Supplemental Information:

An exome-wide sequencing study of lipid response to high-fat meal and fenofibrate in Caucasians: the GOLDN cohort

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Supplemental Figure S1. **Average read depth of each exonic SNP.**

- min: 1
- max: 281
- mean: 52
Supplemental Table S1: Regression models used in the analyses.

| **Full model**                          |
|-----------------------------------------|
| baseline ~ covariates + SNP             |
| fenofibrate-response ~ baseline + covariates + SNP |
| postprandial clearance ~ value at draw2 + covariates + SNP |
| postprandial uptake ~ baseline + covariates + SNP |
| postprandial AUI ~ baseline + covariates + SNP |
| postprandial clearance response to FFB ~ clearance + fenofibrate-response + covariates + SNP |
| postprandial uptake response to response to FFB ~ uptake + fenofibrate-response + covariates + SNP |
| postprandial AUI response to FFB ~ AUI + fenofibrate-response + covariates + SNP |

| **Minimal model**                          |
|-----------------------------------------|
| baseline ~ covariates + SNP             |
| fenofibrate-response ~ covariates + SNP |
| postprandial clearance ~ covariates + SNP |
| postprandial uptake ~ covariates + SNP |
| postprandial AUI ~ covariates + SNP     |
| postprandial clearance response to FFB ~ covariates + SNP |
| postprandial uptake response to response to FFB ~ covariates + SNP |
| postprandial AUI response to FFB ~ covariates + SNP |

Covariates included sex, age, age$^2$, age$^3$, and recruiting center. For post-fenofibrate phenotypes, covariates also included pills per day in addition to those covariates. The postprandial phenotype response to FFB were the values of post-fenofibrate treatment subtracted by the values of pre-fenofibrate treatment. For example, postprandial AUI response to FFB = post-fenofibrate AUI – pre-fenofibrate AUI.
### Supplemental Table S2: Demographic and clinical characteristics of samples in GOLDN, and HAPI Heart Study.

|                          | GOLDN          | HAPI Heart Study |
|--------------------------|----------------|------------------|
| **Gender**               | male: 435      | male: 404        |
|                          | female: 459    | female: 366      |
| **Age**                  | 50.2 ± 6.1     | 43.50 ± 13.90    |
| **BMI (kg/m^2)**         | 28.5 ± 5.6     | 26.62 ± 4.46     |
| **LDL 0h (mg/dL)**       | 122.77 ± 31.88 | —                |
| **HDL 0h (mg/dL)**       | 46.73 ± 13.06  | —                |
| **TG 0h (mg/dL)**        | 139.34 ± 97.63 | 68.56 ± 41.37    |
| **Glucose (mg/dL)**      | 101.51 ± 18.74 | —                |
| **Systolic blood pressure** | 116.08 ± 16.82 | 121.5 ± 0.7     |
|  (mmHg)                  |                |                  |
| **Diastolic blood pressure** | 68.57 ± 9.6   | 76.75 ± 0.4    |
|  (mmHg)                  |                |                  |
Supplemental Table S3 Single variant association test for candidate genes whose common variants were found to be associated with lipid response phenotypes in previous GOLDN study

| Chr | Position | Reference allele | Alternative allele | Number of samples analyzed | Alternative allele frequency | Effect size direction | Phenotype variance explained | P-Value | Trait | Gene |
|-----|----------|-----------------|-------------------|---------------------------|-----------------------------|-----------------------|-----------------------------|---------|-------|-------|
| 11  | 116662407 | G               | C                 | 885                       | 0.052542                    | +                      | 0.017992                    | 6.60E-05 | TG baseline | APOA5 |
| 19  | 45411941  | T               | C                 | 764                       | 0.169503                    | +                      | 0.019979                    | 9.35E-05 | LDL fasting level response to FFB | APOE  |
| 11  | 116662407 | G               | C                 | 782                       | 0.056266                    | -                      | 1.23E-02                    | 0.001906 | TG fasting level response to FFB | APOA5 |
| 11  | 116661001 | G               | A                 | 890                       | 0.000562                    | +                      | 0.008184                    | 0.006958 | TG baseline | APOA5 |
| 11  | 116662407 | G               | C                 | 782                       | 0.056266                    | +                      | 0.008108                    | 0.0118  | HDL fasting level response to FFB | APOA5 |
| 11  | 116662407 | G               | C                 | 808                       | 0.054455                    | +                      | 0.007701                    | 0.012617 | TG clearance | APOA5 |
| 11  | 116662407 | G               | C                 | 885                       | 0.052542                    | -                      | 0.00661                      | 0.015576 | HDL baseline | APOA5 |
| 11  | 116662407 | G               | C                 | 782                       | 0.056266                    | +                      | 0.007291                    | 0.016953 | LDL fasting level response to FFB | APOA5 |
| 11  | 116660983 | T               | A                 | 815                       | 0.000613                    | +                      | 0.006112                    | 0.02562  | TG uptake | APOA5 |
| 19  | 45411941  | T               | C                 | 865                       | 0.165896                    | +                      | 0.005091                    | 0.035864 | LDL baseline | APOE  |
| 11  | 116660983 | T               | A                 | 789                       | 0.000634                    | -                      | 0.005364                    | 0.039667 | LDL fasting level response to FFB | APOA5 |
| 11  | 1166701353| C               | T                 | 884                       | 0.000566                    | -                      | 0.003883                    | 0.06392  | TG AUI | APOA5 |
| 11  | 116661001 | G               | A                 | 890                       | 0.000562                    | -                      | 0.003784                    | 0.066472 | HDL baseline | APOC3 |
| 11  | 116660983 | T               | A                 | 815                       | 0.000613                    | -                      | 0.004053                    | 0.069135 | TG clearance | APOA5 |
| 19  | 45411110  | T               | C                 | 788                       | 0.005076                    | +                      | 0.003958                    | 0.077397 | TG clearance | APOE  |
| 19  | 45411941  | T               | C                 | 865                       | 0.165896                    | +                      | 0.003438                    | 0.084608 | LDL baseline | APOE  |
| 11  | 116701353 | C               | T                 | 884                       | 0.000566                    | +                      | 0.003195                    | 0.09286  | TG AUI response to FFB | APOC3 |
| 11  | 116660983 | T               | A                 | 707                       | 0.000707                    | -                      | 0.00366                     | 0.107684 | TG AUI response to FFB | APOA5 |
| Chr | Chromosome Name | Gene | SNP | Minor Allele | Major Allele | Minor Allele Frequency | Major Allele Frequency | Beta Coefficient | SE | P Value | Gene Function |
|-----|-----------------|------|-----|-------------|--------------|------------------------|------------------------|-------------------|----|---------|--------------|
| 11  | 116661001       | G    | A   | 787        | 0.000635     | +                      | 0.002951               | 0.127506          |     |         | HDL fasting level response to FFB | APOA5 |
| 11  | 116661001       | G    | A   | 890        | 0.000562     | -                      | 0.002456               | 0.139278          |     |         | LDL baseline | APOA5 |
| 11  | 116703575       | G    | C   | 812        | 0.001225     | -                      | 0.002501               | 0.153117          |     |         | TG AUI       | APOC3 |
| 11  | 116661001       | G    | A   | 812        | 0.000615     | +                      | 0.002457               | 0.157579          |     |         | TG clearance | APOA5 |
| 11  | 116703575       | G    | C   | 790        | 0.000633     | -                      | 0.002485               | 0.161165          |     |         | HDL baseline | APOC3 |
| 19  | 45411110        | T    | C   | 766        | 0.004587     | +                      | 0.001944               | 0.203881          |     |         | LDL fasting level response to FFB | APOE |
| 11  | 116703575       | G    | C   | 766        | 0.000706     | -                      | 0.002039               | 0.229502          |     |         | TG clearance response to FFB | APOC3 |
| 11  | 116662407       | G    | C   | 764        | 0.056429     | +                      | 0.001971               | 0.240196          |     |         | TG clearance response to FFB | APOA5 |
| 11  | 116703575       | G    | C   | 764        | 0.000706     | -                      | 0.001818               | 0.256569          |     |         | TG uptake response to FFB | APOC3 |
| 11  | 116660983       | T    | A   | 789        | 0.000634     | -                      | 1.60E-03               | 0.260847          |     |         | TG fasting level response to FFB | APOA5 |
| 11  | 116662407       | G    | C   | 808        | 0.054455     | +                      | 0.001562               | 0.261226          |     |         | TG AUI       | APOA5 |
| 19  | 45411941        | T    | C   | 865        | 0.165896     | -                      | 0.00145               | 0.262679          |     |         | HDL baseline | APOE |
| 11  | 116703575       | G    | C   | 816        | 0.001225     | -                      | 0.001492               | 0.269892          |     |         | TG clearance | APOC3 |
| 19  | 45411941        | T    | C   | 790        | 0.164557     | +                      | 0.001522               | 0.272878          |     |         | TG clearance | APOE |
| 19  | 45411941        | T    | C   | 764        | 0.169503     | -                      | 0.001537               | 0.278564          |     |         | HDL fasting level response to FFB | APOE |
| 11  | 116703575       | G    | C   | 893        | 0.001122     | +                      | 0.001226               | 0.295312          |     |         | HDL baseline | APOC3 |
| 11  | 116703575       | G    | C   | 816        | 0.001225     | -                      | 0.001278               | 0.3071            |     |         | TG uptake | APOC3 |
| 19  | 45411941        | T    | C   | 764        | 0.169503     | +                      | 0.001338               | 0.312013          |     |         | HDL fasting level response to FFB | APOE |
| 19  | 45411110        | T    | C   | 763        | 0.004587     | +                      | 0.001325               | 0.314738          |     |         | HDL fasting level response to FFB | APOE |
|   | ID          | SNP | Genotype | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Trait Description | Gene  |
|---|-------------|-----|----------|---------|---------|---------|---------|---------|-------------------|--------|
| 11| 116703575   | G   | C        | 893     | 0.00112 | -       | 0.00107 | 0.328385| LDL fasting level response to FFB | APOC3  |
| 11| 116701353   | C   | T        | 781     | 0.00064 | -       | 0.001214| 0.330222| LDL fasting level response to FFB | APOC3  |
| 19| 45411110    | T   | C        | 682     | 0.003666| +       | 0.00137 | 0.33371 | TG clearance response to FFB | APOE   |
| 11| 116660983   | T   | A        | 707     | 0.000707| -       | 0.001299| 0.337852| TG clearance response to FFB | APOA5  |
| 11| 116701353   | C   | T        | 781     | 0.00064 | -       | 0.00105 | 0.365117| HDL fasting level response to FFB | APOC3  |
| 19| 45411110    | T   | C        | 864     | 0.005787| +       | 0.000889| 0.380761| LDL baseline | APOE   |
| 11| 116703561   | G   | C        | 817     | 0.001224| -       | 0.000865| 0.400512| TG uptake | APOC3  |
| 19| 45411941    | T   | C        | 684     | 0.166667| +       | 0.00098 | 0.412888| TG clearance response to FFB | APOE   |
| 11| 116703561   | G   | C        | 817     | 0.001224| +       | 0.000816| 0.412444| TG clearance response to FFB | APOE   |
| 11| 116703575   | G   | C        | 790     | 0.000633| +       | 0.000788| 0.430186| HDL fasting level response to FFB | APOC3  |
| 11| 116703561   | G   | C        | 791     | 0.001264| +       | 0.000738| 0.431323| HDL fasting level response to FFB | APOC3  |
| 11| 116662407   | G   | C        | 885     | 0.052542| +       | 0.000535| 0.491532| LDL baseline | APOA5  |
| 11| 116703575   | G   | C        | 708     | 0.000706| -       | 0.000639| 0.501067| TG AUI response to FFB | APOC3  |
| 11| 116662407   | G   | C        | 700     | 0.056429| +       | 0.000613| 0.512319| TG AUI response to FFB | APOA5  |
| 11| 116660983   | T   | A        | 789     | 0.000634| +       | 0.000525| 0.519923| HDL fasting level response to FFB | APOA5  |
| 19| 45411110    | T   | C        | 864     | 0.005787| +       | 0.000475| 0.521623| TG baseline | APOE   |
| 11| 116661001   | G   | A        | 705     | 0.000709| -       | 0.000515| 0.546985| TG uptake response to FFB | APOA5  |
| 11| 116703561   | G   | C        | 817     | 0.001224| -       | 0.000424| 0.556186| TG AUI | APOC3  |
| 19| 45411110    | T   | C        | 763     | 0.004587| +       | 0.000451| 0.55731 | TG fasting level response to FFB | APOE   |
| 11| 116661001   | G   | A        | 787     | 0.000635| +       | 4.29E-04| 0.561354| TG fasting level response to FFB | APOA5  |
| Chromosome | Variation | Allele 1 | Allele 2 | AA1 | AA2 | G WAS Developed for | Genes |
|------------|-----------|----------|----------|-----|-----|-------------------|-------|
| 11         | 116703561 | G        | C        | 894 | 0.001678 | LDL baseline     | APOC3 |
|            | 116703561 | G        | C        | 894 | 0.001678 | LDL baseline     | APOC3 |
|            | 116703575 | G        | C        | 893 | 0.001112 | LDL baseline     | APOC3 |
|            | 116662407 | G        | C        | 808 | 0.054455 | TG uptake        | APOA5 |
|            | 116703561 | G        | C        | 791 | 0.001264 | LDL fasting level response to FFB | APOC3 |
| 19         | 45411110  | T        | C        | 682 | 0.003666 | TG AUI response to FFB | APOE |
|            | 45411110  | T        | C        | 788 | 0.005076 | TG AUI           | APOE |
|            | 45411941  | T        | C        | 684 | 0.166667 | TG uptake response to FFB | APOE |
| 11         | 116660983 | T        | A        | 892 | 0.000561 | LDL baseline     | APOA5 |
|            | 116661001 | G        | A        | 813 | 0.000615 | TG uptake        | APOA5 |
|            | 116661001 | G        | A        | 787 | 0.000635 | LDL fasting level response to FFB | APOA5 |
| 11         | 116703561 | G        | C        | 709 | 0.000705 | LDL AUI response to FFB | APOC3 |
|            | 116660983 | T        | A        | 892 | 0.000561 | HDL baseline     | APOA5 |
|            | 116703561 | G        | C        | 709 | 0.000705 | TG clearance response to FFB | APOC3 |
| 19         | 45411941  | T        | C        | 790 | 0.164557 | TG uptake        | APOE |
|            | 116661001 | G        | A        | 705 | 0.000709 | TG AUI response to FFB | APOA5 |
|            | 116703561 | G        | C        | 894 | 0.001678 | TG baseline      | APOC3 |
|            | 116703575 | G        | C        | 790 | 0.000633 | LDL fasting level response to FFB | APOC3 |
|            | 116660983 | T        | A        | 707 | 0.000707 | TG uptake response to FFB | APOA5 |
|            | 45411941  | T        | C        | 684 | 0.166667 | TG AUI response to FFB | APOE |
| 11         | 116703561 | G        | C        | 791 | 0.001264 | HDL fasting level response to FFB | APOC3 |
|   | Gene         | Chromosome | Position | Effect | p-Value | Beta   | OR     | Trait                  | SNP          |
|---|--------------|------------|----------|--------|---------|--------|--------|------------------------|--------------|
| 11| APOA5        | 11         | 16661001 | G > A  | 0.000709| 5.39E-05| 0.845436| TG clearance response to FFB |
| 11| APOC3        | 11         | 16701353 | C > T  | 0.00064 | 4.44E-05| 0.852299| TG fasting level response to FFB |
| 11| APOA5        | 11         | 16662407 | G > C  | 0.056429| 4.09E-05| 0.865681| TG uptake response to FFB |
| 11| APOA5        | 11         | 16661001 | G > A  | 0.000615| 2.71E-05| 0.882057| TG AUI response to FFB |
| 19| APOE         | 19         | 45411110 | T > C  | 0.005076| 2.07E-05| 0.898277| TG uptake response to FFB |
| 19| APOE         | 19         | 45411941 | T > C  | 0.164557| 2.01E-05| 0.899607| TG AUI response to FFB |
| 19| APOE         | 19         | 45411110 | T > C  | 0.003666| 1.19E-05| 0.928248| TG uptake response to FFB |
| 11| APOC3        | 11         | 16703561 | G > C  | 0.000705| 3.86E-06| 0.958301| TG uptake response to FFB |
Supplemental Table S4 Gene-based association test for candidate genes whose common variants were found to be associated with lipid response phenotypes in previous GOLDN study

| Group name | Number of variants | Variant position | Minor alleles of frequencies | Single variant P-values | Gene based P-value | Method | Minor allele frequency threshold | Trait                      |
|------------|--------------------|------------------|------------------------------|-------------------------|-------------------|--------|---------------------------------|---------------------------|
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000560538, 0.000561798   | 0.203037, 0.0069579    | 0.011655      | SKAT   | 0.05                            | TG baseline               |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000560538, 0.000561798   | 0.203037, 0.0069579    | 0.011655      | SKAT   | 0.01                            | TG baseline               |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000613497, 0.000615006   | 0.157579, 0.070623     | 0.070623     | SKAT   | 0.05                            | TG clearance              |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000613497, 0.000615006   | 0.157579, 0.070623     | 0.070623     | SKAT   | 0.01                            | TG clearance              |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000613497, 0.000615006   | 0.256204, 0.729661     | 0.078039     | SKAT   | 0.05                            | TG uptake                 |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000613497, 0.000615006   | 0.256204, 0.729661     | 0.078039     | SKAT   | 0.01                            | TG uptake                 |
| APOA5      | 2                  | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000565611, 0.00167785, 0.001111982 | 0.0639202, 0.798134, 0.328385 | 0.10998 | MB   | 0.05                            | TG baseline               |
| APOC3      | 3                  | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000565611, 0.00167785, 0.001111982 | 0.0639202, 0.798134, 0.328385 | 0.10998 | MB   | 0.01                            | TG baseline               |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000633714, 0.000635324   | 0.0396668, 0.747714    | 0.114423     | SKAT   | 0.05                            | LDL fasting level response to FFB |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000633714, 0.000635324   | 0.0396668, 0.747714    | 0.114423     | SKAT   | 0.01                            | LDL fasting level response to FFB |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000633714, 0.000635324   | 0.519923, 0.127506     | 0.125074     | Burden | 0.05                            | HDL fasting level response to FFB |
| APOA5      | 2                  | 11:11660983:T:A; 11:11661001:G:A | 0.000633714, 0.000635324   | 0.519923, 0.127506     | 0.125172     | MB     | 0.05                            | HDL fasting level response to FFB |
| Gene   | SNPs                                                                 | p-value 1 | p-value 2 | p-value 3 | p-value 4 | p-value 5 | p-value 6 | p-value 7 | p-value 8 | p-value 9 | p-value 10 | p-value 11 | p-value 12 | p-value 13 | p-value 14 |
|--------|----------------------------------------------------------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000633714, 0.125172 | 0.519923, 0.127506 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | HDL fasting level response to FFB |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | 0.000561798, 0.130345 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | HDL baseline |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | HDL baseline |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | HDL baseline |
| APOA5  | 11:116703561:G:C; 11:116703575:G:C                                  | 0.00122399, 0.151966 | 0.556186, 0.151966 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | TG AUI |
| APOA5  | 11:116703561:G:C; 11:116703575:G:C                                  | 0.00122399, 0.151966 | 0.556186, 0.151966 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | TG AUI |
| APOA5  | 11:116703561:G:C; 11:116703575:G:C                                  | 0.00122399, 0.151966 | 0.556186, 0.151966 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | TG AUI |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000633714, 0.125172 | 0.519923, 0.127506 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | SKAT 0.05 |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | 0.130345 Burden, 0.130345 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | SKAT 0.05 |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | 0.130345 Burden, 0.130345 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | SKAT 0.05 |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | 0.130345 Burden, 0.130345 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | SKAT 0.05 |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | 0.130345 Burden, 0.130345 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | SKAT 0.05 |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A                                  | 0.000560538, 0.130345 | 0.762318, 0.0664718 | 0.130345 Burden, 0.130345 | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | &nbsp; | SKAT 0.05 |
| Gene   | Symbol | Chromosome   | Position   | Minor Allele Frequency | Major Allele Frequency | Haplotype Score | Annotation     | p-value | FDR    | Type   |
|--------|--------|--------------|------------|------------------------|------------------------|-------------------|---------------|---------|-------|--------|
| APOC3  | 11:116701353:C:T | 11:116703561:G:C | 11:116703575:G:C | 0.000565611, 0.0928598, 0.214563, 0.295312 | 0.00111982 | 0.170713 SKAT | 0.05 HDL baseline |
| APOC3  | 11:11660983:T:A | 11:11661001:G:A | 0.000615006 | 0.0256204, 0.729661, 0.181605 MB | 0.01 TG uptake |
| APOA5  | 11:11660983:T:A | 11:11661001:G:A | 0.000615006 | 0.0256204, 0.729661, 0.181972 Burden | 0.05 TG uptake |
| APOA5  | 11:116701353:C:T | 11:116703561:G:C | 11:116703575:G:C | 0.000640205, 0.00126422, 0.835961, 0.161165 | 0.365117, 0.185653 | Burden 0.05 HDL fasting level response to FFB |
| APOA5  | 11:116701353:C:T | 11:116703561:G:C | 11:116703575:G:C | 0.000640205, 0.00126422, 0.835961, 0.161165 | 0.365117, 0.185653 | Burden 0.05 HDL fasting level response to FFB |
| APOC3  | 11:116703561:G:C | 11:116703575:G:C | 0.00122399, 0.400512, 0.3071 | 0.187232 Burden | 0.05 TG uptake |
| APOC3  | 11:116703561:G:C | 11:116703575:G:C | 0.00122399, 0.400512, 0.3071 | 0.187232 Burden | 0.01 TG uptake |
| APOC3  | 11:116703561:G:C | 11:116703575:G:C | 0.00122399, 0.400512, 0.3071 | 0.187244 MB | 0.05 TG uptake |
| APOC3  | 11:116703561:G:C | 11:116703575:G:C | 0.00122399, 0.400512, 0.3071 | 0.187244 MB | 0.01 TG uptake |
| APOA5  | 11:11660983:T:A | 11:11661001:G:A | 0.000561798 | 0.139278 | Burden 0.05 LDL baseline |
| Gene | Repeat | Chromosome | Position | AUI | Level | Type | Baseline | Response to FFB |
|------|--------|------------|----------|-----|-------|------|----------|-----------------|
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000560538, 0.000561798 | 0.715625, 0.139278 | 0.192215 Burden | 0.01 | LDL baseline |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000560538, 0.000561798 | 0.715625, 0.139278 | 0.192366 MB | 0.05 | LDL baseline |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000560538, 0.000561798 | 0.715625, 0.139278 | 0.192366 MB | 0.01 | LDL baseline |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.00633714, 0.00635324 | 0.519923, 0.127506 | 0.197549 VT | 0.01 | HDL fasting level response to FFB |
| APOA5 | 2      | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00565611, 0.00167785, 0.00111982 | 0.0639202, 0.798134, 0.328385 | 0.203458 Burden | 0.05 | TG baseline |
| APOC3 | 3      | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00565611, 0.00167785, 0.00111982 | 0.0639202, 0.798134, 0.328385 | 0.203458 Burden | 0.01 | TG baseline |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000560538, 0.000561798 | 0.762318, 0.0664718 | 0.205309 VT | 0.01 | HDL baseline |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000633714, 0.000635324 | 0.396668, 0.747714 | 0.21896 MB | 0.05 | LDL fasting level response to FFB |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000633714, 0.000635324 | 0.396668, 0.747714 | 0.21896 MB | 0.01 | LDL fasting level response to FFB |
| APOC3 | 2      | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000640205, 0.000632911 | 0.365117, 0.161165 | 0.218966 VT | 0.01 | HDL fasting level response to FFB |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000633714, 0.000635324 | 0.396668, 0.747714 | 0.219361 Burden | 0.05 | LDL fasting level response to FFB |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000613497, 0.000615006 | 0.0601213, 0.882057 | 0.220165 MB | 0.05 | TG AUI |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000613497, 0.000615006 | 0.0601213, 0.882057 | 0.220497 Burden | 0.05 | TG AUI |
| APOA5 | 2      | 11:11660983:T:A; 11:116661001:G:A | 0.000613497, 0.000615006 | 0.0601213, 0.882057 | 0.220497 Burden | 0.01 | TG AUI |
| Gene   | Chromosome | Position | rsID   | Type  | p-value | MAF    | IBD Score | p-value | Annotation |
|--------|------------|----------|--------|-------|---------|--------|-----------|---------|------------|
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | TG AUI  |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A | 0.000633714, 0.519923, 0.254543 | SKAT   | 0.05   | HDL fasting level response to FFB |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A | 0.000633714, 0.519923, 0.254543 | SKAT   | 0.01   | HDL fasting level response to FFB |
| APOA5  | 11:116660983:T:A; 11:116661001:G:A | 0.000707214, 0.519923, 0.254543 | SKAT   | 0.01   | HDL fasting level response to FFB |
| APOA5  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | TG AUI  |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | TG uptake |
| APOA5  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| APOC3  | 11:116703561:G:C; 11:116703575:G:C | 0.00122399, 0.556186, 0.237561 | VT     | 0.01   | LDL baseline |
| Gene  | SNP Information | p-values | q-values | p-values | Measures | p-values | Measures |
|-------|----------------|----------|----------|----------|----------|----------|----------|
| APOC3 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00640205, 0.852299, 0.431323 | 0.00632911, 0.430186 | 0.312202 | MB | 0.01 | TG fasting level response to FFB |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | LDL baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | LDL baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.05 | TG baseline |
| APOA5 | 11:116660983:T:A; 11:116661001:G:A | 0.000561798, 0.715625 | 0.0069579, 0.139278 | 0.313713 | MB | 0.01 | TG baseline |
| Gene   | p-value  | q-value | Statistic | p-value  | q-value | Statistic | p-value  | q-value | Statistic | p-value  | q-value | Statistic |
|--------|----------|---------|-----------|----------|---------|-----------|----------|---------|-----------|----------|---------|-----------|
| APOC3  | 0.005661 | 0.5995  | 0.36242   | 0.01     | LDL baseline |
| APOC3  | 0.005661 | 0.5995  | 0.364874  | 0.05     | LDL baseline |
| APOC3  | 0.005661 | 0.5995  | 0.364874  | 0.01     | LDL baseline |
| APOC3  | 0.001224 | 0.414244| 0.386484  | 0.05     | TG clearance |
| APOC3  | 0.001224 | 0.414244| 0.386484  | 0.01     | TG clearance |
| APOC3  | 0.0007052| 0.9583  | 0.406303  | 0.05     | TG uptake response to FFB |
| APOC3  | 0.0007052| 0.9583  | 0.406303  | 0.01     | TG uptake response to FFB |
| APOC3  | 0.0007052| 0.9583  | 0.406458  | 0.05     | TG uptake response to FFB |
| APOC3  | 0.0007052| 0.9583  | 0.406458  | 0.01     | TG uptake response to FFB |
| APOA5  | 0.0007072| 0.337852| 0.414152  | 0.05     | TG clearance response to FFB |
| APOA5  | 0.0007072| 0.337852| 0.414152  | 0.01     | TG clearance response to FFB |
| APOA5  | 0.0007072| 0.337852| 0.414371  | 0.05     | TG clearance response to FFB |
| APOA5  | 0.0007072| 0.337852| 0.414371  | 0.01     | TG clearance response to FFB |
| APOC3  | 0.001224 | 0.400512| 0.416295  | 0.05     | TG uptake |
| APOC3  | 0.001224 | 0.400512| 0.416295  | 0.01     | TG uptake |
| Gene   | n | Chromosome | Position | Minor Allele | Major Allele | Minor Allele Frequency | Major Allele Frequency | p-Value (SKAT) | p-Value (BURDEN) | p-Value (MB) | Analysis | p-Value (VT) | Baseline | p-Value (VT) | Baseline | Fasting Level Response to FFB | Clearance Response to FFB | Uptake Response to FFB | Baseline | Response to FFB |
|--------|---|------------|----------|--------------|--------------|------------------------|------------------------|----------------|----------------|-------------|----------|---------------|----------|----------------|----------|---------------------------------|-----------------------------|------------------------|----------------|-----------------|
| APOA5  | 2 | 11:11660983;A:T | 0.000633714, 0.000635324 | 0.260847, 0.561354 | 0.448957 | SKAT 0.05 | TG fasting level response to FFB |
| APOA5  | 2 | 11:11660983;A:T | 0.000633714, 0.000635324 | 0.260847, 0.561354 | 0.448957 | SKAT 0.01 | TG fasting level response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.468632 | SKAT 0.01 | TG clearance response to FFB |
| APOC3  | 3 | 11:116701353;C:T | 0.000640205, 0.000632911 | 0.365117, 0.161165 | 0.501333 | SKAT 0.05 | HDL fasting level response to FFB |
| APOC3  | 3 | 11:116701353;C:T | 0.000640205, 0.000632911 | 0.365117, 0.161165 | 0.501333 | SKAT 0.01 | HDL fasting level response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514237 | Burden 0.05 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514237 | Burden 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.05 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 2 | 11:116703561;G:C | 0.000705219, 0.000706215 | 0.781578, 0.229502 | 0.514475 | MB 0.01 | TG clearance response to FFB |
| APOC3  | 3 | 11:116701353;C:T | 0.000565611, 0.000632911 | 0.0928598, 0.430186 | 0.547126 | VT 0.01 | HDL baseline |
| APOC3  | 3 | 11:116701353;C:T | 0.000565611, 0.000632911 | 0.0928598, 0.430186 | 0.547126 | VT 0.01 | HDL baseline |
| APOC3  | 3 | 11:116701353;C:T | 0.000565611, 0.000632911 | 0.0928598, 0.430186 | 0.547126 | VT 0.01 | HDL baseline |
| APOC3  | 3 | 11:116701353;C:T | 0.000565611, 0.000632911 | 0.0928598, 0.430186 | 0.547126 | VT 0.01 | HDL baseline |
| APOC3  | 3 | 11:116701353;C:T | 0.000565611, 0.000632911 | 0.0928598, 0.430186 | 0.547126 | VT 0.01 | HDL baseline |
| Gene  | Count | Position | Score 1 | Score 2 | Score 3 | p-value | Haplotype | Trait Description |
|-------|-------|----------|---------|---------|---------|----------|-----------|------------------|
| APOC3 | 2     | 11:116703561:G:C; 11:116703575:G:C | 0.000705219, 0.958301 | 0.256569 | 0.574537 | 0.01 | VT         | TG uptake response to FFB |
| APOC3 | 3     | 11:116703561:G:C; 11:116703575:G:C | 0.000705219, 0.958301 | 0.256569 | 0.574537 | 0.01 | VT         | LDL baseline     |
| APOC3 | 3     | 11:116703561:G:C; 11:116703575:G:C | 0.000705219, 0.958301 | 0.256569 | 0.574537 | 0.01 | VT         | TG fasting level response to FFB |
| APOC3 | 3     | 11:116703561:G:C; 11:116703575:G:C | 0.000705219, 0.958301 | 0.256569 | 0.574537 | 0.01 | VT         | TG AUI response to FFB |
| APOC3 | 2     | 11:116703561:G:C; 11:116703575:G:C | 0.000705219, 0.958301 | 0.256569 | 0.574537 | 0.01 | SKAT       | TG clearance response to FFB |

**Note:** The table lists genetic variations and their associated scores, p-values, and trait descriptions. Each row represents a different gene and its associated trait response to FFB (Fasting Free Breakfast). The traits include TG (Triglycerides) and LDL (Low-Density Lipoprotein). The scores are derived from statistical methods such as VT and SKAT. The p-values indicate the significance of the association between the genetic variations and the traits.
| Gene   | Count | SNP 1                          | SNP 2                          | P-value 1 | P-value 2 | MB / Burden | P-value | Trait                  |
|--------|-------|--------------------------------|--------------------------------|-----------|-----------|-------------|---------|------------------------|
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.000613497 | 0.000615006 | 0.0691347 | 0.773747 | MB                     |
|        |       | 0.0691347                      | 0.15759                        |           |           |             |         | TG clearance            |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.000613497 | 0.000615006 | 0.0691347 | 0.773747 | MB                     |
|        |       | 0.0691347                      | 0.15759                        |           |           |             |         | TG clearance            |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.000613497 | 0.000615006 | 0.0691347 | 0.774822 | Burden                 |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.000613497 | 0.000615006 | 0.0691347 | 0.774822 | Burden                 |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.794356 | Burden                 |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.794356 | Burden                 |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.794679 | MB                     |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.794679 | MB                     |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.794739 | Burden                 |
| APOA5  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.794739 | Burden                 |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00705219 | 0.00705219 | 0.758373   | 0.797299 | Burden                 |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00705219 | 0.00705219 | 0.758373   | 0.797299 | Burden                 |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00705219 | 0.00705219 | 0.758373   | 0.797488 | MB                     |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00705219 | 0.00705219 | 0.758373   | 0.797488 | MB                     |
| APOC3  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.811603 | SKAT                   |
| APOC3  | 2     | 11:116660983:T:A               | 11:116661001:G:A               | 0.0070922  | 0.0070922  | 0.546985   | 0.811603 | SKAT                   |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00122399 | 0.00122549 | 0.414244   | 0.821382 | Burden                 |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00122399 | 0.00122549 | 0.414244   | 0.821382 | Burden                 |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00122399 | 0.00122549 | 0.414244   | 0.823504 | MB                     |
| APOC3  | 2     | 11:116703561:G:C               | 11:116703575:G:C               | 0.00122399 | 0.00122549 | 0.414244   | 0.823504 | MB                     |
| Gene  | Tag   | Position | p1   | p2   | p3   | p4   | p5   | p6   | p7   | p8   | p9   | p10  | p11  | p12  | p13  | p14  | p15  | p16  | p17  | p18  |
|-------|-------|----------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| APOC3 | 2     | 11:116703561:G:C; 11:116703575:G:C | 0.00122399 | 0.414244 | 0.269892 | 0.823504 | MB | 0.01 | TG clearance |
| APOC3 | 3     | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.000640205 | 0.330222 | 0.613145 | 0.800372 | 0.872221 | MB | 0.05 | LDL baseline |
| APOC3 | 3     | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00126422 | 0.599513 | 0.591086 | 0.604023 | 0.835549 | SKAT | 0.01 | LDL baseline |
| APOC3 | 3     | 11:116660983:T:A; 11:116661001:G:A | 0.00070922 | 0.546985 | 0.941536 | VT | 0.01 | TG uptake response to FFB |
| APOC3 | 3     | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00640205 | 0.330222 | 0.613145 | 0.800372 | 0.887423 | VT | 0.01 | LDL fasting level response to FFB |
| APOC3 | 3     | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00632911 | 0.330222 | 0.613145 | 0.800372 | 0.887423 | VT | 0.01 | LDL fasting level response to FFB |
| APOC3 | 2     | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00640205 | 0.330222 | 0.613145 | 0.800372 | 0.965708 | Burden | 0.05 | LDL fasting level response to FFB |
| APOC3 | 3     | 11:116701353:C:T; 11:116703561:G:C; 11:116703575:G:C | 0.00632911 | 0.330222 | 0.613145 | 0.800372 | 0.965708 | Burden | 0.01 | LDL fasting level response to FFB |
Supplemental Table S5 Single variant association results for SIPA1L2 with GOLDN and HAPI Heart Study for the trait of triglyceride postprandial area under increase.

| gene  | chr | variant position | reference allele | alternative allele | number of samples analyzed | minor allele frequency | P value     | cohort | mutation effect | direction of effect |
|-------|-----|------------------|------------------|-------------------|---------------------------|-----------------------|------------|--------|----------------|---------------------|
| SIPA1L2 | 1   | 232534919        | C                | T                 | 803                       | 0.00996               | 0.117317   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232538214        | C                | T                 | 799                       | 0.00313               | 0.815151   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232539219        | C                | T                 | 728                       | 0.0158                | 0.738418   | HAPI   | Missense       | +                   |
| SIPA1L2 | 1   | 232539219        | C                | T                 | 812                       | 0.00554               | 0.999854   | GOLDN | Missense       | -                   |
| SIPA1L2 | 1   | 232539246        | G                | T                 | 813                       | 0.00062               | 0.434327   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232539255        | C                | A                 | 815                       | 0.00184               | 0.216915   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232561520        | G                | A                 | 797                       | 0.00565               | 0.199456   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232564162        | T                | C                 | 728                       | 0.02198               | 0.101433   | HAPI   | Missense       | +                   |
| SIPA1L2 | 1   | 232564162        | T                | C                 | 817                       | 0.0202                | 0.885149   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232564197        | A                | G                 | 817                       | 0.00245               | 0.069999   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232564288        | T                | G                 | 728                       | 0.00137               | 0.800378   | HAPI   | Missense       | -                   |
| SIPA1L2 | 1   | 232564288        | T                | G                 | 817                       | 0.00734               | 0.262417   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232564297        | T                | A                 | 728                       | 0.23764               | 0.83474    | HAPI   | Missense       | +                   |
| SIPA1L2 | 1   | 232564297        | T                | A                 | 817                       | 0.19584               | 0.444758   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232568041        | G                | A                 | 728                       | 0.11607               | 0.703457   | HAPI   | Missense       | +                   |
| SIPA1L2 | 1   | 232568041        | G                | A                 | 815                       | 0.1092               | 0.091871   | GOLDN | Missense       | -                   |
| SIPA1L2 | 1   | 232568146        | A                | C                 | 817                       | 0.00122               | 0.117251   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232574921        | T                | C                 | 728                       | 0.25962               | 0.966404   | HAPI   | Missense       | +                   |
| SIPA1L2 | 1   | 232574968        | G                | C                 | 780                       | 0.00128               | 0.593174   | HAPI   | Missense       | +                   |
| SIPA1L2 | 1   | 232575166        | T                | C                 | 816                       | 0.00061               | 0.425115   | GOLDN | Missense       | -                   |
| SIPA1L2 | 1   | 232581366        | C                | T                 | 811                       | 0.00247               | 0.097609   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232600762        | T                | C                 | 797                       | 0.00063               | 0.217873   | GOLDN | Missense       | +                   |
| SIPA1L2 | 1   | 232600796        | A                | C                 | 793                       | 0.00063               | 0.243738   | GOLDN | Missense       | +                   |
| SNP         | Chromosome | Position | Reference | Alternate | Allele Ratio Base Frequency | Allele Ratio Larger Frequency | Gene Symbol | Effect Type | Validity |
|-------------|------------|----------|-----------|-----------|-----------------------------|-----------------------------|-------------|-------------|----------|
| SIPA1L2     | 1          | 232615429| C         | T         | 0.00122                     | 0.583783                    | GOLDN       | Missense    | +        |
| SIPA1L2     | 1          | 232626760| C         | T         | 0.00245                     | 0.068269                    | GOLDN       | Missense    | +        |
| SIPA1L2     | 1          | 232649974| G         | A         | 0.00069                     | 0.844218                    | HAPI        | Missense    | +        |
| SIPA1L2     | 1          | 232650253| A         | C         | 0.00062                     | 0.879694                    | GOLDN       | Missense    | +        |
| SIPA1L2     | 1          | 232650307| C         | G         | 0.00184                     | 0.042398                    | GOLDN       | Missense    | +        |
| SIPA1L2     | 1          | 232650454| A         | G         | 0.00245                     | 0.647498                    | GOLDN       | Missense    | +        |
| SIPA1L2     | 1          | 232650624| G         | T         | 0.00061                     | 0.376787                    | GOLDN       | Missense    | +        |
| SIPA1L2     | 1          | 232650662| C         | T         | 0.00123                     | 0.884476                    | GOLDN       | Missense    | -        |
| SIPA1L2     | 1          | 232650941| T         | C         | 0.00062                     | 0.004215                    | GOLDN       | Missense    | +        |
Supplemental Table S6 Gene-based association results for SIPA1L2 with GOLDN and HAPI Heart Study for the trait of triglyceride postprandial area under increase.

| Joint meta-analysis of HAPI and GOLDN | GOLDN | HAPI |
|--------------------------------------|-------|------|
| Burden                              | MB    | SKAT | VT  | Burden | MB | SKAT | VT | Burden | MB | SKAT | VT |
| 6.31E-06                            | 1.73E-06 | 0.0739029 | 2.86E-05 | 6.38E-06 | 2.31E-06 | 0.0713718 | 1.79E-04 | 0.925908 | 0.968225 | 1 | 0.970485 |