SUPPLEMENTARY ONLINE MATERIAL

Identification of ten loci associated with height highlights new biological pathways in human growth

Guillaume Lettre, Anne U. Jackson¶, Christian Gieger¶, Fredrick R. Schumacher¶, Sonja I. Berndt¶, Serena Sanna¶, Susana Eyheramendy, Benjamin F. Voight, Johannah L. Butler, Candace Guiducci, Rachel Hackett, Iris M. Heid, Thomas Illig, Kevin B. Jacobs, Valeriya Lyssenko, Manuela Uda, The Diabetes Genetics Initiative, FUSION, KORA, The Prostate, Lung Colorectal and Ovarian Cancer Screening Trial, The Nurses' Health Study, SardiNIA, Michael Boehnke, Stephen J. Chanock, Leif C. Groop, Frank B. Hu, Bo Isomaa, Peter Kraft, Leena Peltonen, Veikko Salomaa, David Schlessinger, David J. Hunter, Richard B. Hayes, Gonçalo R. Abecasis, H.-Erich Wichmann, Karen L. Mohlke, Joel N. Hirschhorn†

¶ These authors contributed equally

† <u>Correspondence to:</u>
Joel N. Hirschhorn
Division of Genetics and Program in Genomics
Children's Hospital
300 Longwood Avenue, Boston, MA 02115
Phone: 617-919-2129
Fax: 617-730-0253
E-mail: joelh@broad.mit.edu

Supplementary Methods

Protocols from each group were approved by the respective Institutional Review Board, and informed consent was obtained for all subjects.

1. Description of genome-wide association study samples

a. Diabetes Genetics Initiative (DGI)

The individuals analyzed by the DGI have been described elsewhere[1] and a description of the sample is also available online (http://www.broad.mit.edu/diabetes/). In total, 1,464 T2D cases and 1,467 matched controls of European ancestry from Finland and Sweden were genotyped on the Affymetrix 500K platform. This includes 2,097 unrelated individuals (1,022 cases and 1,075 controls) and 326 discordant sibships (834 individuals: 442 cases and 392 controls). Genotyping data, as well as body mass index (BMI), and its components, height and weight, were available for 3,025 individuals (2,931 individuals from the T2D study, and an extra 94 individuals which were not used in the T2D association analysis).

b. Finland-United States Investigation of Non-Insulin-Dependent Diabetes Mellitus Genetics (FUSION)

The FUSION genome-wide association (GWA) study included 1,161 Finnish type 2 diabetes (T2D) cases, 1,174 normal glucose tolerant (NGT) controls, and 122 offspring of case/control pairs[2]. Cases and controls were matched as previously described, taking into account age, sex, and birth province within Finland. For the height analysis, our sample consisted of 1,084 T2D individuals and 1,287 NGT individuals with height measurements from clinical exams.

c. KORA S3/F3 500K

The KORA research platform (Cooperative health research in the Region of Augsburg) has evolved from the WHO MONICA study (Monitoring of Trends and Determinants of Cardiovascular Disease). The KORA genome-wide association study was recruited from the KORA S3 survey, which is a population-based sample from the general population living in the region of Augsburg, Southern Germany. The study participants had a German passport and were of European origin. The participants were examined in 1994/95 by applying standardized examinations that have been described in detail elsewhere[3]. In the KORA S3 study 4,856 subjects, aged 25 to 74 years, have been examined. 3,006 subjects participated in a follow-up examination of S3 in 2004/05 (KORA F3). Informed consent has been given and the study has been approved by the local ethical committee. For the genome-wide KORA S3/F3 500K study we selected 1,644 subjects of KORA S3/F3 and genotyped them using the Affymetrix 500K Array Set. The phenotypes were taken from KORA S3.

d. Nurses' Health Study (NHS)

The NHS is a longitudinal study established in 1976 when 121,700 female registered nurses between the ages of 30 and 55 completed a self-administered questionnaire on their medical histories and baseline health related exposures[4]. Between 1989 and 1990, blood samples were collected from 32,826 of the cohort members. Subsequent follow-up has been greater than 98% for this subcohort. Height and weight information was collected by self-report on the baseline questionnaire and available for 2,286 women. As previously reported[5], 1,145 postmenopausal women of European ancestry with invasive breast cancer and 1,142 matched controls of European ancestry were genotyped at the NCI Core Genotyping Facility using the Sentrix HumanHap550 genotyping assay according to the manufacturer's protocol.

e. Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial (PLCO)

PLCO is a multicenter, randomized trial to evaluate screening methods for the early detection of prostate, lung, colorectal and ovarian cancer[6]. Between 1993 and 2001, over 150,000 men and women ages 55-74 years were recruited from ten centers in the United States (Birmingham, AL; Denver, CO; Detroit, MI; Honolulu, HI; Marshfield, WI; Minneapolis, MN; Pittsburgh, PA; Salt Lake City, UT; St. Louis, MO; and Washington, D.C.). As described elsewhere[7], 1,172 non-Hispanic white prostate cancer cases and 1,105 matched, non-Hispanic white controls (by single sampling) were selected and genotyped using the Illumina HumanHap300 and HumanHap240 platforms. Information on height and weight was collected by self-report on the baseline questionnaire and available for 2,261 men.

f. SardiNIA

The SardiNIA GWAS examined a total of 4,305 related individuals participating in a longitudinal study of aging-related quantitative traits in the Ogliastra region of Sardinia, Italy[8]. As part of the initial clinical exam for the SardiNIA study, height was measured with a scale-mounted height rod. Due to medical conditions, height was not measurable on three individuals, and the height of another four participants was dropped because of short stature related to the Morquio syndrome. Genotyped individuals had four Sardinian grandparents and were selected for genotyping without regard to their phenotypic values.

2. Description of follow-up samples

a. FINRISK97

FINRISK 1997 is one of the population-based risk factor surveys carried out by the National Public Health Institute of Finland every five years[9], and was approved by The Ethical Committee of the National Public Health Institute on Oct. 30th, 1996, decision number 38/96. The sample was drawn from the National Population register for five geographical areas (North Karelia, Kuopio, Oulu province, Helsinki and Vantaa, and Turku/Loimaa area) in Finland, and stratified so that the cell size was 250 per each sex, 10-year age group (range 25-64 years), and study area. In addition, there was a separate 'senior sample', which included 250 men and 500 women aged 65-74 years in the North Karelia and Helsinki/Vantaa area. Altogether, the sample size was 11,500 individuals. Of them, 8,447 (73.5%) participated. DNA sample and informed consent are available from 8,141 participants. Height was measured using a stadiometer with the participant standing straight, back against the height rule, without shoes, heavy outer garments, and hair ornaments. The result was recorded to a precision of 0.5 cm.

b. European American and Poland extreme height panels

The European American (N=2,189) sample is a tall-short study with subjects ranking in the 5th-10th percentiles in adult height (short) and in the 90th-95th percentiles in adult height (tall)[10]. All individuals were self-described "white" or "Caucasian". All subjects were US-born and all of their grandparents were born in either the US or Europe. All subjects gave informed consent and approval was obtained from the Institutional Review Board of Children's Hospital, Boston.

c. FUSION stage 2

The FUSION study includes a series of cases and controls matched to take into account age, sex, and birth province within Finland[2]. FUSION stage 2 samples do not overlap with the individuals used in the initial genome-wide association scan. Clinical height measurements were available for 1,208 type 2 diabetic and 1,258 normal glucose tolerant individuals.

d. KORA S4

The participants of KORA S4 were examined in 1999/2001 by applying the same standardized protocols than for the KORA S3 survey, and KORA S4 individuals do not overlap with genotyped individuals of the KORA F3 500K study. For KORA S4, 4,130 subjects (25-74 years old) were genotyped. Informed consent was given and the study was approved by the local ethical committee.

e. PPP

Prevalence, Prediction and Prevention of Diabetes (PPP) in the Botnia study – a population-based study started in 2004 aiming 1) to study diabetes prevalence in the Botnia population, 2) to test whether genetic and metabolic risk factors previously identified in the Botnia study can be used to identify high risk individuals and 3) to study whether incidence of T2D can be prevented in these high risk using intervention program. The PPP study today includes 3500 individuals.

3. Genotyping and quality-control assessment

DGI. The genotyping of the DGI samples was performed using the Affymetrix 500K array. The DGI data SNP quality control and exclusion criteria are reported in detail elsewhere[1]. The quality-control (QC) criteria for sample and SNP exclusion were: (1) SNPs mapping to multiple locations in the genome, (2) SNPs with genotype call rate <95% in the unrelated component and <90% in the related component, (3) minor allele frequency (MAF) <1% in the DGI cases and <1% in both population and familial subsets of the data, and (4) Hardy-Weinberg equilibrium (HWE) P-value $<1\text{x}10^{-6}$. This resulted in 386,731 SNPs being used for analyses.

FUSION. For the Fusion GWA scan, samples were genotyped with the Illumina Infinium II HumanHap300 BeadChip (version 1.0) and with an Illumina GoldenGate Custom Panel (1,536 SNPs) designed to improve genomic coverage around T2D candidate genes[2]. The QC criteria for sample and SNP exclusion were: SNPs with genotype call rate <95%, (2) MAF <1%, (3) HWE P-value $<1\text{x}10^{-6}$, and (4) reproducibility in duplicate samples and Mendelian inheritance (<3 total discrepancies in a combined set of 79 duplicate samples and 122 parent-offspring sets).

KORA. Genotyping of the KORA S3/F3 500K samples was performed using the Affymetrix 500K Array Set according to the manufacturer's recommendations. Genotypes were called using the BRLMM clustering algorithm. The QC criteria for sample and SNP exclusion were: (1) samples with genotype completeness <93% and (2) samples with at most one discordant call for 50 SNPs common to both chips.

NHS. The genotyping and quality control methods for the NHS samples have been described previously[5]. The samples were genotyped at the NCI Core Genotyping Facility using the Sentrix HumanHap550 genotyping assay. The QC criteria for sample and SNP exclusion were: (1) sample with genotype completeness <90%, (2) genotype call rate <90%, and (3) MAF <1%.

PLCO. Genotyping and quality control methods for the PLCO samples have been described elsewhere[7]. In brief, samples were genotyped using the Illumina HumanHap300 and HumanHap240. The QC criteria for sample and SNP exclusion were: (1) sample with genotype completeness <90%, (2) genotype call rate <94%, and (3) MAF <1%.

SardiNIA. Among the individuals examined, 1,412 were genotyped with the Affymetrix Mapping 500K Array Set. The QC criteria for sample and SNP exclusion were: (1) sample with genotype completeness <90%, (2) MAF <5%, (3) Mendelian transmission (<3 inconsistencies), and (4) HWE P-value $<1\text{x}10^{-6}$. This passing set of 356,359 SNPs was used to impute all polymorphic SNPs genotyped by the HapMap consortium. In the SardiNIA GWAS, the average predicted r^2 between imputed allele counts and true genotypes was 0.86. We compared imputed genotypes with those obtained by genotyping the Affymetrix Mapping 10K array in 436 individuals across 5,305 markers and observed an error rate of 2.17% per allele, similar to expectations (Y. Li and G.R.A., unpublished). Taking advantage of the relatedness among individuals in the SardiNIA sample, we conducted a second round of computational analysis to impute genotypes for analysis in an additional 2,893 individuals who were genotyped only with the Affymetrix Mapping 10K Array. In this second round, we identified large stretches of chromosome shared within each family and probabilistically "filled-in" genotypes within each stretch whenever one or more of its carriers was genotyped with the 500K Array Set[11]. These 2,893 individuals were mostly offspring and siblings of the 1,412 individuals genotyped at high density; typically, we genotyped two or three family members with the 500K Array Set in each large nuclear family and then imputed results for the remaining individuals.

Replication panels. Genotyping in the European American height panel and the replication panels FINRISK97, FUSION stage 2, and KORA S4 was performed using the platform iPLEX™ Sequenom MassARRAY® (P. Oeth, /http://www.sequenom.com/Assets/pdfs/appnotes/8876-006.pdf /(2005).). For the European American height panels, 78 SNPs were attempted and six failed. For the

FINRISK97 panel, 29 SNPs were attempted and two failed. For the PPP panel, 23 SNPs were attempted and 2 failed. For the FUSION stage 2 panel, 27 SNPs were attempted and one failed. For the KORA S4 panel, five SNPs were attempted and one failed. For all passing SNPs, the genotyping success rare was >96% and the consensus error rate, estimated from replicates, was <0.1%.

4. Genotype imputation

Because the GWA scans used different genotyping platforms, we imputed genotypes for all polymorphic HapMap SNPs in each scan, using a Hidden Markov Model as programmed in MACH (Y. Li and G.R.A., unpublished). This approach allowed us to evaluate association at the same SNPs in all scans. The imputation method combines genotype data from each sample with the HapMap CEU samples (July 2006 phased haplotype release) and then infers the unobserved genotypes probabilistically. The inference relies on the identification of stretches of haplotype shared between study samples and individuals in HapMap CEU reference panel. For each SNP in each individual, imputation results are summarized as an "allele dosage" defined as the expected number of copies of the minor allele at that SNP (a fractional value between 0.0 and 2.0). As previously described, r^2 between each imputed genotype and the true underlying genotype is estimated and serves as a QC metric (rsq_hat in Supplementary Table 6). We chose an estimated $r^2>0.3$ as a threshold to flag and discard low quality imputed SNPs (ref. 2, and Y. Li and G.R.A, unpublished). For association testing of imputed genotypes, we used the program MACH2QTL, which uses dosage value (0.0 - 2.0) as predictor in a linear regression framework.

5. Statistical methods

a. Phenotype modeling and association testing

DGI. The height dataset was parsed into four groups to account for possible gender and disease status effects. Individuals with heights greater than four standard deviations from the mean were excluded (N=1). Within each sub-group, height was corrected for age, and Z-scores were calculated based on the mean and standard deviation of the corrected height. Z-scores from the four sub-groups were then pooled, and regressed against the recruiting centers; the residuals were used as quantitative phenotypes in the analysis. Linear regression, as implemented in the software PLINK[12] or MACH2QTL, was used to test the association between SNP genotype and height Z-scores. To account for the presence of sibships in the dataset, we used a genomic control correction factor estimated from the median of the overall association statistics across the genome-wide association data. The inflation factors (λ_{GC}) for both DGI controls and cases are 1.05.

FUSION (stage 1 and stage 2). Height was analyzed separately in type 2 diabetic and normal glucose tolerant individuals. For each sample, height was adjusted for sex, age, age^2, birth province, and study group, then converted to Z-scores using quantile normalization. The Z-scores were then regressed against SNP reference allele counts using a score test that accounts for relatedness among samples[11]. The inflation factors

(λ_{GC}) for FUSION stage 1 NGT and cases are 1.02 and 1.01, respectively.

KORA (S3 and S4). Linear regression, as implemented in PLINK[12] or MACH2QTL, was used to test the correlation between genotype and height Z-scores, correcting for sex and age. The inflation factor (λ_{GC}) for KORA F3 is 1.03.

NHS. After individuals with heights greater than four standard deviations from the mean were excluded (N=1), Z-scores were estimated using the mean and standard deviation from the remaining sample set. All analyses were adjusted for the top four eigenvectors estimated using EIGENSTRAT[13] and age at baseline. The Pearson's correlation coefficient for height vs. cancer is -0.033 (P-value=0.12). The association between height and the genotype dosage for imputed SNPs was evaluated using the linear regression model implemented in MACH2QTL. The inflation factor (λ_{GC}) for NHS is 1.01.

PLCO. Individuals with heights greater than four standard deviations from the mean were excluded (N=3). To account for possible differences by disease status, height was corrected for age and Z-scores calculated using the mean and standard deviation separately for cases and controls. The Pearson's correlation coefficient for height vs. cancer is 0.008 (P-value=0.71). The pooled Z-scores were then regressed against the top four eigenvectors estimated using EIGENSTRAT[13] and the residuals were used for the analysis. The association between the SNPs and height was evaluated using the linear regression model implemented in PLINK[12] or MACH2QTL. The inflation factor (λ_{GC}) for PLCO is 1.01.

SardiNIA. At each SNP, height was related to allele counts for a reference allele in a regression model that also included sex, age, and age^2 as covariates. For SNPs genotyped in the laboratory, allele counts were discrete (0, 1, or 2), whereas for imputed SNPs, allele counts were fractional (between 0.0 and 2.0, depending on the expected number of copies of the allele for each individual). To allow for relatedness, regression coefficients were estimated in the context of a variance components model that can handle imputed genotypes and accounts for background polygenic effects[11]. This method is implemented as a score test that is used to scan the genome in a computationally efficient manner[11]. To avoid inflation of type I error due to deviation from normality, we used quantile normalization (inverse normal scores), by ranking all height values and then converted them to Z-scores according to quantiles of the standard normal distribution.

European American height panel. Association analysis was performed using a Cochran-Mantel-Haenszel test. The dataset was stratified according to the European region of origin of the grandparents.

FINRISK97. Height Z-scores were generated after regressing the height measurements against sex, age, and regions of recruitment. Statistical analysis was performed using linear regression as implemented in PLINK[12].

PPP. Height Z-scores were generated after regressing the height measurements against sex and age. Statistical analysis was performed using linear regression as implemented in

PLINK[12].

b. Meta-analysis and SNP selection for replication genotyping

Association results presented in this manuscript take into account the posterior probability on each imputed genotype. To combine results, we used a weighted Z-score method:

$$z_w = z_i \times \sqrt{N_i / N_{tot}} \ ,$$

where z_w is the weighted Z-score from which the meta-analytic 2-tailed P-value is calculated, z_i is the Z-score from study i (calculated as the cumulative normal probability density for the corresponding 1-tailed P-value, adjusted if needed by subtracting the P-value from one when the directionality of the effect is reversed), N_i is the sample size of study i and N_{tot} is the total sample size. In total, we combined association results at 2,260,683 autosomal SNPs in 15,821 individuals (DGI, N=2,978; FUSION, N=2,371; KORA, N=1,639; NHS, N=2,286; PLCO, N=2,244; SardiNIA, N=4,305). To select markers for follow-up genotyping, we first ranked SNPs based on their meta-analytic P-value, and then clustered them based on the linkage disequilibrium pattern from the HapMap phase II European American (CEU) population to minimize redundant genotyping (SNPs with $r^2 > 0.5$ to a SNP with a lower P-value were binned together with that SNP).

c. Eigenstrat analysis

For DGI, EIGENSTRAT[13] was run on a LD-pruned set of markers (~190,000 SNPs) using genotypes from unrelated individuals only (N=2,364). Similar results were obtained when including the first three or ten main eigenvectors as covariates in the association analysis.

References

1. Saxena, R. et al. Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science* **316**, 1331-6 (2007).
2. Scott, L.J. et al. A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. *Science* **316**, 1341-5 (2007).
3. Lowel, H. et al. The MONICA Augsburg surveys--basis for prospective cohort studies. *Gesundheitswesen* **67 Suppl 1**, S13-8 (2005).
4. Colditz, G.A. & Hankinson, S.E. The Nurses' Health Study: lifestyle and health among women. *Nat Rev Cancer* **5**, 388-96 (2005).
5. Hunter, D.J. et al. A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. *Nat Genet* **39**, 870-4 (2007).
6. Prorok, P.C. et al. Design of the Prostate, Lung, Colorectal and Ovarian (PLCO) Cancer Screening Trial. *Control Clin Trials* **21**, 273S-309S (2000).
7. Yeager, M. et al. Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. *Nat Genet* **39**, 645-9 (2007).
8. Pilia, G. et al. Heritability of cardiovascular and personality traits in 6,148 Sardinians. *PLoS Genet* **2**, e132 (2006).
9. Vartiainen, E. et al. Cardiovascular risk factor changes in Finland, 1972-1997. *Int J Epidemiol* **29**, 49-56 (2000).
10. Campbell, C.D. et al. Demonstrating stratification in a European-American population. *Nature Genet*, 37:868-872 (2005).
11. Chen, W.M. & Abecasis, G.R. Family-based association tests for genomewide association scans. *Am J Hum Genet* **81**, 913-26 (2007).
12. Purcell, S. et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* **81**, 559-75 (2007).
13. Price, A.L. et al. Principal components analysis corrects for stratification in genome-wide association studies. *Nat Genet* **38**, 904-9 (2006).

Supplementary Table 1. Demographics of the populations used in this study

STUDY	SAMPLE SIZE	PERCENTAGE MALE (%)	MALES, AGE AT STUDY (years; mean, SD)	FEMALES, AGE AT STUDY (years; mean, SD)	MALES, HEIGHT AT STUDY (cm; mean, SD)	FEMALES, HEIGHT AT STUDY (cm; mean, SD)
GWA study samples						
DGI (T2D)	1728	50.6	63.1 (10.3)	65.4 (10.5)	174.3 (6.4)	161.1 (6.2)
DGI (Controls)	1648	48.6	58.4 (10.5)	59.2 (10.3)	175.6 (6.2)	162.4 (5.9)
Fusion (T2D)	1084	56.9	62.1(7.3)	63.6(7.8)	173.2(6.1)	159.5(5.6)
Fusion (NGT)	1287	49.7	60.4(11.6)	61.5(10.8)	174.2(6.6)	160.7(6.1)
KORA S3 500K	1644	49.5	53.0 (10.1)	52.1 (10.1)	173.7 (6.5)	161.1 (6.0)
NHS	2286	0	Not applicable	44.4 (6.4)	Not applicable	164.0 (6.8)
PLCO	2261	100	64.3 (5.1)	Not applicable	178.4 (6.7)	Not applicable
SardiNIA	4305	43.8	44.1 (18.1)	43.2 (17.3)	166.3 (7.3)	154.9 (6.5)
Replication samples						
European American (5th-10th percentile)	1057	48.0	57 (9)	55 (10)	167.1 (1.4)	153.2 (1.5)
European American (90th-95th percentile)	1132	51.9	56 (9)	54 (10)	186.9 (2.0)	172.0 (1.8)
FINRISK97	7803	46.3	47.9 (13.1)	47.1 (12.7)	175.6 (7.1)	162.3 (6.3)
Fusion2 T2D	1208	59.4	58.2(9.0)	61.1(8.0)	174.8(6.8)	160.2(5.8)
Fusion2 NGT	1258	61.0	57.2(7.6)	60.5(7.4)	174.5(6.2)	160.5(6.3)
KORA S4	4130	49.4	49.6 (14.0)	48.8 (13.8)	174.8 (7.0)	161.9 (6.6)
PPP	3402	47.4	49.3 (16.0)	49.1 (16.0)	177.0 (6.7)	163.9 (6.2)

Supplementary Table 2. Association results in the European American (USHT) tall-short height panel. Allele 1 corresponds to the minor allele in the USHT panel (minor allele frequency (MAF) is given for allele 1). The panel is treated as a case-control short (5^{th}-10^{th} percentiles in adult height) / tall (90^{th}-95^{th} percentiles in adult height) panel and analyzed using the stratified Cochran-Mantel-Haenszel test to account for the geographic origin of the grandparents (N=2,189). The odds ratio corresponds to the increased odds of being in the group of tall individuals for each additional minor allele (allele 1, positive strand in build NCBI35). SNPs in bold were promoted for genotyping in FINRISK97, KORA S4, PPP, and FUSION stage 2.

Chromosome	Physical position	SNP	Allele 1	Allele 2	MAF	P-value	Odds ratio	95% CI OR
1	17268067	rs2076599	G	A	0.40	0.61	0.97	0.86 - 1.09
1	78840137	rs1413358	A	G	0.23	0.34	0.93	0.81 - 1.08
1	118775455	rs6428750				FAILED		
1	225920244	rs6426470	A	G	0.19	0.21	0.92	0.81 - 1.05
2	54707033	rs4671964				FAILED		
2	103976172	rs935070	T	C	0.15	0.15	1.11	0.96 - 1.28
2	113826562	rs2008324	G	A	0.48	0.34	1.05	0.95 - 1.16
2	121684502	rs4076519	A	G	0.14	0.35	0.92	0.78 - 1.09
2	229919505	rs6728087	C	A	0.44	0.58	1.03	0.93 - 1.14
2	232514563	rs2580823	G	A	0.30	0.06	1.11	0.99 - 1.24
3	119581601	rs575566	A	C	0.29	0.04	0.89	0.80 - 0.99
3	128012494	rs9858948	A	G	0.23	0.51	1.05	0.91 - 1.21
3	139231669	rs6780412	T	G	0.40	0.15	1.09	0.97 - 1.24
3	142585523	rs6763931	A	G	0.42	$1.2x10^{-7}$	1.39	1.23 - 1.56
3	142588260	**rs724016**	G	A	0.42	$7.8x10^{-8}$	1.39	1.23 - 1.57
4	4327819	**rs2916448**	C	T	0.12	0.25	0.90	0.75 - 1.08
4	4330015	rs2916446	A	T	0.13	0.24	0.90	0.76 - 1.07
4	72695625	rs17763915	C	T	0.12	0.54	1.05	0.90 - 1.23
4	82373306	**rs1662845**	T	A	0.45	$8.5x10^{-6}$	1.31	1.17 - 1.48
4	145794294	**rs1812175**	A	G	0.16	$5.1x10^{-8}$	0.68	0.59 - 0.78
4	145869471	**rs1492820**	G	A	0.47	0.0015	0.82	0.73 - 0.93
4	145873947	rs7692915	T	G	0.49	0.0018	1.21	1.07 - 1.36
4	146058714	rs4240326	A	G	0.46	0.015	1.16	1.03 - 1.31
4	174559706	rs17325472	C	A	0.49	0.94	1.00	0.88 - 1.12
5	4573856	**rs1450822**	A	G	0.49	0.21	1.08	0.96 - 1.22
5	32802174	rs1173734	C	T	0.25	0.89	1.01	0.88 - 1.16
5	77467642	rs10514136				FAILED		
5	171463952	rs6868347	T	C	0.14	0.39	1.08	0.91 - 1.27
6	26341366	**rs10946808**	G	A	0.31	$3.4x10^{-8}$	0.74	0.66 - 0.82
6	31617191	rs3094001	T	C	0.17	0.22	1.10	0.94 - 1.29
6	105514355	**rs314277**	A	C	0.14	0.26	1.10	0.93 - 1.31
6	142733242	rs11155242				FAILED		

6	142745570	**rs4896582**	A	G	0.32	2.2×10^{-5}	0.76	0.67 - 0.86
7	42501378	rs1991769	T	C	0.34	0.019	0.88	0.79 - 0.98
7	50632416	**rs12540874**	G	A	0.40	0.98	1.00	0.90 - 1.11
7	92094841	**rs2040494**	C	T	0.46	0.18	0.92	0.82 - 1.04
7	158417550	**rs2730245**	G	C	0.30	0.99	1.00	0.88 - 1.14
8	41596148	**rs11786297**	G	A	0.09	0.39	1.10	0.89 - 1.35
8	57318152	**rs9650315**	T	G	0.14	9.0×10^{-6}	0.68	0.57 - 0.81
8	76362525	rs12681390	G	A	0.44	0.45	1.05	0.93 - 1.18
8	76364801	rs982442	T	C	0.42	0.29	1.07	0.95 - 1.20
8	80009731	rs1443899	G	A	0.12	0.68	1.03	0.88 - 1.21
8	129118629	**rs13249999**	T	C	0.08	0.59	0.94	0.75 - 1.18
9	118174617	**rs7869550**	G	A	0.18	0.58	0.96	0.82 - 1.12
9	132453905	**rs7466269**	G	A	0.34	0.48	0.96	0.87 - 1.07
10	27944181	rs2451928	G	A	0.39	0.50	0.96	0.85 - 1.08
10	124069073	rs7081388	T	C	0.05	0.42	0.91	0.72 - 1.14
10	124154644	rs10082476	G	A	0.22	0.66	0.97	0.86 - 1.10
11	25426266	rs2618792	G	A	0.47	0.82	0.99	0.87 - 1.11
12	64644614	**rs1042725**	T	C	0.48	4.2×10^{-6}	0.79	0.71 - 0.87
13	19621698	rs1041028	T	C	0.46	0.023	0.87	0.77 - 0.98
13	37037260	rs9315503	G	A	0.35	0.38	0.95	0.86 - 1.06
13	49405945	rs4942899	C	T	0.22	0.036	1.16	1.01 - 1.33
14	36069800	**rs17104630**	G	A	0.09	0.018	0.77	0.62 - 0.96
14	91477446	**rs3783937**	T	C	0.23	0.015	0.86	0.77 - 0.97
14	91520137	rs2295164				FAILED		
14	91529711	**rs8007661**	T	C	0.43	0.64	0.97	0.86 - 1.10
14	93843698	rs8022616	G	A	0.10	0.99	1.00	0.84 - 1.19
15	77391837	**rs11858942**	G	A	0.40	0.54	1.04	0.92 - 1.17
15	82055408	rs2585071	G	A	0.35	0.46	0.95	0.84 - 1.08
15	82077496	**rs2562784**	G	A	0.24	0.28	1.07	0.95 - 1.20
15	97798792	rs4965490	T	C	0.18	0.11	1.13	0.97 - 1.32
16	615681	**rs763014**	C	T	0.42	0.046	1.13	1.00 - 1.28
16	2225358	**rs26840**	T	C	0.40	0.015	1.16	1.03 - 1.31
17	51785154	**rs12449568**	C	T	0.45	0.49	1.04	0.93 - 1.18
17	68208939	rs9905659	G	A	0.19	0.14	0.91	0.80 - 1.03
17	76303498	rs7211818	G	A	0.23	0.12	1.10	0.98 - 1.24
18	48613000	**rs12958987**	T	G	0.28	0.69	0.97	0.85 - 1.11
19	2121954	**rs12986413**	T	A	0.48	0.20	0.93	0.82 - 1.04
20	5034939	**rs6116651**	T	A	0.11	0.0035	0.75	0.62 - 0.91
20	32065590	rs6141443	G	C	0.16	0.021	0.83	0.71 - 0.97
20	33194125	rs3746427	A	G	0.46	0.019	0.87	0.77 - 0.98
20	33262941	rs6088765	G	T	0.42	0.23	1.08	0.95 - 1.21
20	33370575	**rs6060369**	C	T	0.38	0.012	1.17	1.04 - 1.32
20	33431481	rs725908				FAILED		
20	33489397	rs143383	G	A	0.37	0.034	1.14	1.01 - 1.29
20	39154787	rs2076574	G	A	0.13	0.52	1.05	0.91 - 1.22
22	40075301	rs2281331	A	G	0.49	0.75	0.98	0.87 - 1.11

Supplementary Table 3. Association results in the FINRISK97 panel. Allele 1 corresponds to the minor allele in FINRISK97 (N=7803). Effect sizes and standard errors are given in s.d. units. The direction of the effect is for allele 1 (positive strand in build NCBI35).

Chromosome	Physical position	SNP	Allele 1	Allele 2	MAF	P-value	Effect size	Standard error
3	142588260	rs724016	G	A	0.44	$4.3\text{x}10^{-8}$	0.087	0.016
4	4327819	rs2916448	C	T	0.06	0.41	0.028	0.034
4	82373306	rs1662845	T	A	0.43	0.93	-0.001	0.016
4	145869471	rs1492820	G	A	0.41	0.035	-0.034	0.016
5	4573856	rs1450822	A	G	FAILED			
6	26341366	rs10946808	G	A	0.43	$4.9\text{x}10^{-5}$	-0.065	0.016
6	105514355	rs314277	A	C	0.17	0.41	0.018	0.021
6	142745570	rs4896582	A	G	0.29	$1.4\text{x}10^{-9}$	-0.105	0.017
7	50632416	rs12540874	G	A	0.31	0.62	-0.009	0.017
7	92094841	rs2040494	C	T	0.47	0.0050	-0.045	0.016
7	158417550	rs2730245	G	C	0.25	0.38	0.016	0.018
8	41596148	rs11786297	G	A	0.04	0.063	0.072	0.039
8	57318152	rs9650315	T	G	0.12	0.021	-0.056	0.024
8	129118629	rs13249999	T	C	0.07	0.30	-0.032	0.031
9	118174617	rs7869550	G	A	0.21	0.10	-0.032	0.019
9	132453905	rs7466269	G	A	0.44	0.047	-0.032	0.016
12	64644614	rs1042725	T	C	0.47	$5.1\text{x}10^{-5}$	-0.064	0.016
14	36069800	rs17104630	G	A	0.10	0.021	-0.061	0.026
14	91477446	rs3783937	T	C	0.24	0.59	-0.010	0.018
14	91529711	rs8007661	T	C	0.47	0.0015	-0.051	0.016
15	77391837	rs11858942	G	A	0.33	0.96	0.001	0.017
15	82077496	rs2562784	G	A	0.26	0.00055	0.062	0.018
16	615681	rs763014	T	C	0.50	0.96	-0.001	0.016
16	2225358	rs26840	T	C	FAILED			
17	51785154	rs12449568	C	T	0.48	0.64	0.007	0.016
18	48613000	rs12958987	T	G	0.33	0.16	0.024	0.017
19	2121954	rs12986413	T	A	0.46	0.21	0.020	0.016
20	5034939	rs6116651	T	A	0.06	0.67	0.014	0.032
20	33370575	rs6060369	C	T	0.45	0.0014	0.051	0.016

Supplementary Table 4. Association results in KORA S4. Allele 1 corresponds to the minor allele in KORA S4 (N=4130). Effect sizes and standard errors are given in s.d. units. The direction of the effect is for allele 1 (positive strand, build NCBI35).

Chromosome	Physical position	SNP	Allele 1	Allele 2	MAF	P-value	Effect size	Standard error
3	142588260	rs724016	G	A	0.43	0.021	0.024	0.011
4	145869471	rs1492820	G	A	0.44	0.0045	-0.030	0.011
6	26341366	rs10946808	G	A	0.29	0.035	-0.024	0.012
6	142745570	rs4896582	A	G	0.31	0.0047	-0.033	0.012
20	33370575	rs6060369	C	T	FAILED			

Supplementary Table 5. Association results in PPP. Allele 1 corresponds to the minor allele in PPP (N=3402). Effect sizes and standard errors are given in s.d. units. The direction of the effect is for allele 1 (positive strand, build NCBI35).

Chromosome	Physical position	SNP	Allele 1	Allele 2	MAF	P-value	Effect size	Standard error
3	142588260	rs724016	A	G	0.496	0.00059	-0.083	0.024
4	4327819	rs2916448	G	A	0.07	0.26	-0.056	0.049
4	82373306	rs1662845	A	T	0.44	0.16	0.033	0.024
4	145869471	rs1492820	C	T	0.44	0.051	-0.048	0.025
5	4573856	rs1450822				FAILED		
6	26341366	rs10946808	G	A	0.35	0.0022	-0.078	0.025
6	105514355	rs314277	A	C	0.17	0.12	0.050	0.032
7	50632416	rs12540874	G	A	0.36	0.54	-0.016	0.025
7	92094841	rs2040494	C	T	0.49	0.35	-0.023	0.024
8	41596148	rs11786297	G	A	0.05	0.16	0.076	0.054
8	129118629	rs13249999				FAILED		
9	118174617	rs7869550	G	A	0.29	0.050	-0.052	0.027
9	132453905	rs7466269	G	A	0.39	0.11	-0.039	0.025
12	64644614	rs1042725	T	C	0.49	9.5×10^{-6}	-0.106	0.024
14	36069800	rs17104630	G	A	0.09	0.54	0.026	0.043
14	91477446	rs3783937	A	G	0.26	0.39	-0.023	0.027
15	77391837	rs11858942	G	A	0.31	0.94	0.0021	0.026
16	615681	rs763014	T	C	0.48	0.0045	-0.070	0.025
16	2225358	rs26840	T	C	0.45	0.065	0.045	0.024
17	51785154	rs12449568	T	C	0.49	0.022	-0.055	0.024
19	2121954	rs12986413	T	A	0.45	0.0029	0.073	0.025
20	5034939	rs6116651	T	A	0.09	0.42	-0.034	0.042
20	33370575	rs6060369	C	T	0.42	0.0014	0.078	0.024

Supplementary Table 6. Association results in the FUSION stage 2 panel (N=2466). Effect sizes and standard errors are given in s.d. units. The direction of the effect is for the reference allele (positive strand in build NCBI35).

Chr	Physical position	SNP	Ref. allele	FUSION2 CTRL			FUSION2 T2D		
				MAF	Beta (se)	P-value	MAF	Beta (se)	P-value
3	142588260	rs724016	A	0.45	-0.055 (0.04)	0.17	0.45	-0.006 (0.042)	0.88
4	4327819	rs2916448	T	0.07	0.014 (0.08)	0.86	0.07	-0.12 (0.082)	0.14
4	82373306	rs1662845	A	0.43	-0.121 (0.041)	0.0034	0.44	-0.069 (0.042)	0.099
4	145794294	rs1812175	G	0.16	0.03 (0.054)	0.58	0.16	-0.099 (0.056)	0.077
4	145869471	rs1492820	A	0.41	0.051 (0.041)	0.21	0.41	-0.025 (0.041)	0.54
5	4573856	rs1450822	G	0.5	0.012 (0.041)	0.78	0.49	-0.058 (0.042)	0.17
6	26341366	rs10946808	A	0.46	0.123 (0.04)	0.0022	0.43	0.086 (0.041)	0.035
6	105514355	rs314277	C	0.14	-0.095 (0.061)	0.12	0.17	-0.073 (0.055)	0.18
6	142745570	rs4896582	G	0.28	0.056 (0.045)	0.21	0.27	0.084 (0.048)	0.080
7	50632416	rs12540874	A	0.3	-0.05 (0.044)	0.26	0.3	-0.041 (0.045)	0.36
7	92094841	rs2040494	T	0.46	0.078 (0.041)	0.053	0.47	-0.01 (0.041)	0.80
7	158417550	rs2730245	C	0.24	-0.097 (0.047)	0.040	0.23	-0.046 (0.05)	0.36
8	41596148	rs11786297	A	0.04	-0.023 (0.107)	0.83	0.04	0.189 (0.108)	0.080
8	57318152	rs9650315	G	0.13	0.069 (0.062)	0.27	0.12	0.033 (0.062)	0.59
9	118174617	rs7869550	A	0.22	-0.002 (0.049)	0.97	0.21	0.022 (0.051)	0.66
9	132453905	rs7466269	A	0.45	0.043 (0.039)	0.27	0.47	-0.029 (0.041)	0.47
12	64644614	rs1042725	C	0.48	0.091 (0.041)	0.026	0.47	0.061 (0.041)	0.14
14	36069800	rs17104630	A	0.1	0.037 (0.068)	0.59	0.11	0.06 (0.067)	0.37
14	91477446	rs3783937	C	0.23	0.049 (0.047)	0.30	0.25	0.053 (0.046)	0.24
15	77391837	rs11858942	A	0.33	0.001 (0.044)	0.97	0.33	0.039 (0.045)	0.38
15	82077496	rs2562784				FAILED			
16	615681	rs763014	C	0.48	0.077 (0.04)	0.056	0.49	0.013 (0.04)	0.75
16	2225358	rs26840	C	0.45	0.053 (0.043)	0.22	0.45	-0.009 (0.042)	0.83
17	51785154	rs12449568	C	0.49	0.048 (0.04)	0.23	0.49	-0.016 (0.042)	0.70
19	2121954	rs12986413	A	0.46	-0.032 (0.042)	0.44	0.45	-0.124 (0.041)	0.0023
20	5034939	rs6116651	A	0.07	0.101 (0.078)	0.20	0.07	0.082 (0.079)	0.30
20	33370575	rs6060369	T	0.45	-0.103 (0.04)	0.0090	0.46	-0.071 (0.041)	0.084

Supplementary Table 7. Height information and association results from all cohorts for the 12 SNPs with combined P-values $<5\text{x}10^{-7}$ (see Table 1)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per G-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AG	GG				
3 (142588260)	rs724016	**A) GWA**											
		DGI CTRL	Imputed (0.996)	0.48 (A)	Male	709	175.0 (174.0, 175.9)	175.7 (175.1, 176.4)	175.8 (175.0, 176.7)	0.002	0.062 (0.042)		0.008
					Female	758	162.1 (161.2, 162.9)	162.3 (161.7, 162.9)	163.2 (162.4, 164.1)				
		DGI T2D		0.50 (A)	Male	768	174.2 (173.3, 175.0)	174.4 (173.8, 175.0)	174.2 (173.2, 175.1)	0.0001	0.017 (0.039)		0.58
					Female	743	160.5 (159.7, 161.4)	160.9 (160.3, 161.5)	161.2 (160.3, 162.1)				
		FUSION CTRL	Imputed(0.969)	0.45(G)	Male	640	173.9 (173.4, 174.4)	174.2 (173.6, 174.7)	174.7 (174.1, 175.2)	0.00245	0.07 (0.04)		0.082
					Female	647	160.4 (159.9, 160.8	160.7 (160.2, 161.2)	161.1 (160.6, 161.5)				
		FUSION T2D		0.47(G)	Male	617	159.1 (158.6, 159.5)	159.4 (158.9, 159.9)	160.4 (159.9, 160.8)	0.0045	0.095 (0.043)		0.029
					Female	467	171.9 (166.5, 177.4)	173.2 (168.6, 177.7)	172.4 (165.3, 179.4)				
		KORA S3	Imputed (0.99)	0.42 (G)	Male	813	173.0 (172.2, 173.8)	174.0 (173.4, 174.7)	174.1 (173.1, 175.2)	Not available	0.115 (0.036)		0.0014
					Female	830	160.5 (159.8, 161.1)	161.3 (160.7, 161.9)	161.6 (160.6, 162.5)				
		NHS	Imputed (0.994)	0.44 (G)	Male		Not applicable			0.0039	0.089 (0.029)		0.002
					Female	2,286	163.4 (163.2, 163,6)	164.1 (163.9, 164.3)	164.6 (164.3, 164.9)				
		PLCO	Imputed (0.998)	0.43 (G)	Male	2244	178.2 (177.7, 178.7)	178.3 (177.9, 178.7)	178.9 (178.2, 179.6)	0.001	0.046 (0.03)		0.13
					Female		Not applicable						
		SardiNIA	Genotyped	0.311 (G)	Male	1,883	158.1 (157.2, 159.0)	158.0 (156.0, 159.1)	155.3 (153.5, 157.1)	0.0054	0.075 (0.017)		5.96×10^{-5}
					Female	2,415	157.8 (156.9, 158.7)	158.3 (157.4, 159.2)	157.2 (155.3, 159.1)				
		Combined GWA (N=15,821)[b]										0% (0.79)	$5.0\text{x}10^{-12}$
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.42 (G)	Male Female	1094 1095	Not applicable				OR=1.4 [1.2-1.6]		$7.8\text{x}10^{-8}$
		FINRISK97	Genotyped	0.44 (G)	Male	3933	174.8 (174.4, 175.2)	175.4 (175.1, 175.7)	175.8 (175.3, 176.2)	0.004	0.087 (0.016)		$4.3\text{x}10^{-8}$
					Female	3869	161.8 (161.4, 1162.1)	162.6 (162.3, 162.8)	162.9 (162.4, 163.4)				
		FUSION2 CTRL	Genotyped	0.45(G)	Male	745	173.7 (173.3, 174.1)	174.8 (174.3, 175.2)	175 (174.5, 175.4)	0.00149	0.055 (0.04)		0.17
					Female	470	160.6 (160, 161.2)	160.4 (159.8, 161)	160.6 (160.1, 161.2)				
		FUSION2 T2D	Genotyped	0.45(G)	Male	693	174.6 (174.1, 175.1)	174.9 (174.4, 175.4)	175.2 (174.7, 175.7)	0.00002	0.006 (0.04)		0.88
					Female	482	160.2 (159.7, 160.7)	160.1 (159.6, 160.6)	160.2 (159.7, 160.8)				

KORA S4	Genotyped	0.43 (G)	Male	2026	174.5 (174.0, 175.0)	174.8 (174.3, 175.2)	175.6(174.9, 176.4)	Not available	0.024 (0.011)		0.021
			Female	2077	161.3 (160.8, 161.8)	162.4 (162.0, 162.8)	162.0 (161.4, 162.7)				
PPP	Genotyped	0.50 (A)	Male	1611	176.5 (175.9, 177.2)	177.2 (176.7, 177.7)	177.2 (176.6, 177.9)	0.003	0.083 (0.024)		0.00059
			Female	1791	163.1 (162.5, 163.7)	164.1 (163.7, 164.5)	164.2 (163.7, 164.8)				
Combined follow-up studies (N=17,697) [b]										71% (0.005)	$2.5x10^{-11}$
All studies (N=33.,518) [b]											$8.3x10^{-22}$

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per G-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AG	GG				
4 (145869471)	rs1492820	**A) GWA**											
		DGI CTRL	Imputed (0.975)	0.43 (G)	Male	709	176.1 (175.2, 176.9)	175.6 (175.0, 176.2)	174.5 (173.4, 175.6)	0.004	-0.144 (0.043)		0.010
					Female	758	163.0 (162.2, 163.8)	162.2 (161.6, 162.8)	162.5 (161.5, 163.5)				
		DGI T2D		0.43 (G)	Male	768	174.4 (173.6, 175.2)	174.4 (173.7, 175.0)	173.9 (172.9, 174.9)	0.001	-0.067 (0.04)		0.12
					Female	743	161.7 (160.9, 162.5)	160.3 (159.7, 160.9)	161.0 (160.0, 162.0)				
		FUSION CTRL	Imputed(0.978)	0.41(G)	Male	640	173.3 (172.8, 173.9)	174.6 (174, 175.1)	174.1 (173.6, 174.6)	0.0027	-0.074 (0.04)		0.066
					Female	647	159.9 (159.4, 160.3)	160.8 (160.3, 161.3)	160.9 (160.4, 161.3)				
		FUSION T2D		0.41(G)	Male	617	172.7 (172.3, 173.2)	173.4 (172.9, 173.9)	173.2 (172.7, 173.6)	0.00001	-0.004 (0.045)		0.93
					Female	467	159.4 (159, 159.9)	159.7 (159.2, 160.2)	159.3 (158.8, 159.8)				
		KORA S3	Imputed (0.99)	0.44 (G)	Male	813	174.6 (173.8, 175.4)	173.2 (172.6, 173.9)	173.5 (172.4, 174.5)	Not available	-0.096 (0.036)		0.0082
					Female	830	161.6 (160.8, 162.3)	160.8 (160.2, 161.4)	161 (160.1, 161.8)				
		NHS	Imputed (0.983)	0.46 (G)	Male			Not applicable		0.0029	-0.080 (0.029)		0.007
					Female	2,286	164.6 (164.4, 164.8)	163.7 (163.5, 163.9)	163.7 (163.4, 164.0)				
		PLCO	Imputed (0.990)	0.44 (G)	Male	2244	178.8 (178.3, 179.3)	178.3 (177.9, 178.7)	177.9 (177.3, 178.5)	0.002	-0.065 (0.029)		0.03
					Female			Not applicable					
		SardiNIA	Imputed (0.970)	0.373 (A)	Male	1,883	158.2 (156.2,160.1)	157.3 (156.3,158.2)	158.4 (157.3,159.4)	0.0024	-0.047 (0.22)		0.0582
					Female	2,415	158.1 (156.6, 159.6)	158.1 (157.2, 159.1)	157.8 (156.8, 158.7)				
		Combined GWA (N=15,821)[b]										0% (0.58)	$3.6x10^{-8}$
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.47 (G)	Male Female	1,094 1,095		Not applicable			OR=0.8 [0.7-0.9]		0.0015
		FINRISK97	Genotyped	0.41 (G)	Male	3839	175.4 (175.0 175.8)	175.2 (174.9, 175.5)	175.3 (174.7, 175.8)	0.0006	-0.034 (0.016)		0.035
					Female	3859	162.5 (162.1, 162.8)	162.4 (162.1, 162.7)	162.2 (161.7, 162.6)				
		FUSION2 CTRL	Genotyped	0.41(G)	Male	743	174.7 (174.2, 175.1)	174.4 (174, 174.9)	174.2 (173.8, 174.6)	0.0013	-0.051 (0.041)		0.21
					Female	469	160.5 (159.9, 161.1)	160.6 (160, 161.1)	160.5 (159.9, 161)				
		FUSION2 T2D	Genotyped	0.41(G)	Male	693	174.8 (174.3, 175.3)	174.9 (174.4, 175.4)	174.8 (174.3, 175.4)	0.00031	0.025 (0.41)		0.54
					Female	482	160.2 (159.6,	159.9 (159.4,	160.7 (160.3,				

					160.7)	160.5)	161.2)				
PPP	Genotyped	0.44 (G)	Male	1611	177.2 (176.6, 177.8)	177.3 (176.8, 177.8)	176.2 (175.6, 176.9)	0.001	-0.048 (0.025)		0.050
			Female	1791	164.1 (163.6, 164.6)	163.7 (163.3, 164.1)	164.1 (163.5, 164.8)				
KORA S4	Genotyped	0.44 (G)	Male	2015	175.2 (174.6, 175.8)	174.9 (174.4, 175.3)	174.2 (173.5, 174.9)	Not available	-0.030 (0.011)		0.0045
			Female	2066	162.3 (161.8, 162.9)	161.8 (161.4, 162.2)	161.8 (161.2, 162.4)				
Combined follow-up studies (N=17,697) [b]										0% (1)	3.9×10^{-5}
All studies (N=33,518) [b]											1.2×10^{-11}

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per G-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AG	GG				
6 (26341366)	rs10946808	**A) GWA**											
		DGI CTRL	Imputed (0.872)	0.33 (G)	Male	709	175.5 (174.8, 176.2)	175.9 (175.2, 176.5)	174.6 (173.1, 176.1)	0.0002	-0.035 (0.049)		0.92
					Female	758	162.9 (162.3, 163.5)	162.1 (161.4, 162.7)	162.4 (161.1, 163.7)				
		DGI T2D		0.33 (G)	Male	768	174.8 (174.2, 175.4)	174.2 (173.5, 175.0)	172.4 (171.3, 173.5)	0.007	-0.179 (0.045)		4.8x10^{-5}
					Female	743	161.7 (161.0, 162.3)	160.5 (159.9, 161.2)	159.4 (158.1, 160.7)				
		FUSION CTRL	Genotyped	0.43 (G)	Male	640	174.6 (174.1, 175.1)	174 (173.5, 174.5)	173.9 (173.4, 174.5)	0.0006	-0.034 (0.03)		0.38
					Female	647	160.9 (160.4, 161.3)	160.6 (160.1, 161.1)	160.5 (160, 161.1)				
		FUSION T2D		0.42 (G)	Male	617	173.9 (173.4, 174.4)	172.9 (172.4, 173.3)	172.9 (172.5, 173.4)	0.004	-0.094 (0.043)		0.0296
					Female	467	160.3 (159.8, 160.8)	159.2 (158.7, 159.7)	159.1 (158.5, 159.6)				
		KORA S3	Imputed (0.83)	0.29 (G)	Male	813	173.7 (173.1, 174.4)	174.0 (173.3, 174.7)	172.1 (170.7, 173.6)	Not available	-0.085 (0.044)		0.056
					Female	830	161.3 (160.7, 161.9)	161.1 (160.4, 161.7)	159.3 (157.6, 161.0)				
		NHS	Imputed (1.00)	0.30 (G)	Male		Not applicable			0.0024	-0.075 (0.032)		0.019
					Female	2,286	164.3 (164.1, 164.5)	163.8 (163.6, 164.0)	162.9 (162.0, 163.8)				
		PLCO	Genotyped	0.29 (G)	Male	2244	178.6 (178.3, 179.0)	178.2 (177.7, 178.6)	177.6 (176.7, 178.6)	0.002	-0.063 (0.032)		0.05
					Female		Not applicable						
		SardiNIA	Imputed(0.801)	0.244 (G)	Male	1,883	157.6 (156.7, 158.5)	158.1 (157.0, 159.2)	156.8 (154.5, 159.1)	0.0038	-0.068 (0.026)		0.0172
					Female	2,415	157.9 (157.2, 158.7)	158.6 (157.6, 159.6)	154.2 (151.5, 156.8)				
		Combined GWA (N=15,821)[b]										40% (0.15)	3.3x10^{-8}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.31 (G)	Male Female	1,094 1,095	Not applicable				OR=0.7 [0.7-0.8]		3.4x10^{-8}
		FINRISK97	Genotyped	0.43 (G)	Male	3932	175.6 (175.3, 176.0)	175.2 (174.9, 175.6)	174.8 (174.3, 175.3)	0.002	-0.065 (0.016)		4.9x10^{-5}
					Female	3876	163.0 (162.6, 163.4)	162.1 (161.8, 162.4)	162.1 (161.6, 162.5)				
		FUSION2 CTRL	Genotyped	0.46(G)	Male	745	175.3 (174.9, 175.8)	174.2 (173.8, 174.7)	174.1 (173.6, 174.5)	0.0075	-0.123 (0.04)		0.0022
					Female	473	160.9 (160.3, 161.5)	160.7 (160.2, 161.3)	159.5 (158.9, 160)				
		FUSION2 T2D		0.43(G)	Male	697	175.9 (175.4, 176.4)	174.2 (173.7, 174.7)	174.7 (174.2, 175.2)	0.00367	-0.086 (0.041)		0.035
					Female	477	161 (160.4, 161.5)	159.6 (159.1, 160.1)	160.1 (159.6, 160.7)				

PPP	Genotyped	0.35 (G)	Male	1611	177.6 (177.1, 178.1)	176.6 (176.1, 177.1)	176.8 (175.8, 177.7)	0.003	-0.078 (0.025)		0.0022
			Female	1791	164.4 (163.9, 164.8)	163.5 (163.0, 163.9)	163.9 (163.0, 164.7)				
KORA S4	Genotyped	0.29 (G)	Male	2027	175.2 (174.8, 175.6)	174.6 (174.2, 175.1)	173.8 (172.9, 174.8)	Not available	-0.024 (0.012)		0.035
			Female	2077	162.0 (161.6, 162.4)	162.1 (161.7, 162.6)	161.1 (160.2, 162.1)				
Combined follow-up studies (N=17,697) [b]										63% (0.03)	1.9x10^{-10}
All studies (N=33,518) [b]											3.8x10^{-17}

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per A-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AC	CC				
6 (105514355)	rs314277	**A) GWA**											
		DGI CTRL	Imputed (0.599)	0.13 (A)	Male	709	174.9 (170.6, 179.3)	176.1 (175.2, 177.0)	175.4 (174.9, 176.0)	0.0009	0.052 (0.079)		0.24
					Female	758	164.0 (161.5, 166.6)	162.7 (161.8, 163.7)	162.4 (161.9, 162.9)				
		DGI T2D		0.13 (A)	Male	768	174.7 (172.4, 177.0)	174.3 (173.3, 175.2)	174.3 (173.8, 174.8)	0.001	0.096 (0.074)		0.10
					Female	743	160.4 (154.8, 166.0)	161.3 (160.5, 162.2)	160.8 (160.2, 161.3)				
		FUSION CTRL	Genotyped	0.16 (A)	Male	640	176.1 (175.7, 176.6)	174.3 (173.8, 174.8)	174.1 (173.5, 174.6)	0.0028	0.104 (0.055)		0.059
					Female	647	161.3 (160.9, 161.7)	161.5 (161.1, 162)	160.4 (159.9, 160.8)				
		FUSION T2D		0.14 (A)	Male	617	174.3 (173.8, 174.8)	174.2 (173.7, 174.7)	172.9 (172.4, 173.4)	0.0093	0.192 (0.061)		0.0016
					Female	467	162.6 (162.3, 162.9)	159.8 (159.3, 160.4)	159.4 (158.8, 159.9)				
		KORA S3	Imputed (0.598)	0.11 (A)	Male	813	173.5 (160.7, 186.3)	174.0 (173.1, 174.9)	173.6 (173.1, 174.1)	Not available	0.177 (0.073)		0.015
					Female	830	158.7 (148.6, 168.8)	162.1 (161.2, 163.0)	160.8 (160.3, 161.3)				
		NHS	Imputed (1.00)	0.14 (A)	Male		Not applicable			0.0024	0.100 (0.042)		0.017
					Female	2,286	161.3 (157.6, 165.0)	164.5 (164.2, 164.8)	163.9 (163.8, 164.0)				
		PLCO	Genotyped	0.15 (A)	Male	2243	178.3 (176.4, 180.1)	178.7 (178.2, 179.3)	178.2 (177.9, 178.6)	0.001	0.062 (0.041)		0.13
					Female		Not applicable						
		SardiNIA	Imputed (0.614)	0.09(A)	Male	1,883	158.5 (147.7, 169.3)	157.2 (155.7, 158.8)	157.9 (157.2, 158.6)	0.0024	0.079 (0.028)		0.0105
					Female	2,415	168.5 (159.7, 177.3)	157.8 (156.5, 159.1)	158.0 (157.3, 158.7)				
		Combined GWA (N=15,821)[b]										0% (0.76)	5.9×10^{-9}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.14 (A)	Male Female	1,094 1,095	Not applicable				OR=1.1 [0.9-1.3]		0.26
		FINRISK97	Genotyped	0.17 (A)	Male	3935	175.3 (174.0, 176.6)	175.2 (174.8, 175.6)	175.3 (175.1, 175.6)	8×10^{-5}	0.018 (0.021)		0.41
					Female	3875	163.8 (162.6, 165.0)	162.2 (161.8, 162.6)	162.4 (162.2, 162.7)				
		FUSION2 CTRL	Genotyped	0.14 (A)	Male	745	173.1 (173, 173.3)	174.9 (174.4, 175.4)	174.4 (174, 174.8)	0.0024	0.095 (0.061)		0.12
					Female	473	164 (163.4, 164.7)	161.3 (160.6, 161.9)	160.3 (159.7, 160.8)				
		FUSION2 T2D		0.17 (A)	Male	697	177.6 (177.2, 178.1)	175.6 (175.1, 176.1)	174.5 (174, 175)	0.0014	0.073 (0.055)		0.18
					Female	477	157.6 (157.1, 158.2)	160 (159.5, 160.6)	160.4 (159.9, 161)				

PPP	Genotyped	0.17 (A)	Male	1611	177.5 (175.7, 179.4)	177.4 (176.8, 178.0)	176.9 (176.5, 177.3)	0.0007	0.050 (0.032)		0.12
			Female	1791	164.4 (162.5, 166.2)	163.9 (163.3, 164.4)	163.9 (163.6, 164.3)				
Combined follow-up studies (N=13,604) [b]										0% (0.82)	0.035
All studies (N=29,425) [b]											$1.1x10^{-8}$

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per A-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AG	GG				
6 (142745570)	rs4896582	**A) GWA**											
		DGI CTRL	Imputed (0.974)	0.26 (A)	Male	709	174.7 (172.8, 176.7)	175.1 (174.4, 175.8)	176.0 (175.4, 176.6)	0.0001	-0.021 (0.048)		0.067
					Female	758	162.0 (160.6, 163.4)	162.7 (162.0, 163.3)	162.4 (161.9, 163.0)				
		DGI T2D		0.27 (A)	Male	768	174.4 (172.7, 176.1)	173.8 (173.1, 174.5)	174.7 (174.0, 175.3)	0.002	-0.058 (0.045)		0.032
					Female	743	161.2 (159.6, 162.7)	160.4 (159.6, 161.1)	161.3 (160.7, 161.9)				
		FUSION CTRL	Imputed (0.978)	0.27 (A)	Male	640	173 (172.5, 173.5)	174.2 (173.7, 174.7)	174.3 (173.8, 174.8)	0.0033	-0.092 (0.046)		0.044
					Female	647	159.9 (159.4, 160.3)	160.3 (159.9, 160.8)	161.1 (160.6, 161.5)				
		FUSION T2D		0.26 (A)	Male	617	171.1 (170.7, 171.6)	173.2 (172.7, 173.6)	173.6 (173.1, 174.1)	0.0032	-0.09 (0.049)		0.063
					Female	467	159.2 (158.6, 159.8)	159.8 (159.3, 160.3)	159.5 (159, 160)				
		KORA S3	Imputed (0.96)	0.30 (A)	Male	813	171.9 (170.4, 173.3)	173.9 (173.2, 174.5)	173.9 (173.2, 174.5)	Not available	-0.092 (0.039)		0.019
					Female	830	160.0 (158.7, 161.3)	161.0 (160.4, 161.6)	161.3 (160.7, 161.9)				
		NHS	Imputed (0.978)	0.32 (A)	Male			Not applicable		0.0015	-0.056 (0.032)		0.077
					Female	2,286	163.7 (163.3, 164.1)	163.8 (163.6, 164.0)	164.2 (164.0, 164.4)				
		PLCO	Imputed (0.981)	0.29 (A)	Male	2244	177.5 (176.6, 178.4)	178.4 (177.9, 178.8)	178.5 (178.1, 178.9)	0.002	-0.056 (0.032)		0.08
					Female			Not applicable					
		SardiNIA	Imputed (0.977)	0.366 (A)	Male	1,883	157.7 (155.7, 159.7)	157.2 (156.3, 158.1)	158.5 (157.5, 159.6)	0.0032	-0.055 (0.022)		0.0244
					Female	2,415	158.6 (157.0, 160.2)	157.9 (157.0, 158.8)	157.8 (156.8, 158.7)				
		Combined GWA (N=15,821)[b]										0% (0.96)	3.2×10^{-8}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.32 (A)	Male	1,094		Not applicable			OR=0.8 [0.7-0.9]		2.2×10^{-5}
					Female	1,095							
		FINRISK97	Genotyped	0.29 (A)	Male	3930	174.3 (173.6, 175.0)	175.1 (174.7, 175.4)	175.6 (175.3, 175.9)	0.005	-0.105 (0.017)		1.4×10^{-9}
					Female	3874	160.6 (160.0, 161.3)	162.3 (162.0, 162.6)	162.8 (162.5, 163.1)				
		FUSION2 CTRL	Genotyped	0.28 (A)	Male	744	174.6 (174.2, 175)	174 (173.6, 174.5)	174.9 (174.5, 175.4)	0.0013	-0.056 (0.045)		0.21
					Female	472	159.8 (159.3, 160.3)	160.4 (159.9, 161)	160.7 (160.1, 161.3)				
		FUSION2 T2D	Genotyped	0.27 (A)	Male	692	174.3 (173.6, 174.9)	174.2 (173.7, 174.6)	175.4 (174.9, 175.9)	0.0028	-0.084 (0.04)		0.080
					Female	472	160 (159.5, 160.5)	160.1 (159.6, 160.6)	160.3 (159.8, 160.8)				

KORA S4	Genotyped	0.31 (A)	Male	2027	174.1 (173.0, 175.3)	174.7 (174.3, 175.2)	175.0 (174.6, 175.5)	Not available	-0.033 (0.012)		0.0047
			Female	2079	160.7 (159.7, 161.7)	161.9 (161.4, 162.3)	162.3 (161.9, 162.7)				
Combined follow-up studies (N=14,290) [b]										24% (0.29)	$6.3x10^{-12}$
All studies (N=30,111) [b]											$2.4x10^{-18}$

---

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the ‘Follow-up studies’ or ‘All studies’ did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per C-allele effect size (s.e.)^a	Hetero-geneity I^2 (P-value)	P-value
							CC	CT	TT				
7 (92094841)	rs2040494	**A) GWA**											
		DGI CTRL	Imputed (0.976)	0.47 (C)	Male	709	175.2 (174.3, 176.1)	175.7 (175.1, 176.3)	175.7 (174.8, 176.6)	0.0003	-0.026 (0.042)		0.090
					Female	758	162.3 (161.4, 163.2)	162.4 (161.9, 163.0)	162.8 (161.9, 163.6)				
		DGI T2D		0.49 (C)	Male	768	174.2 (173.3, 175.2)	174.2 (173.5, 174.8)	174.5 (173.7, 175.4)	0.0005	-0.033 (0.039)		0.21
					Female	743	160.4 (159.4, 161.5)	160.9 (160.3, 161.5)	161.3 (160.4, 162.2)				
		FUSION CTRL	Imputed (0.972)	0.49 (C)	Male	640	173.7 (173.2, 174.1)	174.1 (173.5, 174.6)	174.8 (174.3, 175.3)	0.00035	-0.027 (0.04)		0.51
					Female	647	160.6 (160.1, 161)	160.6 (160.2, 161.1)	160.9 (160.4, 161.4)				
		FUSION T2D		0.47 (C)	Male	617	172.5 (172, 173)	174.1 (173.6, 174.5)	172.2 (171.7, 172.7)	0.00069	0.037 (0.044)		0.39
					Female	467	160 (159.5, 160.5)	159.2 (158.7, 159.7)	159.7 (159.1, 160.2)				
		KORA S3	Imputed (0.972)	0.46 (C)	Male	813	173.8 (172.7, 174.9)	173.6 (172.9, 174.2)	173.9 (173.1, 174.8)	Not available	0 (0.036)		1
					Female	830	161.2 (160.4, 162.0)	161.0 (160.4, 161.6)	161.1 (160.4, 161.8)				
		NHS	Imputed (0.980)	0.46 (C)	Male		Not applicable			0.0007	-0.038 (0.029)		0.19
					Female	2,286	163.3 (162.9, 163.7)	164.2 (164.0, 164.4)	164.1 (163.9, 164.3)				
		PLCO	Imputed (0.980)	0.46 (C)	Male	2244	177.7 (177.1, 178.3)	178.4 (178.0, 178.8)	178.8 (178.3, 179.3)	0.003	-0.087 (0.03)		0.004
					Female		Not applicable						
		SardiNIA	Imputed (1.000)	0.354 (C)	Male	1,883	156.8 (155.1, 158.5)	157.9 (156.9, 158.9)	158.0 (157.1, 159.0)	0.0062	-0.078 (0.022)		0.00189
					Female	2,415	158.5 (147.7, 169.3)	157.2 (155.7, 158.9)	157.9 (157.2, 158.6)				
		Combined GWA (N=15,821)^b										29% (0.29)	4.8x10^{-5}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.46 (C)	Male Female	1,094 1,095	Not applicable				OR=0.9 [0.8-1.0]		0.18
		FINRISK97	Genotyped	0.47 (C)	Male	3934	175.0 (174.5, 175.5)	175.2 (174.9, 175.5)	175.6 (175.2, 176.1)	0.001	-0.045 (0.016)		0.0050
					Female	3874	162.0 (161.5, 162.4)	162.6 (162.3, 162.8)	162.3 (162.0, 162.8)				
		FUSION2 CTRL	Genotyped	0.46 (C)	Male	747	173.8 (173.4, 174.2)	174.6 (174.1, 175)	174.9 (174.5, 175.4)	0.003	-0.078 (0.041)		0.053
					Female	474	159.8 (159.2, 160.3)	160.8 (160.3, 161.4)	160.6 (160, 161.1)				
		FUSION2 T2D	Genotyped	0.47 (C)	Male	695	175.6 (175.1, 176.1)	174.5 (174, 175)	174.9 (174.4, 175.4)	0.00005	0.01 (0.041)		0.80
					Female	476	159.8 (159.3, 160.2)	160.2 (159.6, 160.7)	160.7 (160.1, 161.2)				

PPP	Genotyped	0.49 (C)	Male	1611	176.4 (175.8, 177.1)	177.0 (176.5, 177.5)	177.7 (177.0, 178.3)	0.0003	-0.023 (0.024)		0.35
			Female	1791	164.0 (163.4, 164.5)	164.0 (163.6, 164.4)	163.7 (163.1, 164.3)				
Combined follow-up studies (N=13,604) [b]										0% (0.62)	0.0020
All studies (N=29,425) [b]											$3.8x10^{-7}$

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per T-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							GG	GT	TT				
8 (57318152)	rs9650315	**A) GWA**											
		DGI CTRL	Imputed (0.909)	0.12 (T)	Male	709	175.6 (175.1, 176.1)	175.5 (174.5, 176.6)	173.1 (168.5, 177.8)	0.002	-0.087 (0.069)		0.71
					Female	758	162.5 (162.0, 163.0)	162.5 (161.6, 163.4)	160.9 (156.4, 165.4)				
		DGI T2D		0.11 (T)	Male	768	174.5 (174.0, 175.0)	173.6 (172.6, 174.6)	175.0 (167.2, 182.8)	0.004	-0.177 (0.064)		0.0089
					Female	743	161.1 (160.6, 161.6)	160.1 (159.2, 161.0)	159.3 (155.9, 162.7)				
		FUSION CTRL	Imputed (0.969)	0.11 (T)	Male	640	174.1 (173.6, 174.6)	174.6 (174.1, 175.1)	173.1 (172.6, 173.7)	0.00003	0.012 (0.064)		0.85
					Female	647	160.7 (160.2, 161.2)	160.5 (160.1, 161)	161 (160.4, 161.6)				
		FUSION T2D		0.12 (T)	Male	617	173.2 (172.7, 173.7)	173.3 (172.9, 173.7)	173.9 (173.5, 174.3)	0.00088	-0.066 (0.069)		0.34
					Female	467	159.6 (159.1, 160.1)	159.6 (159.1, 160.1)	157 (156.2, 157.7)				
		KORA S3	Imputed (0.922)	0.14 (T)	Male	813	173.8 (173.3, 174.3)	173.5 (172.6, 174.5)	172.6 (169.7, 175.6)	Not available	-0.154 (0.053)		0.0037
					Female	830	161.3 (160.8, 161.7)	160.5 (159.6, 161.4)	159.1 (155.2, 162.9)				
		NHS	Imputed (0.960)	0.15 (T)	Male		Not applicable			0.0005	-0.047 (0.043)		0.27
					Female	2,286	164.1 (164.0, 164.2)	163.6 (163.2, 164.0)	162.9 (162.1, 163.7)				
		PLCO	Imputed (0.956)	0.13 (T)	Male	2244	178.6 (178.3, 178.9)	177.6 (177.1, 178.2)	178.6 (177.0, 180.2)	0.0006	-0.063 (0.044)		0.15
					Female		Not applicable						
		SardiNIA	Imputed (0.900)	0.226 (T)	Male	1,883	157.4 (156.6, 158.2)	158.5 (157.3, 159.6)	157.6 (154.8, 160.4)	0.0060	-0.088 (0.025)		0.00183
					Female	2,415	157.9 (157.1, 158.7)	158.4 (157.4, 159.4)	154.9 (152.1, 157.8)				
		Combined GWA (N=15,821)[b]										46% (0.10)	9.6×10^{-6}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.14 (T)	Male	1,094	Not applicable				OR=0.7 [0.6-0.8]		9.0×10^{-6}
					Female	1,095							
		FINRISK97	Genotyped	0.12 (T)	Male	3935	175.3 (175.1, 175.6)	175.2 (174.7, 175.6)	175.4 (173.3, 177.5)	0.0007	-0.056 (0.024)		0.021
					Female	3877	162.5 (162.3, 162.8)	161.9 (161.4, 162.3)	162.2 (160.5, 163.9)				
		FUSION2 CTRL	Genotyped	0.13 (T)	Male	739	174.6 (174.2, 175.1)	174.3 (173.9, 174.8)	170.9 (170.4, 171.4)	0.00103	-0.069 (0.062)		0.27
					Female	470	160.6 (160, 161.2)	160 (159.5, 160.6)	160.8 (160.3, 161.3)				
		FUSION2 T2D	Genotyped	0.12 (T)	Male	685	174.9 (174.4, 175.4)	175.1 (174.6, 175.6)	174.6 (174, 175.2)	0.00024	-0.033 (0.062)		0.59
					Female	476	160.2 (159.7, 160.8)	160.2 (159.7, 160.7)	159.3 (158.6, 159.9)				

Combined follow-up studies (N=10,182) [b]	26% (0.27)	0.010
All studies (N=26,003) [b]		3.8×10^{-7}

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per T-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							CC	CT	TT				
12 (64644614)	rs1042725	**A) GWA**											
		DGI CTRL	Genotyped	0.46 (T)	Male	725	175.7 (174.9, 176.5)	175.9 (175.3, 176.5)	174.9 (173.9, 175.9)	0.003	-0.083 (0.042)		0.0027
					Female	771	163.3 (162.6, 164.1)	162.4 (161.8, 163.0)	161.6 (160.7, 162.5)				
		DGI T2D		0.48 (T)	Male	779	174.8 (174.0, 175.7)	174.1 (173.5, 174.8)	174.0 (173.1, 174.9)	0.006	-0.108 (0.037)		0.0030
					Female	750	161.8 (160.9, 162.7)	160.8 (160.2, 161.4)	160.0 (159.2, 160.9)				
		FUSION CTRL	Imputed (0.985)	0.47 (T)	Male	640	174.8 (174.3, 175.4)	173.7 (173.2, 174.2)	174.3 (173.8, 174.8)	0.0019	-0.061 (0.039)		0.12
					Female	647	161 (160.6, 161.5)	160.7 (160.2, 161.2)	160.2 (159.8, 160.7)				
		FUSION T2D		0.48 (T)	Male	617	173.9 (173.4, 174.4)	172.8 (172.3, 173.3)	173.3 (172.9, 173.8)	0.00031	-0.025 (0.043)		0.57
					Female	467	158.9 (158.4, 159.4)	159.9 (159.4, 160.4)	159.6 (159.1, 160.1)				
		KORA S3	Genotyped	0.49 (C)	Male	813	174.5 (173.6, 175.5)	173.8 (173.1, 174.4)	172.9 (172.0, 173.7)	Not available	-0.097 (0.036)		0.0066
					Female	830	161.3 (160.5, 162.1)	161.1 (160.5, 161.7)	160.7 (159.9, 161.5)				
		NHS	Imputed (0.995)	0.50 (T)	Male		Not applicable			0.0079	-0.122 (0.029)		2.5x10^{-5}
					Female	2,286	164.9 (164.7, 165.1)	163.9 (163.7, 164.1)	163.2 (163.0, 163.4)				
		PLCO	Imputed (0.995)	0.49 (T)	Male	2244	179.0 (178.5, 179.6)	178.2 (177.9, 178.6)	177.9 (177.4, 178.5)	0.002	-0.062 (0.030)		0.04
					Female		Not applicable						
		SardiNIA	Genotyped	0.447 (C)	Male	1,883	157.9 (156.5, 159.3)	158.2 (157.2, 159.1)	157.0 (157.1, 159.3)	0.00024	-0.046 (0.022)		0.0584
					Female	2,415	157.3 (156.0, 158.6)	158.0 (157.1, 158.9)	158.2 (157.1, 159.3)				
		Combined GWA (N=15,821)[b]										8% (0.51)	2.6x10^{-11}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.48 (T)	Male Female	1,094 1,095	Not applicable				OR=0.8 [0.7-0.9]		4.2x10^{-6}
		FINRISK97	Genotyped	0.47 (T)	Male	3955	175.8 (175.4, 176.2)	175.3 (175.0, 175.6)	174.7 (174.2, 175.1)	0.002	-0.064 (0.016)		5.1x10^{-5}
					Female	3895	162.6 (162.2, 163.0)	162.4 (162.1, 162.7)	161.9 (161.5, 162.3)				
		FUSION2 CTRL	Genotyped	0.48 (T)	Male	736	175.2 (174.8, 175.7)	174.7 (174.2, 175.1)	173.6 (173.2, 174)	0.0042	-0.091 (0.041)		0.026
					Female	460	161.4 (160.9, 162)	160.1 (159.5, 160.7)	160.7 (160.2, 161.2)				
		FUSION2 T2D	Genotyped	0.47 (T)	Male	691	174.8 (174.3, 175.3)	174.8 (174.3, 175.3)	174.6 (174.1, 175)	0.0018	-0.061 (0.041)		0.14
					Female	468	161 (160.5, 161.5)	160.1 (159.5, 160.6)	159.7 (159.2, 160.2)				

PPP	Genotyped	0.49 (T)	Male	1611	177.8 (177.2, 178.5)	176.9 (176.4, 177.4)	176.4 (175.8, 177.1)	0.006	-0.106 (0.024)		$9.5x10^{-5}$
			Female	1791	164.5 (163.9, 165.0)	164.0 (163.5, 164.4)	163.3 (162.7, 163.8)				
Combined follow-up studies (N=13,604) [b]										0% (0.71)	$1.7x10^{-10}$
All studies (N=29,425) [b]											$2.7x10^{-20}$

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per T-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							CC	CT	TT				
14 (91529711)	rs8007661	**A) GWA**											
		DGI CTRL	Imputed (0.590)	0.25 (T)	Male	709	175.8 (175.1, 176.4)	175.2 (174.6, 175.9)	176.8 (174.5, 179.1)	0.00008	-0.027 (0.062)		0.15
					Female	758	162.5 (161.9, 163.0)	162.7 (162.0, 163.3)	161.2 (159.3, 163.2)				
		DGI T2D		0.24 (T)	Male	768	174.2 (173.6, 174.7)	174.6 (173.8, 175.3)	173.0 (171.0, 175.0)	0.0006	-0.03 (0.058)		0.83
					Female	743	161.0 (160.4, 161.6)	160.7 (160.0, 161.4)	160.5 (158.5, 162.6)				
		FUSION CTRL	Imputed (0.670)	0.24 (T)	Male	640	174.6 (174.1, 175.1)	173.8 (173.3, 174.4)	172.1 (171.6, 172.6)	0.0027	-0.084 (0.05)		0.12
					Female	647	160.8 (160.3, 161.2)	160.7 (160.3, 161.1)	159.9 (159.4, 160.4)				
		FUSION T2D		0.23 (T)	Male	617	173.5 (173.1, 174)	172.8 (172.3, 173.3)	172.8 (172.3, 173.3)	0.0034	-0.096 (0.062)		0.12
					Female	467	159.8 (159.3, 160.3)	159 (158.5, 159.6)	160.5 (160, 160.9)				
		KORA S3	Imputed (0.50)	0.26 (T)	Male	813	174 (173.4 , 174.6)	173.3 (172.6, 174)	174.2 (172.2, 176.2)	Not available	-0.092 (0.054)		0.086
					Female	830	161.2 (160.6, 161.7)	161.1 (160.4, 161.7)	159.9 (158 , 161.9)				
		NHS	Genotyped	0.46 (T)	Male		Not applicable			0.0008	-0.039 (0.029)		0.18
					Female	2,286	164.1 (163.8, 164.4)	163.9 (163.7, 164.1)	163.9 (163.6, 164.2)				
		PLCO	Genotyped	0.49 (T)	Male	2243	179.0 (178.5, 179.6)	178.5 (178.1, 178.8)	177.4 (176.8, 177.9)	0.009	-0.130 (0.030)		0.00001
					Female		Not applicable						
		SardiNIA	Imputed (0.450)	0.217 (T)	Male	1,883	157.7 (156.8, 158.5)	158.1 (157.0, 159.2)	156.1 (152.3, 159.9)	0.0040	-0.072 (0.026)		0.0135
					Female	2,415	157.8 (157.0, 158.6)	158.2 (157.2, 159.2)	158.0 (155.0, 161.0)				
		Combined GWA (N=15,821)[b]										0% (0.63)	8.9x10^{-8}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.43 (T)	Male Female	1,094 1,095	Not applicable				OR=1.0 [0.9-1.1]		0.64
		FINRISK97	Genotyped	0.47 (T)	Male	3933	175.6 (175.2, 176.0)	175.4 (175.1, 175.7)	174.5 (174.0, 175.0)	0.001	-0.051 (0.016)		0.0015
					Female	3874	162.5 (162.2, 162.9)	162.3 (162.1, 162.6)	162.2 (161.8, 162.7)				
		Combined follow-up studies (N=7,803) [b]										n.a.	0.0015
		All studies (N=23,624) [b]											5.5x10^{-10}

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per G-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AG	GG				
15 (82077496)	rs2562784	**A) GWA**											
		DGI CTRL	Genotyped	0.25 (G)	Male	717	175.3 (174.7, 175.9)	175.7 (175.0, 176.5)	177.6 (175.8, 179.4)	0.005	0.109 (0.048)		0.0047
					Female	768	162.2 (161.6, 162.8)	162.9 (162.3, 163.5)	163.0 (161.4, 164.6)				
		DGI T2D		0.25 (G)	Male	771	173.9 (173.3, 174.5)	174.8 (174.1, 175.6)	175.1 (173.3, 176.9)	0.006	0.123 (0.044)		0.0089
					Female	745	160.5 (159.9, 161.1)	161.5 (160.8, 162.2)	160.3 (158.6, 162.0)				
		FUSION CTRL	Imputed (0.973)	0.26 (G)	Male	640	173.9 (173.3, 174.4)	174.5 (174, 175)	175.2 (174.7, 175.7)	0.0018	0.069 (0.046)		0.13
					Female	647	160.5 (160, 161)	160.5 (160, 160.9)	163.2 (162.7, 163.7)				
		FUSION T2D		0.24 (G)	Male	617	173.7 (173.2, 174.2)	172.4 (172, 172.9)	173.2 (172.7, 173.7)	0.00058	-0.039 (0.051)		0.45
					Female	467	159.3 (158.8, 159.8)	160 (159.5, 160.5)	159.5 (159.1, 160)				
		KORA S3	Genotyped	0.26 (G)	Male	813	173.6 (173, 174.2)	173.8 (173.1, 174.5)	174.3 (172.5, 176)	Not available	0.073 (0.042)		0.079
					Female	830	160.7 (160.2, 161.3)	161.5 (160.8, 162.2)	161.2 (159.6, 162.9)				
		NHS	Imputed (1.00)	0.23 (G)	Male		Not applicable			0.00005	-0.012 (0.035)		0.74
					Female	2,286	164.1 (163.9, 164.3)	163.9 (163.6, 164.2)	163.1 (162.5, 163.7)				
		PLCO	Genotyped	0.23 (G)	Male	2240	178.2 (177.8, 178.5)	178.6 (178.1, 179.0)	178.9 (177.7, 180.2)	0.002	0.074 (0.036)		0.04
					Female		Not applicable						
		SardiNIA	Genotyped	0.306 (G)	Male	1,883	157.8 (156.9, 158/7)	157.6 (156.8, 158.9)	157.4 (155.6, 159.2)	0.0012	0.036 (0.022)		0.152
					Female	2,415	157.7 (156.8, 158.5)	157.8 (156.9, 158.8)	159.8 (157.9, 161.6)				
		Combined GWA (N=15,821)[b]										3% (0.54)	$2.9x10^{-5}$
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.24 (G)	Male Female	1,094 1,095	Not applicable				OR=1.1 [1.0-1.2]		0.28
		FINRISK97	Genotyped	0.26 (G)	Male	3961	175.1 (174.8, 175.4)	175.5 (175.1, 175.8)	176.1 (175.3, 176.9)	0.002	0.062 (0.018)		0.00055
					Female	3905	162.1 (161.8, 162.4)	162.6 (162.3, 162.9)	162.8 (162.0, 163.6)				
		Combined follow-up studies (N=7,803) [b]										n.a.	0.00055
		All studies (N=23,624) [b]											6.4x10-8

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per T-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							AA	AT	TT				
19 (2121954)	rs12986413	**A) GWA**											
		DGI CTRL	Imputed (0.966)	0.49 (T)	Male	709	174.9 (174.0, 175.7)	175.8 (175.1, 176.4)	176.1 (175.2, 177.0)	0.001	0.05 (0.043)		0.24
					Female	758	162.3 (161.5, 163.2)	162.6 (162.0, 163.2)	162.5 (161.7, 163.3)				
		DGI T2D		0.47 (T)	Male	768	173.8 (173.0, 174.6)	174.4 (173.7, 175.1)	174.6 (173.7, 175.4)	0.0002	-0.021 (0.039)		0.70
					Female	743	161.4 (160.6, 162.2)	160.7 (160.1, 161.3)	160.5 (159.6, 161.5)				
		FUSION CTRL	Imputed (0.990)	0.47 (T)	Male	640	173.5 (173, 174)	174.5 (173.9, 175)	174.4 (173.9, 174.9)	0.0016	0.056 (0.039)		0.16
					Female	647	159.9 (159.4, 160.3)	161 (160.5, 161.5)	161.1 (160.6, 161.5)				
		FUSION T2D		0.48 (T)	Male	617	173 (172.6, 173.5)	173.2 (172.7, 173.7)	173.5 (173, 174)	0.00059	0.034 (0.044)		0.43
					Female	467	159.3 (158.7, 159.8)	159.6 (159.1, 160.1)	159.7 (159.2, 160.2)				
		KORA S3	Imputed (0.895)	0.50 (A)	Male	813	172.7 (171.9, 173.5)	174.1 (173.4, 174.7)	173.9 (172.9, 174.8)	Not available	0.096 (0.037)		0.0097
					Female	830	160.7 (159.9, 161.5)	160.9 (160.3, 161.4)	161.9 (161.0, 162.7)				
		NHS	Imputed (0.969)	0.47 (T)	Male		Not applicable			0.0024	0.069 (0.030)		0.019
					Female	2,286	163.3 (163.0, 163.6)	164.2 (164.0, 164.4)	164.3 (164.0, 164.6)				
		PLCO	Imputed (0.971)	0.48 (T)	Male	2244	178.2 (177.7, 178.7)	178.5 (178.1, 178.9)	178.3 (177.7, 178.9)	0.00005	0.008 (0.030)		0.79
					Female		Not applicable						
		SardiNIA	Imputed (0.881)	0.43 (A)	Male	1,883	159.4 (157.9, 160.9)	157.4 (156.5, 156.3)	157.4 (156.2, 158.5)	0.0069	0.080 (0.023)		0.0026
					Female	2,415	157.2 (155.9, 158.6)	158.0 (157.1, 158.9)	158.4 (157.3, 159.4)				
		Combined GWA (N=15,821)[b]										23% (0.36)	2.0×10^{-5}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.48 (T)	Male Female	1,094 1,095	Not applicable				OR=1.1 [1.0-1.2]		0.20
		FINRISK97	Genotyped	0.46 (T)	Male	3932	174.9 (174.5, 175.3)	175.5 (175.2, 175.8)	175.5 (175.0, 176.0)	0.0002	0.020 (0.016)		0.20
					Female	3871	162.4 (162.0, 162.7)	162.2 (161.9, 162.5)	162.8 (162.4, 163.3)				
		FUSION2 CTRL	Genotyped	0.46 (T)	Male	718	174.6 (174.1, 175.1)	174.4 (174, 174.9)	174.9 (174.5, 175.3)	0.00052	0.032 (0.042)		0.44
					Female	452	160.3 (159.8, 160.9)	160.7 (160.1, 161.3)	160.7 (160.2, 161.3)				
		FUSION2 T2D	Genotyped	0.45 (T)	Male	681	173.6 (173.1, 174.1)	175.6 (175.1, 176.1)	175 (174.4, 175.5)	0.00765	0.124 (0.041)		0.0023
					Female	465	159.3 (158.8, 159.8)	160.2 (159.6, 160.7)	161.6 (161, 162.1)				

PPP	Genotyped	0.45 (T)	Male	1611	176.9 (176.4, 177.5)	177.1 (176.6, 177.5)	177.2 (176.4, 177.9)	0.003	0.073 (0.025)		0.0029
			Female	1791	163.3 (162.8, 163.8)	164.0 (163.6, 164.4)	164.6 (163.9, 165.2)				
Combined follow-up studies (N=13,604) [b]										60% (0.08)	3.7×10^{-4}
All studies (N=29,425) [b]											2.9×10^{-8}

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 7 (continued)

Chr (position)	SNP	Study	Imputation (rsq_hat)	MAF (allele)	Gender	Sample size	Mean height in cm (95% c.i.) by genotype			Variance explained	Per C-allele effect size (s.e.)[a]	Hetero-geneity I^2 (P-value)	P-value
							CC	CT	TT				
20 (33370575)	rs6060369	**A) GWA**											
		DGI CTRL	Genotyped	0.43 (C)	Male	725	175.2 (174.0, 176.3)	176.0 (175.4, 176.6)	175.2 (174.5, 176.0)	0.002	0.068 (0.042)		0.037
					Female	771	163.3 (162.3, 164.3)	162.5 (161.9, 163.2)	162.0 (161.3, 162.7)				
		DGI T2D		0.45 (C)	Male	779	175.2 (174.2, 176.2)	174.2 (173.6, 174.8)	173.9 (173.0, 174.7)	0.002	0.061 (0.038)		
					Female	750	161.1 (160.2, 162.0)	160.9 (160.2, 161.5)	160.9 (160.1, 161.7)				
		FUSION CTRL	Genotyped	0.46 (C)	Male	636	175.1 (174.5, 175.6)	174 (173.5, 174.6)	173.8 (173.3, 174.3)	0.00695	0.118 (0.04)		0.0028
					Female	642	161.3 (160.8, 161.7)	160.9 (160.5, 161.4)	159.9 (159.4, 160.4)				
		FUSION T2D		0.42 (C)	Male	610	173.9 (173.4, 174.4)	173.2 (172.7, 173.6)	173.1 (172.6, 173.5)	0.00261	0.073 (0.04)		0.093
					Female	464	159.8 (159.2, 160.3)	159.8 (159.3, 160.3)	159 (158.5, 159.5)				
		KORA S3	Genotyped	0.40 (C)	Male	813	174.3 (173.3, 175.4)	173.9 (173.3, 174.6)	173.1 (172.4, 173.8)	Not available	0.056 (0.037)		0.13
					Female	830	161.4 (160.2, 162.5)	160.9 (160.3, 161.4)	161.2 (160.5, 161.9)				
		NHS	Imputed (0.985)	0.39 (C)	Male		Not applicable			0.0001	0.011 (0.030)		0.72
					Female	2,286	164.2 (163.9, 164.5)	163.9 (163.7, 164.1)	163.9 (163.6, 164.2)				
		PLCO	Imputed (0.984)	0.38 (C)	Male	2244	179.0 (178.2, 179.7)	178.5 (178.2, 178.9)	177.9 (177.5, 178.3)	0.003	0.095 (0.031)		0.002
					Female		Not applicable						
		SardiNIA	Genotyped	0.384 (C)	Male	1,883	157.6 (155.7, 159.5)	157.7(156.9, 158.6)	157.9 (156.8, 159.0)	0.0072	0.083 (0.021)		0.000435
					Female	2,415	158.5 (156.8, 160.2)	157.6 (156.8, 158.4)	158.2 (157.1, 159.3)				
		Combined GWA (N=15,821)[b]										0% (0.58)	1.9×10^{-10}
		B) Follow-up studies											
		USHT tall-short	Genotyped	0.38 (C)	Male Female	1,094 1,095	Not applicable				OR=1.2 [1.0-1.3]		0.012
		FINRISK97	Genotyped	0.45 (C)	Male	3930	175.5 (175.1, 176.0)	175.3 (174.9, 175.6)	175.1 (174.7, 175.5)	0.001	0.051 (0.016)		0.0014
					Female	3869	162.8 (162.4, 163.3)	162.4 (162.1, 162.7)	162.0 (161.6, 162.4)				
		FUSION2 CTRL	Genotyped	0.45 (C)	Male	728	175.6 (175.2, 176.1)	174.3 (173.9, 174.8)	174.4 (173.9, 174.8)	0.0053	0.103 (0.04)		0.0090
					Female	475	161 (160.4, 161.6)	160.3 (159.8, 160.9)	160.4 (159.9, 161)				
		FUSION2 T2D	Genotyped	0.46 (C)	Male	690	175.5 (175, 175.9)	175.1 (174.6, 175.6)	174 (173.5, 174.5)	0.0025	0.071 (0.041)		0.084
					Female	464	160.7 (160.2, 161.1)	160.3 (159.7, 160.8)	160.2 (159.6, 160.7)				

PPP	Genotyped	0.42 (C)	Male	1611	177.1 (176.4, 177.9)	177.4 (176.9, 177.8)	176.5 (176.0, 177.1)	0.003	0.078 (0.024)		0.0014
			Female	1791	164.3 (163.6, 165.1)	164.0 (163.6, 164.4)	163.6 (163.1, 164.0)				
Combined follow-up studies (N=13,604) [b]										0% (0.78)	1.3×10^{-7}
All studies (N=29,425) [b]											1.4×10^{-16}

[a] Effect size and standard error are expressed in s.d. units. For the DGI GWAS, only the unrelated component of the study (N=2,448) was used to estimate the effect size. Combined effect sizes for the 'Follow-up studies' or 'All studies' did not use data from the case-control tall-short USHT panel. [b] Combined P-values were calculated using a weighted Z-score method. Combined effect sizes were calculated using the inverse variance method, assuming a fixed effect.

Supplementary Table 8. Analysis of stratification in the DGI panel. Association results in DGI unrelated (N=2,364) before and after correction for residual population stratification using principal component methods implemented in EIGENSTRAT.

SNP	**Uncorrected P-value**	**Adjusted P-value**
rs724016	0.1649	0.1517
rs2916448	0.1601	0.1767
rs1662845	0.8320	0.6040
rs1812175	0.0055	0.0024
rs1492820	0.0009	0.0006
rs1450822	0.1173	0.1027
rs10946808	0.0438	0.0914
rs314277	0.1747	0.1314
rs4896582	0.1343	0.1393
rs12540874	0.1521	0.1170
rs2040494	0.3577	0.4139
rs2730245	0.0026	0.0035
rs11786297	0.1608	0.2084
rs9650315	0.3131	0.2582
rs13249999	0.1279	0.1265
rs7869550	0.0396	0.0312
rs7466269	0.0038	0.0086
rs1042725	0.0002	0.0005
rs17104630	0.0244	0.0260
rs3783937	0.0010	0.0010
rs8007661	0.4482	0.4949
rs11858942	0.1367	0.1178
rs2562784	0.0010	0.0011
rs763014	0.8326	0.7391
rs26840	0.6592	0.8011
rs12449568	0.1972	0.1750
rs12958987	0.0218	0.0163
rs12986413	0.7586	0.8531
rs6116651	0.0250	0.0273
rs6060369	0.0288	0.0309

Supplementary Table 9. Stratified analysis by geographical regions in the FINRISK97 DNA panel.

SNP	Unstratified analysis P-value	Stratified analysis by region P-value
rs724016	4.3×10^{-8}	3.5×10^{-8}
rs2916448	0.41	0.40
rs1662845	0.93	0.96
rs1812175	0.00012	1.4×10^{-4}
rs1492820	0.035	0.035
rs1450822	FAILED	FAILED
rs10946808	4.9×10^{-5}	4.6×10^{-5}
rs314277	0.41	0.38
rs4896582	1.4×10^{-9}	1.2×10^{-9}
rs12540874	0.62	0.59
rs2040494	0.0050	0.0049
rs2730245	0.38	0.43
rs11786297	0.063	0.069
rs9650315	0.021	0.023
rs13249999	0.30	0.28
rs7869550	0.10	0.11
rs7466269	0.047	0.049
rs1042725	5.1×10^{-5}	7.4×10^{-5}
rs17104630	0.021	0.020
rs3783937	0.59	0.63
rs8007661	0.0015	0.0017
rs11858942	0.96	0.97
rs2562784	0.00055	3.4×10^{-4}
rs763014	0.96	0.92
rs26840	FAILED	FAILED
rs12449568	0.64	0.66
rs12958987	0.16	0.13
rs12986413	0.21	0.19
rs6116651	0.67	0.66
rs6060369	0.0014	0.0013

Supplementary Note

Membership of DGI

Diabetes Genetics Initiative of Broad Institute of Harvard and Massachusetts Institute of Technology, Lund University and Novartis Institutes for BioMedical Research

** NPB, PIWdB, VL, RS and BFV contributed equally to the original DGI scan and are listed alphabetically.*

Site 1 (Massachusetts General Hospital, Children's Hospital, Harvard Medical School, Broad Institute of Harvard and MIT)
*Noël P. Burtt[1,3], *Paul I.W. de Bakker[1,2,4,5,10], *Richa Saxena[1,3-5,10], *Benjamin F. Voight[1,4], Kristin Ardlie[1], Rachel Barry[2], Brendan Blumenstiel[2], Wendy Brodeur[2], Jody Camarata[2], Nancy Chia[2], Matthew DeFelice[2], Mary Fava[2], Jose C. Florez[1,3-5,9,11], Stacey B. Gabriel[2], Diane Gage[2], Casey Gates[2], John Gibbons[2], Lauren Gianniny[1], Candace Guiducci[1], Rachel Hackett[1], Bob Handsaker[2], Claire Healy[2], Sekar Kathiresan[1,3,7,8,11], Guillaume Lettre[1,3,13,14], Helen N. Lyon[1,3,12,14], Vamsi K. Mootha[3,4], Christopher Newton-Cheh[1,8], Marcia Nizzari[2], Kieu Nguyen[2], Melissa Parkin[2], Shaun Purcell[1,4], Carrie Sougnez[2], Elizabeth K. Speliotes[1,3,11], Aarti Surti[1], Ryan Tewhey[1], Joel N. Hirschhorn[1,3,10,12-14], Mark J. Daly[1,3,4,6,11], David Altshuler[1,3-6,9-11]

Site 2 (Lund University, University of Helsinki)
*Valeriya Lyssenko[15], Peter Almgren[15], Anna Berglund[15], Johan Holmkvist[15], Bo Isomaa[16,19], Esa Laurila[15], Olle Melander[15], Marju Orho-Melander[15], Peter Nilsson[15], Hemang Parikh[15], Marketa Sjögren[15], Malin Svensson[15], Margareta Svensson[15], Kristina Bengtsson[17], Ulf Lindblad[17], Marja-Riitta Taskinen[16], Tiinamaija Tuomi[18,19], Leif Groop[15,18]

Site 3 (Novartis Institutes for BioMedical Research)
Hong Chen[20], Gung-Wei Chirn[20], Qicheng Ma[20], Darrell Ricke[20], Delwood Richardson[20], Jeffrey J. Roix[20], Joanne Meyer[20], Thomas E. Hughes[20]

[1]Program in Medical and Population Genetics, [2]Genetic Analysis Platform, and [3]Metabolic Disease Initiative, Broad Institute of Harvard and Massachusetts Institute of Technology, Seven Cambridge Center, Cambridge, Massachusetts 02142, USA. [4] Center for Human Genetic Research, [5]Department of Molecular Biology and [6]Medicine, [7]Cardiovascular Disease Prevention Center, [8]Cardiology Division, and [9]Diabetes Unit, Massachusetts General Hospital, 185 Cambridge Street, CPZN-6818, Boston, Massachusetts 02114-2790, USA. [10] Department of Genetics, [11]Medicine and [12]Pediatrics, Harvard Medical School, Boston, Massachusetts, USA. [13] Division of Endocrinology and [14]Genetics, Children's Hospital, Boston, Massachusetts, USA. [15] Department of Clinical Sciences, Diabetes and Endocrinology Research Unit, University Hospital Malmö, Lund University, Malmö, Sweden. [16]Malmska Municipal Health Center and Hospital, Jakobstad, Finland. [17]Skaraborg Institute, Skövde, Sweden. [18]Department of Medicine, Helsinki University Hospital, University of Helsinki, Helsinki, Finland. [19]Folkhälsan Research Center, Helsinki, Finland. [20] Diabetes and Metabolism Disease Area, Novartis Institutes for BioMedical Research, 100 Technology Square, Cambridge, Massachusetts, USA.

Membership of FUSION

Finland United States Investigation of NIDDM Genetics

Anne U. Jackson[1], Cristen J. Willer[1], Lori L. Bonnycastle[2], Amy J. Swift[2], Heather M. Stringham[1], William L. Duren[1], Laura J. Scott[1], Michael R. Erdos[2], Parimal A. Deodhar[2], Kari A. Kubalanza[2], Mario A. Morken[2], Matthew G. Rees[2], Narisu Narisu[2], Peter S. Chines[2], Peggy P. White[1], Timo T. Valle[3], Thomas A. Buchanan[4], Richard M. Watanabe[5,6], Richard N. Bergman[6], Jaakko Tuomilehto[3,7,8], Francis S. Collins[2], Michael Boehnke[1], and Karen L. Mohlke[9]

[1]Department of Biostatistics and Center for Statistical Genetics, University of Michigan, Ann Arbor, Michigan
[2]Genome Technology Branch, National Human Genome Research Institute, Bethesda, Maryland
[3]Diabetes Unit, Department of Epidemiology and Health Promotion, National Public Health Institute, Helsinki, Finland
[4]Division of Endocrinology, Keck School of Medicine, University of Southern California, Los Angeles, California
[5]Department of Preventive Medicine, Keck School of Medicine, University of Southern California, Los Angeles, California
[6]Department of Physiology and Biophysics, Keck School of Medicine, University of Southern California, Los Angeles, California
[7]Department of Public Health, University of Helsinki, Helsinki, Finland
[8]South Ostrobothnia Central Hospital, Seinäjoki, Finland
[9]Department of Genetics, University of North Carolina, Chapel Hill, North Carolina

Membership of SardiNIA

Gene-finding and longitudinal study for age-associated conditions in a Sardinian population cohort.

Authors are listed by site, and within each site alphabetically, with the exception that within each site team leaders are listed at the front, and PI's are at the end.

Site 1 (Istituto di Neurogenetica e Neurofarmacologia, CNR, Monserrato, Italy)
Manuela Uda[1], Giuseppe Albai[1], Angelo Scuteri[1,2], Marcello Argiolas[1], Monica Balloi[1], Fabio Busonero[1], Anna Cau[1], M. Valeria Cerchi[1], Laura Crisponi[1], Marina D'aquila[1], Mariano Dei[1], Barbara Deiana[1], Manila Deiana[1], Liana Ferreli[1], Pietro Figus[1], Danilo Fois[1], Monica Lai[1], Sandra Lai[1], Francesco Loi[1], Paola Loi[1], Marco Masala[1,3], Andrea Maschio[1], Massimo Muggianu[1], Antonella Mulas[1], Silvia Naitza[1], Nazario Olla[1], Marco Orrú[1], M. Grazia Pilia[1], M. Grazia Piras[1], Natascia Sestu[1], M. Cristina Spada[1], Gianluca Usala[1], Antonio Cao[1]

Site 2 (National Institute of Aging, Baltimore, MD)
Nagaraja Ramaiah[4], Luigi Ferrucci[5], Edward Lakatta[4], Samer S. Najjar[4], James Strait[4], Kirill Tarasov[4], Alan B. Zonderman[4], David Schlessinger[4]

Site 3 (University of Michigan, Ann Arbor, MI)
Serena Sanna[1,6], Wei-Min Chen[6], Paul Scheet[6], Gonçalo R. Abecasis[6]

[1]Istituto di Neurogenetica e Neurofarmacologia (INN), Consiglio Nazionale delle Ricerche, c/o Cittadella Universitaria di Monserrato, Monserrato, Cagliari 09042, Italy
[2]Unitá Operativa Geriatria, Istituto per la Patologia Endocrina e Metabolica, Rome, Italy
[3]U.O. Semplice Cardiologia, Div. Medicina, P.O. S. Barabara, Iglesias, Italy;
[4]Gerontology Research Center, National Institute on Aging, 5600 Nathan Shock Drive, Baltimore, MD 21224, USA
[5]Clinical Research Branch, National Institute on Aging, Baltimore, Maryland, United States of America
[6]Center for Statistical Genetics, Department of Biostatistics, University of Michigan, Ann Arbor, MI 48109

Membership of KORA

Cooperative health research in the Region of Augsburg (KORA)

KORA study group consists of H.-Erich Wichmann[1,2] (speaker), Rolf Holle[3], Jürgen John[3], Thomas Illig[2], Christa Meisinger[1], Annette Peters[1], and their coworkers, who are responsible for the design and conduct of the KORA studies. The KORA S3/F3 500K study was conducted by Christian Gieger[1,2], Guido Fischer[1], Iris M. Heid[1,2],Susana Eyheramendy[1,2], Norman Klopp[1,2], Peter Lichtner[4], Gertrud Eckstein[4], Thomas Illig[2], H.-Erich Wichmann[1,2], and Thomas Meitinger[4,5]

[1]Institute of Epidemiology, GSF - National Research Center for Environment and Health, 85764 Neuherberg, Germany.[2]Chair of Epidemiology, IBE, University of Munich, 81377 Munich, Germany. [3]Institute of Health Economics and Health Care Management, GSF-National Research Centre for Environment and Health, 85764 Neuherberg, Germany. [4]Institute of Human Genetics, GSF National Research Center for Environment and Health, 85764 Neuherberg, Germany, [5]Institute of Human Genetics, Technical University, 81765 Munich, Germany

Membership of PLCO-CGEMS Prostate Cancer GWAS and Anthropometry Initiative

Sonja Berndt[1], Meredith Yeager[1,2], Kevin B. Jacobs[3], Sholom Wacholder[1], Kai Yu[1], Nilanjan Chatterjee[1], Robert Welch[1,2], Gerald L. Andriole[4], E. David Crawford[5], Margaret Tucker[1], Daniela S. Gerhard[6], Joseph F. Fraumeni, Jr.[1], Robert Hoover[1], David J. Hunter[1,7], Gilles Thomas[1], Stephen J Chanock[1,8], Richard B. Hayes[1]

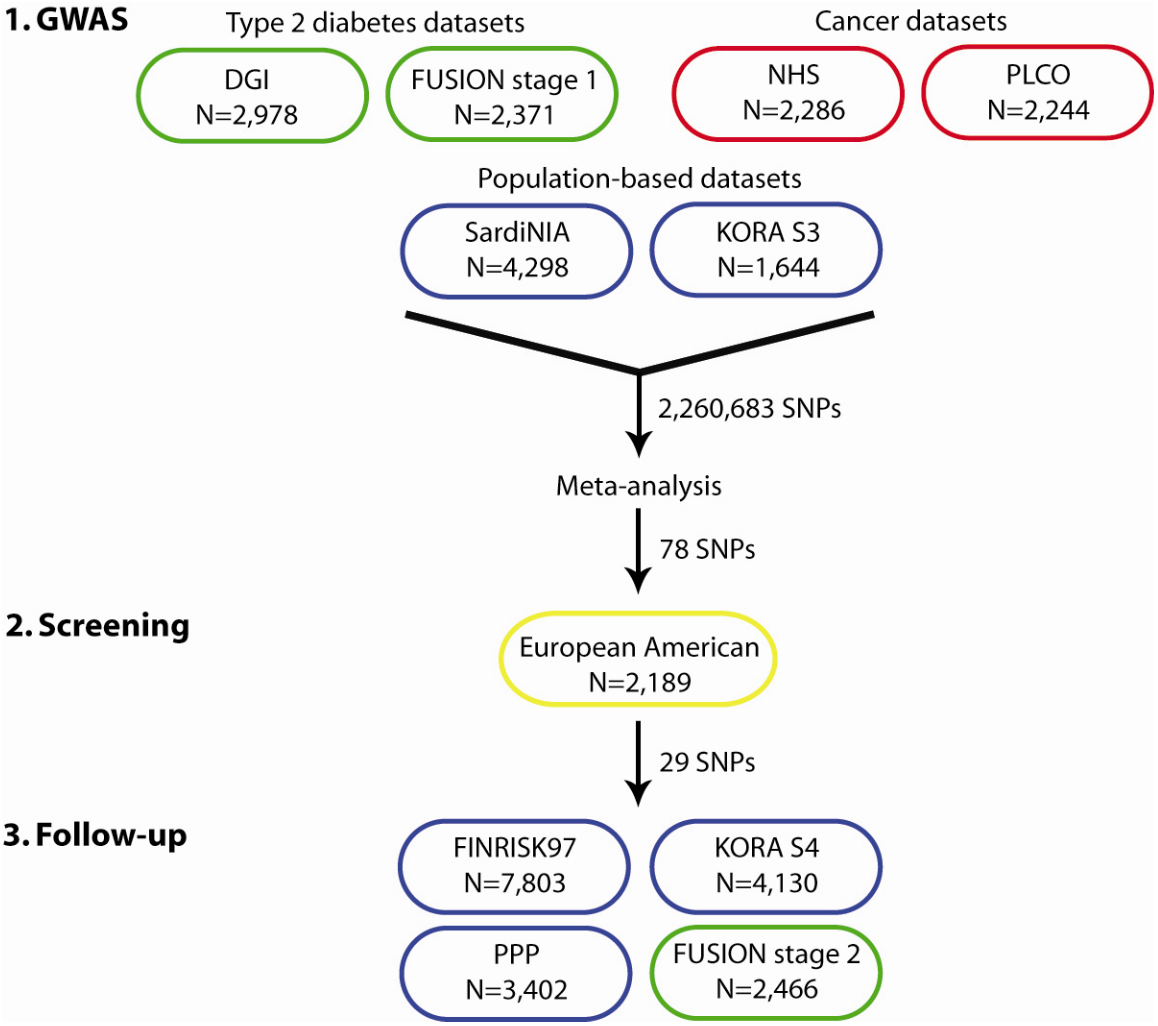
[1] Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health, Department of Health and Human Services
[2] SAIC-Frederick, NCI-FCRDC, Frederick, MD
[3] Bioinformed Consulting Services, Gaithersburg, MD
[4] Division of Urologic Surgery, Washington University School of Medicine, St. Louis, MO
[5] Department of Urologic Oncology, University of Colorado Health Sciences Center, Aurora, CO
[6] Office of Cancer Genomics, NCI, NIH, DHHS
[7] Program in Molecular and Genetic Epidemiology, Department of Epidemiology, Harvard School of Public Health, Boston, Massachusetts
[8] Pediatric Oncology Branch, Center for Cancer Research, NCI, NIH, DHHS

Supplementary Figure Legends

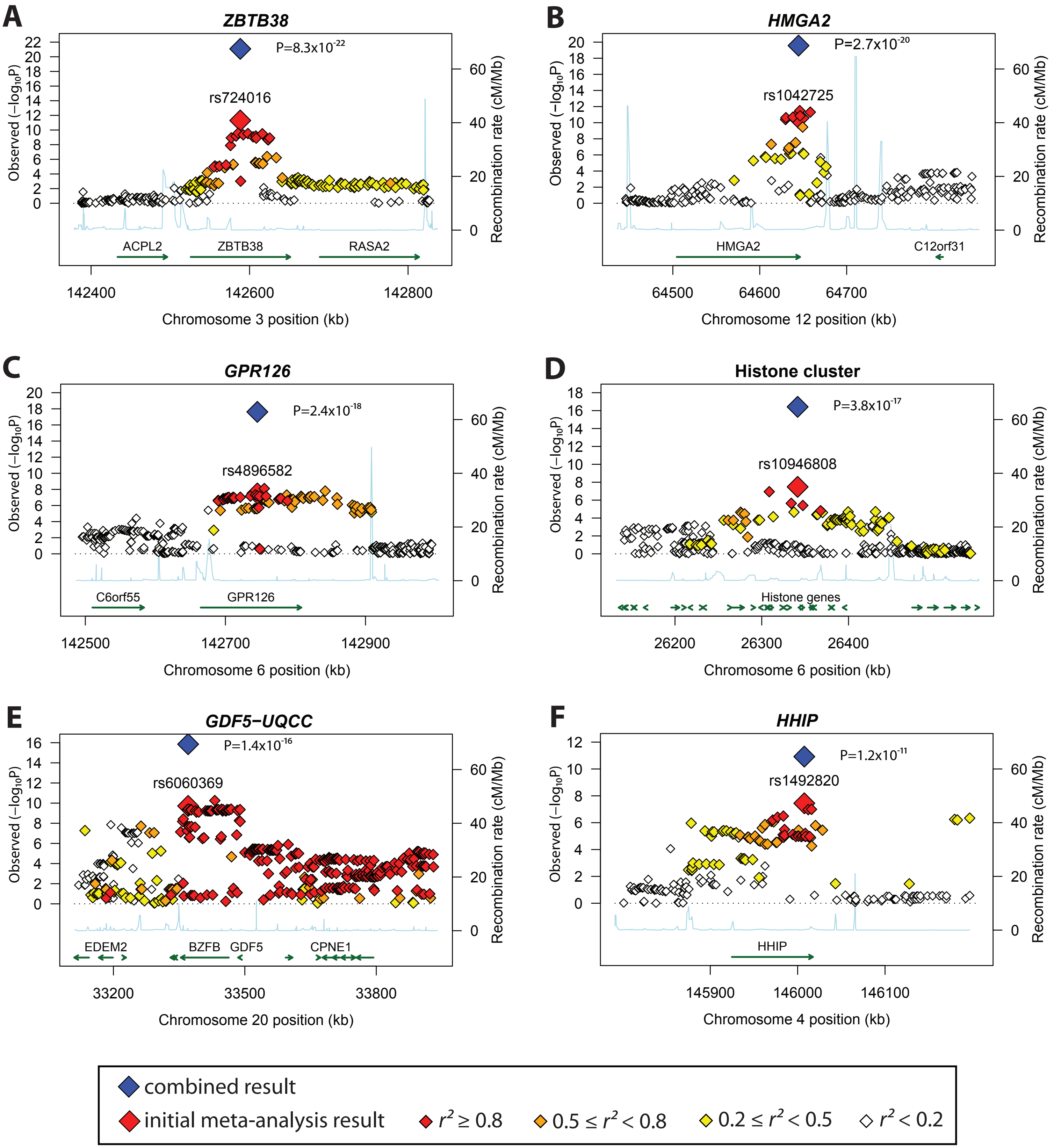
Supplementary Figure 1. Overall study design to identify and validate new height loci. Height association results from six GWA scans (N=15,821) were combined using a meta-analytic Z-score-based method. Top ranking SNPs were then genotyped in a European American tall-short (5th-10th and 90th-95th percentiles of the height distribution) screening panel (N=2,189). SNPs with odds ratio consistent with the direction of the effect observed in the meta-analysis were finally genotyped in large follow-up panels.

Supplementary Figure 2. Regional plots of 12 replicated associations to adult height. Genotyped or imputed SNPs are plotted with their meta-analytic P-values ($-\log_{10}$(P-value)) versus their genomic postion (NCBI build 35). In each panel, the SNP with the most significant association in the combined analysis is listed (blue diamond) and its initial P-value in the height meta-analysis (red diamond). Estimated recombination rates (taken from HapMap CEU) are plotted to reflect the local LD structure around the associated SNPs and their correlated proxies (red = $r^2 \geq 0.8$; orange = $0.5 \leq r^2 < 0.8$; yellow = $0.2 \leq r^2 < 0.5$). Gene annotations were taken from the UCSC genome browser.

- Supplementary Figure 1 -



Lettre et al., Supplementary Figure 2 (I)



Lettre et al., Supplementary Figure 2 (II)