

Supplementary material

Genome-Wide Association Studies of Estimated Fatty Acid Desaturase Activity in Serum and Adipose Tissue in Elderly Individuals: Associations with Insulin Sensitivity

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Supplementary Figures

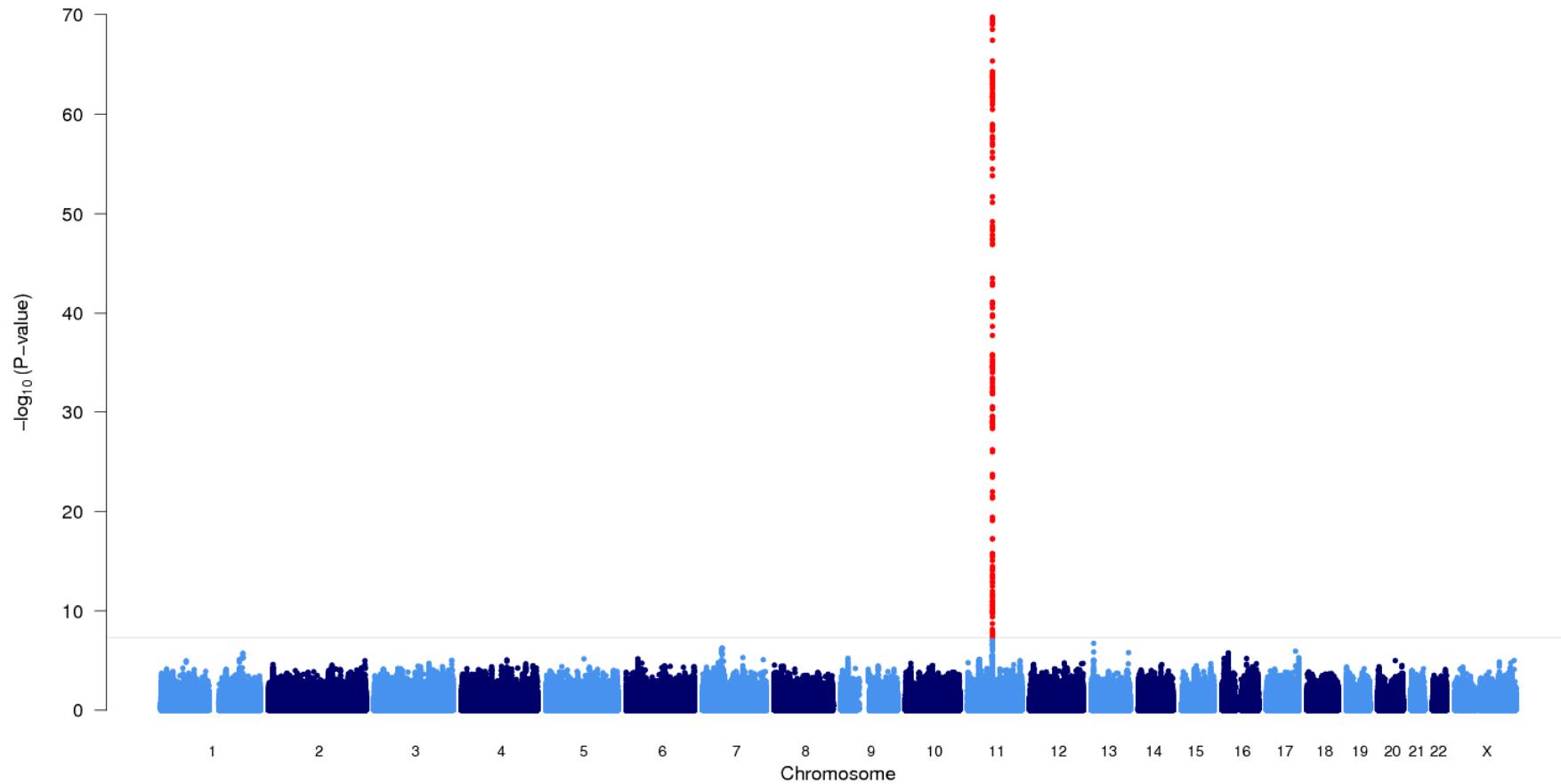


Figure S1. Manhattan plot of the meta-analysis of the single-variant association results of serum D5D.

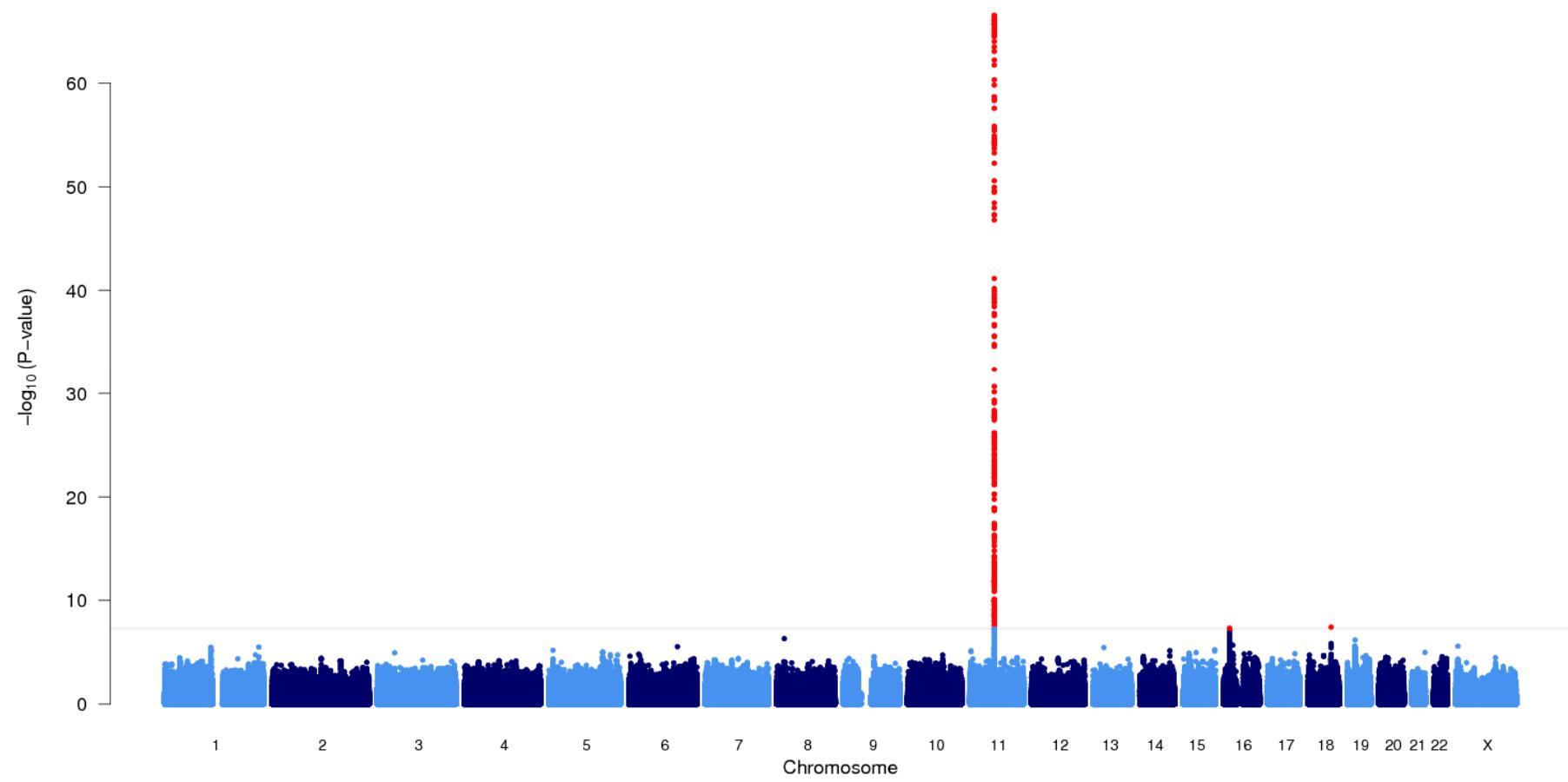


Figure S2. Manhattan plot of the meta-analysis of the single-variant association results of serum D6D.

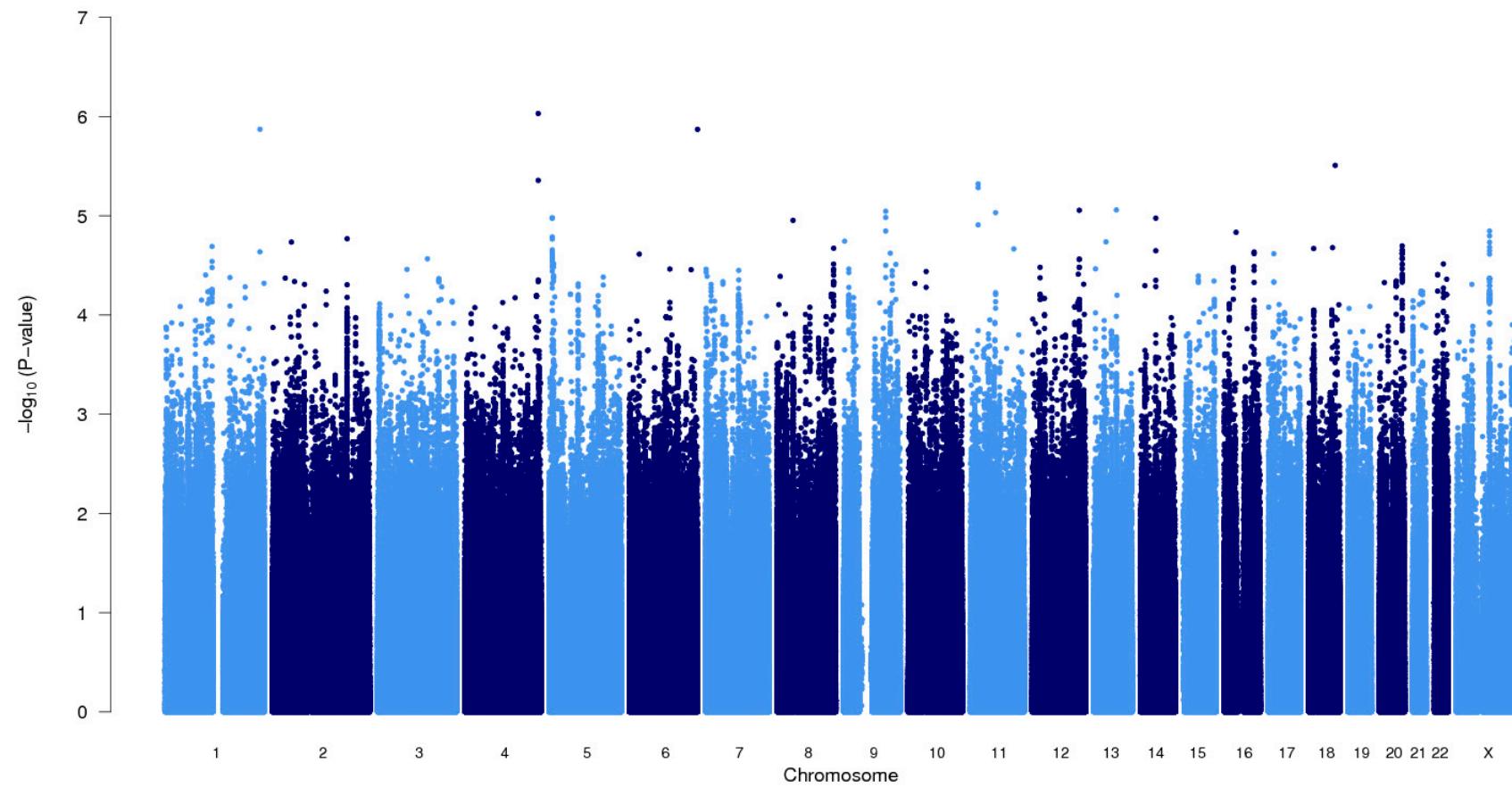


Figure S3. Manhattan plot of the meta-analysis of the single-variant association results of serum SCD.

Supplementary Tables

Table S1. Sample exclusion criteria and number of samples excluded after quality control in PIVUS and ULSAM.^a

| Cohort | Genotyping platform | Sample exclusion criteria | | | | | |
|--------|---------------------|---------------------------|----------------------|--------------------|------------|-----------|-----------------|
| | | Call rate<95% | Heterozygosity >3 SD | Gender discordance | Duplicates | IBD match | Ethnic outliers |
| PIVUS | Illumina | 7 | 14 | 3 | 0 | 0 | 0 |
| | OmniExpress | 0 | 6 | 0 | 3 | 0 | 0 |
| | Illumina Metabochip | 0 | 0 | 0 | 0 | 0 | 0 |
| ULSAM | Illumina | 6 | 7 | 1 | 0 | 1 | 22 |
| | OmniExpress | 0 | 0 | 0 | 0 | 0 | 0 |
| | Illumina Metabochip | 0 | 0 | 0 | 0 | 0 | 0 |

^aIBD, identity by descent; PIVUS, Prospective Investigation of Uppsala Seniors; SD, standard deviation; ULSAM, Uppsala Longitudinal Study of Adult Men.

Table S2. Secondary signals significant at P-value $\sim 10^{-5}$ after adjustment for the lead variant.^a

| Desaturase | lead variant | rs# | Chr:Position (b37) | EAF | Effect allele / Other allele | Before adjustment | | After adjustment | |
|------------|--------------|-----------|--------------------|------|------------------------------|-------------------|-----------------------|------------------|----------------------|
| | | | | | | Direction | P-value | Direction | P-value |
| D5D | rs174549 | rs968567 | 11:61595564 | 0.15 | T / C | - | 4.8×10^{-49} | - | 1.7×10^{-5} |
| D6D | rs138194593 | rs2072113 | 11:61604967 | 0.17 | T / C | - | 3.8×10^{-55} | - | 3.3×10^{-9} |

^ab37, NCBI build 37; Chr, chromosome; D5D, δ-5-desaturase; D6D, δ-6-desaturase; EAF, effect allele frequency; FADS, fatty acid desaturase.

Table S3. Results for the significant loci in the single variant analysis extracted from published meta-analyses of GWAS for HOMA-IR, HDL cholesterol, triglycerides, and BMI.^a

| Gene | rs# | Effect | | HDL ^b | | | Triglycerides ^b | | | BMI ^c | | | HOMA-IR ^d | | |
|-----------|-----------|--------|------|------------------|-----------------------|--------|----------------------------|-----------------------|--------|------------------|-----------------------|--------|----------------------|---------|-------|
| | | Allele | EAF | Direction | P-value | N | Direction | P-value | N | Direction | P-value | N | Direction | P-value | N |
| FADS1 | rs174549 | a | 0.32 | - | 4.3×10 ⁻²³ | 186973 | + | 6.9×10 ⁻³⁴ | 177673 | + | 0.47 | 321655 | + | 0.60 | 46186 |
| FADS2 | rs968567 | t | 0.16 | - | 6.2×10 ⁻⁰⁴ | 172673 | + | 3.4×10 ⁻⁰⁹ | 163958 | + | 0.40 | 309670 | + | 0.14 | 46186 |
| FADS2 | rs2072113 | c | 0.85 | + | 9.1×10 ⁻⁰⁵ | 90617 | - | 1.0×10 ⁻⁰⁶ | 84618 | N/A | N/A | N/A | N/A | N/A | N/A |
| PDXDC1 | rs6498540 | a | 0.67 | + | 0.03 | 92820 | - | 9.8×10 ⁻⁰⁴ | 89485 | + | 1.3×10 ⁻⁰³ | 233998 | + | 0.55 | 46186 |
| near MC4R | rs9957425 | c | 0.39 | - | 0.24 | 92820 | + | 0.04 | 89485 | + | 0.55 | 220175 | - | 1.00 | 46186 |
| PKD2L1 | rs603424 | a | 0.19 | + | 0.52 | 187113 | + | 0.49 | 177807 | - | 0.73 | 309733 | + | 0.28 | 46186 |

^aBMI, body mass index; EAF, Effect allele frequency; HDL, high-density lipoprotein; HOMA-IR, homeostasis model assessment of insulin resistance. ^bResults from (PubMed ID: 24097068). ^cResults from (PubMed ID: 25673413). ^dResults from (PubMed ID: 20081858).