variance. Box plots at the top and side of the plot represent the overall distribution of X and Y axes, respectively.
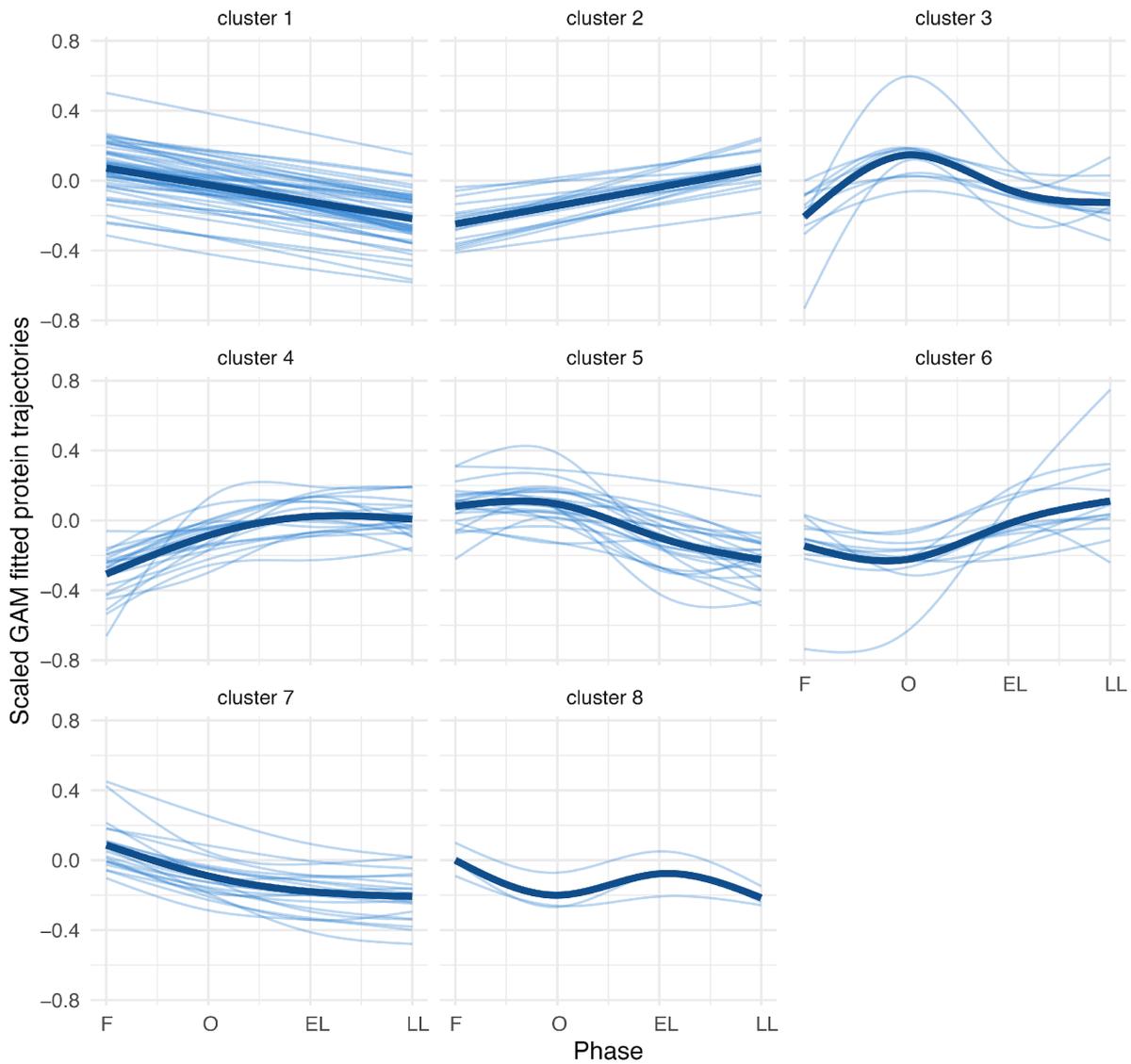
Figure S5. Clustering of protein trajectories.
Hierarchical clustering was performed separately on linear (cluster 1 and 2) and non-linear (cluster 3-8) fitted trajectories. Light blue lines reflect GAM curves predicted for eah protein at 100 time points, while the bold line represents the average for all trajectories of the cluster.
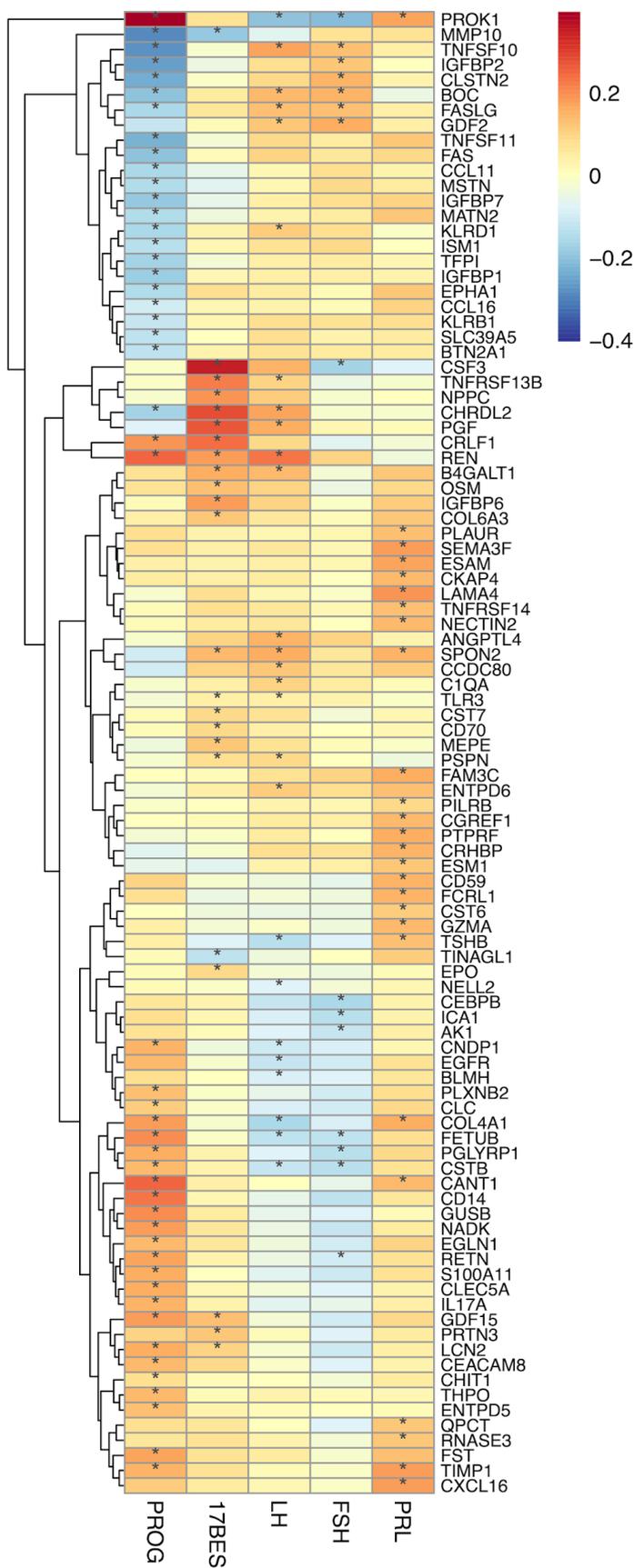
Figure S6. Heatmap of all associations between proteins and sex hormones.
The heatmap shows associations between proteins and sex hormones, with squares coloured
according to effect estimates obtained from the GAM model as indicated in the colour code bar.
Rectangles are marked with an asterisk if the p-value adjusted for multiple testing is below 0.05.
Clustering on the left side is performed based on association effect estimates using hierarchical
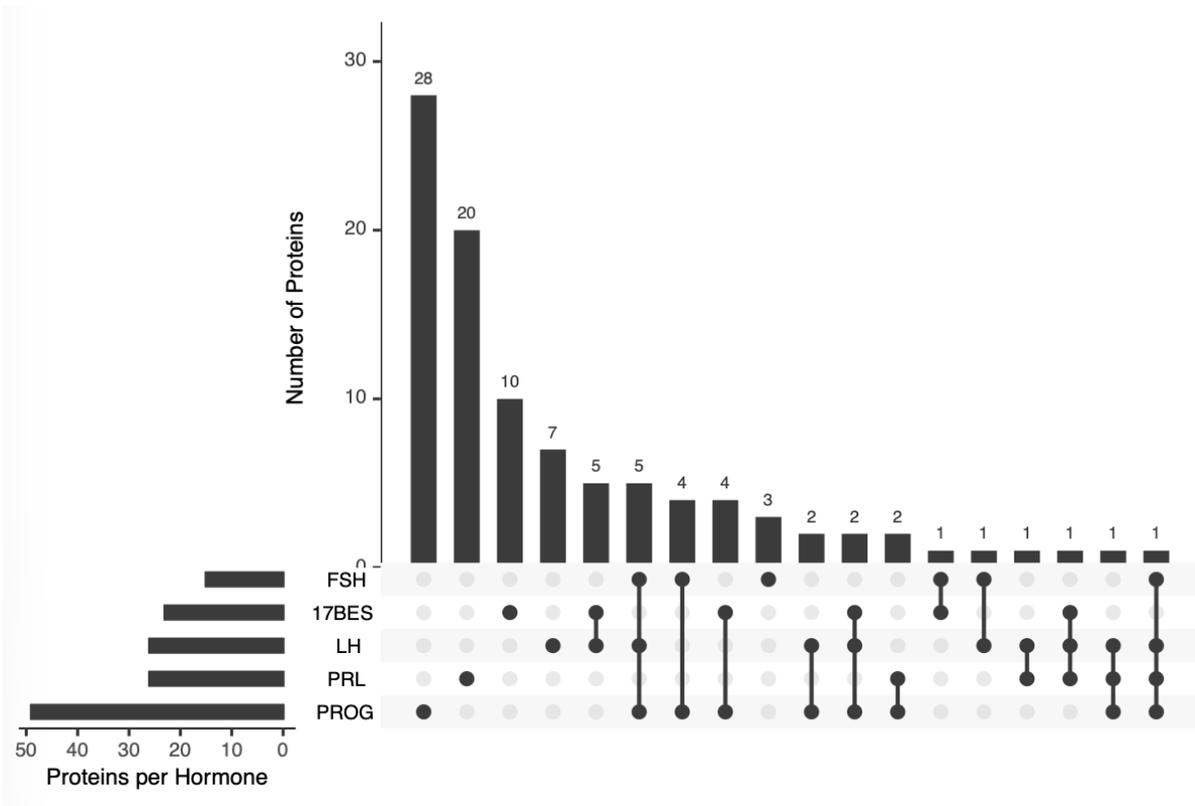clustering.

Figure S7. Overlap of the associated proteins between sex hormones

The figures shows the distribution of the number of proteins associated with each or multiple sex hormones. On the left side, the histogram shows total number of proteins associated with each hormone
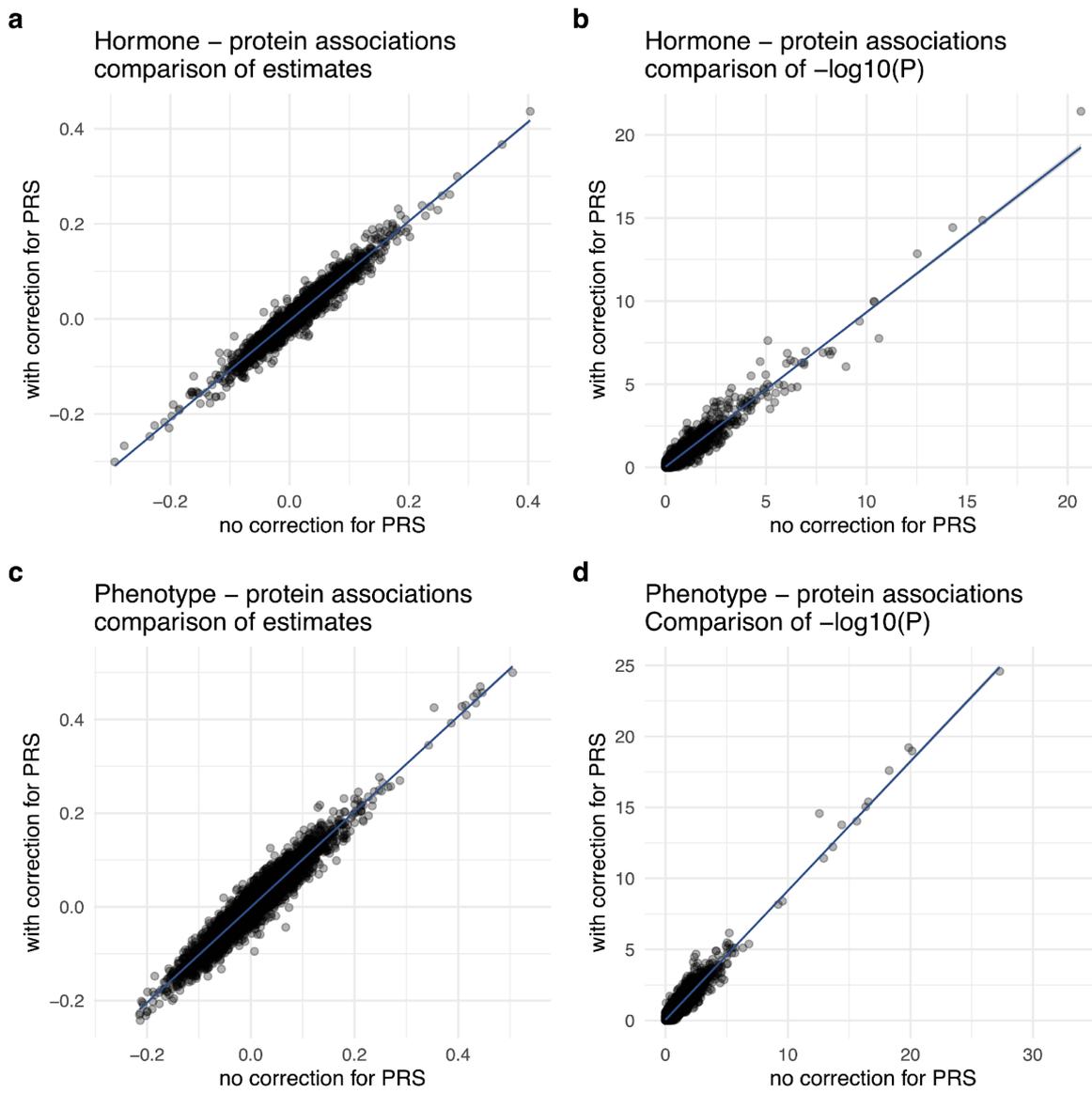
a Hormone − protein associations comparison of estimates

b Hormone − protein associations comparison of −log10(P)

c Phenotype − protein associations comparison of estimates

d Phenotype − protein associations Comparison of −log10(P)

Figure S8. Comparison of association results with and without correction for PRS.
Scatter plot for the comparison of association results between hormones − protein (a,b) and phenotype − protein (c,d) associations. We plotted model estimates (a, c) and −log10(p-values) (b,d).
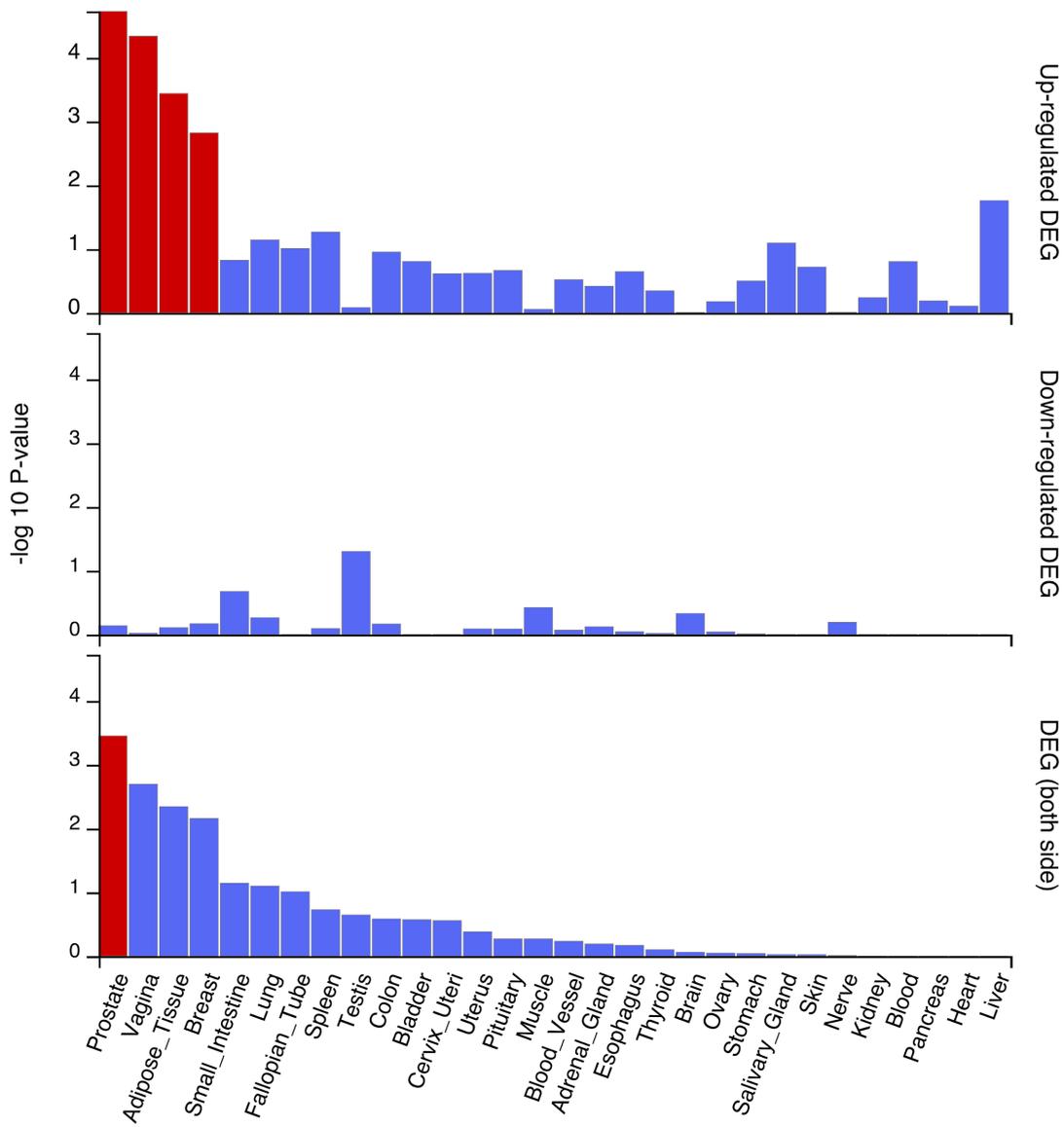
Figure S9. Tissue enrichment analysis of hormone-associated proteins
Tissue enrichment for significant hormone-associated proteins combined from both main analysis and batch 2 analysis done using FUMA based on GTEx v.8 gene sets.
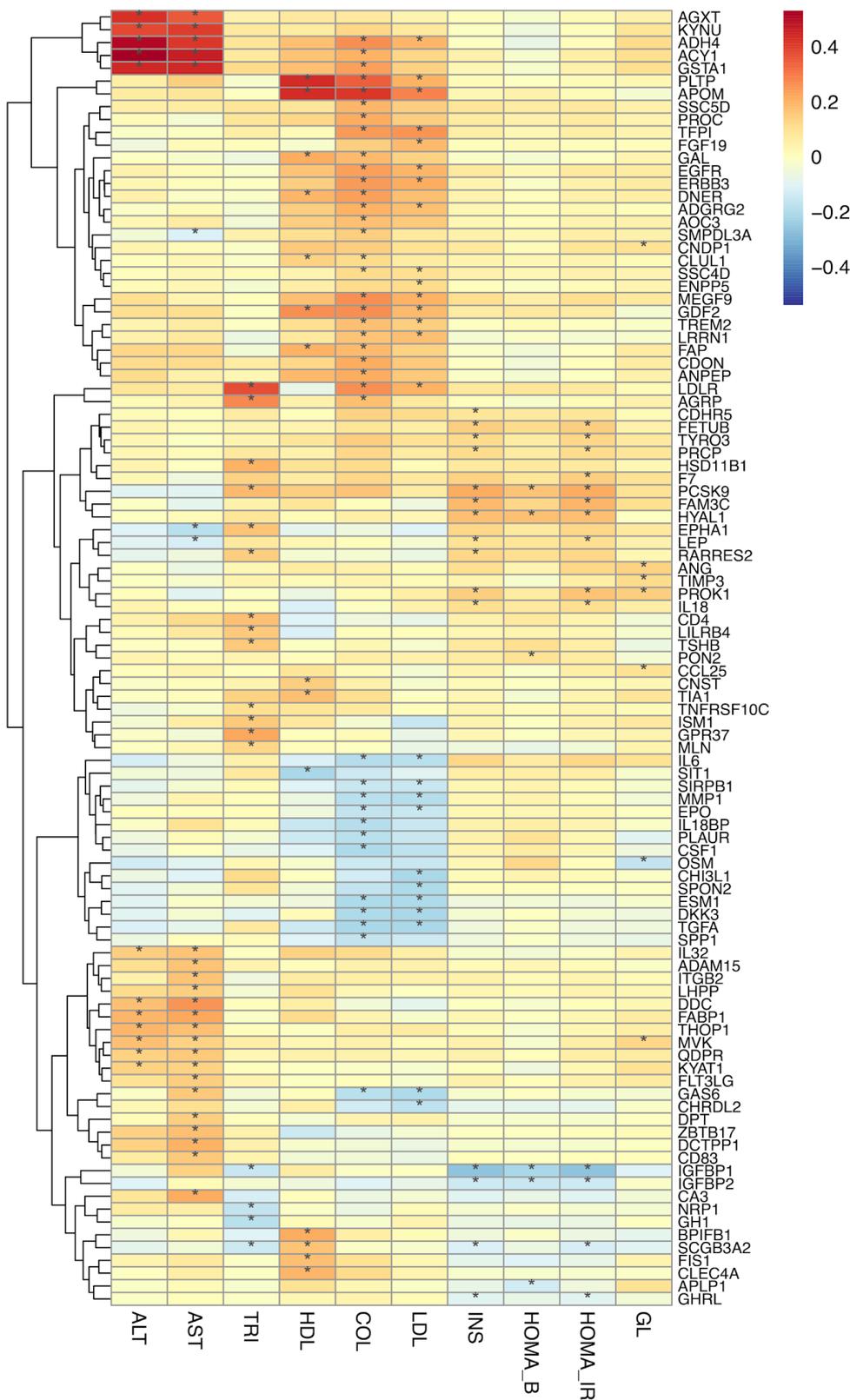
Figure S10. Heatmap of proteins associated with CMD-related phenotypes.
The heatmap shows associations between CMD-related phenotypes and sex hormones, with rectangles coloured according to effect estimates obtained from the GAM model as indicated in the colour code bar. Rectangles are marked with an asterisk if the p-value adjusted for multiple testing is below 0.05. Clustering on the left side is performed based on association effect estimates using hierarchical clustering.
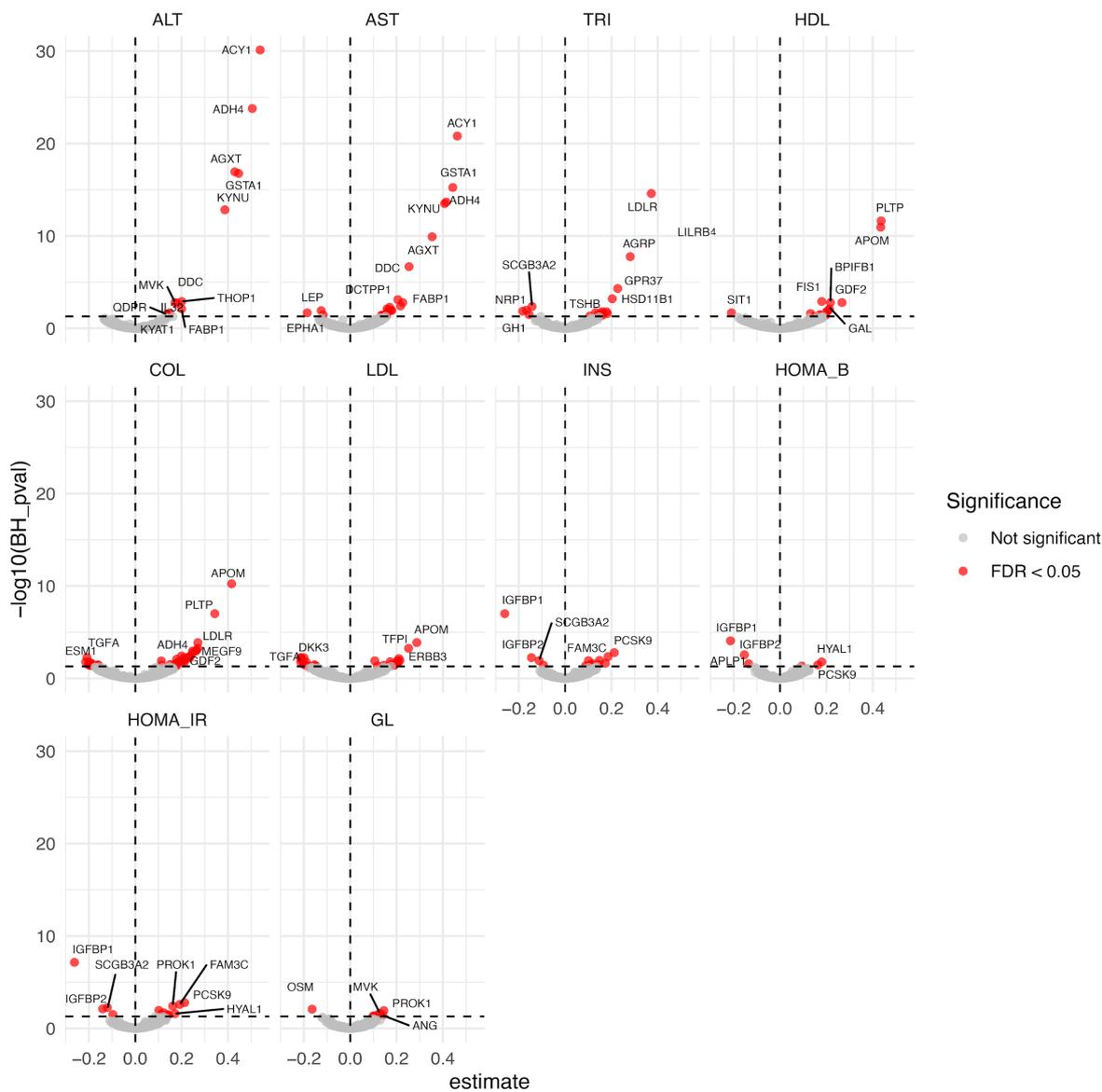
Figure S11. Volcano plots of associations between proteins and other phenotypes.
The plot shows a volcano plot of all associations, with X-axis showing the magnitude of the association and Y axis showing -log10 of adjusted p-values. Significant proteins are marked in red and for some of them their name is indicated.