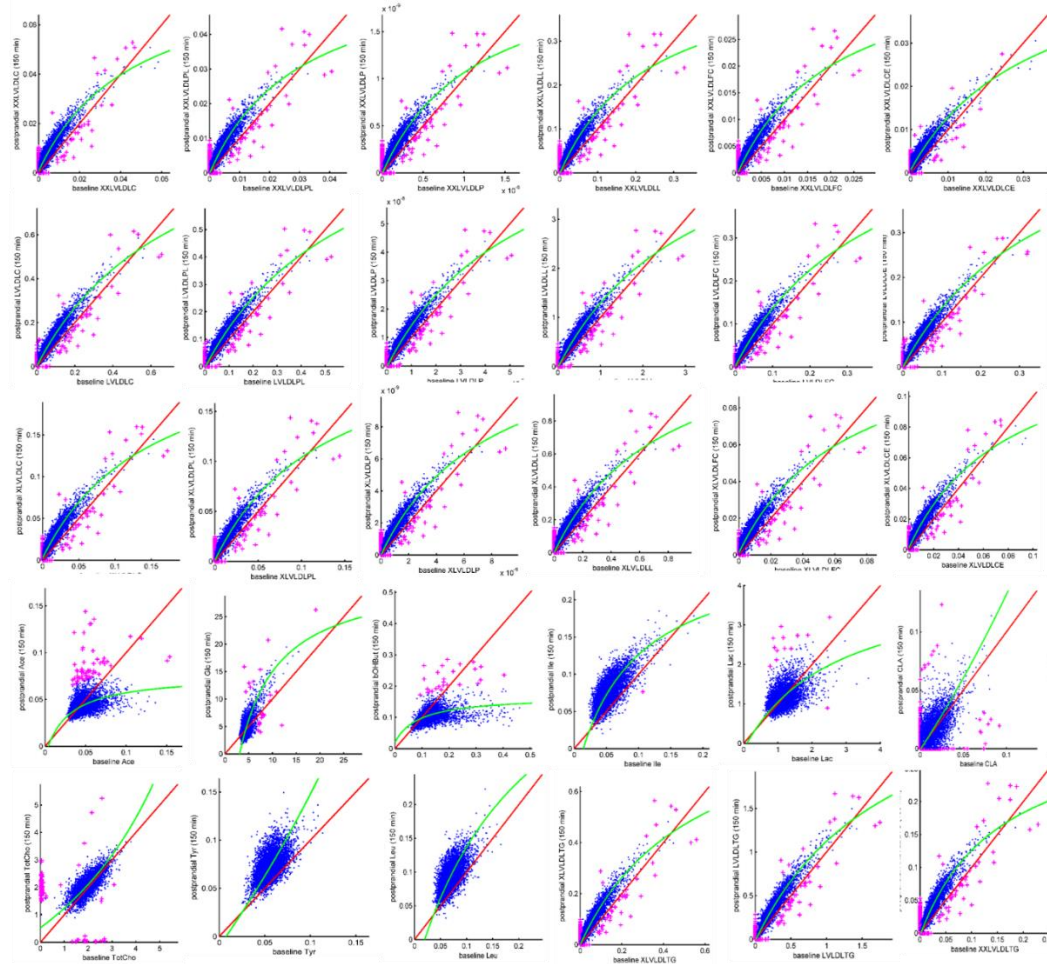
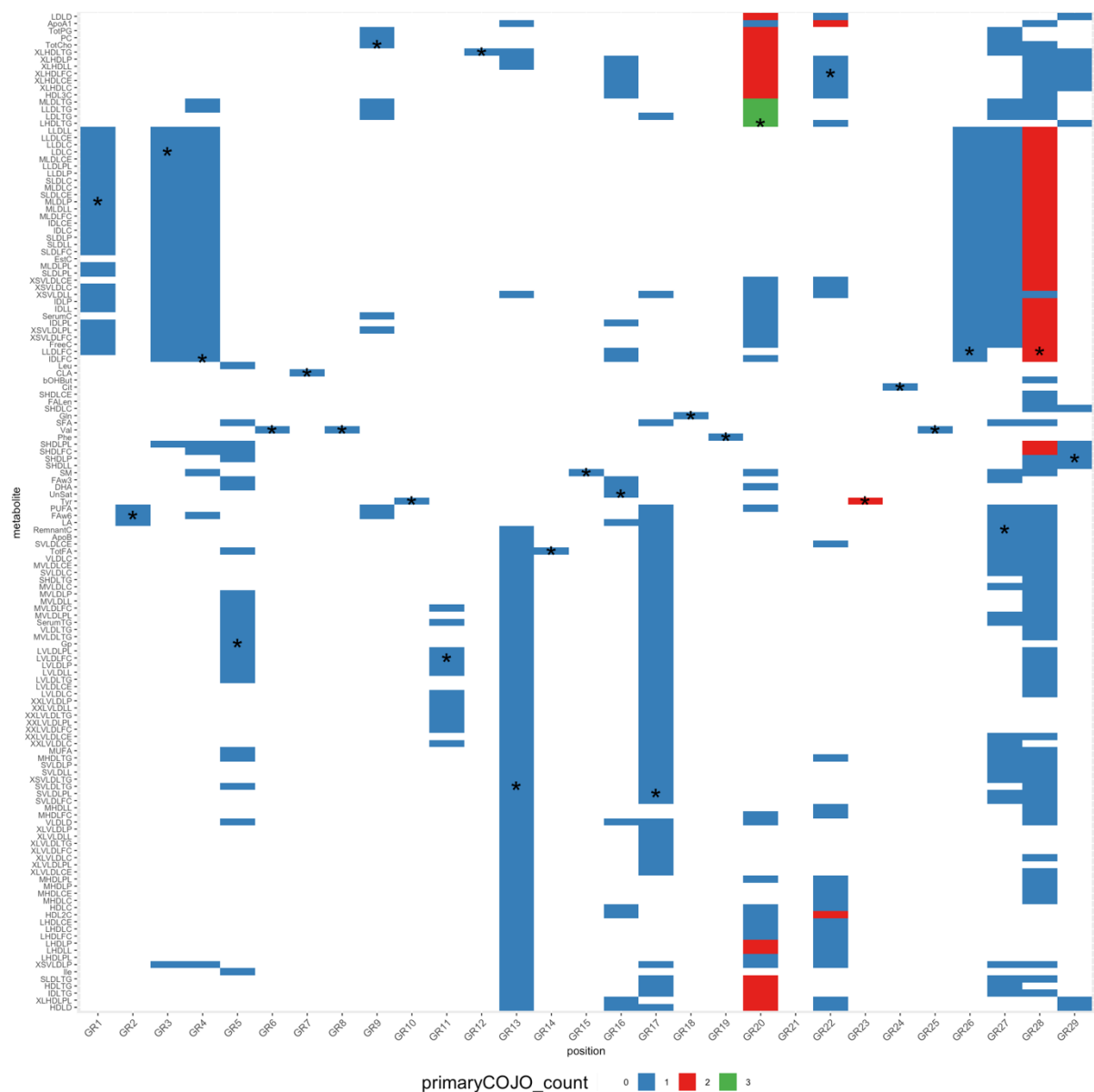


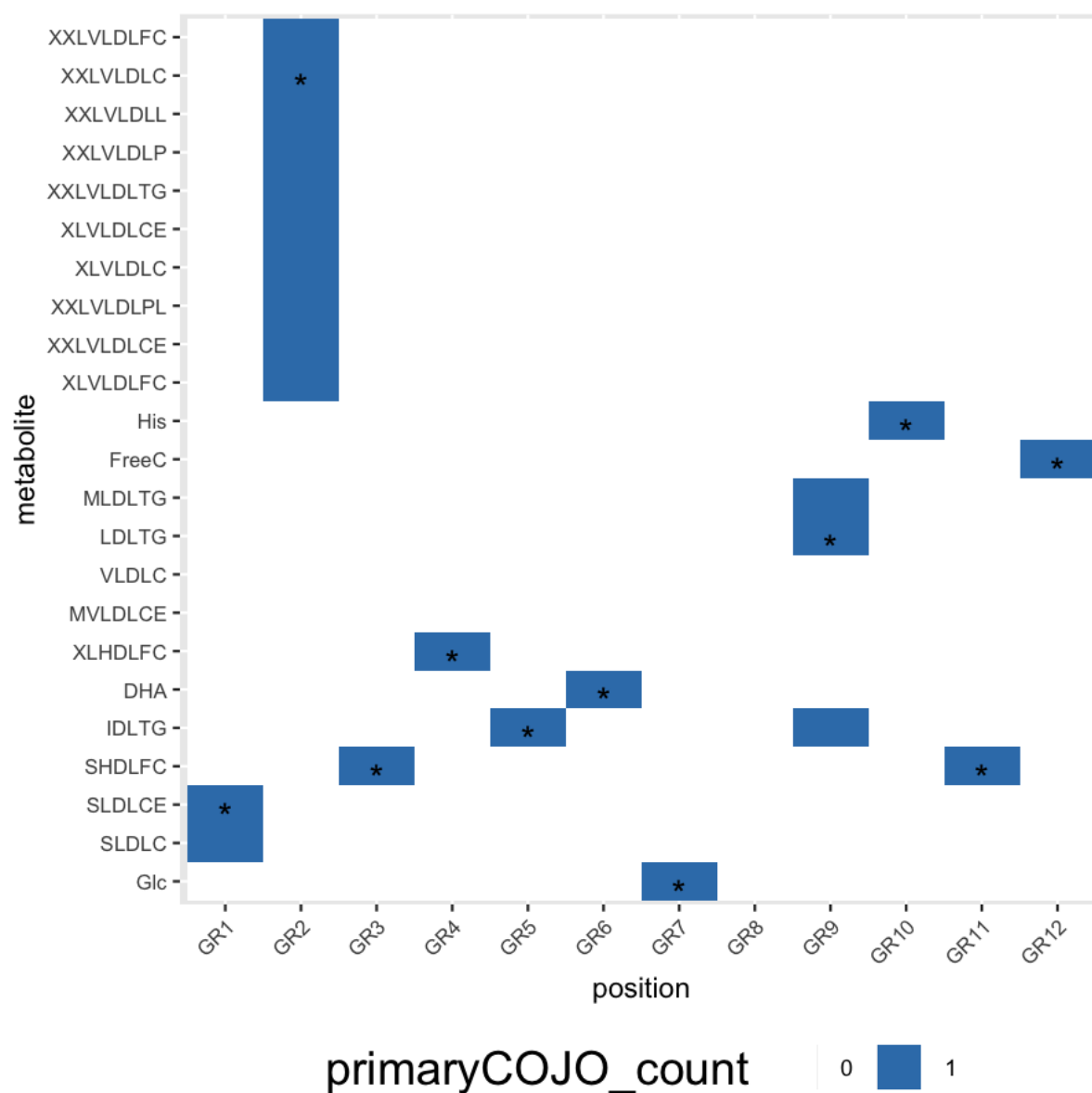
Supplemental Information



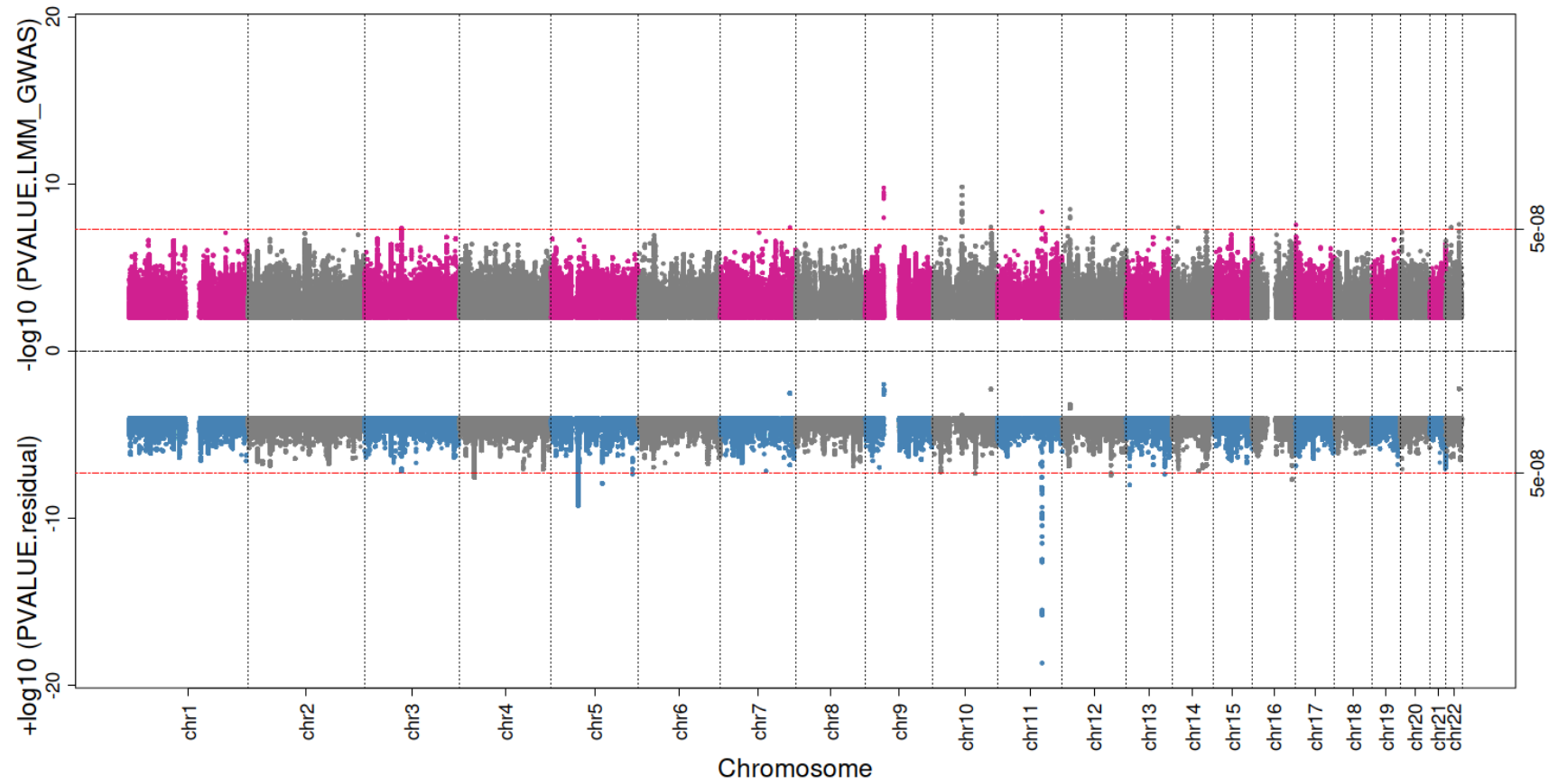
Supplemental Figure 1. Metabolite concentrations (N=30) between fasting and postprandial states with non-linear associations. The x-axis represents fasting metabolite concentrations, and y-axis represents postprandial metabolite concentrations. The red line corresponds to the $y=x$, and green line corresponds to the non-linear orthogonal fitting line. The blues dots correspond to each individual, and pink crosses represent the outliers that were removed from the model fitting.



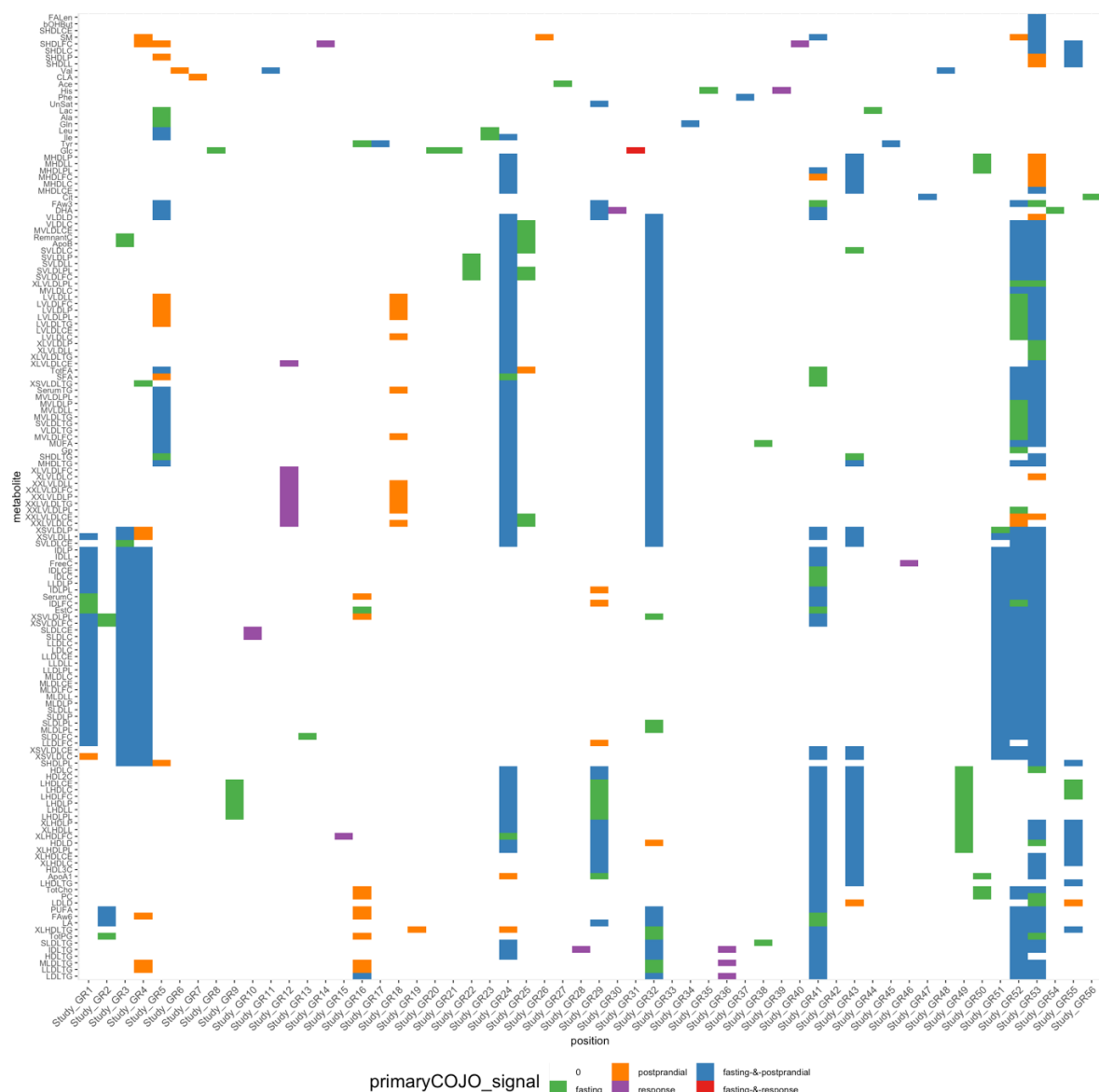
Supplemental Figure 4. Primary COJO association signals in the postprandial NEO data set. Genomic regions, defined by physical distance between associated SNPs (Supplemental Table 5), are along the x-axis. The associated metabolites are along the y-axis. The number of primary COJO associations for a metabolite in a genomic region are indicated by the tile color: blue = 1, red = 2, green = 3. The metabolite with the smallest p-value for each genomic region is indicated with an asterisk. Please note that postprandial-GR21, while containing genome-wide associations, does not contain any independent primary association.



Supplemental Figure 5. Primary COJO association signals in the OrNLSr response NEO data set. Genomic regions, defined by physical distance between associated SNPs (Supplemental Table 6), are along the x-axis. The associated metabolites are along the y-axis. Primary COJO associations for a metabolite in a genomic region are indicated a blue tile. The metabolite with the smallest p-value for each genomic region is indicated with an asterisk.



Supplemental Figure 6. Miami plot of 148 metabolite response measured by linear mixed model (LMM) (top) and OrNLSr nonlinear residuals (bottom).



Supplemental Figure 7. Study wide genomic regions, built by identifying fasting-, postprandial-, and response-genomic-regions that overlapped with each other, or did not. Primary COJO association signals in each dietary state and shared across states in the NEO data set are presented. Study wide genomic regions, defined by physical distance between associated SNPs (Supplemental Table 8), are along the x-axis. The associated metabolites are along the y-axis. The dietary state(s) carrying a primary COJO associations for a metabolite in a study genomic region are indicated by the tile color: green = fasting, orange = postprandial, purple = response, fasting-&-postprandial = blue, and fasting-&-response = red.