Online Supporting Material

Supplemental Tables

Supplemental Figures

Abbreviations for Supplemental Tables and Figures

AOAC, Association of Official Analytical Chemists; ARIC, Atherosclerosis Risk in Communities Study; CHARGE, Cohorts for Heart and Aging Research in Genomic Epidemiology; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FG, fasting glucose; FHS, Framingham Heart Study; FI, fasting insulin; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; GWAS, genome-wide association study; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MAGIC, Meta-Analyses of Glucose and Insulin-Related Traits Consortium; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; SNP, single nucleotide polymorphism; T2D, type 2 diabetes; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

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Supplemental Table 1. Cohort-Specific Dietary, Outcome, and Covariate Definitions*

Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
ARIC	66-item, interviewer-administered, modified Willett FFQ [Willett WC, *et al. Am J Epidemiol.* 1985; 122(1):51–65. and Stevens J, *et al. Nutrition Research* 1996;16:735–745.]	Harvard	≥8-h fasting blood samples were drawn from an antecubital vein into tubes containing a serum separator gel. Serum glucose concentrations were assessed with a hexokinase/glucose -6-phosphate dehydrogenase method.	≥8-h fasting insulin was quantified by radioimmunoassay (125Insulin Kit; Cambridge Medical Diagnosis, Billerica, MA), with a 7 pmol/L lower limit of sensitivity and 33% cross-reactivity with proinsulin.	ARIC samples were genotyped using the Affymetrix Genome-Wide Human SNP Array 6.0 (Santa Clara, CA). Imputation was performed with MACH software. 11 SNPs studied in the present analyses were imputed; 6 SNPs were directly genotyped: rs340874, rs560887, rs11765, rs4506565, rs10830963, and rs7944584.	Categorized into 6 groups: grade school or none, some high school, high school graduate, vocational school, college, graduate/ professional school	Classified as current, former, never smoker or missing/ unknown	Assessed as both sport and leisure time using the Baecke questionnaire. A sports activity score and a leisure activity score ranged from low to high. Each score ranged from 1–5 in 0.25 increments.	Quantified as g/d (Association of Official Analytical Chemists [AOAC] method)	Quantified as mg/d	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$
CHS	99-item, self-administered, picture-sort version of National Cancer Institute FFQ [Kumanyika S, *et al. J Am Diet Assoc.* 1996;96(2):137–144.]	Harvard	≥8-h fasting glucose was quantified using a Kodak Ektachem 700 analyzer with reagents (Eastman Kodak, Rochester, NY). The overall CV was 1.86%, and the correlation coefficient between 169 pairs of blind replicates was 0.997.	≥8-h fasting insulin was quantified by radioimmunoassay (Coat-A-Count Insulin assay (Diagnostics Products Corp, Los Angeles, CA)	CHS samples were genotyped using the Illumina HumanCNV370-Duo BeadChip system. Imputation was performed using BIMBAM10 v0.91 with reference to HapMap CEU using release 21A, build 35 using one round of imputations and the default expectation-maximization warm-ups and runs; 12 SNPs studied in the present analyses were imputed; 4 SNPs were directly genotyped: rs340874, rs4607517, rs560887, and rs780094.	Categorized into 3 groups: no high school degree, high school or vocational school degree, college degree	Classified as current, former, never smoker	Derived from a questionnaire; exercise intensity was classified into 3 categories: none, low/moderate, high	Quantified as g/d (AOAC method)	Quantified as mg/d	Quantified as drinks/wk (1 drink equivalent to 14 g alcohol)	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
FamHS	66-item, interviewer-administered, modified Willett FFQ [Willett WC, *et al. Am J Epidemiol.* 1985; 122(1):51–65. and Stein AD, *et al*. *Am J Epidemiol.* 1992; 135(6):667–677.]	Harvard	≥8-h fasting blood samples were collected, allowed to clot, centrifuged, aliquoted, and frozen at -70 degrees Celsius before shipment to a central processing laboratory. At the central processing laboratory, glucose was quantified by a thin film adaptation of a glucose oxidase enzymatic, spectrophotometric procedure using the Vitros analyzer (Ortho Clinical Diagnostics, Rochester, NY).	≥8-h fasting insulin was quantified using the coated-tube radioimmunoassay method (Diagnostic Products Corp., Los Angeles, CA).	All participants were typed on an Illumina HumMap chip. The initial 974 were typed with 550K density; 249 were typed at 610K, and the remaining 1482 at 1M. Of these, 34 (3.3%) were excluded due to technical errors, call rates below 98%, and discrepancies between reported sex and sex-diagnostic markers. There was no significant plate-to-plate variation in allele frequencies. Imputation was performed with MACH software.	Categorized into 3 groups: high school graduate or less, vocational school, college or more	Classified as current, former, never smoker or missing/ unknown	Quantified as min/d spent exercising	Quantified as g/d (AOAC method)	Quantified as mg/d	Quantified as drinks/wk (1 drink equivalent to approx-imately 14 g alcohol) and modeled as 0, 1–3, 4–7, 8–14, ≥14 drinks/wk	Calculated from measured weight (kg) / height $(m)^2$
FHS	126-item, self-administered Willett FFQ [Rimm EB, *et al. Am J Epidemiol.* 1992;135:1114–1126, 1127–1136. and Salvini S, *et al*. *Int J Epidemiol.* 1989; 18:858–867.]	USDA	≥8-h fasting plasma glucose was quantified with a hexokinase reagent kit (A-gent glucose test, Abbott Laboratories, South Pasadena, CA). Glucose assays were run in duplicate, and the intra-assay coefficient of variation ranged from 2–3%, depending on the assayed glucose concentration.	≥8-h fasting insulin concentrations were quantified in plasma using human-specific RIA at exam 7 in the Framingham Offspring Cohort and using human-specific insulin ELISA in the Framingham Generation 3 cohort (both assays from Linco Inc., St. Louis, MO).	Framingham study samples were genotyped using Affymetrix 500K (250K Nsp and 250K Sty) and MIPS 50K. Imputation was performed using MACH software. Ratio of variance of dosage to expected variance under binomial model: >0.3.	Continuous, ranging from 0–30 years of education	Classified as regular cigarette smoking in last year (yes/no)	Quantified as a weighted average of the proportion of a typical day spent sleeping and performing sedentary, slight, moderate, or heavy physical activities (expressed in metabolic equivalent units	Quantified as g/d (AOAC method)	Quantified as mg/d	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
GENDAI	Two 24-h recalls	USDA and Greek Food Composition Tables (Nutritionist Pro, v2.2, Axxya Systems- Nutritionist Pro, Stafford, TX, USA)	≥8-h fasting serum glucose concentrations were assessed using commercially available enzymatic colorimetric assays (Sigma Diagnostics, St. Louis, MO) on an automated ACE analyzer (Schiapparelli Biosystems, Inc., Fairfield, NJ).	≥8-h fasting serum insulin was quantified via immunofluorescence on an automatic AIA 600II analyzer (Tosoh Corp., Tokyo, Japan) using a commercially available kit for this purpose (ST AIA-PACK IRI, Tosoh Corp.).	Genotyping was performed using Taqman (Applied Biosystems) in accordance with the recommended protocols. The mean call rate for all SNPs was >95%.	Not applicable, all were in 5th or 6th grade of school	Not applicable	Determined from the Sallis physical activity recall checklist and quantified as m/d of physical activity	Quantified as g/d (AOAC method)	Not applicable	Not applicable	Calculated from measured weight (kg) / height $(m)^2$
GHRAS	55-item, interviewer administered FFQ	USDA	≥8-h fasting serum glucose concentrations were assessed using commercially available enzymatic colorimetric assays (Sigma Diagnostics, St. Louis, MO) on an automated ACE analyzer (Schiapparelli Biosystems, Inc., Fairfield, NJ).	≥8-h fasting serum insulin was quantified via immunofluorescence on an automatic AIA 600II analyzer (Tosoh Corp., Tokyo, Japan) using a commercially available kit for this purpose (ST AIA-PACK IRI, Tosoh Corp.).	Genotyping was performed using Taqman (Applied Biosystems) in accordance with the recommended protocols. The mean call rate for all SNPs was >95%.	Categorized into 4 groups: no degree, primary degree, secondary degree, higher degree	Classified as current, former, never smoker	Metabolic equivalent units of all activities commonly performed in a week, including time spent walking, in vigorous, moderate-intensity, and in sedentary activity (sedentary work, outdoor activities, leisure time and sleep). Based on self-reported responses to the Harokopio Physical Activity Questionnaire.	Not available	Not available	Calculated as mL/d with a concen-tration of 12 g ethanol / 100 mL	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
GLACIER	66-item, self-administered FFQ [Johansson I, *et al*. *Public Health Nutr*. 2002;5(3):487–496. and Johansson G, *et al*. *Public Health Nutr*. 2001;4(4):919–927. and Wennberg M, *et al*. *Public Health Nutr*. 2009;12(9):1477–1484.]	Swedish National Food Administration Database	≥8-h fasting plasma glucose was assayed using fresh capillary plasma on a benchtop analyzer (Reflotron; Boehringer Mannheim, Mannheim, Germany). A threshold glucose value of ≤1 mmol/L was used to exclude potentially spurious values.	≥8-h fasting serum insulin was quantified on a Roche Modular E170 analyzer (Diagnostics GmbH, Mannheim, Germany) with limits of detection of 2.6–24.9 mIU/L.	DNA was extracted at the Medical Biobank in Umeå from peripheral white blood cells. Genomic DNA samples were subsequently diluted to 4 ng/μL. Genotyping was undertaken using Sequenom iPLEX platform (Sequenom Inc., CA, USA), in accordance with the recommended protocols. Approximately 10% duplicate samples were included for the assessment of genotyping concordance. The mean concordance was 99.3% and the mean success rate was 98.4%.	Categorized into 3 groups: total of 6–7 years of compulsory school education, total 12–13 years of education (school + college), school + college + university	Classified as current, former, never smoker	Based on a questionnaire response and classified into 2 exercise frequency categories (never/ infrequently vs. medium/high levels)	Quantified as g/d (AOAC method)	Quantified as mg/d from coffee, tea, and soda	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
Health ABC	108-item, interviewer-administered Block FFQ [Houston, *et al. Am J Clin Nutr*. 2008; 87(1):150–155.]	Block Dietary Data Systems	≥8-h fasting plasma glucose was quantified by an automated glucose oxidase reaction (YSI 2300, Yellow Springs, OH).	≥8-h fasting plasma insulin was assayed with a microparticle enzyme immunoassay (Abbott IMx, Abbott Laboratories, South Pasadena, CA).	Genotyping was performed by the Center for Inherited Disease Research (CIDR) using the Illumina Human1M-Duo BeadChip system. Samples were excluded from the dataset for the reasons of sample failure, genotypic sex mismatch, and first-degree relative of an included individual based on genotype data. Imputation was based on the HapMap CEU (release 22, build 36) using the MACH software (version 1.0.16); 11 SNPs studied in the present analyses were imputed; 6 SNPs were directly genotyped: rs340874, rs780094, rs560887, rs4607517, rs11558471, and rs35767.	Categorized into 3 groups: <high school degree, high school degree, postsecondary degree	Classified as current, former, never smoker	Physical activity over previous 7 d assessed by interviewer-administered questionnaire. Time spent gardening, heavy household chores, light house work, grocery shopping, laundry, climbing stairs, walking for exercise, walking for other purposes, aerobic exercise, weight or circuit training, and moderate- and high-intensity exercise activities obtained in addition to intensity level of activity. Approximate metabolic equivalent unit values assigned to each activity category to calculate weekly energy expenditure (kcal/kg body weight) which was multiplied by each participants' weight, for kcal/wk.	Quantified as g/d of total dietary fiber	Not available	Quantified as g/d	Calculated from measured weight (kg) and height (m^2), at baseline

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
InCHIANTI	236-item, interviewer-administered FFQ [Bartali, *et al*. *Arch Gerontol Geriatr*. 2004;38: 51–60. and Pisani, et al. Int J Epidemiol. 1997; 26:152–160.]	Italian Food Composition Database for Epidemio-logical Studies	≥8-h fasting blood glucose was determined by an enzymatic colorimetric assay using a modified glucose oxidase-peroxidase method (Roche Diagnostics GmbH, Mannheim, Germany) and a Roche-Hitachi 917 analyzer.	Fasting plasma fasting insulin concentrations were determined with a double-antibody, solid-phase radioimmunoassay (intra-assay CV: 3.1 ± 0.3%) (Sorin Biomedica, Milan, Italy).	Genotyping was conducted using Illumina 550K. Samples QC: call rate filter was set at >98.5%; sex misspecification. SNPs QC: MAF >1%; HWE $>10^{-4}$; call rate >99%. Imputation was made using MACH software. Ratio of variance of dosage to expected variance under binomial model: >0.3, MAF >1%.	Categorized into 3 groups: elementary, secondary, or undocu-mented; high school or professional school degree; university degree or higher	Classified as current, former, never smoker	Physical activity in 12 mo prior to interview was assessed through a modified standard interview-administered questionnaire. Based on responses to 7 questions, physical activity was collapsed into 3 categories: sedentary (inactivity or light-intensity activity <1 h/wk); light physical activity (light intensity activity 2–4 h/wk); moderate-high physical activity (light-intensity activity at least 5 h/wk or moderate activity at least 1–2 h/wk)	Quantified as g/d	Quantified as servings/d of coffee, cappuc-cino, latte, or tea (1 cup of coffee contains approx-imately 100 mg caffeine).	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
Malmö	7-d food diary combined with a 168-item FFQ followed by a 1-h diet interview [Elmstahl, *et al*. *Eur J Clin Nutr.* 1996; 50:134–142. and Elmstahl, *et al. Eur J Clin Nutr*. 1996; 50:143–151. and Riboli, *et al. Int J Epidemiol*. 1997;26 Suppl 1:S161–173. and Callmer, *et al. J Intern Med*. 1993; 233:53–57.]	Swedish National Food Administration Database	Fasting glucose was quantified in overnight fasting whole blood samples by a hexokinase-glucose-6-phosphate dehydrogenase method. Blood glucose was converted to plasma glucose using a correction factor of 1.13.	Fasting insulin was quantified by non-specific radioimmunoassay in overnight fasting blood samples.	SNPs were genotyped using either the iPLEX Sequenom MassARRAY platform (GCK, TCF7L2, FADS1) or allelic discrimination (GCKR) on an ABI 7900 instrument (Applied Biosystems). All genotyped SNPs had a genotyping call rate >95% (mean 97.8%) and a HWE p <0.10.	Categorized into 5 groups: elementary, primary and secondary, upper secondary, further education without a degree, university degree	Classified as current, former, never smoker	Leisure-time physical activity was obtained from a list of 18 different activities. The duration of each activity was multiplied by an intensity factor creating a score. The score was divided into six categories.	Quantified as g/d (AOAC method)	No information on caffeine. Coffee intake was used, as g/d. De-caffeinated coffee is very rare in Sweden.	Quantified as g/d (over 7 consec-utive days)	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
MESA	120-item, self-administered, modified-Block FFQ [Mayer-Davis E, *et al*. *Ann Epidemiol.* 1999;9:314–324. and Nettleton JA, *et al*. *Br J Nutr.* 2009;102: 1220–1227.]	Nutrition Data Systems for Research (NDS-R) software database	≥8-h fasting serum glucose was quantified by rate reflectance spectrophotometry using thin film adaptation of the glucose oxidase method on the Vitros analyzer (Johnson & Johnson Clinical Diagnostics, Rochester, NY) at the Collaborative Studies Clinical Laboratory at Fairview-University Medical Center (Minneapolis, MN). Values from the baseline examination were recalibrated after reanalyzing 200 samples from each of the 4 examinations (each approximately 2 y apart).	≥8-h fasting insulin was quantified by raidoimmunoassay (Linco Human Insulin Specific RIA Kit; Linco Research, Inc., St. Charles, MO) at the Collaborative Studies Clinical Laboratory at Fairview-University Medical Center (Minneapolis, MN).	MESA participants were genotyped using the Affymetrix Genome-Wide Human SNP Array 6.0 (Santa Clara, CA); for the current meta-analysis only self-reported Caucasian participants were analyzed. IMPUTE version 2.1.0 was used to perform imputation for the MESA SHARe Caucasian participants (chromosomes 1–22) using HapMap Phase I and II CEU as the reference panel (release 24, build 36 (dbSNP b126)).	Categorized into 3 groups: high school not completed; completion of high school, some college or technical school certificate; completion or Associate's degree, Bachelor's degree or higher	Classified as current, former, never smoker	Quantified as metabolic equivalent-minutes in sedentary leisure activity and active leisure activity (included walking, conditioning, doing sport/dance)	Quantified as g/d (AOAC method)	Quantified as mg/d	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
PIVUS	7 one-d food records [Becker W, Lennernäs MM, Gustafsson I-B, *et al*. *Food intake. The Sixth Nordic Conference in Nutrition.* Göteborg, Sweden, 1996.]	Swedish National Food Administration Database	Reference method at Uppsala University Hospital	Enzymatic-immunological assay at Uppsala University Hospital	SNPs were genotyped by multiplex mini-sequencing (fluorescent single base extension) using the SNPstream system (Beckman Coulter). SNPstream UHT: ultra-high throughput SNP genotyping for pharmacogenomics and drug discovery. (*Biotechniques* 2002;30:S70–77). SNP QC filters: MAF>5%; HWE $<10^{-3}$; call rate >93%. Average SNP call rate: 0.97777335625. Sample QC filters: call rate >95%. Average sample call rate: 0.97629158.	Categorized into 3 groups: elementary school only, secondary school only, college or graduate degree	Classified as current smoker (yes/no)	Leisure time physical activity was assessed using a questionnaire and participants were classified into four categories and referred to as sedentary, moderate, regular and athletic physical activity	Not available	Not available	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
Rotterdam	Two-step procedure: (1) A simple self-administered questionnaire was first completed at home, only questions were asked about which food items were consumed; no questions about portion sizes (or frequency) were asked during this step. (2) A subsequent interviewer-administered FFQ [Klipstein-Grobusch K, *et al*. *Eur J Clin Nutr.* 1998;52(8):588–596]	NEVO Dutch Food Composition Table	In 1997–1999 (approximately 6 years after the baseline exam where FFQ data were gathered), ≥8-h fasting blood collected and glucose was quantified enzymatically using the hexokinase method (Boehringer Mannheim, Mannheim, Germany).	In 1997–1999 (approximately 6 years after the baseline exam where FFQ data were gathered), ≥8-h fasting blood samples were drawn and stored at -80 degrees Celsius. In 2008, insulin concentrations were quantified on a Modular Analytics E170 analyzer, using a Cobas Roche electrochemi-luminescence immunoassay (12017547 122).	Genotyping was conducted using the Illumina 550K array among participants of self-reported European descent, and succeeded in 6,240 participants (sample call rate 97.5%). We excluded participants for excess autosomal heterozygosity, mismatch between called and phenotypic gender, or being outliers identified by the IBS clustering analysis.	Categorized into 4 groups: completed primary education; lower vocational training or general education; inter-mediate vocational training or inter-mediate and higher general education; higher vocational training, college, or university	Classified as current, former, never smoker	Not available	Total dietary fiber, quantified as g/d	Quantified as mg/d	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$

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Cohort Study	Dietary assessment method	Nutrient database	Fasting glucose	Fasting insulin	GWAS/ genotyping	Education	Smoking status	Physical activity	Fiber intake	Caffeine intake	Alcohol intake	Body mass index
ULSAM	7 one-d food records [Becker W, Lennernäs MM, Gustafsson I-B, *et al*. *Food intake. The Sixth Nordic Conference in Nutrition.* Göteborg, Sweden, 1996.]	Swedish National Food Administration Database	≥8-h fasting venous plasma samples were obtained from the antecubital vein. Glucose was quantified by the glucose dehydrogenase method (Gluc-DH, Merck, Darmstadt, Germany). The intra-individual CV for fasting plasma glucose was 3.2%.	≥8-h fasting plasma insulin was assayed using an enzymatic-immunological assay (Enzymmun, Boehringer Mannheim, Mannheim, Germany) performed in an ES300 automatic analyzer (Boehringer Mannheim) and the concentrations were originally given in mU/L.	SNPs were genotyped by multiplex mini-sequencing (fluorescent single base extension) using the SNPstream system (Beckman Coulter). SNPstream UHT: ultra-high throughput SNP genotyping for pharmacogenomics and drug discovery. (*Biotechniques* 2002;30:S70–77). SNP QC filters: MAF >5%; HWE $<10^{-3}$; call rate >93%. Average SNP call rate: 0.97777335625. Sample QC filters: call rate >95%. Average sample call rate: 0.97629158.	Categorized into 3 groups: elementary school only, secondary school only, college or graduate degree	Classified as current smoker (yes/no)	Leisure time physical activity was assessed using a questionnaire and participants were classified into four categories and referred to as sedentary, moderate, regular, and athletic physical activity	Not available	Not available	Quantified as g/d	Calculated from measured weight (kg) / height $(m)^2$
YFS	131-item FFQ [Paalanen L, *et al*. *J Clin Epid.* 2006;59(9):994–1001.]	Finnish food composition database	≥8-h fasting glucose concentrations were analyzed enzymatically (Olympus Diagnostica GmbH, Hamburg, Germany).	≥8-h fasting serum insulin was quantified by microparticle enzyme immunoassay kit (Abbott Laboratories, Diagnostic Division, Dainabot, South Pasadena, CA).	Genotyping was performed at the Sanger Institute (UK) using the custom-built Illumina BeadChip Human670K. Genotypes were called using Illumina's clustering algorithm. SNPs that were present on HapMap and that passed quality control measures were used for imputation with MACH version 1.0.	Continuous, as sum of all education years (elementary through graduate, as applicable)	Classified into current or former smoker vs. never smoker	Frequency of moderate to intense exercise in leisure time (6 categories): never, 1 time/mo, 1 time/wk, 2–3 times/wk, 4–6 times/wk, daily	Total fiber, quantified as g/d	From coffee only in servings/d, quantified as mg/d caffeine (1 cup of coffee contains 100 mg caffeine)	Quantified as drinks/d (1 drink equivalent to approx-imately 14 g alcohol)	Calculated from measured weight (kg) / height $(m)^2$

*AOAC, Association of Official Analytical Chemists; ARIC, Atherosclerosis Risk in Communities Study; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FG, fasting glucose; FHS, Framingham Heart Study; FI, fasting insulin; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; GWAS, genome-wide association study; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; SNP, single nucleotide polymorphism; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

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Supplemental Table 2. Meta-Analyzed Associations of SNPs on Fasting Glucose (mmol/L) and Fasting Insulin (ln-pmol/L)*

SNP	Nearest Gene	Coded / Other Allele	*n*	Coded Allele Frequency	β	SE	*P*	I^2 (95% CI)
Outcome is FASTING GLUCOSE (mmol/L)								
Glucose-related SNPs								
rs10830963	*MTNR1B*	G/C	51,735	0.28	0.083	0.004	5.4E-99	54 (18 to 74)
rs10885122	*ADRA2A*	G/T	52,546	0.88	0.022	0.005	2.9E-05	0 (0 to 35)
rs11071657	*C2CD4B*	A/G	52,576	0.61	0.009	0.004	0.01	15 (0 to 53)
rs11558471	*SLC30A8*	A/G	50,807	0.69	0.035	0.004	1.7E-19	0 (0 to 50)
rs11605924	*CRY2*	A/C	52,742	0.48	0.023	0.003	1.6E-11	0 (0 to 52)
rs11708067	*ADCY5*	A/G	51,172	0.78	0.026	0.004	1.7E-10	30 (0 to 63)
rs11920090	*SLC2A2*	T/A	51,784	0.86	0.031	0.005	5.8E-10	28 (0 to 62)
rs174550	*FADS1*	T/C	52,783	0.67	0.017	0.004	2.5E-06	0 (0 to 13)
rs2191349	*DGKB-TMEM195*	T/G	52,719	0.53	0.029	0.003	2.7E-17	0 (0 to 51)
rs340874	*PROX1*	C/T	51,792	0.53	0.020	0.004	9.7E-09	42 (0 to 69)
rs4506565	*TCF7L2*	T/A	49,731	0.29	0.025	0.004	5.2E-11	0 (0 to 39)
rs4607517	*GCK*	A/G	52,948	0.17	0.063	0.005	1.1E-44	0 (0 to 33)
rs560887	*G6PC2*	C/T	51,957	0.70	0.076	0.004	5.7E-95	0 (0 to 25)
rs7034200	*GLIS3*	A/C	52,494	0.48	0.018	0.003	9.3E-08	0 (0 to 13)
rs780094	*GCKR*	C/T	52,920	0.61	0.031	0.004	8.5E-19	20 (0 to 57)
rs7944584	*MADD*	A/T	51,741	0.73	0.024	0.004	6.0E-10	6 (0 to 42)
Magnesium-related SNPs								
rs11144134	*TRPM6*	T/C	30,432	0.92	0.007	0.008	0.39	0 (0 to 55)
rs2274924	*TRPM6*	A/G	29,734	0.84	-0.013	0.006	0.03	0 (0 to 58)
rs3740393	*CNNM2*	G/C	31,382	0.85	-0.003	0.006	0.63	0 (0 to 41)
rs3750425	*TRPM6*	C/T	30,432	0.91	-0.014	0.008	0.07	0 (0 to 62)
rs4072037	*MUC1*	C/T	31,383	0.45	-0.005	0.004	0.29	0 (0 to 11)
rs6746896	*CNNM4*	A/G	30,688	0.67	0.004	0.005	0.44	0 (0 to 48)
rs8042919	*TRPM7*	G/A	31,383	0.90	0.001	0.007	0.92	28 (0 to 65)
rs994430	*CNNM3*	A/T	31,383	0.60	0.003	0.004	0.54	0 (0 to 49)

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SNP	Nearest Gene	Coded / Other Allele	*n*	Coded Allele Frequency	β	SE	*P*	I^2 (95% CI)
Outcome is FASTING INSULIN (ln-pmol/L)								
Insulin-related SNPs								
rs35767	*IGF1*	G/A	37,862	0.84	0.016	0.005	0.003	20 (0 to 56)
rs780094	*GCKR*	C/T	38,181	0.59	0.028	0.004	4.3E-13	20 (0 to 56)
Magnesium-related SNPs								
rs11144134	*TRPM6*	T/C	29,902	0.92	0.010	0.009	0.26	0 (0 to 18)
rs2274924	*TRPM6*	A/G	29,204	0.83	0.003	0.006	0.61	0 (0 to 23)
rs3740393	*CNNM2*	G/C	30,844	0.85	-0.003	0.006	0.60	0 (0 to 39)
rs3750425	*TRPM6*	C/T	29,902	0.91	0.0004	0.008	0.95	0 (0 to 37)
rs4072037	*MUC1*	C/T	30,845	0.45	-0.003	0.005	0.59	0 (0 to 36)
rs6746896	*CNNM4*	A/G	30,150	0.68	0.002	0.005	0.60	0 (0 to 58)
rs8042919	*TRPM7*	G/A	30,845	0.90	-0.005	0.007	0.50	0 (0 to 55)
rs994430	*CNNM3*	A/T	30,845	0.61	0.0003	0.004	0.94	0 (0 to 48)

*In an additive allele model, adjusted for age, sex, study center (in ARIC, CHS, FamHS, Health ABC, InCHIANTI, MESA), and family or population substructure (in CHS, FamHS, FHS, MESA, YFS). β represents the change in fasting glucose (mmol/L) or fasting insulin (ln-pmol/L) per each additional coded allele. I^2 represents the heterogeneity statistic, presented as %. AOAC, Association of Official Analytical Chemists; ARIC, Atherosclerosis Risk in Communities Study; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FG, fasting glucose; FHS, Framingham Heart Study; FI, fasting insulin; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; GWAS, genome-wide association study; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MAGIC, Meta-Analyses of Glucose and Insulin-Related Traits Consortium; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; SNP, single nucleotide polymorphism; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

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Supplemental Table 3. Cohort Study Acknowledgements*

Cohort Study	Country	Description and Acknowledgements	Consortium Membership(s)
ARIC	US	The **A**therosclerosis **R**isk **I**n **C**ommunities Study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute contracts (HHSN268201100005C, HHSN268201100006C, HHSN268201100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C, and HHSN268201100012C), R01HL087641, R01HL59367 and R01HL086694; National Human Genome Research Institute contract U01HG004402; and National Institutes of Health contract HHSN268200625226C. The authors thank the staff and participants of the ARIC study for their important contributions. Infrastructure was partly supported by Grant Number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research. Dr. Nettleton is supported by a K01 from the National Institutes of Health, National Institute of Diabetes and Digestive and Kidney Diseases (5K01DK082729-04). [representing authors: JAN, KEN, JSP, WHLK]	CHARGE, MAGIC
CHS	US	The **C**ardiovascular **H**ealth **S**tudy research was supported by NHLBI contracts N01-HC-85239, N01-HC-85079 through N01-HC-85086; N01-HC-35129, N01 HC-15103, N01 HC-55222, N01-HC-75150, N01-HC-45133, HHSN268201200036C and NHLBI grants HL080295, HL087652, HL105756 with additional contribution from NINDS. Additional support was provided through AG-023629, AG-15928, AG-20098, and AG-027058 from the NIA. See also http://www.chs-nhlbi.org/pi.htm. DNA handling and genotyping was supported in part by National Center of Advancing Translational Technologies CTSI grant UL1TR000124 and National Institute of Diabetes and Digestive and Kidney Diseases grant DK063491 to the Southern California Diabetes Endocrinology Research Center. [representing authors: RNL, DM, LD, KM, DSS]	CHARGE, MAGIC
FamHS	US	The **Fam**ily **H**eart **S**tudy work was supported in part by NIH R01-HL-087700 and R01-HL-088215 (Michael A. Province, PI) from NHLBI; and R01-DK-8925601 and R01-DK-075681 (Ingrid B. Borecki, PI) from NIDDK. The investigators thank the staff and participants of the Family Heart Study for their important contributions. [representing authors: MKW, IBB]	MAGIC

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Cohort Study	Country	Description and Acknowledgements	Consortium Membership(s)
FHS	US	The Framingham Offspring Study (Exam 7) and Framingham Third Generation Study (Exam 1) analyses were conducted in part using data and resources from the **F**ramingham **H**eart **S**tudy of the National Heart, Lung, and Blood Institute of the National Institutes of Health and Boston University School of Medicine. The analyses reflect intellectual input and resource development from the Framingham investigators participating in the SNP Health Association Resource (SHARe) project. This work was partially supported by the National Heart, Lung, and Blood Institute's Framingham Heart Study (contract no. N01-HC-25195) and its contract with Affymetrix, Inc. for genotyping services (contract no. N02-HL-6-4278). A portion of this research utilized the Linux Cluster for Genetic Analysis (LinGA-II) funded by the Robert Dawson Evans Endowment of the Department of Medicine at Boston University School of Medicine and Boston Medical Center. Also supported by National Institute for Diabetes and Digestive and Kidney Diseases (NIDDK) R01 DK078616 and NIDDK K24 DK080140 to JBM. NMM is supported by USDA agreement no. 58-1950-7-707. AH is an American Heart Association Predoctoral Fellow. The authors thank the participants of the Framingham Heart Study. [representing authors: AH, JSN, PFJ, JBM, NMM, LAC]	CHARGE, MAGIC
GENDAI	Greece	The **Gen**e-**D**iet **A**ttica **I**nvestigation on childhood obesity thank all the field investigators for samples and data collection and all the children, their parents and the elderly people for participation in the study. Diabetes UK (grant RD08/0003704). The research of Inga Prokopenko is funded through the European Community's Seventh Framework Programme (FP7/2007-2013), ENGAGE project, grant agreement HEALTH-F4-2007-201413. The GENDAI cohort was supported by a research grant from Coca Cola Hellas. [representing authors: IN, GVD, MY, CP, CJG, IP, NH, MIM]	MAGIC
GHRAS	Greece	The **G**reek **H**ealth **R**andomized **A**ging **S**tudy would like to thank all the field investigators for samples and data collection and all the children, their parents and the elderly people for participation in the study. Diabetes UK (grant RD08/0003704). The research of Inga Prokopenko is funded in part through the European Community's Seventh Framework Programme (FP7/2007-2013), ENGAGE project, grant agreement HEALTH-F4-2007-201413. [representing authors: SK, GVD, EG, CJG, IP, NH, MIM]	MAGIC

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Cohort Study	Country	Description and Acknowledgements	Consortium Membership(s)
GLACIER	Sweden	The **G**ene-**L**ifestyle interactions **A**nd **C**omplex traits **I**nvolved in **E**levated Disease **R**isk study is nested within the Northern Swedish Health and Disease Study cohort and the Västerbotten Intervention Programme (VIP). We are indebted to the study participants who dedicated their time and samples to these studies. We also thank the VIP and Umeå Medical Biobank staff for biomedical data collection and preparation. We specifically thank John Hutiainen, Åsa Ågren and Sara Nilsson (Umeå Medical Biobank) for data organization, Kerstin Enqvist and Thore Johansson (Västerbottens County Council) for expert technical assistance with DNA preparation, and David Hunter, Patrice Soule and Hardeep Ranu (Harvard School of Public Health) for expert assistance with planning and undertaking genotyping of GLACIER samples. The GLACIER Study was funded by project grants from Novo Nordisk (PWF), the Swedish Heart-Lung Foundation (PWF), the Swedish Diabetes Association (to PWF), Påhlssons Foundation (PWF), the Swedish Research Council (PWF), Umeå University Career Development Award (PWF), and The Heart Foundation of Northern Sweden (PWF). FR was supported by a post-doctoral stipend from the Swedish Heart-Lung Foundation. [representing authors: FR, GH, IJ, FBH, PWF]	
Health ABC	US	The **Health**, **A**ging and **B**ody **C**omposition study was supported in part by the Intramural Research Program of the NIH, National Institute on Aging contracts N01AG62101, N01AG62103, and N01AG62106. The genome-wide association study was funded by NIA grant R01 AG032098 to Wake Forest University Health Sciences and genotyping services were provided by the Center for Inherited Disease Research (CIDR). CIDR is fully funded through a federal contract from the National Institutes of Health to The Johns Hopkins University, contract number HHSN268200782096C. [representing authors: DKH, KKL, YL, SBK]	
InCHIANTI	Italy	**In**vecchiare in **Chianti** (aging in the Chianti area; **InCHIANTI**) study investigators thank the Intramural Research Program of the NIH, National Institute on Aging who are responsible for the InCHIANTI samples. Investigators also thank the InCHIANTI participants. The InCHIANTI study baseline (1998–2000) was supported as a “targeted project” (ICS110.1/RF97.71) by the Italian Ministry of Health and in part by the US National Institute on Aging (contracts 263 MD 9164 and 263 MD 821336). [representing authors: TT, SB, LF]	MAGIC

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Cohort Study	Country	Description and Acknowledgements	Consortium Membership(s)
Malmö	Sweden	The **Malmö** Diet & Cancer Study was initiated and planned in collaboration with the International Agency for Research on Cancer, the Swedish Cancer Society, and Swedish Medical Research Council and the Faculty of Medicine Lund University, Sweden. The study is also funded by Region Skåne, City of Malmö, Påhlsson Foundation and the Swedish Heart and Lung Foundation. [representing authors: ES, MO-M]	
MESA	US	The **M**ulti-**E**thnic **S**tudy of **A**therosclerosis and MESA SHARe project are conducted and supported by contracts N01-HC-95159 through N01-HC-95169 and RR-024156 from the National Heart, Lung, and Blood Institute (NHLBI). Funding for MESA SHARe genotyping was provided by NHLBI Contract N02-HL-6-4278. The authors thank the participants of the MESA study, the Coordinating Center, MESA investigators, and study staff for their valuable contributions. A full list of participating MESA investigators and institutions can be found at http://www.mesa-nhlbi.org. [representing authors: AM, JAN, JIR]	CHARGE, MAGIC
PIVUS	Sweden	The participants in the **P**rospective **I**nvestigation of the **V**asculature in **U**ppsala **S**eniors were randomly sampled from all men and women at age 70 living in Uppsala County in 2001 (www.medsci.uu.se/PIVUS). Of the 2025 individuals invited, 1016 participated. The participants underwent a medical examination including a detailed questionnaire on lifestyle and socioeconomic factors, fasting blood sampling, blood pressure measurement and anthropometric measurements, as previously described.18 Blood and plasma samples have been frozen until analysis, and blood tests performed include a wide variety of traditional and more recent CVD risk factors, along with DNA extraction. In addition, the individuals have also undergone extensive phenotyping including whole body MRI, echocardiography, endothelial function measurements, carotid ultrasound, DXA, and spirometry. Genotyping was performed by the SNP&SEQ Technology Platform in Uppsala (www.genotyping.se). We thank Tomas Axelsson, Ann-Christine Wiman and Caisa Pöntinen for their excellent assistance with genotyping. The SNP Technology Platform is supported by Uppsala University, Uppsala University Hospital and the Swedish Research Council for Infrastructures. E.I. is supported by grants from the Swedish Research Council, the Swedish Heart-Lung Foundation, the Swedish Foundation for Strategic Research, and the Royal Swedish Academy of Science. [representing authors: AG, UR, ACS, LL, EI]	MAGIC

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Cohort Study	Country	Description and Acknowledgements	Consortium Membership(s)
Rotterdam	The Netherlands	The generation and management of GWAS genotype data for the **Rotterdam Study** is supported by the Netherlands Organisation of Scientific Research NWO Investments (nr. 175.010.2005.011, 911-03-012). This study is funded by the Research Institute for Diseases in the Elderly (014-93-015; RIDE2), the Netherlands Genomics Initiative (NGI)/Netherlands Organisation for Scientific Research (NWO) project nr. 050-060-810. We thank Pascal Arp, Mila Jhamai, Marijn Verkerk, Lizbeth Herrera and Marjolein Peters for their help in creating the GWAS database, and Karol Estrada and Maksim V. Struchalin for their support in creation and analysis of imputed data. The Rotterdam Study is funded by Erasmus Medical Center and Erasmus University, Rotterdam, Netherlands Organization for the Health Research and Development (ZonMw), the Research Institute for Diseases in the Elderly (RIDE), the Ministry of Education, Culture and Science, the Ministry for Health, Welfare and Sports, the European Commission (DG XII), and the Municipality of Rotterdam. The authors are grateful to the study participants, the staff from the Rotterdam Study and the participating general practitioners and pharmacists. [representing authors: FJAvR, MCZ, AGU, AH, OHF, JCMW]	CHARGE, MAGIC
ULSAM	Sweden	Subjects born between 1920 and 1924 in Uppsala, Sweden were invited to participate at age 50 in the the **U**ppsala **L**ongitudinal **S**tudy of **A**dult **M**en, that was started in 1970. Subjects were reinvestigated at the ages of 60, 70, 77, 82 and 88 years.19 Blood samples for DNA extraction and main cardiovascular risk factors were available from the 70-years old investigation (n=1,146 with DNA and data on CHD risk factors). The participants have undergone extensive phenotyping at repeated time points, including for example euglycemic clamps, oral glucose tolerance tests, echocardiography, 24-h ambulatory blood pressure measurement, and a range of biomarkers. Genotyping was performed by the SNP&SEQ Technology Platform in Uppsala (www.genotyping.se). We thank Tomas Axelsson, Ann-Christine Wiman and Caisa Pöntinen for their excellent assistance with genotyping. The SNP Technology Platform is supported by Uppsala University, Uppsala University Hospital and the Swedish Research Council for Infrastructures. EI is supported by grants from the Swedish Research Council, the Swedish Heart-Lung Foundation, the Swedish Foundation for Strategic Research, and the Royal Swedish Academy of Science. [representing authors: AG, UR, ACS, LL, EI]	MAGIC

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Cohort Study	Country	Description and Acknowledgements	Consortium Membership(s)
YFS	Finland	The Cardiovascular Risk in **Y**oung **F**inns **S**tudy has been financially supported by the Academy of Finland: grants 126925, 121584, 124282, 129378 (Salve), 117787 (Gendi), and 41071 (Skidi), the Social Insurance Institution of Finland, Kuopio, Tampere and Turku University Hospital Medical Funds (grant 9M048 for TL), Juho Vainio Foundation, Paavo Nurmi Foundation, Finnish Foundation of Cardiovascular Research and Finnish Cultural Foundation, Tampere Tuberculosis Foundation and Emil Aaltonen Foundation (TL). The expert technical assistance in the statistical analyses by Irina Lisinen and Ville Aalto are gratefully acknowledged. [representing authors: TL, OTR, JV, VM, MK]	

*ARIC, Atherosclerosis Risk in Communities Study; CHARGE, Cohorts for Heart and Aging Research in Genomic Epidemiology; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FHS, Framingham Heart Study; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; GWAS, genome-wide association study; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MAGIC, Meta-Analyses of Glucose and Insulin-Related Traits Consortium; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

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Supplemental Table 4. Authors and Affiliations

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Cohort Study	Author Name	Initials	Institutional Affiliation(s)
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Cohort Study	Author Name	Initials	Institutional Affiliation(s)
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Cohort Study	Author Name	Initials	Institutional Affiliation(s)
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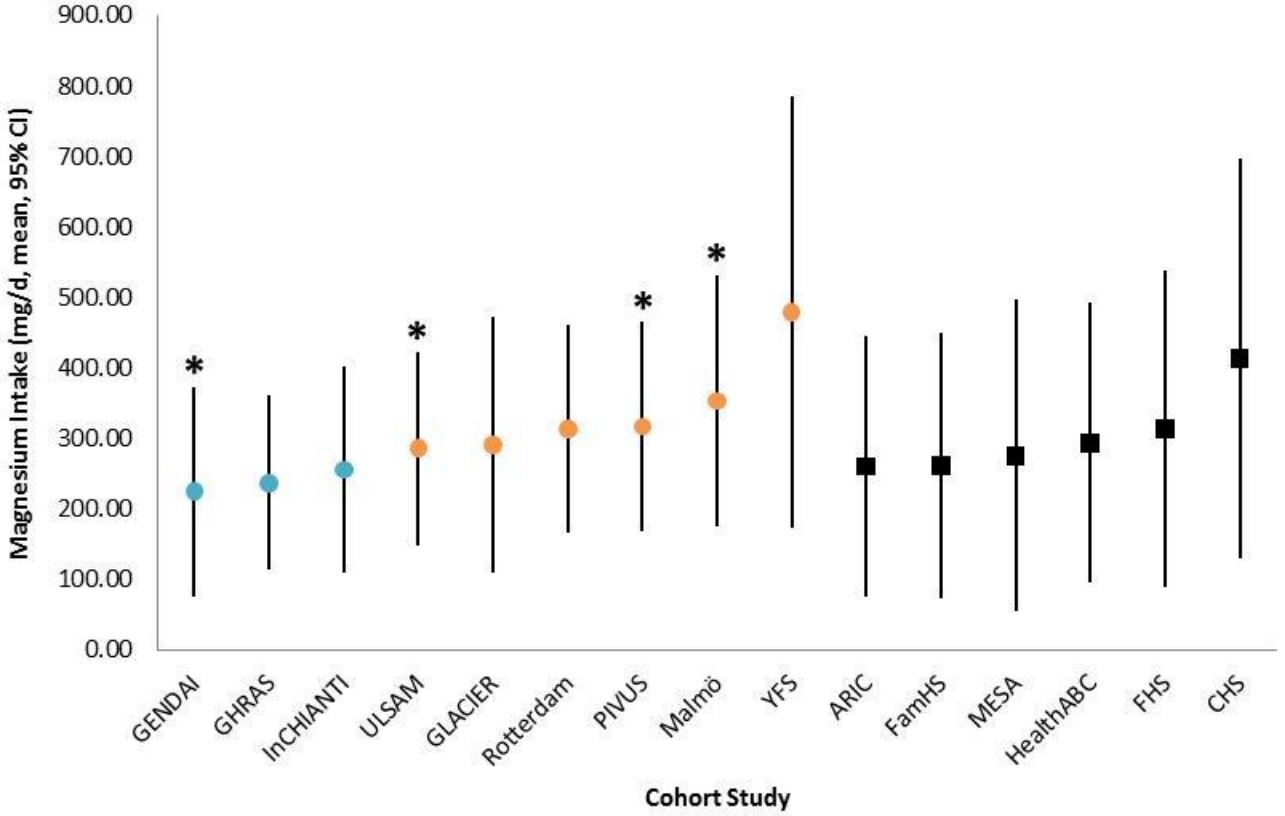
YFS	Vera Mikkilä, PhD	VM	Department of Food and Environmental Sciences, University of Helsinki, Helsinki, Finland
YFS	Mika Kähönen, MD, PhD	MK	Department of Clinical Physiology, Tampere University Hospital and University of Tampere, Tampere, Finland

*ARIC, Atherosclerosis Risk in Communities Study; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FHS, Framingham Heart Study; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

Online Supporting Material

Supplemental Figure 1. Mean Magnesium Intake by Ascending Mean Intake in Each Region, in 15 Cohort Studies



Mean and 95% confidence interval of dietary magnesium intake (mg/d). Values are shown by region in order of ascending intake: Mediterranean cohort studies = aqua circles; Northern European cohort studies = orange circles; North American cohort studies = black squares. All cohort studies estimated intake using food frequency questionnaire, except where starred (*): GENDAI = 24-h dietary recall; Malmö = food diary and FFQ; PIVUS and ULSAM = dietary record. ARIC, Atherosclerosis Risk in Communities Study; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FHS, Framingham Heart Study; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

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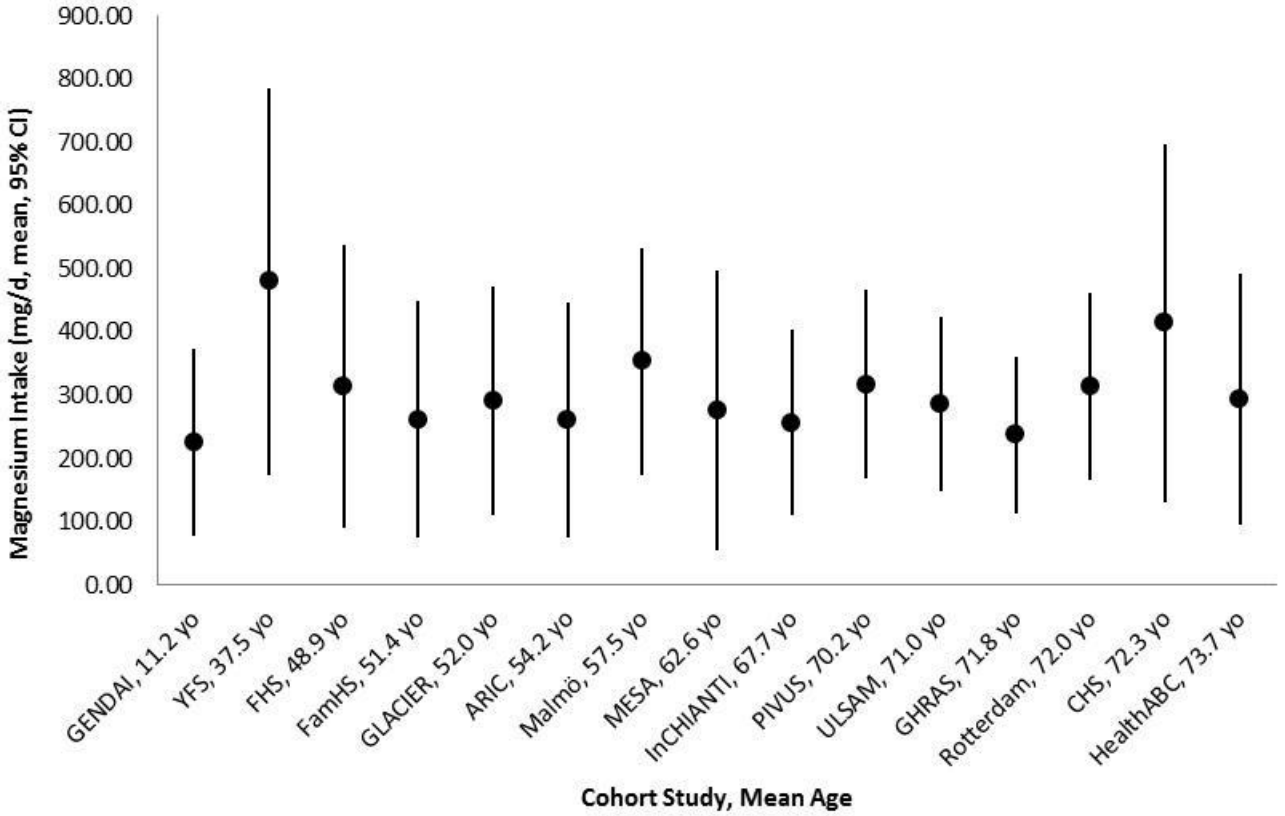
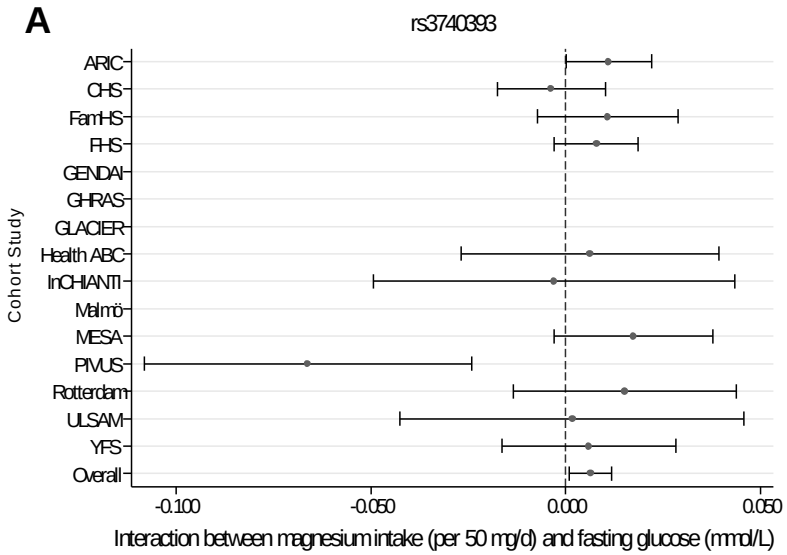
Supplemental Figure 2. Mean Magnesium Intake by Ascending Mean Age, in 15 Cohort Studies

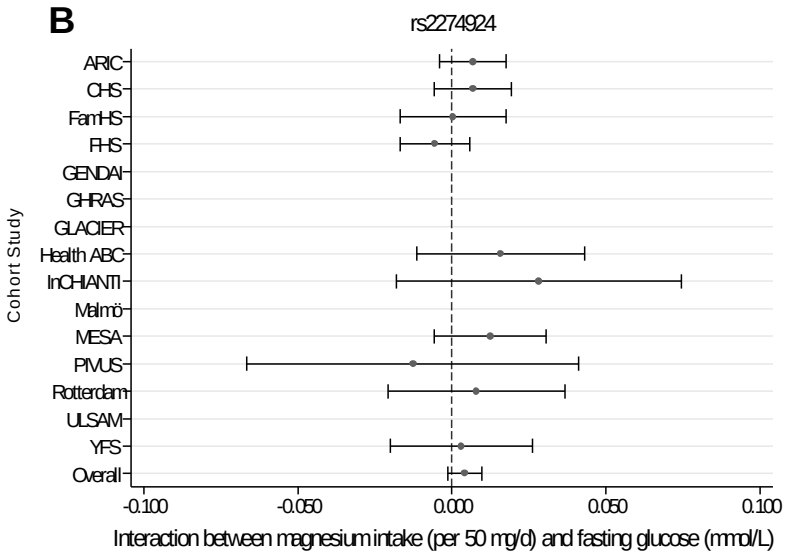


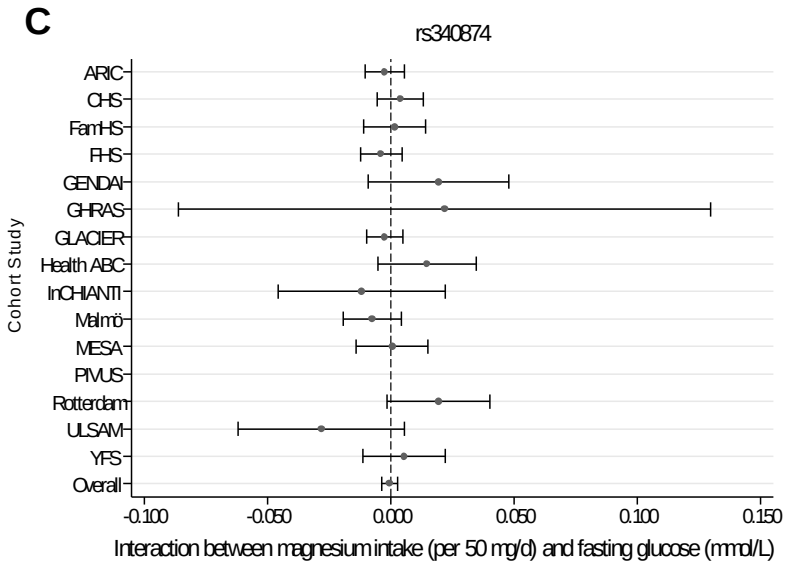
Mean and 95% confidence interval of dietary magnesium intake (mg/d). Values are shown in order of ascending mean age of each cohort study. ARIC, Atherosclerosis Risk in Communities Study; CHS, Cardiovascular Health Study; FamHS, Family Heart Study; FFQ, food frequency questionnaire; FHS, Framingham Heart Study; GENDAI, Gene-Diet Attica Investigation on Childhood Obesity; GHRAS, Greek Health Randomized Aging Study, GLACIER, Gene-Lifestyle interactions And Complex traits Involved in Elevated disease Risk; Health ABC, Health, Aging, and Body Composition Study; InCHIANTI, Invecchiare in Chianti; MESA, Multi-Ethnic Study of Atherosclerosis; PIVUS, Prospective Investigation of the Vasculature in Uppsala Seniors; ULSAM, Uppsala Longitudinal Study of Adult Men; YFS, Cardiovascular Risk in Young Finns Study.

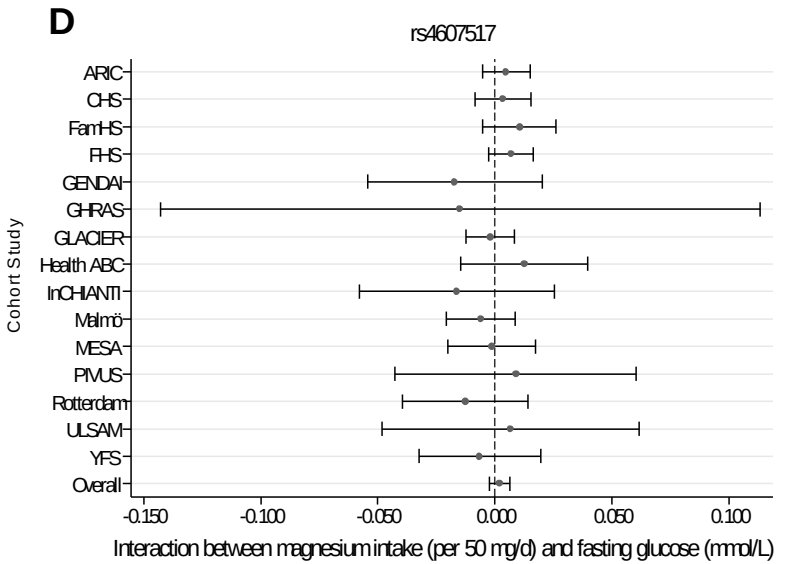
Online Supporting Material

Supplemental Figure 3. Forest Plots of Cohort-Specific and Meta-Analyzed Magnesium × SNP Interactions on Fasting Glucose (24 plots, A–X)









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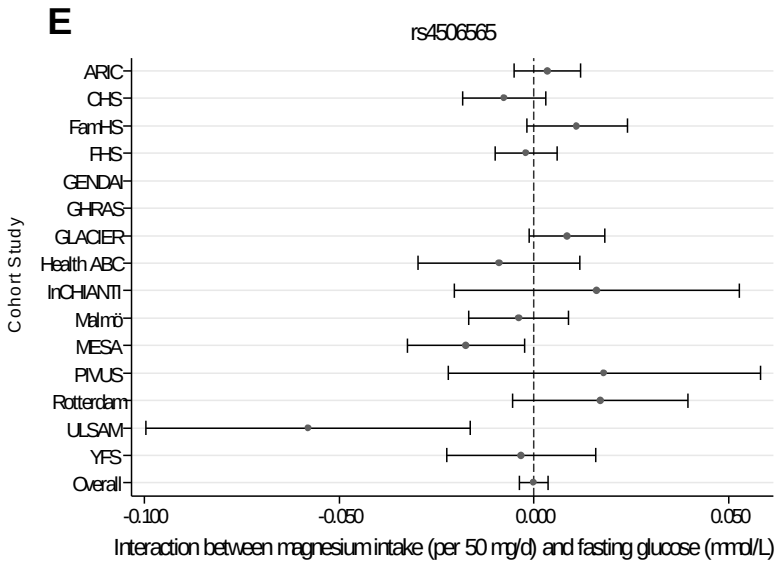

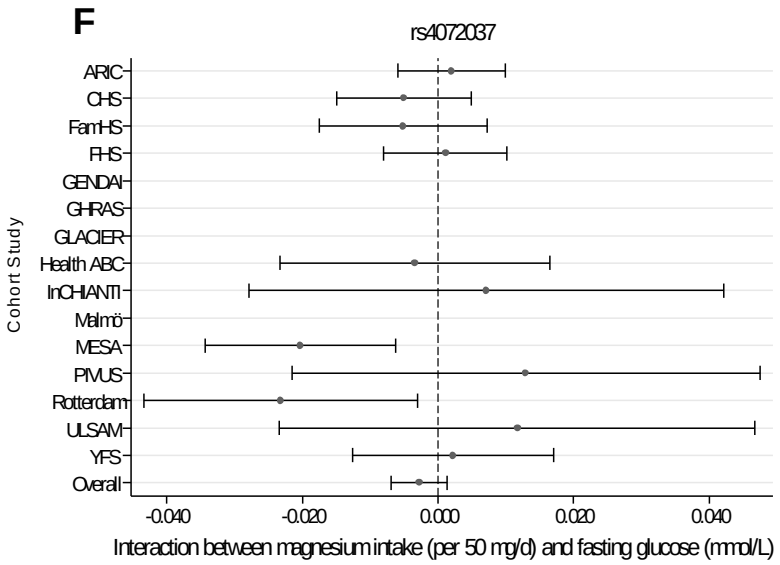

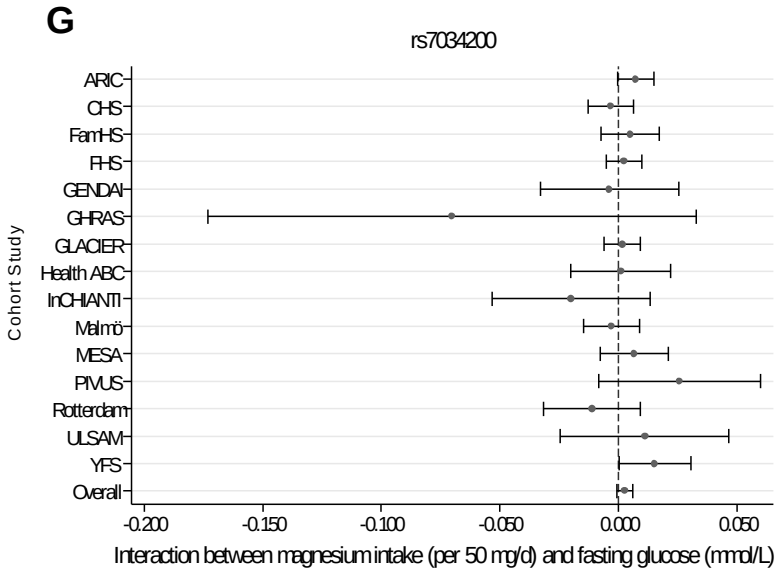

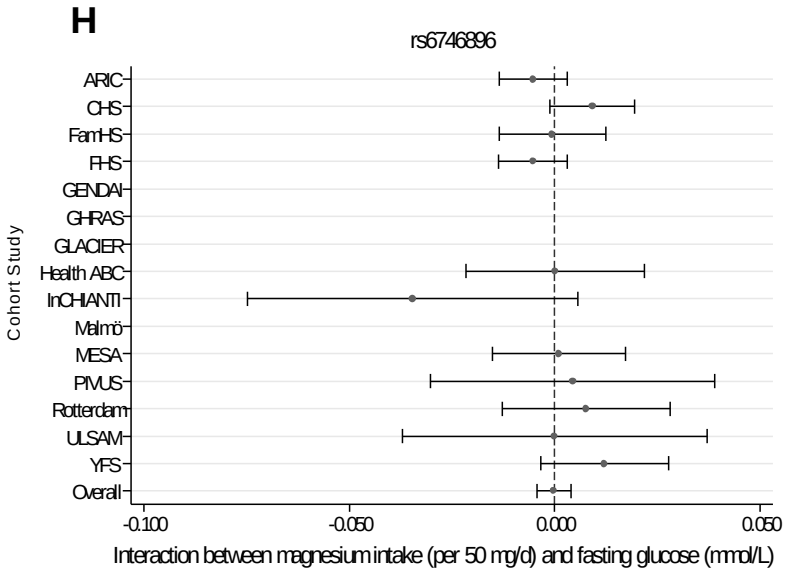

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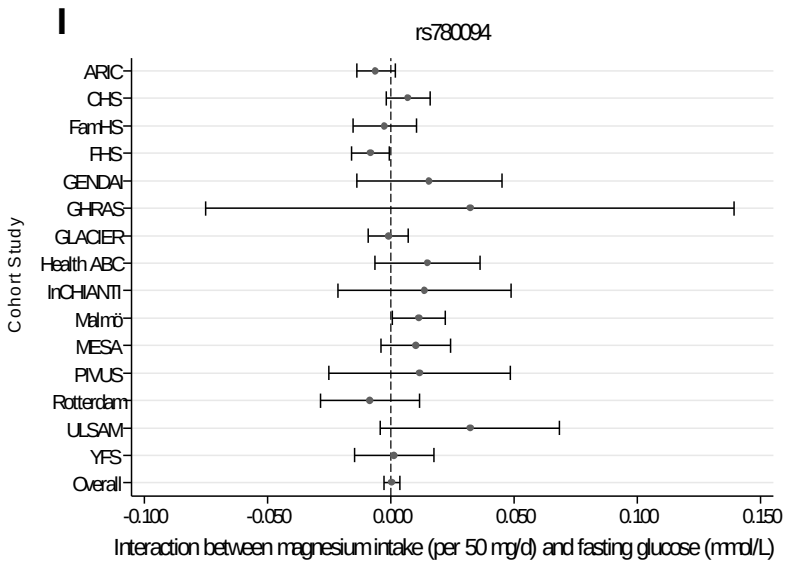

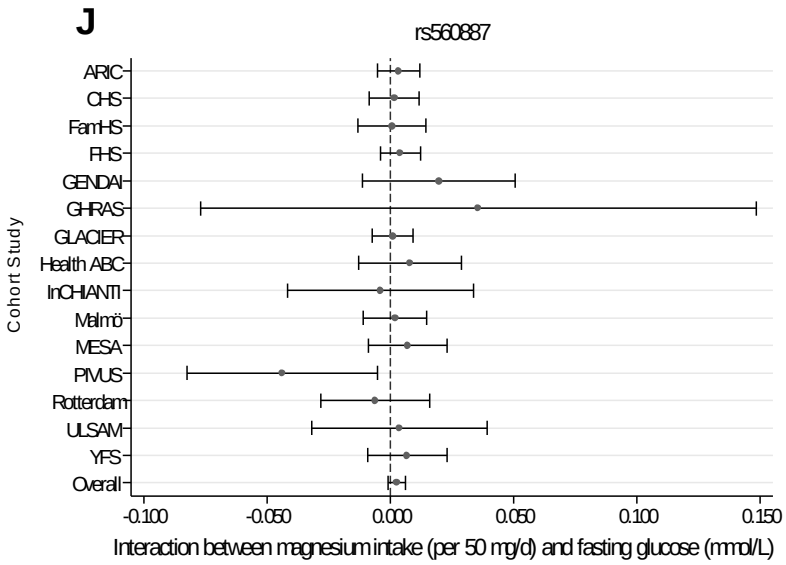

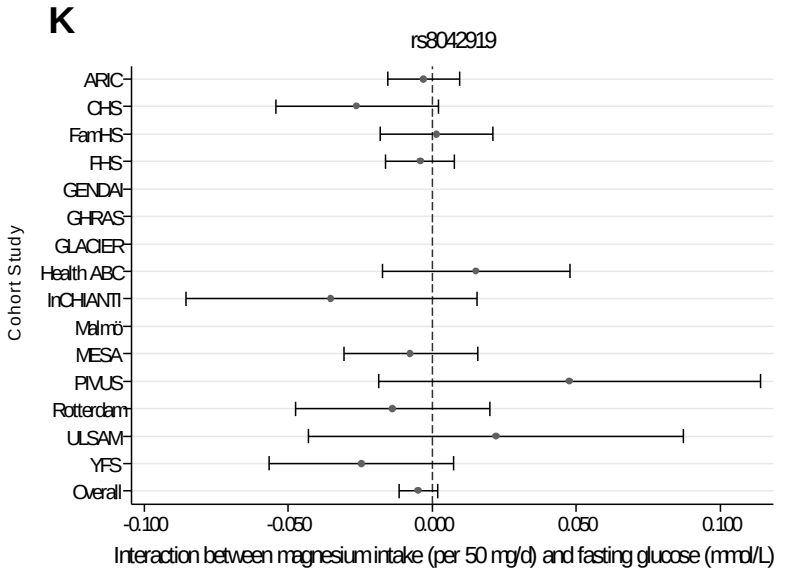

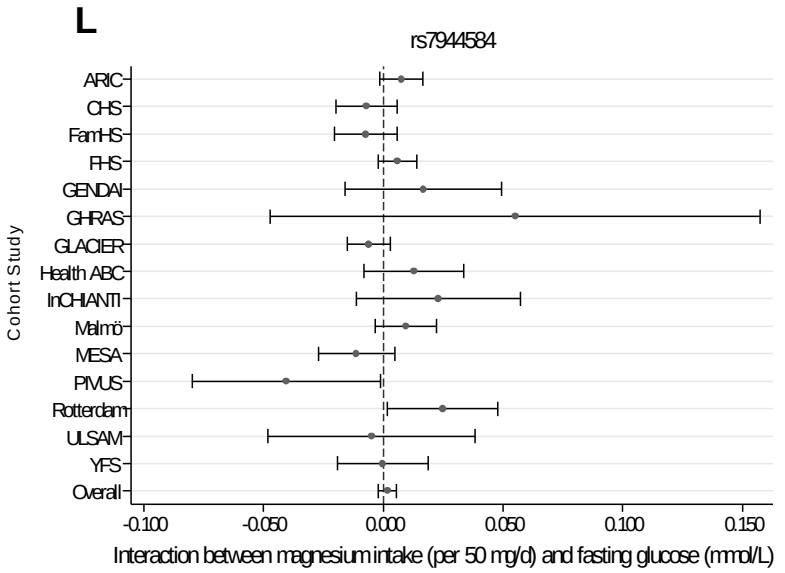

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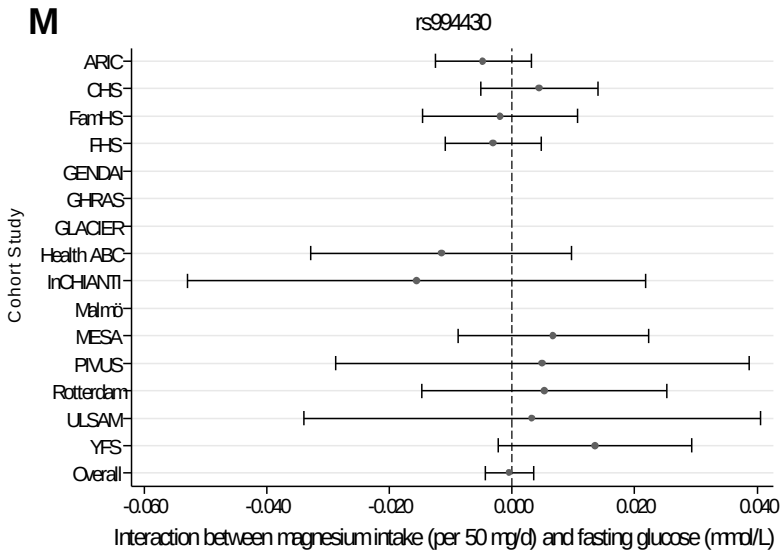

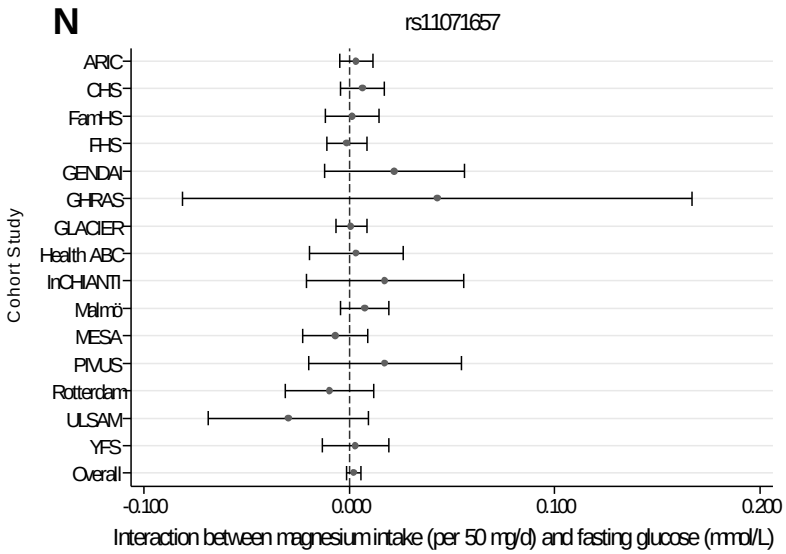

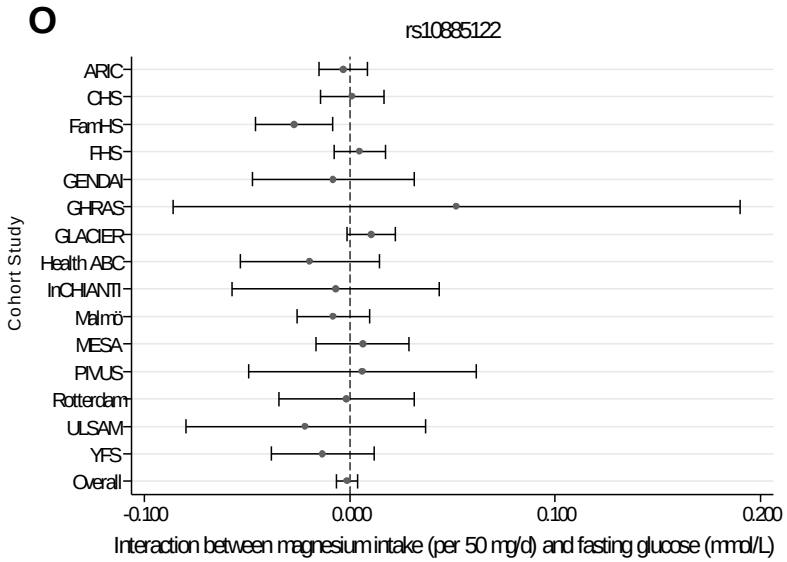

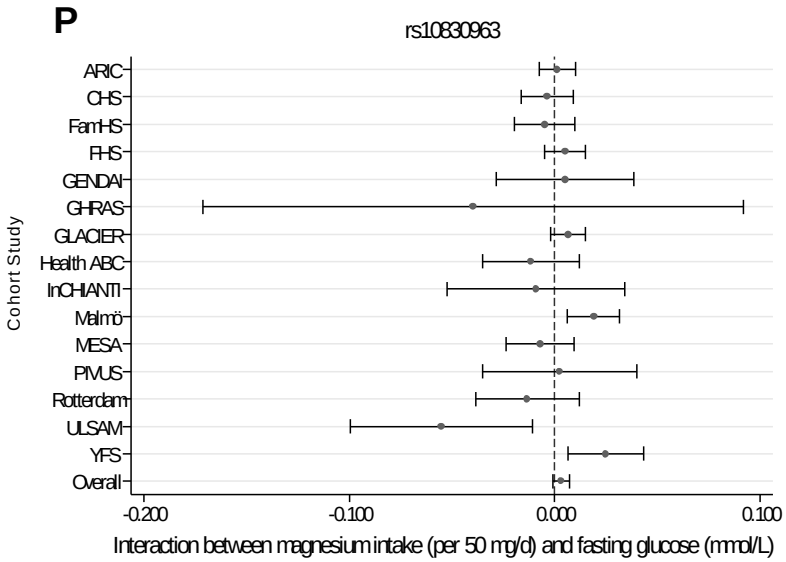

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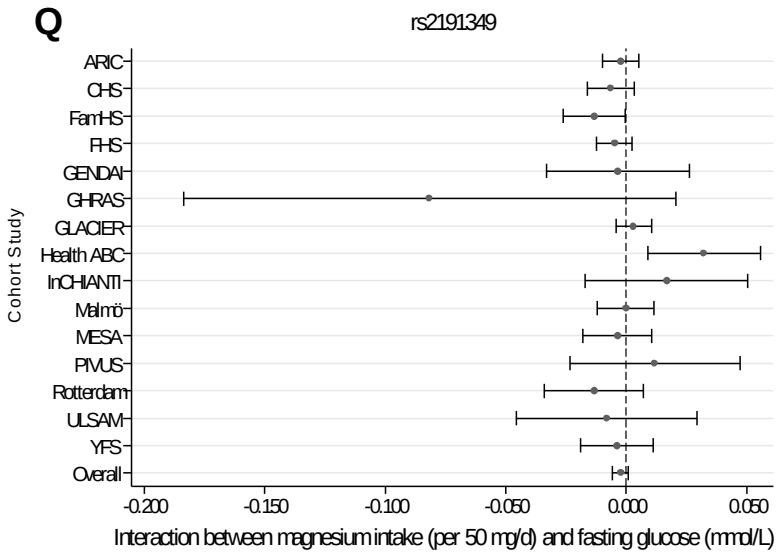

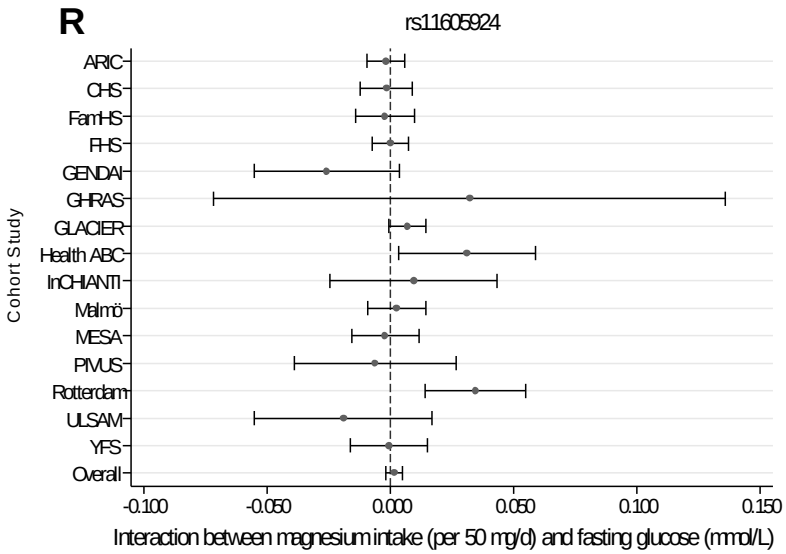

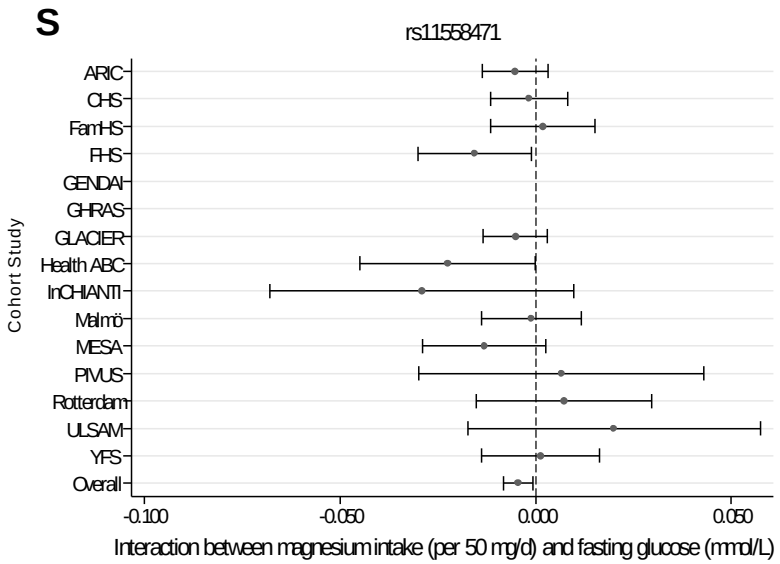

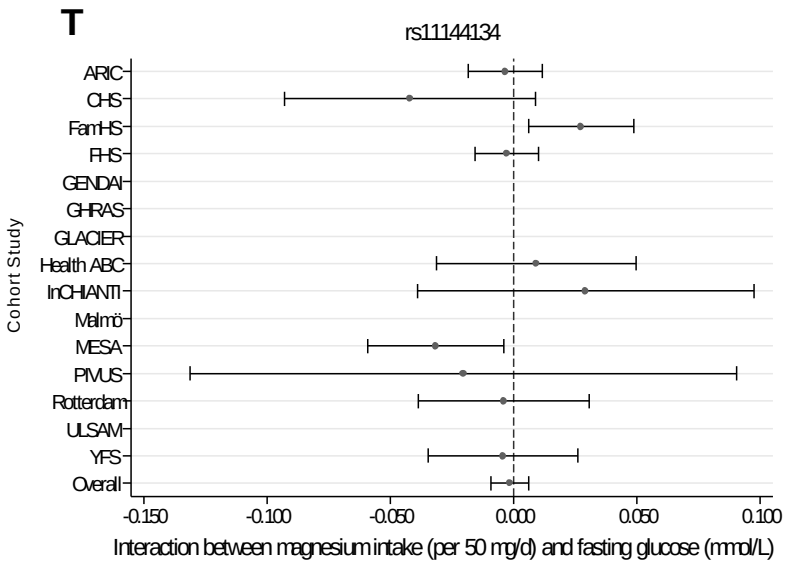

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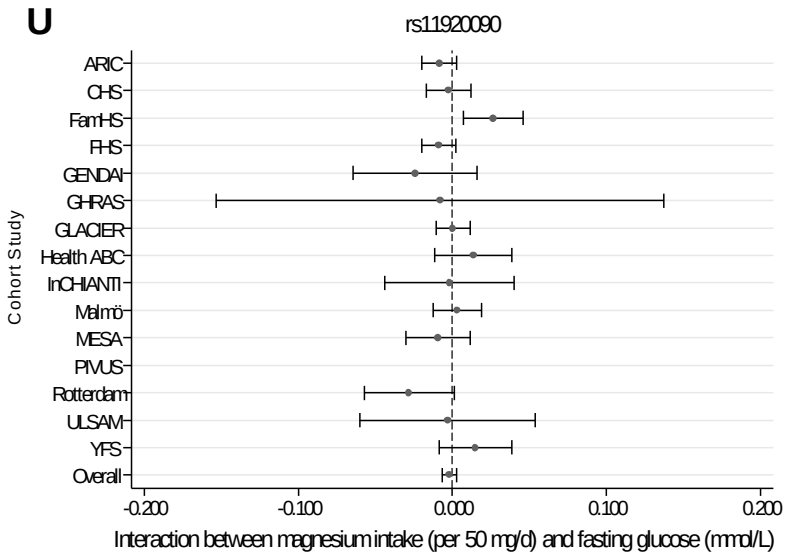
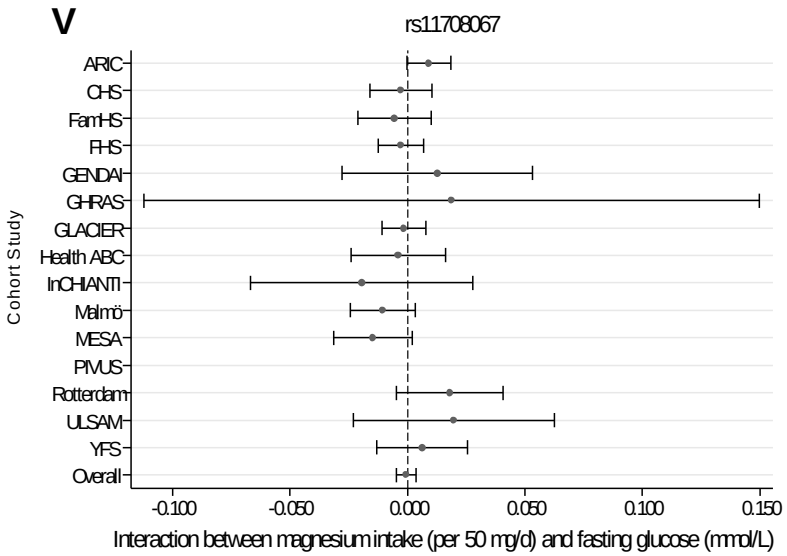
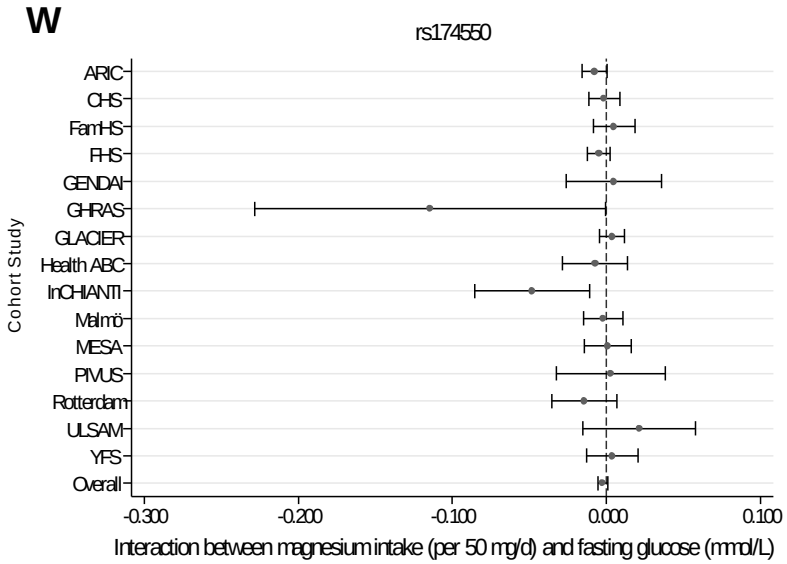
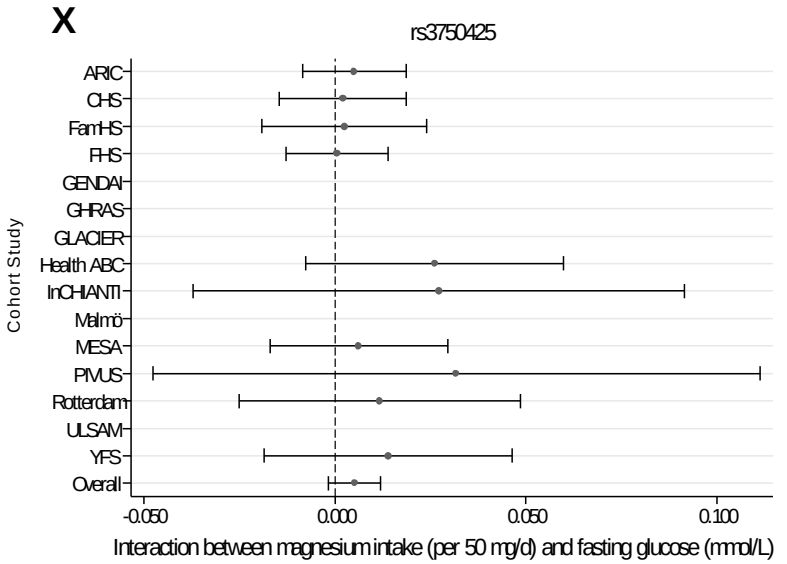


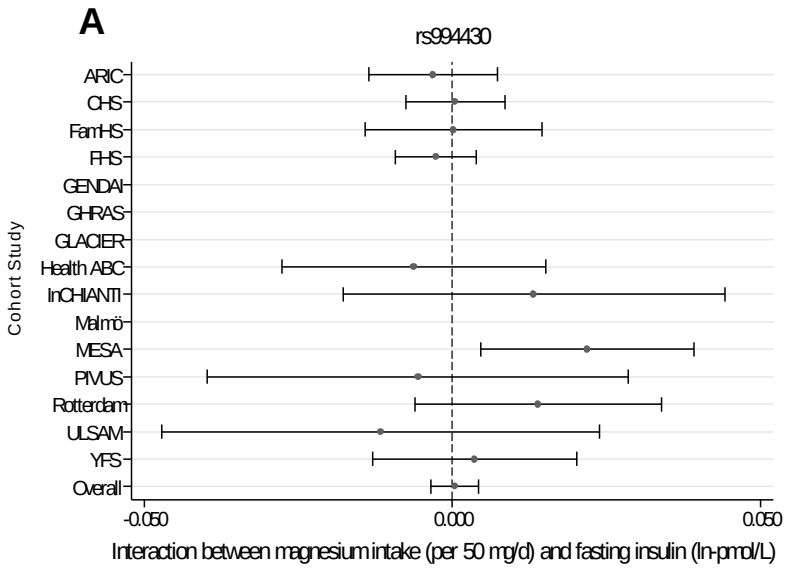


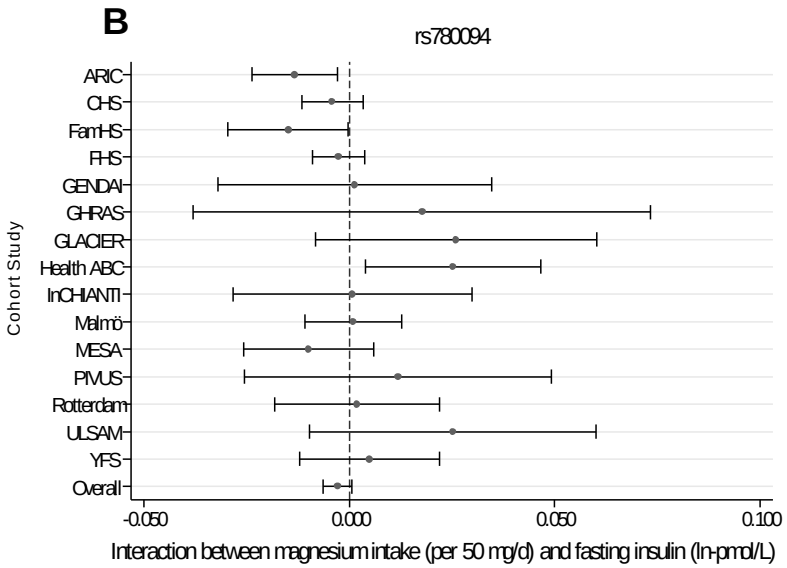


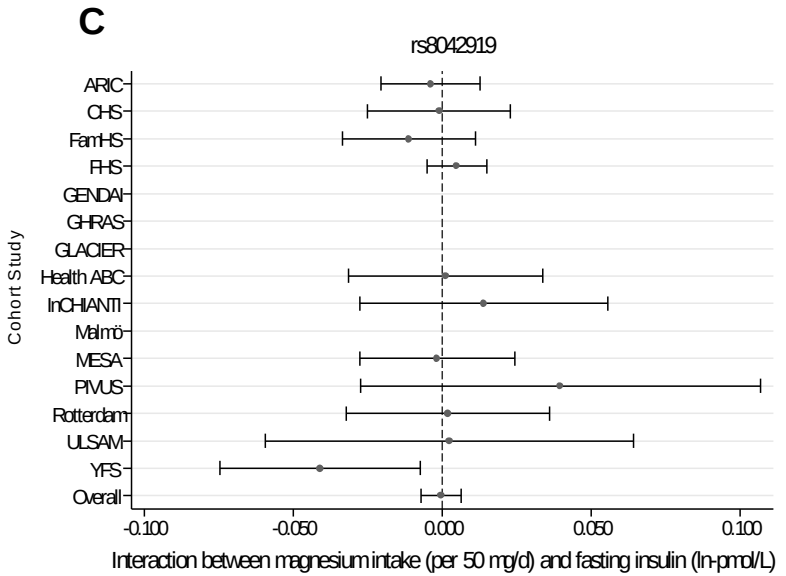


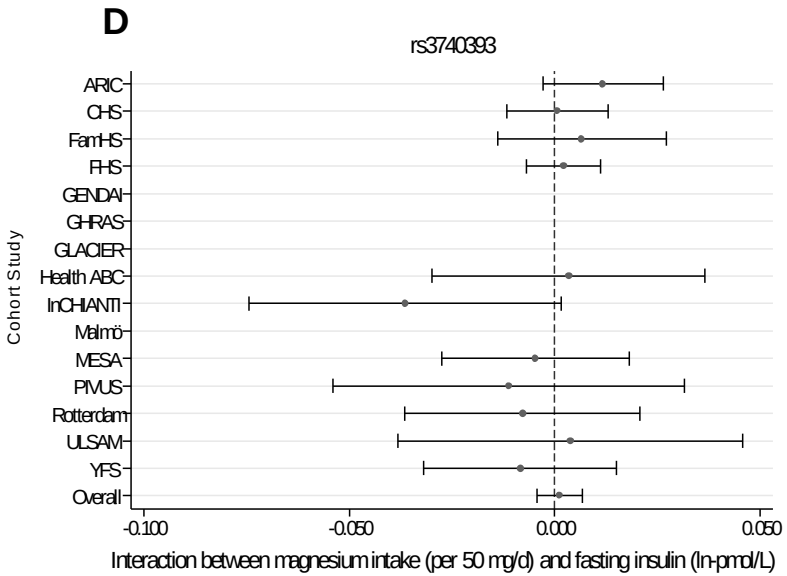
Online Supporting Material

Supplemental Figure 4. Forest Plots of Cohort-Specific and Meta-Analyzed Magnesium × SNP Interactions on Fasting Insulin (10 plots, A–J)









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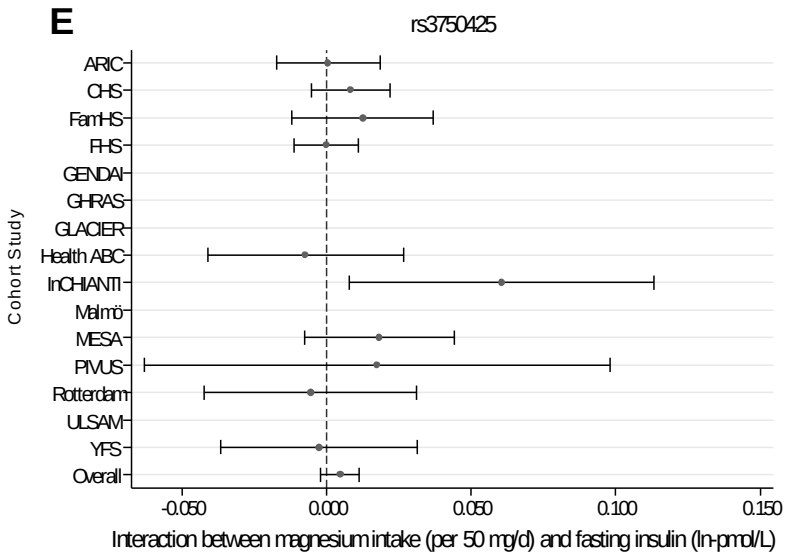

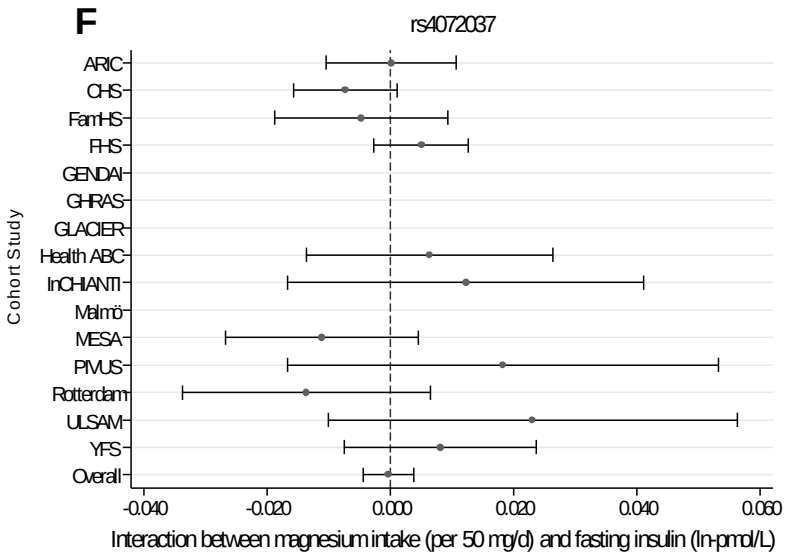

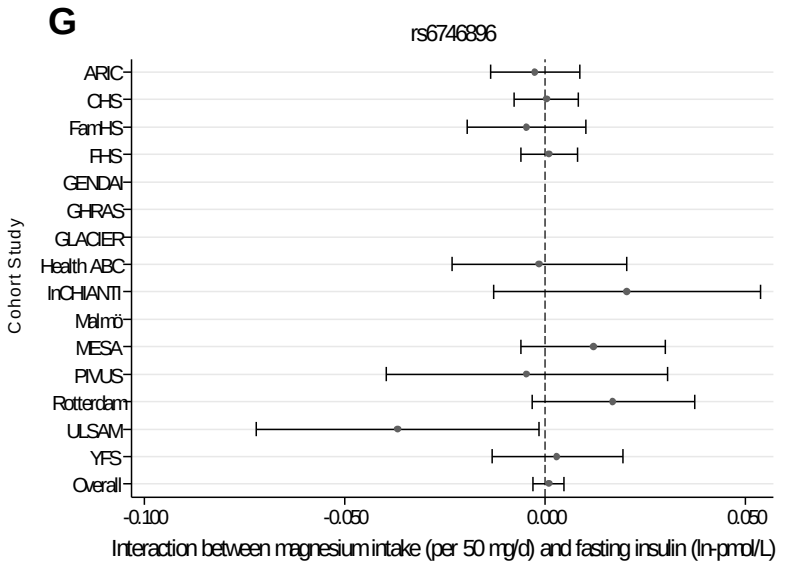

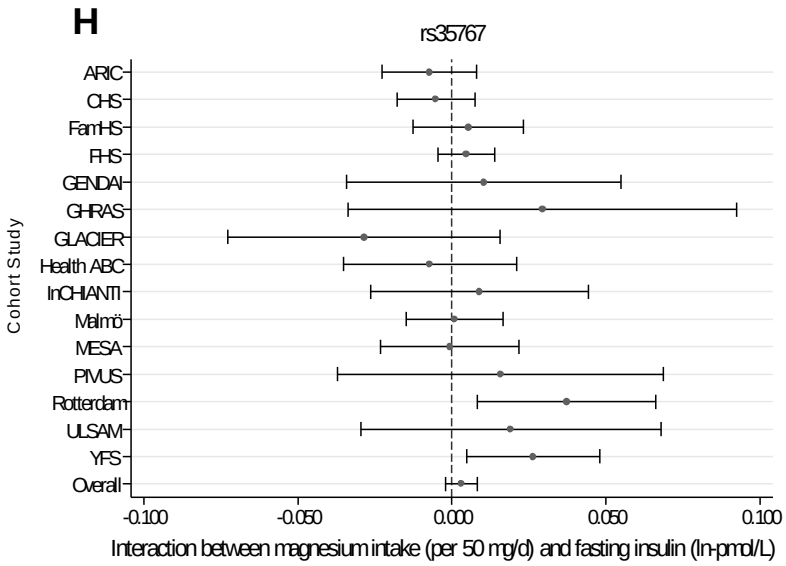

Online Supporting Material