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Methods Summary

The primary meta-analysis (Stage 1) included 46 GWA studies of 133,653 individuals. The *in-silico* follow up (Stage 2) included 15 studies of 50,074 individuals. All individuals were of European ancestry and >99.8% were adults. Details of genotyping, quality control, and imputation methods[1-3] of each study are given below and in **Supplementary Methods Table 1-2**. Each study provided summary results of a linear regression of age-adjusted, within-sex Z scores of height against the imputed SNPs, and an inverse-variance meta-analysis was performed in METAL (http://www.sph.umich.edu/csg/ abecasis/METAL/).

Validation of selected SNPs was performed through direct genotyping in an extreme height panel (N=3,190) using Sequenom iPLeX, and in 492 Stage 1 samples using the KASPar SNP System. Family-based testing was performed using QFAM, a linear regression-based approach that uses permutation to account for dependency between related individuals[4], and FBAT, which uses a linear combination of offspring genotypes and traits to determine the test statistic[5].

We used a previously described method[6] to estimate the amount of genetic variance explained by the nominally associated loci (using significance threshold increments from $P<5\times10^{-8}$ to $P<0.05$). To predict the number of height susceptibility loci, we took the height loci that reached a significance level of $P<5\text{x}10^{-8}$ in Stage 1 and estimated the number of height loci that are likely to exist based on the distribution of their effect sizes observed in Stage 2 and the power to detect their association in Stage 1 (see ref. 7). These analyses, as well as gene-by-gene interaction, dominant, recessive, conditional analyses, and pathway analyses are described in more detail below.

Empirical assessment of enrichment for coding SNPs used permutations of random sets of SNPs matched to the 180 height-associated SNPs on the number of nearby genes, gene proximity, and minor allele frequency. GRAIL text-mining and MAGENTA pathway-based methods have been described previously[8,9]. To assess possible enrichment for genes known to be mutated in severe growth defects, we identified such genes in the OMIM database (**Supplementary Table 10**), and evaluated the extent of their overlap with the 180 height-associated regions through comparisons with 1000 random sets of regions with similar gene content ($\pm$10%).

Supplementary Methods

1. Primary genome-wide association meta-analysis (Stage 1)

In Stage 1, we combined the height summary statistics from 46 genome-wide association (GWA) studies in a meta-analysis of 133,653 individuals (60,587 males and 73,066 females).

1.1 Description of individual cohorts and genotyping methods

Descriptive characteristics, study design, sample size, sample quality control (QC) and anthropometric measurement technique for the studies included in Stage 1 are provided in **Supplementary Methods Table 1.** All individuals were Caucasians of European ancestry. Approximately 45% of the individuals were male, and the ages ranged from 14 to 103 years (99.7% of the samples were $\geq$18 years old). All participants provided written informed consent and the studies were approved by the respective Local Research Ethics committees or Institutional Review Boards.

Details on the genotyping platform used and genotype quality control procedures employed for each study are presented in **Supplementary Methods Table 2**, while the basic anthropometric measures are summarised in **Supplementary Methods Table 3**.

1.2 Imputation

All cohorts were genotyped using commercially available Affymetrix (Affymetrix, Inc., Santa Clara, CA, USA), Illumina (Illumina, Inc., San Diego, CA, USA) genotyping arrays, or custom Perlegen (Perlegen Sciences, Inc., Mountain View, CA, USA) arrays. Quality control was performed independently for each study. To facilitate meta-analysis, each group performed genotype imputation using BIMBAM[1], IMPUTE[2], or MACH[3] and genotypes from the Phase II CEU HapMap[10]. Each imputation software estimates an overall imputation quality score for each SNP. For example, IMPUTE calculates the 'proper info' statistic which is a measure of the observed statistical information for the estimate of allele frequency of the SNP, while MACH calculates the 'rsq_hat', which is the estimated r^2 between each imputed genotype and its true underlying genotype. Study-specific details are presented in **Supplementary Methods Table 2**.

1.3 GWA analyses in individual cohorts

Details on study-specific analysis software are summarized in **Supplementary Methods Table 2.** Each GWA study tested association between each imputed or genotyped SNP and sex-standardized height, assuming an additive inheritance model and adjusting for age and other appropriate covariates specific to the study (e.g. genotype-based principal components). Studies with unrelated individuals tested association under a linear regression framework. Studies with related samples used variance component or other linear mixed effects modeling to account for relatedness in the regression. The uncertainty of the imputed genotypes was taken into account in the association analysis using methods appropriate for the imputation software used.

The genomic control (GC) inflation factor was calculated for each of the GWA scans separately. The average GC inflation factor was 1.03 (**Supplementary Methods Table 2**). Genomic control correction was applied to results for each study prior to meta-analysis by multiplying SNP standard errors by the square root of the inflation factor.

1.4 Quality control checks of individual studies

Where applicable, the Stage 1 studies calculated separate summary GWA data in males and females and disease cases and controls. Except for studies with related individuals, we used the sex-

specific summary results. Each file going into meta-analysis had the following information (columns): SNP, strand, N (sample size), effect allele (allele to which regression coefficient refers), other allele, EAF (effect allele frequency), imputation (posterior probability of imputed genotype, available from some programs), information type (imputation software used), information (imputation quality scores), *P*-value, beta (regression coefficient), standard error, and NxMAF (sample size multiplied by minor allele frequency). Each file was processed through a cleaning script that performed several quality checks, including calculating the number of markers, ranges of test statistics, the genomic correction inflation factor, and NxMAF. From each study we excluded monomorphic SNPs and SNPs with poor imputation quality: rsq_hat < 0.3 (BIMBAM and MACH) or proper info < 0.4 (IMPUTE).

1.5 Meta-analysis of GWA studies

A total of 2,836,010 autosomal SNPs were meta-analyzed across 98 input files (many of the 46 cohorts had separate male-female and/or case-control files). We did not apply a minor allele frequency cut-off, but we did apply an arbitrary cut-off of NxMAF > 3 (equivalent to a minor allele count of 6) to guard against extremely rare variants present in only one or two samples (possible genotyping/imputation errors or private mutations), for which regression coefficients are not estimated well using the standard statistical methods employed in most GWA statistical programs.
We used the inverse-variance fixed effects meta-analysis method to combine the results from the individual studies. For comparison purposes, we also performed a sample size weighted *Z*-score-based fixed effects meta-analysis. The correlation coefficient between the $\log_{10}$ of the *P*-values of the inverse variance and sample size weighted meta-analysis was 0.99. SNP selection for follow-up was based on the meta-analysis of the inverse variance meta-analysis results. Meta-analyses were performed using the software program METAL (www.sph.umich.edu/csg/abecasis/metal).

1.6 Overall genomic control correction

After genomic control applied in each study the overall genomic control inflation factor (λ_{GC}) for the meta-analysis was 1.42. The possibility that such high inflation is due to effects of population stratification or genotyping biases alone is unlikely, considering the different results presented in Supplementary section 4 which argue against this. In an attempt to identify other sources for such inflation, we removed all SNPs within 1Mb from the leading SNP in loci with SNPs reaching $P<5\times10^{-8}$, which yielded a similarly high λ_{GC}=1.33. Next, in a simulated phenotype dataset we evaluated the potential role of multiple causal variants failing to reach genome-wide significance. Using a model comprising 120,000 subjects, 294,831 SNPs, and 1000 causal variants, the λ_{GC} increased in a near linear way from 1.15 to 1.32, as heritability (h^2) increased from 0.2 to 0.8. Alternatively, increasing the number of causal variants from 100 to 4000 while keeping heritability constant (at 0.52) increased the λ_{GC} from 1.1 to 1.6 (see ref. 11). The latter observed data are consistent with a model containing many causal variants that are in LD with multiple SNPs resulting in inflated test statistics. Although our data imply that a second GC correction on the meta-analysis statistics may be overly conservative, we decided to apply anyway a second genomic control correction to the meta-analysis standard errors and P-values.

1.7 Selection of SNPs for subsequent analyses

SNP selection criteria for validation by genotyping, *in silico* replication, and all additional analyses and simulations, based on the results of Stage 1 GWA meta-analysis, are described below.

2. *In silico* follow-up (Stage 2)

2.1 SNP selection

We took forward for replication 309 SNPs. These included the 207 index SNPs representing each of the 207 2Mb loci reaching $P<5x10^{-6}$ in Stage 1 and 102 SNPs that lie within the same 2Mb windows as the 207, but which were poorly correlated ($r^2<0.05$) with the index SNP in CEU HapMap II samples. No minimum sample size was used for SNPs taken forward for replication, although we note that the minimum N for the 207 variants taken forward from Stage 1 to Stage 2 was 78,550 (for SNP rs11714558 that reached Stage 1+2 *P*-value of $1.7x10^{-10}$). Subsequent analyses are based on the index SNPs from the 207 loci and the 19 SNPs within the 2 Mb windows that were confirmed to be independent by the conditional analysis described below.

2.2 Description of Stage 2 populations

Our *in silico* replication (Stage 2) included 50,074 individuals (12,651 males, 37,423 females) from 15 additional GWA studies. Approximately 26% of the subjects were male (one large study was entirely female), and ages ranged from 17 to 113 years (all but 5 individuals were $\geq$18 years old). Brief study descriptions, details on sample quality control, genotyping and imputation methods, and descriptive statistics, are provided in **Supplementary Methods Tables 1-3**.

2.3 Quality control checks of individual studies in Stage 2

The Stage 2 studies provided the same summary GWA statistics as Stage 1 studies, but only for the requested 309 SNPs. In addition to the QC checks performed in the stage 1 studies (section 1.4 above), we checked the direction of effects for the 309 SNPs in replication studies compared to the overall effects in the Stage 1 meta-analysis. In only one of the cohorts (Sorbs), fewer than 50% of the SNPs had effects in the same direction (47% for males, N=371; 50% for females, N=536). As expected, the largest study showed greatest consistency with the stage 1 meta-analysis results: 98% of SNPs in the same direction in the WGHS, N=32,099). We meta-analyzed these studies in METAL assuming a fixed effects model. When we examined the heterogeneity between Stage 2 studies, only one SNP (rs7567288) had a heterogeneity *P*-value smaller that that expected by chance (P_{het} = $5.6x10^{-6}$) (see **Supplementary Table 1**).

3. Meta-analysis of Stage 1 and Stage 2

The overall meta-analysis combined Stage 1 and Stage 2 results for the 309 SNPs using a fixed effects model. No SNP showed evidence of heterogeneity between Stage 1 and Stage 2 after accounting for the number of tests performed, and only a single SNP had the opposite direction of effect in Stage 2 compared to Stage 1. We report results of fixed-effect meta-analyses only, considering that low evidence of heterogeneity was observed across the 180 SNPs that reached overall genome-wide significance (no SNPs with $I^2>50$ and there were only 8 with $I^2>25$).

3.1 Age and sex-specific analyses of associated signals

We also performed sex-specific analyses of the associated signals and observed no differences between their effects in males compared to females (**Supplementary Table 1**). Because of the wide age range in our GWA studies (**Supplementary Methods Table 3**), we performed a sensitivity analysis by splitting the Stage 1 samples into two approximately equally sized groups around the overall mean age. There was no evidence that any of the 180 effect sizes for the index SNPs were stronger in either the younger half or older half of studies – 84 SNPs were stronger in the younger half and 91 stronger in the older half (*P*=0.65).

4. Validation by genotyping and population stratification analyses

4.1 Imputation validation

To validate genotype imputation, we directly genotyped 27 height associated SNPs from the 207 loci in 492 subjects from the WTCCC-T2D study. These 27 SNPs were tested because they were not present on any of the most commonly used arrays (used by >2 studies) and did not have any perfect directly-typed proxies (HapMap r^2=1). We also genotyped a random subset of 18 additional height associated SNPs from these 207 loci in the same samples. Genotyping was performed by Kbioscience (Herts, UK) using a KASPar-based singleplex assay (details of which are available on their website www.kbioscience.co.uk/chemistry/chemistry_Kasp_intro.htm). Forty-three SNPs passed genotyping quality control (HWE P>0.01; genotype success rate > 0.9; duplicate error rate <0.5%). We assessed imputation quality by determining the correlation between the directly ascertained genotypes and the genotype dosages produced by IMPUTE (the imputation program used in WTCCC-T2D). We then compared the observed R^2 to the proper_info statistic produced by IMPUTE (which is essentially a predicted R^2 between imputed genotype and actual genotype). The correlation between the predicted and the observed R^2 was high for both the random set of SNPs (r=0.92) and for SNPs that were not well captured (r=0.84). This suggests that imputation uncertainty has been appropriately accounted for in our analyses.

4.2 Direct genotyping in subjects from tails of height distribution

For additional validation, we genotyped randomly chosen SNPs representing 33 of the 207 associated loci in an independent samples of 2,181 European-American and 1,009 Polish subjects from the tails of the height distribution (5-10th and 90-95th percentile). These height case-control samples and the genotyping methods have been described previously[12]. For both panels, all individuals were self-described "white" or "Caucasian." For the US panel, all subjects were born in the US, and all of their grandparents were born in either the US or Europe. All subjects in the Polish panel were born in Poland, and all grandparents were born in Europe or Russia. All subjects gave informed consent, and approval was obtained from the Institutional Review Board of Children's Hospital, Boston. Statistical analysis was performed using a Cochran-Mantel-Haenszel test, as implemented in PLINK[4]. The data set was stratified according to the country of origin of the grandparents to account for population stratification within the European American height panel[12].

Power to replicate the direction of effect of the top 180 height SNPs in the extreme height panel was calculated using the Genetic Power Calculator (http://pngu.mgh.harvard.edu/~purcell/gpc/) based on the following assumptions: a sample size of 3,190 equally divided between individuals in the lower tail (5th-10th percentile) and the upper tail (90th-95th percentile) of the height distribution, variance explained between 0.005-0.3% of the height variation (consistent with our effect size estimates of Stage 2 data, using the equation from quantitative genetics $\sigma^2_g = 2*p*q*\alpha^2$, where σ^2_g is the additive genetic variance, p and q are the allele frequencies, and α is the effect size in SD units), and 3 different minor allele frequencies. Under these assumptions, power is minimally affected by minor allele frequency.

Variance explained	MAF=5%	MAF=25%	MAF=50%
0.005%	56%	56%	56%
0.01%	62%	62%	62%
0.05%	88%	88%	88%
0.1%	97%	97%	97%
0.2%	>99%	>99%	>99%
0.3%	>99%	>99%	>99%

4.3 Family-based association analyses

The family-based analysis performed to assess the influence of population stratification as a potential source of false positive associations in the discovered 180 loci, comprised the Framingham Heart (FramHS) and the Erasmus Rucphen Family-based (ERF) studies. The design of the studies has been described elsewhere[13,14]. The family-based analyses was performed in FramHS (n=5,510) using the QFAM --within procedure from PLINK[6], running 100,000 permutations to account for the dependence between related individuals. Effect sizes and directions in FramHS were the betas reported by PLINK from the within component but p values were empirical, based on the permutation testing. The extended pedigree of ERF was broken into nuclear families (totaling 1,826 individuals) and analyzed with FBAT[5] which uses a linear combination of offspring genotypes and traits to determine the test statistic. For imputed SNPs, only those with MACH rsq_hat>0.3 were analyzed, using the best guess genotypes from dosages (for FramHS, directly genotyped proxies were also analyzed for comparison and gave similar results). *P*-values were meta-analyzed using a weighted Z-score–based meta-analysis implemented in METAL; if data were only available from one study, the *P*-value from that study was used. Weights were defined based on effective sample size (actual sample size/lambda, where lambda is the genomic control inflation factor calculated from the GWA data of the family-based samples when ignoring relatedness). The direction of the effect allele in the FHS/ERF meta-analysis was compared to that observed in the GIANT meta-analysis using an exact sign-test statistic based on a binomial distribution. The average estimated effect sizes were essentially identical in the GIANT meta-analysis and the FramHS family-based sample (**Supplementary Table 3**), suggesting that there is minimal if any inflation of the GIANT effect sizes due to stratification.

4.4 Other population stratification analyses

We checked if the 180 height-associated variants included ancestry informative marker (AIM) SNPs previously identified as highly informative of the sub-structure in European populations. We tested the correlations between height loci and 683 AIMs from 3 different sources[15,16,17]. These included AIMs from both the HLA and lactase loci. The largest HapMap CEU r^2 correlations between height SNPs and AIMs were observed for the *GDF5* and *EFEMP1* variants (r^2 = 0.3 and 0.35, respectively). All other pairwise correlations, including those at the HLA locus, had r^2<0.2.

We also assessed the absolute values of EIGENSTRAT[18] loading scores along the principal component of ancestry that corresponds roughly to the North-South intra-European axis that is correlated with height[6] (absolute values of loading scores are a measure of allele frequency differentiation along this axis). The absolute values of loading scores for the height-associated SNPs was not significantly greater than those of 1,000 sets of allele frequency matched SNPs (*P*=0.08). We also compared F_{st} values (a measure of the proportion of genetic diversity due to differences among populations) for the 180 SNPs with sets of matched SNPs and the F_{st} values of the height-associated SNPs were not different when calculated by cohort, although they were nominally significantly higher (*P*=0.04) when grouped by country. Together with the family-based analysis, these results strongly suggest that the observed associations with height are unlikely to be appreciably affected by population stratification.

5. Percentage variation explained and number of loci

5.1 Estimation of variance explained and polygene analysis

We used a method recently proposed by the International Schizophrenia Consortium[6] to evaluate the amount of phenotypic variance explained by our associated loci in an independent validation set including the Fingesture (Finland), RS-II & RS-III (Netherlands), GOOD (Sweden) and QIMR (Australia or UK origin) studies. To avoid the influence of potential cryptic relatedness between discovery and validation set, a “leave one out” analysis was performed, namely excluding in the

discovery set in turn, all studies from one of the four European countries of the validation set (Finland, Netherlands, Sweden and UK).

The method followed three steps: 1) selection of markers to build a prediction model, 2) scoring each individual based on model and 3) estimation of variation explained using the scores as predictor.

First, we re-ran the meta-analysis using the "leave one out" approach and selected the SNPs that were genotyped in each validation study. For each of these four meta-analysis, a list of independent SNPs associated with height at various *P*-value thresholds (from $P<5\times10^{-8}$ to $P<0.05$) was computed (using the clumping procedure implemented in PLINK, with an LD-based threshold of $r^2\geq0.05$, and a physical distance of 1 Mb from the top hit).

Second, using the selected SNPs from the revised meta-analyses described above, we performed profile scoring for each individual of the five validation studies as implemented in PLINK, where:

$$Score_i=\sum_{j=1 \text{ to } m} b_j x_{ij}\text{, where}$$

m= number of SNPs

b_j =effect of allele at locus *j*

x_{ij}=number of reference alleles of individual *i* at locus *j*

Third, the measure of variance explained (adjusted R^2) is estimated from a linear regression model incorporating the score as the predictor and the age-adjusted standardized height residuals as outcome.

This approach was applied for the estimation of variance explained by the 43 previously published loci, the discovered 180 genome-wide significant loci and the polygene results incorporating different sets of markers at different significance thresholds.

5.2 Prediction of number of susceptibility loci

We utilized a new method by Park et *al.*[7] to estimate the number of susceptibility loci that are likely to exist based on the distribution of effect sizes observed for established height loci and the power to detect those effects in the original scan. To be conservative and obtain unbiased estimates of the effect sizes, we only utilized the loci that reach a significance threshold of $P<5\text{x}10^{-8}$ in the Stage 1 meta-analysis and were replicated in Stage 2. The Stage 2 replication data was used to estimate the effect sizes for these loci. Power was calculated based on the sample size for Stage 1 accounting for the number of SNPs that could be identified with the particular effect size. Only SNPs that had a power of at least 1% were used in the predication. One outlying SNP was removed from analysis due to a very small effect size. The phenotypic variance explained was estimated by summing the product of each effect size and the number of loci predicted with that particular effect size. The genetic variance explained was estimated assuming heredity accounts for 80% of the variance in height. A parametric bootstrap method was used to obtain an estimate of the variability of the estimated number of loci.

6. Gene by gene (GxG) interaction, dominant and recessive analyses

6.1 Associated loci analyses

To perform the GxG, dominant and recessive analyses for just the associated loci, each individual study extracted genotype imputation dosages for each of the 207 lead SNPs from the Stage 1 meta-analysis (based on 2Mb distance pruning; $P<5\text{x}10^{-6}$). These dosages were also used for the conditional analysis described below.

An R-script (available on request) was provided to each individual study and was run using the extracted dosages. The allele coding was such that the height increasing allele (based on the Stage 1 meta-analysis) was always the dosage increasing allele (*i.e.* the height increasing allele was coded as allele 2). For the additive dosage and pairwise interaction (Y=b0+b1.A+b2.B+b3.AB+e; Test of b3 = 0) analyses, the dosages were then regressed against residuals of sex-standardized Z-score height,

adjusted for age and appropriate covariates (e.g. principal components), as with the primary GWA study, under the appropriate models. For the additive best-guess (performed for quality control purposes), recessive, dominant and dominance deviation analyses "best guess" genotypes were assigned based on genotype dosage, and these genotypes were similarly regressed against Z-score height under the appropriate model.

We meta-analysed individual study results using METAL. We performed meta-analyses for the additive, dominant, recessive, dominant deviation and pairwise interaction terms. We excluded SNPs from individual studies where NxMAF < 10 and/or imputation quality was < 0.4. We also re-ran the meta-analyses excluding SNPs with a NxMAF < 30 and imputation quality < 0.9, because deviation from additivity is harder to detect if the genotype has not been accurately imputed. The results were essentially the same. As an additional quality check we compared the additive dosage and additive best guess results from this meta-analysis to that from obtained from the primary Stage 1 meta-analysis files, and the correlation were very high (r>0.99). Results for the single SNP models, and the top results from the GxG interaction analysis are presented in **Supplementary Table 5 and 6.**

6.2 Genome-wide joint effect analysis

For the genome-wide analysis we used 10,618 individuals from four WTCCC studies (T2D, CAD, HT, NBS) and the EPIC-obesity study where we had access to individual level genotype data and study and sex-standardised, age-adjusted height Z-scores. All the studies were genotyped using the Affymetrix 500K platform (Affymetrix, Inc., Santa Clara, CA, USA). After quality control (including genotype success rate >95%; MAF>1% and HWE P>0.0001), 343,249 autosomal SNPs were used in the analysis.

As a genome-wide pairwise interaction analysis was not computationally feasible we performed two separate analyses. First, we performed a pairwise analysis of all SNPs with individual SNP P<0.01 with each other (Y=b0+b1.A+b2.B+b3.AB+e; Test of b3 = 0). Second, we performed a genome-wide pairwise analysis testing the full model (an 8 d.f. model). SNP pairs generated here will include those driven by main effects as well as interaction. Therefore, we removed the 9 strongest single SNPs which accounted for a large fraction of the associated pairs, and assessed additive by additive interaction of the remaining pairs with a joint effects $P<1x10^{-8}$ using PLINK. A total of 371 pairs of SNPs with an additive by additive interaction $P<1x10^{-5}$ were taken forward into replication in 16,100 samples from 4 cohorts, 3 of which (Rotterdam, CoLaus, DGI) were genotyped on the Affymetrix 500K platform (Affymetrix, Inc., Santa Clara, CA, USA). The fourth replication study, CGEMS, was genotyped on the Illumina platform (Illumina, Inc., San Diego, CA, USA), and where a SNP was not available an r^2 > 0.8 proxy was used. Of the 371 SNP pairs that were taken forward into replication, none showed strong evidence of replication (top $P_{Replication}$ = 0.01; top $P_{Overall}$ = $1x10^{-6}$; N~26,000).

7. Conditional analyses

To perform the conditional analysis, individual Stage 1 studies repeated their genome-wide analysis, this time including a set of 225 imputation dosages as covariates (those from the 180 SNPs representing the novel loci, plus 27 SNPs from the remaining loci reaching $P<5x10^{-6}$ in Stage 1 and an additional 18 SNPs with $P<8x10^{-6}$). For quality control purposes, the files obtained from each of the individual studies were put through the same checks as for the Stage 1 analysis (described in section 1.4). Additional checks were performed to ensure that each of the 225 conditioned SNPs was no longer associated with height (all P>0.2) and that SNPs outside the 225 conditioned loci had similar P-values and effect sizes to the primary Stage 1 analysis. After these quality checks, nearly 80% of the Stage 1 samples ereailable for the meta-analysis, which was performed in the same way as the primary Stage 1 meta-analysis (including a NxMAF>3 cut-off and double GC correction).

8. Functional variant analyses

8.1 eQTL analysis

We examined the association between the 180 height associated SNPs and expression of nearby genes in two different tissues: lymphocyte and osteoblast.

8.1.1 Lymphocyte eQTL analysis

As described previously[19], peripheral blood lymphocytes were transformed into lymphoblastoid cell lines for 206 families of European descent, totaling 830 parents and offspring. Using extracted RNA, gene expression was assessed with the Affymetrix HG-U133 Plus 2.0 chip. Genotyping was conducted using the Illumina Human1M Beadchip and Illumina HumanHap300K Beadchip, and imputation performed using data from Phase II HapMap CEU population. SNPs were tested for *cis* associations (defined as genes within 1 Mb) and trans associations, adjusting for non-genetic effects in the gene expression value. Only cis associations that reached a $P<6.8\text{x}10^{-5}$ (or FDR 1%) are included in the **Supplementary Table 7**. The p-value cutoff corresponding to a 1% FDR was estimated by permuting the data while maintaining the correlation of gene expression among family members, the linkage disequilibrium structure among SNPs, and correlation of expression between different genes, and comparing the distribution of p-values for all SNP-probe pairs within 1Mb. A total of 47 out of 180 height SNPs were associated with cis-eQTLs compared to 20 expected by chance assuming a FDR of 1%.

8.1.2 Osteoblast eQTL analysis

Human primary osteoblasts (N=104) derived from Swedish unrelated donors were cultured under four different conditions (PBS control; dexamethasone; BMP2 treated; PGE2 treated). Global gene expression was measured using the Illumina HumanRef-8 vs.2 Expression BeadChip. Expression profiles for each treatment were performed in biological replicates (independently derived primary lines) and averaged. Genotyping was performed using the Illumina HumanHap550K platform and imputation carried out using MACH based on HapMap CEU population. The height SNPs were tested for cis associations (±100 kb flanking the gene) as well as trans associations using MACH2QTL.

Allelic expression association mapping was carried out using a novel method, which allows measurement of cis-regulatory variation in genome-wide manner with minimal impact from trans-acting or environmental effects and consequently detects 5-10-fold more functional variation in local control of gene expression as compared to similarly sized eQTL studies[20]. The allelic expression mapping dataset used in this comparison are from CEU HapMap lymphoblastoid cell lines. Only cis associations that reached a $P<4.0\text{x}10^{-4}$ (or FDR 5%) are included in the **Supplementary Table 7**.

8.1.3 Liver, omentum, and subcutaneous fat eQTL analysis

The liver tissue was taken from 567 Caucasian patients post mortem or undergoing bariatric surgery at the Massachusetts General Hospital (Boston, MA) as described previously[21]. Subcutaneous fat was acquired from 610 of these patients and omental tissue from 742 of these patients. RNA was isolated from the tissues and gene expression was measured using a custom Agilent 44,000 microarray composed of 39,280 oligonucleotide probes. DNA was also extracted and genotyping was conducted using the Illumina 650K platforms followed by imputation of the common SNPs in the Phase II HapMap CEU population. Each SNP was tested for *cis* associations with genes within 1Mb using linear regression adjusting for age, race, gender, and surgery year. Trans eQTLs were also tested. Only cis associations that reached a $P<6.0\text{x}10^{-6}$ (or FDR 5%) are included in the **Supplementary Table 7**.

8.2 Non-synonymous enrichment analysis

For all 180 height SNPs, we retrieved all proxy SNPs in linkage disequilibrium (r^2≥0.8 in HapMap phase II CEU) and annotated them according to whether they were missense, nonsense or neither (**Supplementary Table 8**). Annotation was based on the NCBI build 36.1. In total for the 180 height SNPs, we identified 2,550 proxies, including 0 nonsense and 31 missense SNPs. We repeated this analysis using 1,000 sets of 180 SNPs that were matched based on allele frequency (± 2.0%), nearby number of genes (± 10% of seed SNP count), and gene proximity (± 20kb). Among these sets, the ranges for the number of proxies, nonsense SNPs, and missense SNPs were, respectively, 2566-4640, 0-1, and 8-49. After accounting for the number of proxy SNPs in each set, there were only four sets with a ratio (number of nonsynonymous SNPs / total number of proxies) equal or above the ratio observed for the 180 height SNPs (ratio: 0.0122, range of ratios observed in matched sets: 0.0024-0.0133). Similar results were obtained using a logistic regression framework, where control SNPs were matched only on allele frequency but the other matching parameters were used as covariates; here the "exposure" is being a height-associated SNP and the "outcome" is having a missense SNP as a proxy.

8.3 Association with other traits

We downloaded from the NHGRI GWA study catalogue (http://www.genome.gov/26525384; accessed on 12th February 2010) all SNPs associated with diseases and traits other than height at genome-wide significance level of $P<5\times10^{-8}$. We then identified all SNPs that mapped within 1Mb of at least one height SNP and had some correlation (HapMap CEU $r^2>0.1$) with the index height SNP for each of the 180 associated loci. There were 22 such overlapping loci, some associated with multiple other traits and diseases (**Supplementary Table 9**). At 6 of the loci the height and 'other' trait SNP were either identical or strongly correlated ($r^2>0.8$). For one of these loci, *LIN28B,* the height effect may be secondary to the large effect on pubertal timing, but the remaining five are likely to represent true pleiotropic effects.

9. Biological enrichment analyses

9.1 OMIM analysis

We searched the Online Mendelian Inheritance in Man (OMIM) database and identified 241 genes that underlie human syndromes characterized by abnormal skeletal growth (**Supplementary Table 10**). The gene list was initially obtained using search keywords 'short stature', 'overgrowth', 'skeletal dysplasia', and 'brachydactyly', and was manually curated blindly to our results. We then grouped the 180 height-associated SNPs into 175 non-overlapping gene regions (to avoid double counting), containing a total of 652 genes. For each region, we set the genomic boundaries using linkage disequilibrium cutoffs (r^2≤0.3 from the index height SNP) and then next recombination hotspots. Although these 175 regions contained only ~3.3% of all human genes, they included 21 genes from the curated OMIM height gene list (8.7%). We assessed the significance of this result by permutation: we generated 1,000 sets of 175 regions with similar gene content (±10%) and counted, in each set, the number of OMIM height genes within the regions. In these 1,000 permutations, the median number of OMIM height genes was 8 and the range was 1-19 (empirical *P*-value for an overlap of 21 OMIM genes is $P<0.001$).

9.2 Text-mining using GRAIL

The GRAIL algorithm was recently described[8]. As in the OMIM analysis, we used LD and recombination hotspots to define boundaries on the left and right of each height index SNP. This identified 652 genes in 175 regions (five regions were overlapping when using our criteria to define genomic interval around height index SNP).

9.3 Pathway analysis

We applied an adaptation of the gene set enrichment analysis (GSEA) framework (Meta-Analysis Gene-set Enrichment of variaNT Associations, MAGENTA[9]) to the height meta-analysis to determine whether the 180 height SNPs cluster near genes that belong to specific biological pathways and potentially to discover new pathways that may be enriched for modest height associations not yet identified. Specifically, for each gene in the genome we calculated a corrected gene association *P*-value based on the most significant SNP height association *P*-value of all SNPs in the gene region (110 kb upstream and 40 kb downstream to gene's most extreme transcript start and end sites, respectively), accounting for confounding effects such as gene size, number of SNPs per gene and linkage-related properties. Genes were grouped into pathways using annotations from the KEGG, PANTHER, INGENUITY and Gene Ontology databases. KEGG, PANTHER and INGENUITY pathways were downloaded from the Molecular Signatures Database (MsigDB, http://www.broad.mit.edu/gsea/msigdb/collections.jsp), PANTHER molecular function gene-sets were downloaded from the PANTHER website (http://www.pantherdb.org/), and Gene Ontology biological process and molecular function categories were downloaded from the Gene Ontology website (http://cvsweb.geneontology.org/).

For each gene set, enrichment of highly ranked gene scores above the 95th percentile of all gene scores in the height meta-analysis was evaluated compared to 10,000 randomly sampled gene sets of identical size from the genome. A false discovery rate (FDR) was also calculated for each gene set *gs*, as the fraction of all randomized gene sets generated across all GSEA tests (10,000 permutations times the total number of real gene sets tested) whose 'leading edge fraction' was equal to or more significant than that of the given gene set *gs*, divided by the fraction of real gene sets tested whose leading edge fraction was equal to or more significant than that of gene set *gs*. The 'leading edge fraction' is defined here as the fraction of genes in a given gene set whose gene *p*-values exceed the 95th percentile of all gene *p*-values in the height meta-analysis, normalized, as follows, to account for differences in gene set size across the real and permuted gene sets: the mean leading edge fraction of all randomized gene sets of identical size to gene set *gs* was subtracted from the leading edge fraction of gene set *gs*, and the resulting value was divided by the standard deviation of the leading edge fractions of all randomized genes sets of identical size to gene set *gs*. FDR was calculated for each database separately. In cases where the estimated FDR was larger than 1, FDR was set to 1. This may occasionally occur for gene sets at the tails of the GSEA *p*-value distribution, partly due to the fact that gene sets in a given database are not completely independent.

Results from this analysis show strong enrichment for genes that belong to the hedgehog signaling pathway (nominal GSEA *P*=0.0009, FDR=0.078) the histone molecular function category (nominal GSEA *P*=0.0001, FDR=0.0028), and growth and development-related gene-sets (nominal GSEA *P*=0.0001-0.002, FDR=0.07-0.17), many of which are near the top GIANT height SNPs. In total, there were 17 pathways, including the TGF-beta pathway, 14 molecular functions and 98 Gene Ontology categories, such as anatomical structure morphogenesis, heart morphogenesis, insulin receptor substrate binding, and mammary gland development, that were nominally significant (*P*=0.05) in our GSEA using MAGENTA (**Supplementary Table 12**)

10. URLs

Bayesian Imputation Based Association Mapping, BIMBAM, http://quartus.uchicago.edu/~yguan/bimbam/index.html; population stratification detection software, EIGENSTRAT, http://genepath.med.harvard.edu/~reich/EIGENSTRAT.htm; genotype imputation program, IMPUTE, http://www.stats.ox.ac.uk/~marchini/software/gwas/impute.html; Markov chain haplotyping package, MACH, http://www.sph.umich.edu/csg/abecasis/MACH; MACH2QTL, http://www.sph.umich.edu/csg/abecasis/MACH/download; pedigree analysis package, MERLIN, http://www.sph.umich.edu/csg/abecasis/Merlin; meta-analysis tool for GWASs, METAL, http://www.sph.umich.edu/csg/abecasis/Metal/index.html; whole-genome association analysis

package, PLINK, http://pngu.mgh.harvard.edu/~purcell/plink; whole-genome association analysis of imputed data, ProbABEL, http://mga.bionet.nsc.ru/~yurii/ABEL; statistical computer software, R, http://www.r-project.org; whole-genome association analysis package, SNPTEST, http://www.stats.ox.ac.uk/~marchini/software/gwas/snptest.html.

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Supplementary Tables

Supplementary Table 1. Association results for Stage 1 (discovery GWAS), Stage 2 (in-silico replication), Stage 1+2 combined, and Stage 1+2 sex-specific meta-analyses, for the 180 independent signals that reached genome-wide significance (P<5x10^{-8}) in the combined Stage 1+2 analysis. I^2 represents the % heterogeneity of effect size between Stage 1 studies. P_{het} is the heterogeneity P-value.

						STAGE 1 up to 133,653 samples				STAGE 2 up to 50,074 samples		STAGE 1 + STAGE 2 up to 183,727 samples		STAGE 1 + STAGE 2 SEX-SPECIFIC up to 73,238 males and 110,489 females				
SNP [a]	Chr	Position (bp)	Nearest/OMIM height gene [b]	Effect / other allele [c]	Frequency (effect allele)	Beta	*P*-value [d]	I^2	P_{het}	Beta	P-value [d]	Beta	*P*-value [d]	Beta (Males)	*P*-value [d] (Males)	Beta (Females)	*P*-value [d] (Females)	P_{het} (MvsF
rs425277	1	2059032	***PRKCZ***	T/C	0.28	0.024	1.70E-06	0	0.73	0.019	3.10E-03	0.022	2.10E-08	0.017	5.90E-03	0.027	6.70E-08	0.15
rs2284746	1	17179262	***MFAP2***	C/G	0.48	-0.035	5.60E-15	17.77	0.07	-0.049	2.50E-16	-0.04	3.90E-29	-0.041	1.60E-13	-0.039	1.80E-18	0.76
rs1738475	1	23409478	***HTR1D***	C/G	0.59	0.022	1.90E-06	0	0.69	0.031	1.60E-07	0.025	3.00E-12	0.02	2.80E-04	0.028	5.20E-10	0.25
rs4601530	1	24916698	***CLIC4***	T/C	0.26	-0.024	2.00E-06	15.60	0.10	-0.036	1.10E-07	-0.028	2.20E-12	-0.03	6.50E-07	-0.025	5.20E-07	0.47
rs7532866	1	26614131	***LIN28***	A/G	0.67	0.022	3.30E-06	0	0.54	0.02	2.60E-03	0.021	3.40E-08	0.017	4.30E-03	0.025	1.30E-07	0.23
rs2154319	1	41518357	***SCMH1***	T/C	0.75	-0.034	4.30E-10	0	0.86	-0.025	4.90E-04	-0.03	1.80E-12	-0.024	2.70E-04	-0.035	4.60E-11	0.13
rs17391694	1	78396214	***GIPC2***	T/C	0.12	0.04	5.90E-07	7.76	0.27	0.045	5.60E-06	0.042	1.70E-11	0.041	7.00E-06	0.042	5.90E-08	0.95
rs6699417	1	88896031	***PKN2***	T/C	0.61	0.022	1.70E-06	0	0.89	0.02	8.60E-04	0.021	5.00E-09	0.02	3.10E-04	0.02	6.40E-06	0.99
rs10874746	1	93096559	***RPL5***	T/C	0.37	-0.022	1.70E-06	0	0.55	-0.027	7.90E-06	-0.024	6.70E-11	-0.024	1.30E-05	-0.022	7.30E-07	0.78
rs9428104	1	118657110	***SPAG17***	A/G	0.24	-0.038	8.90E-13	0	0.98	-0.048	6.40E-12	-0.041	5.60E-23	-0.039	9.10E-10	-0.043	4.10E-17	0.55
rs11205277	1	148159496	**SF3B4**	A/G	0.58	-0.045	1.20E-18	0.02	0.48	-0.048	8.10E-15	-0.046	4.80E-32	-0.042	9.60E-12	-0.049	2.00E-24	0.36
rs17346452	1	170319910	***DNM3***	T/C	0.73	-0.038	3.30E-14	0	0.79	-0.045	4.00E-11	-0.04	1.40E-23	-0.037	1.10E-09	-0.042	6.60E-17	0.56
rs1325598	1	175058872	***PAPPA2***	A/G	0.43	-0.026	1.60E-08	0	0.88	-0.016	9.60E-03	-0.022	1.10E-09	-0.025	4.10E-06	-0.021	2.70E-06	0.52
rs1046934	1	182290152	***TSEN15***	A/C	0.64	-0.046	6.40E-22	0	0.80	-0.042	2.30E-11	-0.044	2.10E-31	-0.043	8.60E-14	-0.044	1.10E-20	0.94
rs10863936	1	210304421	***DTL***	A/G	0.53	-0.022	6.20E-07	3.05	0.40	-0.02	8.40E-04	-0.021	1.90E-09	-0.029	5.40E-08	-0.017	1.10E-04	0.06
rs6684205	1	216676325	***TGFB2***	A/G	0.71	-0.033	2.00E-11	0	0.61	-0.019	4.00E-03	-0.028	1.50E-12	-0.032	7.20E-08	-0.026	8.50E-08	0.41
rs11118346	1	217810342	***LYPLAL1***	T/C	0.47	-0.026	2.20E-09	9.57	0.22	-0.023	2.00E-04	-0.025	1.90E-12	-0.018	9.50E-04	-0.03	3.10E-11	0.05
rs10799445	1	225978506	***JMJD4***	A/C	0.77	0.031	1.20E-08	0	0.51	0.033	2.80E-06	0.032	2.40E-13	0.026	4.00E-05	0.036	7.10E-12	0.21
rs4665736	2	25041103	***DNAJC27***	T/C	0.54	0.034	1.40E-13	0	0.97	0.021	4.30E-04	0.029	7.30E-16	0.022	5.30E-05	0.034	3.40E-14	0.08
rs6714546	2	33214929	***LTBP1***	A/G	0.28	-0.025	2.20E-06	0	0.99	-0.026	1.70E-04	-0.026	1.60E-09	-0.019	3.40E-03	-0.029	2.70E-08	0.19
rs17511102	2	37814117	***CDC42EP3***	A/T	0.91	-0.06	1.30E-12	0	0.67	-0.061	1.70E-07	-0.06	1.60E-18	-0.061	1.80E-09	-0.06	1.20E-12	0.9
rs2341459	2	44621706	***C2orf34***	T/C	0.27	0.028	3.60E-08	0	0.75	0.02	4.40E-03	0.025	7.90E-10	0.031	2.40E-07	0.021	4.70E-05	0.14
rs12474201	2	46774789	***SOCS5***	A/G	0.35	0.023	1.00E-06	0	0.62	0.036	1.00E-08	0.028	2.60E-13	0.026	6.10E-06	0.028	2.90E-09	0.78
rs3791675	2	55964813	***EFEMP1***	T/C	0.23	-0.05	2.40E-20	22.09	0.03	-0.059	3.20E-17	-0.053	2.50E-35	-0.055	1.20E-17	-0.052	3.60E-23	0.71
rs11684404	2	88705737	***EIF2AK3***	T/C	0.67	-0.027	6.40E-09	14.78	0.12	-0.029	2.60E-06	-0.028	9.90E-14	-0.03	7.10E-08	-0.025	4.20E-08	0.46
rs7567288	2	134151294	***NCKAP5***	T/C	0.8	-0.031	6.70E-08	0	0.92	-0.033	8.40E-06	-0.032	2.10E-12	-0.029	2.10E-05	-0.033	4.10E-09	0.6
rs7567851	2	178392966	***PDE11A***	C/G	0.08	0.041	7.50E-07	25.21	0.01	0.028	9.50E-03	0.037	3.30E-08	0.033	8.20E-04	0.038	3.60E-06	0.7
rs1351164	2	217980143	***TNS1***	T/C	0.79	0.028	3.70E-07	0	0.87	0.044	2.70E-09	0.034	2.10E-14	0.033	4.30E-07	0.032	5.90E-09	0.83
rs12470505	2	219616613	***CCDC108/IHH***	T/G	0.9	0.048	1.30E-10	0	0.67	0.028	5.80E-03	0.041	8.90E-12	0.059	1.40E-10	0.032	2.50E-05	0.01
rs2629046	2	224755988	***SERPINE2***	T/C	0.55	0.025	2.20E-08	0	0.89	0.023	1.00E-04	0.024	7.90E-12	0.019	3.80E-04	0.027	7.20E-10	0.2
rs2580816	2	232506210	***NPPC***	T/C	0.19	-0.041	1.80E-12	0	0.80	-0.051	4.60E-11	-0.045	5.80E-22	-0.05	9.30E-13	-0.041	1.70E-12	0.23
rs12694997	2	241911659	***SEPT2***	A/G	0.24	-0.027	1.80E-07	3.06	0.40	-0.018	1.40E-02	-0.024	1.20E-08	-0.021	1.10E-03	-0.025	1.40E-06	0.61
rs2597513	3	13530836	***HDAC11***	T/C	0.9	-0.039	1.10E-07	9.85	0.22	-0.031	1.40E-03	-0.036	7.40E-10	-0.036	4.90E-05	-0.038	1.10E-07	0.83
rs13088462	3	51046753	***DOCK3***	T/C	0.94	-0.054	3.10E-07	0	0.80	-0.048	2.90E-04	-0.052	3.80E-10	-0.057	4.70E-06	-0.048	2.40E-06	0.56

rs2336725	3	53093779	***RTF1***	T/C	0.55	-0.026	3.50E-08	8.25	0.26	-0.028	5.20E-06	-0.027	9.70E-13	-0.028	1.00E-06	-0.026	1.30E-08	0.85
rs9835332	3	56642722	***C3orf63***	C/G	0.46	-0.022	8.70E-07	8.66	0.25	-0.032	5.70E-08	-0.026	5.30E-13	-0.026	2.10E-06	-0.025	2.10E-08	0.91
rs17806888	3	67499012	***SUCLG2***	T/C	0.88	0.04	1.10E-07	7.76	0.28	0.028	3.70E-03	0.036	2.10E-09	0.036	7.10E-05	0.035	1.20E-06	0.93
rs9863706	3	72520103	***RYBP***	T/C	0.22	-0.03	1.50E-08	0	0.69	-0.033	4.70E-06	-0.031	4.10E-13	-0.034	2.50E-07	-0.03	1.80E-08	0.6
rs6439167	3	130533446	***C3orf47***	T/C	0.21	-0.034	7.20E-10	0	0.89	-0.035	2.40E-06	-0.034	8.90E-15	-0.026	1.10E-04	-0.039	4.80E-13	0.09
rs9844666	3	137456906	***PCCB***	A/G	0.25	-0.028	3.10E-08	0	0.77	-0.017	1.70E-02	-0.024	3.50E-09	-0.016	8.60E-03	-0.029	1.80E-08	0.09
rs724016	3	142588260	***ZBTB38***	A/G	0.56	-0.067	4.50E-52	20.23	0.05	-0.075	2.90E-36	-0.07	3.10E-86	-0.066	8.80E-35	-0.071	5.70E-60	0.42
rs572169	3	173648421	***GHSR***	T/C	0.31	0.036	9.90E-14	3.61	0.38	0.03	3.40E-06	0.033	2.80E-18	0.03	2.80E-07	0.036	4.20E-14	0.4
rs720390	3	187031377	***IGF2BP2***	A/G	0.39	0.031	1.60E-10	19.54	0.05	0.026	1.80E-05	0.029	1.90E-14	0.036	4.40E-10	0.026	3.20E-08	0.14
rs2247341	4	1671115	***SLBP/FGFR3***	A/G	0.36	0.025	6.80E-08	17.58	0.08	0.026	3.80E-05	0.025	1.50E-11	0.027	1.60E-06	0.024	1.80E-07	0.67
rs6449353	4	17642586	***LCORL***	T/C	0.85	0.071	1.30E-27	0	0.69	0.081	2.60E-20	0.075	7.10E-46	0.074	2.10E-21	0.076	3.20E-32	0.88
rs17081935	4	57518233	***POLR2B***	T/C	0.2	0.031	4.80E-08	6.60	0.30	0.028	1.80E-04	0.03	3.70E-11	0.038	1.70E-08	0.025	6.60E-06	0.09
rs7697556	4	73734177	***ADAMTS3***	T/C	0.47	0.022	1.30E-06	0	0.71	0.038	2.90E-10	0.028	2.00E-14	0.03	4.80E-08	0.026	5.00E-09	0.56
rs788867	4	82369030	***PRKG2/BMP3***	T/G	0.68	-0.039	1.80E-15	0	0.52	-0.05	2.10E-14	-0.043	8.90E-28	-0.042	9.00E-13	-0.042	1.60E-18	0.95
rs10010325	4	106325802	***TET2***	A/C	0.49	0.021	2.30E-06	0	0.68	0.028	3.20E-06	0.024	3.90E-11	0.025	2.40E-06	0.022	3.40E-07	0.64
rs7689420	4	145787802	***HHIP***	T/C	0.16	-0.069	1.40E-29	10.51	0.20	-0.08	1.40E-23	-0.073	6.20E-51	-0.07	8.90E-22	-0.075	1.10E-35	0.61
rs955748	4	184452669	***WWC2***	A/G	0.24	-0.024	2.20E-06	0	0.52	-0.019	5.70E-03	-0.023	4.40E-08	-0.027	1.50E-05	-0.019	1.60E-04	0.29
rs1173727	5	32866278	***NPR3***	T/C	0.4	0.036	4.00E-15	1.45	0.44	0.032	1.10E-07	0.034	1.60E-21	0.038	4.60E-12	0.031	3.10E-12	0.27
rs11958779	5	55037656	***SLC38A9***	A/G	0.7	-0.028	8.00E-09	0	0.92	-0.026	4.90E-05	-0.027	1.80E-12	-0.028	1.20E-06	-0.027	2.30E-08	0.8
rs10037512	5	88390431	***MEF2C***	T/C	0.56	0.027	3.80E-09	22.57	0.03	0.04	2.20E-11	0.032	2.00E-18	0.035	1.70E-10	0.029	1.40E-10	0.3
rs13177718	5	108141243	***FER***	T/C	0.07	-0.041	4.10E-06	12.78	0.16	-0.037	2.20E-03	-0.04	3.00E-08	-0.051	2.30E-06	-0.034	1.30E-04	0.16
rs1582931	5	122685098	***CEP120***	A/G	0.47	-0.025	2.10E-08	0	0.98	-0.019	1.90E-03	-0.023	1.50E-10	-0.019	3.50E-04	-0.026	8.10E-09	0.31
rs274546	5	131727766	***SLC22A5***	A/G	0.4	-0.028	8.50E-10	0	0.92	-0.032	1.50E-07	-0.029	7.30E-16	-0.035	2.00E-10	-0.025	1.50E-08	0.13
rs526896	5	134384604	***PITX1***	T/G	0.73	0.032	1.90E-09	2.86	0.40	0.029	3.20E-05	0.03	2.30E-13	0.024	1.70E-04	0.035	1.70E-11	0.15
rs4282339	5	168188818	***SLIT3***	A/G	0.2	-0.035	3.40E-10	4.07	0.37	-0.038	3.10E-07	-0.036	6.60E-16	-0.034	4.40E-07	-0.037	1.70E-11	0.69
rs12153391	5	171136043	***FBXW11***	A/C	0.25	-0.033	8.70E-10	0	0.83	-0.024	5.20E-04	-0.03	3.60E-12	-0.027	2.10E-05	-0.032	2.00E-09	0.57
rs889014	5	172916720	***BOD1***	T/C	0.36	-0.029	4.50E-10	8.66	0.25	-0.032	2.10E-07	-0.03	9.40E-16	-0.032	9.70E-09	-0.028	8.30E-10	0.51
rs422421	5	176449932	***FGFR4/NSD1***	T/C	0.22	-0.033	1.40E-09	27.96	0.01	-0.028	1.40E-04	-0.031	1.10E-12	-0.03	7.10E-06	-0.034	5.20E-10	0.64
rs6879260	5	179663620	***GFPT2***	T/C	0.39	-0.028	5.60E-10	0	0.79	-0.01	9.70E-02	-0.022	1.60E-09	-0.02	3.40E-04	-0.025	3.00E-08	0.41
rs3812163	6	7670759	***BMP6***	A/T	0.54	-0.037	6.70E-16	23.10	0.03	-0.035	4.30E-09	-0.036	1.20E-23	-0.033	2.80E-09	-0.039	1.50E-18	0.36
rs1047014	6	19949472	***ID4***	T/C	0.75	-0.029	1.10E-07	0	0.55	-0.037	1.80E-07	-0.032	1.80E-13	-0.033	7.80E-07	-0.032	4.10E-09	0.9
rs806794	6	26308656	**Histone cluster**	A/G	0.7	0.053	5.50E-26	22.95	0.03	0.051	4.30E-15	0.052	1.20E-39	0.046	2.50E-14	0.057	5.30E-31	0.12
rs3129109	6	29192211	***OR2J3***	T/C	0.39	-0.026	3.30E-08	16.96	0.09	-0.041	1.60E-11	-0.032	2.40E-17	-0.029	2.60E-07	-0.032	3.30E-12	0.64
rs2256183	6	31488508	***MICA***	A/G	0.45	0.035	2.70E-14	0	0.54	0.051	8.30E-17	0.04	7.80E-29	0.043	4.40E-14	0.037	3.60E-17	0.43
rs6457620	6	32771977	**HLA locus**	C/G	0.51	-0.024	3.60E-08	0	0.98	-0.037	2.50E-10	-0.029	2.10E-16	-0.03	2.50E-08	-0.028	1.00E-10	0.81
rs2780226	6	34307070	***HMGA1***	T/C	0.92	-0.079	1.00E-18	20.61	0.05	-0.072	1.70E-10	-0.076	8.10E-28	-0.077	1.90E-12	-0.076	2.00E-19	0.96
rs6457821	6	35510783	***PPARD/FANCE***	A/C	0.02	-0.121	1.80E-11	3.24	0.40	-0.068	8.00E-03	-0.104	2.10E-12	-0.084	2.20E-04	-0.112	3.40E-10	0.29
rs9472414	6	45054484	***SUPT3H/RUNX2***	A/T	0.22	-0.031	2.40E-08	26.80	0.01	-0.019	8.70E-03	-0.026	1.80E-09	-0.029	6.90E-06	-0.026	1.70E-06	0.66
rs9360921	6	76322362	***SENP6***	T/G	0.89	-0.048	4.60E-11	17.19	0.08	-0.033	5.00E-04	-0.042	2.60E-13	-0.045	1.20E-07	-0.04	1.40E-08	0.62
rs310405	6	81857081	***FAM46A***	A/G	0.52	0.03	3.60E-11	0	0.89	0.02	8.10E-04	0.026	2.20E-13	0.023	2.60E-05	0.03	1.30E-11	0.25
rs7759938	6	105485647	***LIN28B***	T/C	0.68	-0.042	8.70E-18	6.39	0.30	-0.051	4.10E-15	-0.045	8.30E-31	-0.04	8.70E-12	-0.048	5.20E-23	0.26
rs1046943	6	109890634	***ZBTB24***	A/G	0.58	0.022	8.60E-07	0	0.67	0.016	7.20E-03	0.02	2.50E-08	0.024	1.20E-05	0.019	1.90E-05	0.46
rs961764	6	117628849	***VGLL2***	C/G	0.42	-0.023	2.40E-07	0	0.87	-0.026	1.20E-05	-0.024	1.30E-11	-0.024	1.20E-05	-0.025	8.90E-09	0.79

rs1490384	6	126892853	***C6orf173***	T/C	0.5	0.037	3.20E-16	15.83	0.10	0.028	1.80E-06	0.034	3.90E-21	0.037	5.30E-12	0.033	3.40E-14	0.55
rs6569648	6	130390812	***L3MBTL3***	T/C	0.76	-0.036	8.90E-12	16.88	0.08	-0.047	1.20E-11	-0.04	1.10E-21	-0.046	5.10E-13	-0.035	8.40E-12	0.14
rs7763064	6	142838982	***GPR126***	A/G	0.29	-0.045	6.40E-19	6.91	0.29	-0.055	7.20E-17	-0.048	1.10E-33	-0.044	2.10E-13	-0.051	5.30E-26	0.29
rs543650	6	152152636	***ESR1***	T/G	0.4	-0.032	1.40E-09	16.12	0.11	-0.037	2.10E-09	-0.034	1.20E-17	-0.029	3.30E-06	-0.036	1.30E-13	0.36
rs9456307	6	158849430	***TULP4***	A/T	0.06	-0.05	4.60E-07	0.20	0.47	-0.045	1.20E-03	-0.048	2.20E-09	-0.041	7.90E-04	-0.053	6.20E-08	0.38
rs798489	7	2768329	***GNA12***	T/C	0.3	-0.052	8.50E-25	0	0.55	-0.042	1.70E-10	-0.048	1.90E-33	-0.051	4.50E-17	-0.046	5.10E-21	0.53
rs4470914	7	19583047	***TWISTNB***	T/C	0.18	0.033	3.80E-08	5.76	0.32	0.023	3.40E-03	0.029	9.20E-10	0.03	4.80E-05	0.029	5.50E-07	0.93
rs12534093	7	23469499	***IGF2BP3***	A/T	0.22	-0.03	5.60E-08	3.09	0.39	-0.04	4.10E-08	-0.034	2.00E-14	-0.032	1.70E-06	-0.033	5.30E-10	0.84
rs1708299	7	28156471	***JAZF1***	A/G	0.3	0.042	1.50E-17	14.38	0.12	0.038	5.80E-09	0.04	5.80E-25	0.036	4.10E-10	0.044	3.30E-20	0.25
rs6959212	7	38094851	***STARD3NL***	T/C	0.32	-0.023	2.80E-06	0	0.52	-0.025	1.30E-04	-0.024	1.60E-09	-0.021	3.40E-04	-0.024	5.90E-07	0.66
rs42235	7	92086012	***CDK6***	T/C	0.31	0.055	7.30E-28	21.51	0.04	0.062	1.90E-20	0.057	7.70E-47	0.046	1.60E-14	0.063	3.70E-37	0.01
rs822552	7	148281567	***PDIA4***	C/G	0.74	-0.03	1.30E-07	0	0.48	-0.017	2.70E-02	-0.025	2.60E-08	-0.032	2.30E-06	-0.022	9.40E-05	0.24
rs2110001	7	150147955	***TMEM176A***	C/G	0.69	-0.033	9.80E-10	17.78	0.08	-0.028	4.40E-05	-0.031	3.30E-13	-0.029	3.40E-06	-0.032	4.40E-10	0.71
rs1013209	8	24172249	***ADAM28***	T/C	0.25	-0.029	4.50E-08	10.06	0.21	-0.019	7.30E-03	-0.025	1.60E-09	-0.026	4.80E-05	-0.026	8.90E-07	0.95
rs7460090	8	57356717	***SDR16C5***	T/C	0.87	0.055	9.60E-16	0	0.70	0.064	7.70E-13	0.058	8.20E-27	0.051	7.00E-10	0.064	1.10E-21	0.16
rs6473015	8	78341040	***PEX2***	A/C	0.72	-0.032	1.70E-10	12.48	0.16	-0.023	5.80E-04	-0.029	6.90E-13	-0.03	8.90E-07	-0.028	9.00E-09	0.84
rs6470764	8	130794847	***GSDMC***	T/C	0.2	-0.047	5.90E-17	17.64	0.07	-0.056	3.40E-13	-0.05	1.70E-28	-0.05	1.60E-13	-0.05	4.10E-18	0.95
rs12680655	8	135706519	***ZFAT***	C/G	0.6	0.03	4.80E-11	16.69	0.09	0.024	7.50E-05	0.028	1.60E-14	0.025	5.10E-06	0.029	3.70E-11	0.45
rs7864648	9	16358732	***BNC2***	T/G	0.32	0.025	4.90E-07	3.83	0.37	0.017	7.80E-03	0.022	2.10E-08	0.027	5.40E-06	0.019	9.70E-05	0.23
rs11144688	9	77732106	***PCSK5***	A/G	0.11	-0.055	1.50E-09	0	0.52	-0.04	9.10E-04	-0.049	9.60E-12	-0.044	3.30E-05	-0.057	3.90E-10	0.28
rs7853377	9	85742025	***C9orf64***	A/G	0.77	-0.026	3.10E-06	0	0.65	-0.021	3.50E-03	-0.024	4.50E-08	-0.018	6.10E-03	-0.027	5.00E-07	0.26
rs8181166	9	88306448	***ZCCHC6***	C/G	0.53	0.025	1.10E-07	26.48	0.01	0.028	3.90E-06	0.026	2.70E-12	0.019	8.30E-04	0.031	8.20E-12	0.07
rs2778031	9	90025546	***SPIN1***	T/C	0.24	0.027	3.60E-07	0	0.81	0.037	2.40E-07	0.031	9.00E-13	0.031	1.50E-06	0.029	2.20E-08	0.78
rs9969804	9	94468941	***IPPK***	A/C	0.44	0.028	5.60E-10	0	0.61	0.033	1.90E-08	0.03	7.70E-17	0.028	1.50E-07	0.029	7.30E-11	0.92
rs1257763	9	95933766	***PTPDC1***	A/G	0.04	0.069	2.50E-06	0	0.95	0.07	1.00E-04	0.069	9.90E-10	0.063	2.10E-04	0.075	1.00E-07	0.55
rs473902	9	97296056	***PTCH1/FANCC***	T/G	0.92	0.074	1.70E-14	0	0.61	0.05	6.80E-05	0.065	2.30E-17	0.061	6.70E-08	0.068	9.80E-13	0.62
rs7027110	9	108638867	***ZNF462***	A/G	0.23	0.034	1.30E-10	0	0.85	0.025	3.80E-04	0.031	2.30E-13	0.032	4.80E-07	0.03	8.90E-09	0.72
rs1468758	9	112846903	***LPAR1***	T/C	0.25	-0.026	1.50E-06	0	0.59	-0.026	1.90E-04	-0.026	1.40E-09	-0.031	1.20E-06	-0.022	2.50E-05	0.24
rs751543	9	118162163	***PAPPA***	T/C	0.72	0.029	4.50E-08	0	0.86	0.021	3.40E-03	0.026	6.50E-10	0.027	2.50E-05	0.026	6.70E-07	0.89
rs7466269	9	132453905	***FUBP3***	A/G	0.64	0.036	1.20E-14	37.95	0.00	0.024	7.50E-05	0.032	2.60E-17	0.032	2.70E-08	0.032	2.30E-12	0.92
rs7849585	9	138251691	***QSOX2***	T/G	0.33	0.032	3.40E-11	14.89	0.12	0.024	1.50E-04	0.029	4.70E-14	0.031	1.70E-07	0.028	3.30E-09	0.69
rs7909670	10	12958770	***CCDC3***	T/C	0.44	-0.022	1.30E-06	0	0.85	-0.02	7.30E-04	-0.021	3.20E-09	-0.028	3.60E-07	-0.016	2.60E-04	0.06
rs2145998	10	80791702	***PPIF***	A/T	0.49	-0.025	2.70E-08	2.75	0.40	-0.027	3.80E-06	-0.026	3.60E-13	-0.027	4.80E-07	-0.025	2.60E-08	0.68
rs11599750	10	101795432	***CPN1***	T/C	0.38	-0.023	7.60E-07	0	0.82	-0.036	6.90E-09	-0.028	1.60E-13	-0.023	3.40E-05	-0.03	9.00E-11	0.32
rs2237886	11	2767307	***KCNQ1***	T/C	0.11	0.043	3.10E-08	6.34	0.31	0.05	1.00E-06	0.046	2.20E-13	0.037	7.50E-05	0.05	4.30E-11	0.25
rs7926971	11	12654616	***TEAD1***	A/G	0.55	-0.024	7.30E-08	0	0.91	-0.019	1.40E-03	-0.023	4.40E-10	-0.025	3.50E-06	-0.02	8.30E-06	0.4
rs1330	11	17272605	***NUCB2***	T/C	0.35	0.024	4.40E-07	17.47	0.08	0.019	2.10E-03	0.022	4.90E-09	0.02	4.70E-04	0.024	3.10E-07	0.56
rs10838801	11	48054856	***PTPRJ/SLC39A13***	A/G	0.69	-0.031	1.80E-10	12.10	0.17	-0.02	1.90E-03	-0.027	3.50E-12	-0.024	5.40E-05	-0.031	7.70E-11	0.27
rs1814175	11	49515748	***FOLH1***	T/C	0.34	0.023	2.60E-06	0	0.62	0.02	1.60E-03	0.022	1.60E-08	0.016	5.60E-03	0.027	2.20E-08	0.13
rs5017948	11	51270794	***OR4A5***	A/T	0.18	0.027	4.70E-06	9.62	0.23	0.026	1.60E-03	0.027	3.10E-08	0.016	3.10E-02	0.036	1.60E-09	0.02
rs3782089	11	65093395	***SSSCA1***	T/C	0.06	-0.058	5.90E-09	0	0.63	-0.057	1.40E-05	-0.058	3.60E-13	-0.071	2.00E-09	-0.049	7.70E-07	0.13
rs7112925	11	66582736	***RHOD***	T/C	0.35	-0.023	8.50E-07	0	0.48	-0.023	2.00E-04	-0.023	9.00E-10	-0.026	5.90E-06	-0.022	2.30E-06	0.57
rs634552	11	74959700	***SERPINH1***	T/G	0.14	0.041	1.40E-09	2.32	0.42	0.035	4.40E-05	0.039	3.50E-13	0.036	7.00E-06	0.04	1.60E-09	0.69

rs494459	11	118079885	***TREH***	T/C	0.41	0.021	4.90E-06	19.42	0.05	0.02	1.10E-03	0.02	1.70E-08	0.023	1.90E-05	0.019	2.30E-05	0.5
rs654723	11	128091365	***FLI1***	A/C	0.62	0.024	6.70E-07	0	0.93	0.028	8.00E-06	0.025	3.60E-11	0.026	4.70E-06	0.025	1.30E-07	0.82
rs2856321	12	11747040	***ETV6***	A/G	0.64	-0.03	1.50E-10	0	0.99	-0.029	4.00E-06	-0.029	4.50E-15	-0.029	4.10E-07	-0.03	8.10E-11	0.83
rs10770705	12	20748734	***SLCO1C1***	A/C	0.33	0.031	4.60E-11	0	0.75	0.036	2.20E-08	0.033	8.00E-18	0.031	8.40E-08	0.033	3.80E-12	0.77
rs2638953	12	28425682	***CCDC91***	C/G	0.68	0.036	8.40E-14	2.95	0.40	0.026	5.40E-05	0.032	6.70E-17	0.024	3.10E-05	0.038	1.10E-15	0.04
rs2066807	12	55026949	***STAT2***	C/G	0.93	-0.052	9.60E-09	0	0.71	-0.058	1.90E-06	-0.054	1.00E-13	-0.047	2.20E-05	-0.056	1.30E-10	0.49
rs1351394	12	64638093	***HMGA2***	T/C	0.49	0.054	7.80E-34	24.54	0.02	0.073	1.60E-34	0.06	1.70E-65	0.054	1.40E-23	0.063	9.00E-48	0.14
rs10748128	12	68113925	***FRS2***	T/G	0.35	0.035	3.80E-11	20.87	0.04	0.042	1.20E-10	0.038	2.10E-20	0.043	1.10E-11	0.034	8.10E-12	0.23
rs11107116	12	92502635	***SOCS2***	T/G	0.22	0.052	1.70E-23	10.02	0.21	0.05	2.20E-12	0.052	1.40E-34	0.044	4.70E-12	0.057	1.90E-27	0.1
rs7971536	12	100897919	***CCDC53/GNPTAB***	A/T	0.46	-0.025	1.10E-07	0	0.64	-0.034	4.30E-08	-0.028	8.20E-14	-0.029	3.40E-07	-0.027	1.30E-08	0.75
rs11830103	12	122389499	***SBNO1***	A/G	0.78	-0.035	3.80E-10	0	0.76	-0.035	2.50E-06	-0.035	3.90E-15	-0.041	1.40E-09	-0.032	4.50E-09	0.27
rs7332115	13	32045548	***PDS5B/BRCA2***	T/G	0.62	-0.025	7.60E-08	0	0.86	-0.02	1.10E-03	-0.023	5.50E-10	-0.02	4.80E-04	-0.026	1.70E-08	0.37
rs3118905	13	50003335	***DLEU7***	A/G	0.29	-0.052	3.00E-25	0	0.58	-0.063	3.10E-22	-0.056	1.10E-45	-0.05	4.00E-17	-0.06	1.60E-34	0.15
rs7319045	13	90822575	***GPC5***	A/G	0.4	0.029	4.50E-10	0	0.89	0.019	1.80E-03	0.025	1.20E-11	0.027	8.40E-07	0.024	1.40E-07	0.6
rs1950500	14	23900690	***NFATC4***	T/C	0.29	0.032	3.90E-11	0	0.95	0.038	8.70E-09	0.034	2.20E-18	0.038	2.00E-10	0.031	1.60E-10	0.32
rs2093210	14	60027032	***SIX6***	T/C	0.58	-0.034	2.30E-12	0	0.56	-0.029	3.90E-06	-0.032	6.20E-17	-0.028	2.10E-06	-0.036	1.90E-14	0.23
rs1570106	14	67882868	***RAD51L1***	T/C	0.2	-0.026	4.90E-06	0.50	0.47	-0.026	4.70E-04	-0.026	8.10E-09	-0.023	5.40E-04	-0.027	1.70E-06	0.67
rs862034	14	74060499	***LTBP2***	A/G	0.36	-0.023	1.10E-06	12.90	0.15	-0.037	1.90E-09	-0.028	7.30E-14	-0.032	1.90E-08	-0.024	2.10E-07	0.24
rs7155279	14	91555634	***TRIP11***	T/G	0.36	-0.029	8.90E-10	21.48	0.04	-0.016	9.20E-03	-0.024	1.40E-10	-0.028	8.70E-07	-0.022	1.10E-06	0.38
rs16964211	15	49317787	***CYP19A1***	A/G	0.05	-0.051	2.50E-06	14.06	0.13	-0.049	1.60E-04	-0.05	1.70E-09	-0.067	8.10E-08	-0.036	5.30E-04	0.04
rs7178424	15	60167551	***C2CD4A***	T/C	0.47	-0.024	2.20E-07	0	0.62	-0.017	6.20E-03	-0.021	5.60E-09	-0.02	2.50E-04	-0.021	1.50E-06	0.88
rs10152591	15	67835211	***TLE3***	A/C	0.91	0.045	3.50E-08	0	0.50	0.034	1.50E-03	0.041	2.70E-10	0.033	8.60E-04	0.046	6.60E-09	0.28
rs12902421	15	69948457	***MYO9A***	T/C	0.97	-0.069	1.70E-06	0	0.51	-0.051	3.70E-03	-0.062	2.90E-08	-0.049	2.80E-03	-0.072	2.50E-07	0.25
rs5742915	15	72123686	***PML***	T/C	0.54	-0.031	3.00E-10	0	0.71	-0.031	5.30E-07	-0.031	1.00E-15	-0.039	3.90E-11	-0.027	1.10E-08	0.08
rs11259936	15	82371586	***ADAMTSL3***	A/C	0.48	-0.042	2.20E-21	3.92	0.37	-0.047	1.10E-15	-0.044	1.70E-35	-0.036	1.50E-11	-0.049	1.00E-29	0.03
rs16942341	15	87189909	***ACAN***	T/C	0.03	-0.134	1.30E-17	24.62	0.03	-0.124	4.50E-11	-0.13	3.80E-27	-0.139	1.60E-14	-0.122	1.40E-16	0.43
rs2871865	15	97012419	***IGF1R***	C/G	0.88	0.054	1.10E-12	32.60	0.002	0.062	3.50E-10	0.057	2.90E-21	0.052	1.80E-08	0.058	2.80E-15	0.54
rs4965598	15	98577137	***ADAMTS17***	T/C	0.68	-0.035	1.40E-13	0	0.81	-0.015	2.30E-02	-0.028	4.30E-13	-0.024	5.10E-05	-0.032	9.70E-12	0.21
rs11648796	16	732191	***NARFL***	A/G	0.74	-0.031	2.40E-07	0	0.87	-0.039	6.90E-08	-0.034	1.20E-13	-0.032	7.40E-06	-0.035	5.60E-10	0.71
rs26868	16	2189377	***CASKIN1***	A/T	0.46	0.03	3.50E-08	0	0.78	0.04	2.40E-10	0.034	9.00E-17	0.036	1.20E-08	0.034	9.80E-12	0.73
rs1659127	16	14295806	***MKL2***	A/G	0.34	0.024	2.90E-06	0	0.79	0.033	5.20E-07	0.027	1.10E-11	0.025	7.90E-05	0.027	2.90E-08	0.7
rs8052560	16	87304743	***CTU2/GALNS***	A/C	0.79	0.039	1.40E-08	0	0.63	0.015	7.40E-02	0.029	3.30E-08	0.025	2.20E-03	0.032	1.10E-06	0.47
rs4640244	17	21224816	***KCNJ12***	A/G	0.61	0.028	2.00E-07	13.00	0.15	0.017	1.20E-02	0.024	2.30E-08	0.023	2.80E-04	0.025	1.70E-06	0.78
rs3110496	17	24941897	***ANKRD13B***	A/G	0.33	-0.023	1.60E-06	0	0.69	-0.021	1.10E-03	-0.022	7.30E-09	-0.03	1.10E-07	-0.016	6.40E-04	0.04
rs3764419	17	26188149	***ATAD5/RNF135***	A/C	0.39	-0.037	8.90E-16	16.60	0.09	-0.032	1.50E-07	-0.035	1.80E-21	-0.034	1.30E-09	-0.036	7.80E-16	0.67
rs17780086	17	27367395	***LRRC37B***	A/G	0.15	0.035	4.40E-08	10.44	0.21	0.017	5.50E-02	0.028	2.60E-08	0.03	9.40E-05	0.028	5.30E-06	0.85
rs1043515	17	34175722	***PIP4K2B***	A/G	0.45	-0.022	1.30E-06	0	0.80	-0.024	6.60E-05	-0.023	2.90E-10	-0.028	2.00E-07	-0.019	2.20E-05	0.15
rs4986172	17	40571807	***ACBD4***	T/C	0.35	-0.028	7.10E-09	30.83	0.003	-0.037	2.50E-09	-0.032	2.30E-16	-0.035	1.70E-09	-0.03	3.10E-10	0.41
rs2072153	17	44745013	***ZNF652***	C/G	0.3	0.026	6.70E-08	0	0.86	0.013	4.30E-02	0.021	3.50E-08	0.031	1.60E-07	0.016	8.30E-04	0.03
rs4605213	17	46599746	***NME2***	C/G	0.34	0.023	9.30E-07	0	0.88	0.018	5.90E-03	0.021	2.70E-08	0.026	5.40E-06	0.018	2.10E-04	0.21
rs227724	17	52133816	***NOG***	A/T	0.65	-0.027	1.20E-08	0	0.92	-0.034	6.60E-08	-0.03	7.40E-15	-0.035	8.10E-10	-0.027	1.10E-08	0.2
rs2079795	17	56851431	***TBX2***	T/C	0.33	0.04	1.20E-16	0	0.81	0.04	1.50E-09	0.04	2.10E-24	0.033	7.80E-09	0.044	8.10E-20	0.12
rs2665838	17	59320197	***CSH1/GH1***	C/G	0.73	-0.037	2.00E-13	11.25	0.19	-0.052	7.00E-14	-0.042	5.10E-25	-0.042	2.20E-11	-0.042	3.00E-17	0.92

rs11867479	17	65601802	***KCNJ16/KCNJ2***	T/C	0.34	0.024	4.90E-07	0	0.87	0.026	5.40E-05	0.025	1.50E-10	0.023	7.00E-05	0.026	6.70E-08	0.68
rs4800452	18	18981609	***CABLES1***	T/C	0.79	0.048	2.40E-17	0	0.84	0.056	1.20E-14	0.051	4.20E-30	0.052	7.40E-15	0.05	8.40E-20	0.8
rs9967417	18	45213498	***DYM***	C/G	0.58	-0.038	2.60E-16	30.04	0.004	-0.039	3.20E-10	-0.038	9.30E-25	-0.041	3.40E-13	-0.036	1.30E-15	0.44
rs17782313	18	56002077	***MC4R***	T/C	0.76	-0.025	3.50E-06	13.42	0.14	-0.035	1.20E-06	-0.028	3.80E-11	-0.03	4.00E-06	-0.025	1.20E-06	0.55
rs12982744	19	2128193	***DOT1L***	C/G	0.6	-0.033	2.80E-12	0	0.97	-0.027	1.10E-05	-0.03	3.40E-16	-0.028	4.90E-07	-0.032	3.80E-12	0.6
rs7507204	19	3379834	***NFIC***	C/G	0.24	0.028	2.30E-07	0	0.88	0.049	2.10E-11	0.036	4.30E-16	0.025	1.70E-04	0.041	2.60E-14	0.05
rs891088	19	7135762	***INSR***	A/G	0.74	-0.025	1.70E-06	2.38	0.41	-0.035	1.80E-07	-0.029	2.40E-12	-0.025	6.10E-05	-0.031	1.10E-09	0.45
rs4072910	19	8550031	***ADAMTS10***	C/G	0.46	-0.029	2.50E-07	0	0.76	-0.034	2.20E-07	-0.031	3.60E-13	-0.025	1.30E-04	-0.033	3.10E-10	0.31
rs2279008	19	17144303	***MYO9B***	T/C	0.74	0.031	2.40E-07	0	0.63	0.018	9.50E-03	0.025	2.50E-08	0.022	2.00E-03	0.027	5.00E-07	0.48
rs17318596	19	46628935	***ATP5SL***	A/G	0.36	0.029	3.00E-09	0	0.79	0.037	2.10E-08	0.032	5.00E-16	0.043	1.30E-13	0.024	8.00E-07	0.01
rs1741344	20	4049800	***SMOX***	T/C	0.63	-0.026	3.50E-08	16.74	0.09	-0.016	1.00E-02	-0.023	3.30E-09	-0.02	4.10E-04	-0.024	2.60E-07	0.55
rs2145272	20	6574218	***BMP2***	A/G	0.65	-0.039	5.90E-16	19.29	0.06	-0.04	4.60E-10	-0.039	2.10E-24	-0.039	1.50E-11	-0.04	2.30E-17	0.85
rs7274811	20	31796842	***ZNF341***	T/G	0.23	-0.04	6.80E-14	7.93	0.26	-0.042	1.10E-09	-0.041	5.90E-22	-0.044	1.60E-11	-0.039	1.30E-13	0.52
rs143384	20	33489170	***GDF5***	A/G	0.58	-0.064	4.90E-39	21.58	0.04	-0.061	9.10E-22	-0.063	1.00E-58	-0.066	9.30E-30	-0.061	8.30E-38	0.47
rs237743	20	47336426	***ZNFX1***	A/G	0.21	0.034	7.20E-10	0	0.69	0.053	3.10E-13	0.041	1.30E-20	0.035	1.20E-07	0.043	6.80E-16	0.28
rs2834442	21	34612656	***KCNE2***	A/T	0.65	0.027	7.30E-09	0	0.80	0.024	9.70E-05	0.026	5.10E-12	0.025	9.10E-06	0.026	1.00E-08	0.9
rs4821083	22	31386341	***SYN3***	T/C	0.84	0.033	4.80E-08	0	0.70	0.027	1.40E-03	0.031	3.10E-10	0.036	1.40E-06	0.028	4.20E-06	0.41

[a] SNPs most likely to be representing a previously published height locus are highlighted in green.
[b] Gene regions are named after the gene nearest to the index SNP. A near-by (within 500kb from the index SNP) OMIM height gene (defined as a gene that when mutated results in a monogenic skeletal growth defect) is also included if it is not the nearest. All OMIM height genes are highlighted in blue.
[c] Alleles are indexed to the forward strand of NCBI Build 36.
[d] All p-values are based on the inverse-variance weighted meta-analysis model (fixed effects).

Supplementary Table 2. Association results for 33 SNPs selected randomly among the 180 SNPs that reached genome-wide significance (P=5x10^{-8}) in the Stage 1 meta-analysis and genotyped in European American (N=2,181) and Poland (N=1,009) panels at tails of height distribution. Results are combined using a Cochran-Mantel-Haenszel test.

GIANT height SNP	Chr	Position	GIANT height meta-analysis				Results in extreme height panels				Comment
			Effect allele	Other allele	Effect size (Stage 1)	Stage 1+2 P-value	Effect allele	Other allele	OR [95% CI]	1-tailed P-value	
rs143384	20	33489170	A	G	-0.0639	9.954E-59	G	A	1.2 [1.08-1.33]	0.0002	Same direction, 1-tailed P-value <0.05
rs2580816	2	232506210	T	C	-0.0412	5.837E-22	T	C	0.8 [0.7-0.91]	0.0002	Same direction, 1-tailed P-value <0.05
rs1738475	1	23409478	C	G	0.0216	2.952E-12	G	C	0.86 [0.78-0.96]	0.002	Same direction, 1-tailed P-value <0.05
rs12474201	2	46774789	A	G	0.0233	2.581E-13	A	G	1.16 [1.04-1.29]	0.003	Same direction, 1-tailed P-value <0.05
rs1351164	2	217980143	T	C	0.0279	2.081E-14	C	T	0.84 [0.74-0.96]	0.004	Same direction, 1-tailed P-value <0.05
rs822552	7	148281567	C	G	-0.0302	2.613E-08	G	C	1.15 [1.03-1.29]	0.007	Same direction, 1-tailed P-value <0.05
rs7849585	9	138251691	T	G	0.0324	4.724E-14	T	G	1.13 [1.02-1.26]	0.011	Same direction, 1-tailed P-value <0.05
rs1257763	9	95933766	A	G	0.0685	9.865E-10	A	G	1.33 [1.04-1.69]	0.012	Same direction, 1-tailed P-value <0.05
rs12534093	7	23469499	A	T	-0.0298	2.019E-14	A	T	0.87 [0.77-0.98]	0.012	Same direction, 1-tailed P-value <0.05
rs2871865	15	97012419	C	G	0.0535	2.862E-21	G	C	0.83 [0.71-0.98]	0.013	Same direction, 1-tailed P-value <0.05
rs310405	6	81857081	A	G	0.03	2.245E-13	G	A	0.89 [0.81-0.99]	0.016	Same direction, 1-tailed P-value <0.05
rs10037512	5	88390431	T	C	0.0267	2.011E-18	C	T	0.82 [0.69-0.99]	0.018	Same direction, 1-tailed P-value <0.05
rs1814175	11	49515748	T	C	0.023	1.645E-08	T	C	1.11 [1-1.24]	0.02	Same direction, 1-tailed P-value <0.05
rs16942341	15	87189909	T	C	-0.1335	3.807E-27	T	C	0.74 [0.55-1.01]	0.03	Same direction, 1-tailed P-value <0.05
rs4665736	2	25041103	T	C	0.0335	7.29E-16	C	T	0.92 [0.83-1.02]	0.05	Same direction, 1-tailed P-value <0.05
rs6684205	1	216676325	A	G	-0.0328	1.473E-12	G	A	1.09 [0.97-1.22]	0.07	Same direction
rs7567288	2	134151294	T	C	-0.0309	2.071E-12	C	T	1.11 [0.97-1.26]	0.07	Same direction
rs7697556	4	73734177	T	C	0.0219	1.958E-14	T	C	1.07 [0.96-1.18]	0.11	Same direction
rs11599750	10	101795432	T	C	-0.023	1.604E-13	T	C	0.94 [0.85-1.05]	0.13	Same direction
rs2066807	12	55026949	C	G	-0.052	1.025E-13	G	C	1.12 [0.92-1.35]	0.13	Same direction
rs751543	9	118162163	T	C	0.0287	6.537E-10	C	T	0.94 [0.84-1.05]	0.13	Same direction
rs7532866	1	26614131	A	G	0.0222	3.372E-08	G	A	0.94 [0.85-1.05]	0.14	Same direction
rs11118346	1	217810342	T	C	-0.0264	1.879E-12	T	C	0.96 [0.87-1.06]	0.20	Same direction
rs6439167	3	130533446	T	C	-0.0338	8.925E-15	T	C	0.93 [0.75-1.15]	0.24	Same direction
rs274546	5	131727766	A	G	-0.0278	7.254E-16	A	G	0.97 [0.87-1.07]	0.26	Same direction
rs10863936	1	210304421	A	G	-0.022	1.922E-09	G	A	1.03 [0.93-1.14]	0.27	Same direction
rs9360921	6	76322362	T	G	-0.0479	2.552E-13	G	T	1.05 [0.89-1.25]	0.28	Same direction
rs4986172	17	40571807	T	C	-0.0283	2.333E-16	T	C	0.97 [0.87-1.08]	0.29	Same direction
rs9456307	6	158849430	A	T	-0.0499	2.239E-09	A	T	0.98 [0.78-1.22]	0.42	Same direction
rs572169	3	173648421	T	C	0.0355	2.765E-18	T	C	1.02 [0.84-1.24]	0.42	Same direction
rs2110001	7	150147955	C	G	-0.0328	3.319E-13	G	C	0.99 [0.88-1.1]	0.61	Opposite direction (1-tailed P-value adjusted accordingly)
rs8052560	16	87304743	A	C	0.0392	3.324E-08	C	A	1.08 [0.95-1.23]	0.89	Opposite direction (1-tailed P-value adjusted accordingly)

Supplementary Table 3. Family-based association results for the 180 confirmed height SNPs in the Framingham Heart Study (FHS) and the Erasmus Rucphen Family (ERF) study. For each study, and the meta-analysis FHS+ERF, we compare the direction of effect observed with respect to the effect of the height-increasing allele in the GIANT meta-analysis.

SNP	GIANT meta-analysis			FHS (family-based test)			ERF (family-based test)		Meta-analysis FHS+ERF (family-based test)	
	Height Increasing allele	BETA	*P*-value	Direction of effect relative to GIANT	*P*-value	BETA relative to GIANT	Direction of effect relative to GIANT	*P*-value	Direction of effect relative to GIANT	*P*-value
rs724016	G	0.067	4.5E-52	Same	0.02	0.066	Same	0.61	Same	0.02
rs143384	G	0.064	4.9E-39	Same	3.5E-03	0.081	Same	0.65	Same	4.8E-03
rs1351394	T	0.054	7.8E-34	Same	1.3E-03	0.089	Same	0.73	Same	2.3E-03
rs7689420	C	0.069	1.4E-29	Same	0.06	0.068	Same	0.03	Same	0.01
rs42235	T	0.055	7.3E-28	Opposite	0.91	-0.003	Opposite	0.85	Opposite	0.85
rs6449353	T	0.071	1.3E-27	Same	0.04	0.070	Same	0.43	Same	0.03
rs806794	A	0.053	5.5E-26	Same	1.7E-03	0.106	Same	0.02	Same	1.2E-04
rs3118905	G	0.052	3.0E-25	Same	0.36	0.027	Same	0.57	Same	0.28
rs798489	C	0.052	8.5E-25	Same	0.09	0.052	Same	0.04	Same	0.02
rs11107116	T	0.052	1.7E-23	Same	0.05	0.065	Same	0.33	Same	0.03
rs1046934	C	0.046	6.4E-22	Same	0.03	0.062	Same	0.89	Same	0.05
rs11259936	C	0.042	2.2E-21	Same	0.06	0.053	Same	0.90	Same	0.09
rs3791675	C	0.050	2.4E-20	Same	0.67	0.014	Same	0.25	Same	0.38
rs7763064	G	0.045	6.4E-19	Same	0.43	0.023	Same	0.23	Same	0.22
rs2780226	C	0.079	1.0E-18	Same	6.4E-04	0.171	Same	0.02	Same	4.9E-05
rs11205277	G	0.045	1.2E-18	Same	0.12	0.043	Same	2.0E-03	Same	0.01
rs7759938	C	0.042	8.7E-18	Same	0.15	0.041	Same	0.65	Same	0.13
rs16942341	C	0.134	1.3E-17	Same	2.5E-03	0.236	Same	0.59	Same	3.1E-03
rs1708299	A	0.042	1.5E-17	Same	4.5E-03	0.090	Same	0.29	Same	2.6E-03
rs4800452	T	0.048	2.4E-17	Same	0.01	0.082	Same	0.49	Same	0.01
rs6470764	C	0.047	5.9E-17	Same	0.22	0.041	Same	0.87	Same	0.24
rs2079795	T	0.040	1.2E-16	Same	0.09	0.049	Same	0.69	Same	0.09
rs9967417	G	0.038	2.6E-16	Same	0.22	0.031	Same	0.67	Same	0.20
rs1490384	T	0.037	3.2E-16	Same	0.03	0.060	Opposite	0.45	Same	0.10
rs2145272	G	0.039	5.9E-16	Same	0.01	0.069	Same	0.88	Same	0.02
rs3812163	T	0.037	6.7E-16	Same	0.80	0.007	Same	0.18	Same	0.42
rs3764419	C	0.037	8.9E-16	Same	0.09	0.046	Same	0.49	Same	0.07
rs7460090	T	0.055	9.6E-16	Opposite	0.96	-0.002	Same	0.19	Same	0.60
rs788867	G	0.039	1.8E-15	Same	0.56	0.017	Same	0.36	Same	0.36
rs1173727	T	0.036	4.0E-15	Same	0.03	0.058	Same	0.40	Same	0.02
rs2284746	G	0.035	5.6E-15	Same	0.69	0.011	Same	0.09	Same	0.28
rs7466269	A	0.036	1.2E-14	Same	0.20	0.036	Same	0.05	Same	0.04
rs473902	T	0.074	1.7E-14	Same	0.26	0.056	Same	0.83	Same	0.26
rs2256183	A	0.035	2.7E-14	Same	0.79	0.008	Opposite	0.94	Same	0.84
rs17346452	C	0.038	3.3E-14	Same	0.92	0.003	Same	0.21	Same	0.52
rs7274811	G	0.040	6.8E-14	Same	0.01	0.080	Same	0.42	Same	0.01

SNP	GIANT meta-analysis			FHS (family-based test)			ERF (family-based test)		Meta-analysis FHS+ERF (family-based test)	
	Height Increasing allele	BETA	*P*-value	Direction of effect relative to GIANT	*P*-value	BETA relative to GIANT	Direction of effect relative to GIANT	*P*-value	Direction of effect relative to GIANT	*P*-value
rs2638953	C	0.036	8.4E-14	Same	0.07	0.056	Opposite	0.97	Same	0.11
rs572169	T	0.036	9.9E-14	Same	0.60	0.015	Same	0.03	Same	0.17
rs4665736	T	0.034	1.4E-13	Same	0.28	0.030	Same	0.11	Same	0.09
rs4965598	C	0.035	1.4E-13	Same	0.02	0.069	Same	0.52	Same	0.02
rs2665838	G	0.037	2.0E-13	Same	0.09	0.051	Same	0.40	Same	0.06
rs9428104	G	0.038	8.9E-13	Same	0.06	0.057	Opposite	0.19	Same	0.27
rs2871865	C	0.054	1.1E-12	Same	0.10	0.074	Same	0.08	Same	0.02
rs17511102	T	0.060	1.3E-12	Same	0.23	0.062	Same	0.50	Same	0.17
rs2580816	C	0.041	1.8E-12	Same	0.37	0.031	Opposite	0.67	Same	0.54
rs2093210	C	0.034	2.3E-12	Same	0.20	0.036	Same	0.07	Same	0.05
rs12982744	G	0.033	2.8E-12	Same	0.69	0.012	Opposite	0.46	Same	0.97
rs6569648	C	0.036	8.9E-12	Same	0.06	0.058	Same	0.46	Same	0.04
rs6457821	C	0.121	1.8E-11	Opposite	0.93	-0.009	Same	0.26	Same	0.69
rs6684205	G	0.033	2.0E-11	Same	0.47	0.021	Same	0.08	Same	0.16
rs7849585	T	0.032	3.4E-11	Opposite	0.91	-0.003	Same	0.19	Same	0.64
rs310405	A	0.030	3.6E-11	Opposite	0.81	-0.007	Same	0.16	Same	0.70
rs10748128	T	0.035	3.8E-11	Opposite	0.65	-0.014	Same	0.35	Same	0.99
rs1950500	T	0.032	3.9E-11	Same	0.28	0.033	Same	0.29	Same	0.15
rs10770705	A	0.031	4.6E-11	Opposite	0.29	-0.031	Opposite	0.60	Opposite	0.24
rs9360921	G	0.048	4.6E-11	Same	0.52	0.029	Opposite	0.65	Same	0.70
rs12680655	C	0.030	4.8E-11	Opposite	0.50	-0.019	Same	0.39	Opposite	0.82
rs12470505	T	0.048	1.3E-10	Same	0.22	0.053	Same	0.45	Same	0.15
rs7027110	A	0.034	1.3E-10	Same	0.16	0.046	Opposite	0.81	Same	0.24
rs2856321	G	0.030	1.5E-10	Same	0.32	0.028	Same	0.56	Same	0.25
rs720390	A	0.031	1.6E-10	Same	0.10	0.048	Same	0.19	Same	0.04
rs6473015	C	0.032	1.7E-10	Same	0.55	0.017	Opposite	0.62	Same	0.74
rs10838801	G	0.031	1.8E-10	Same	0.01	0.075	Same	0.04	Same	1.7E-03
rs5742915	C	0.031	3.0E-10	Same	0.05	0.059	Same	0.25	Same	0.02
rs4282339	G	0.035	3.4E-10	Same	0.34	0.032	Same	0.75	Same	0.32
rs2154319	C	0.034	4.3E-10	Same	0.27	0.035	Same	0.01	Same	0.03
rs7319045	A	0.029	4.5E-10	Same	0.01	0.078	Same	0.57	Same	0.01
rs889014	C	0.029	4.5E-10	Same	0.38	0.025	Same	0.70	Same	0.34
rs6879260	C	0.028	5.6E-10	Same	0.99	0.000	Same	0.13	Same	0.50
rs9969804	A	0.028	5.6E-10	Same	0.47	0.021	Opposite	0.71	Same	0.62
rs237743	A	0.034	7.2E-10	Same	0.24	0.041	Same	0.05	Same	0.06
rs6439167	C	0.034	7.2E-10	Same	0.12	0.049	Same	0.73	Same	0.12
rs274546	G	0.028	8.5E-10	Same	0.01	0.066	Opposite	0.41	Same	0.07
rs12153391	C	0.033	8.7E-10	Same	0.55	0.018	Same	0.15	Same	0.25
rs7155279	G	0.029	8.9E-10	Opposite	0.74	-0.009	Same	0.53	Opposite	0.98
rs2110001	G	0.033	9.8E-10	Same	0.15	0.042	Same	0.03	Same	0.03

SNP	GIANT meta-analysis			FHS (family-based test)			ERF (family-based test)		Meta-analysis FHS+ERF (family-based test)	
	Height Increasing allele	BETA	*P*-value	Direction of effect relative to GIANT	*P*-value	BETA relative to GIANT	Direction of effect relative to GIANT	*P*-value	Direction of effect relative to GIANT	*P*-value
rs422421	C	0.033	1.4E-09	Same	9.0E-05	0.126	Same	0.05	Same	1.2E-05
rs543650	G	0.032	1.4E-09	Same	0.27	0.037	Same	0.51	Same	0.20
rs634552	T	0.041	1.4E-09	Same	0.74	0.014	Opposite	0.10	Opposite	0.68
rs11144688	G	0.055	1.5E-09	Same	0.63	0.022	Same	0.34	Same	0.40
rs526896	T	0.032	1.9E-09	Same	0.97	0.001	Opposite	0.37	Opposite	0.72
rs1809889	T	0.032	1.9E-09	Opposite	0.48	-0.023	Same	0.10	Same	0.92
rs11118346	C	0.026	2.2E-09	Same	0.04	0.057	Same	0.68	Same	0.04
rs17318596	A	0.029	3.0E-09	Same	0.72	0.010	Opposite	0.62	Same	0.92
rs10037512	T	0.027	3.8E-09	Same	0.06	0.051	Same	0.73	Same	0.07
rs3782089	C	0.058	5.9E-09	Same	0.99	0.001	Same	0.57	Same	0.80
rs11684404	C	0.027	6.4E-09	Same	0.20	0.038	Same	0.36	Same	0.12
rs4986172	C	0.028	7.1E-09	Same	0.35	0.026	Opposite	0.12	Same	0.88
rs2834442	A	0.027	7.3E-09	Same	0.08	0.049	Opposite	0.82	Same	0.13
rs11958779	G	0.028	8.0E-09	Opposite	0.80	-0.008	Opposite	0.80	Opposite	0.73
rs2066807	G	0.052	9.6E-09	Same	0.03	0.129	Opposite	0.44	Same	0.10
rs10799445	A	0.031	1.2E-08	Same	0.51	0.021	Opposite	0.50	Same	0.77
rs227724	T	0.027	1.2E-08	Same	0.15	0.043	Opposite	0.87	Same	0.23
rs8052560	A	0.039	1.4E-08	Same	0.01	0.031	Opposite	0.34	Same	0.06
rs9863706	C	0.030	1.5E-08	Same	0.01	0.086	Opposite	0.57	Same	0.03
rs1325598	G	0.026	1.6E-08	Same	0.03	0.058	Same	0.62	Same	0.03
rs1582931	G	0.025	2.1E-08	Same	0.01	0.074	Same	0.38	Same	0.01
rs2629046	T	0.025	2.2E-08	Same	0.64	0.013	Same	0.62	Same	0.52
rs9472414	T	0.031	2.4E-08	Same	0.33	0.094	Same	0.48	Same	0.24
rs2145998	T	0.025	2.7E-08	Same	0.35	0.027	Opposite	0.80	Same	0.46
rs2237886	T	0.043	3.1E-08	Same	0.02	0.117	Same	0.52	Same	0.02
rs9844666	G	0.028	3.1E-08	Same	0.25	0.037	Opposite	0.25	Same	0.60
rs3129109	C	0.026	3.3E-08	Opposite	0.43	-0.022	Opposite	0.72	Opposite	0.38
rs10152591	A	0.045	3.5E-08	Same	0.20	0.063	Same	0.10	Same	0.06
rs1741344	C	0.026	3.5E-08	Same	0.05	0.057	Same	0.26	Same	0.02
rs2336725	C	0.026	3.5E-08	Same	0.05	0.051	Same	0.63	Same	0.05
rs26868	A	0.030	3.5E-08	Same	0.79	0.008	Same	0.58	Same	0.63
rs2341459	T	0.028	3.6E-08	Same	0.12	0.050	Opposite	0.82	Same	0.19
rs6457620	G	0.024	3.6E-08	Same	0.93	0.003	Opposite	0.69	Opposite	0.93
rs4470914	T	0.033	3.8E-08	Same	1.00	0.000	Same	1.00	Same	1.00
rs17780086	A	0.035	4.4E-08	Same	0.31	0.041	Opposite	0.97	Same	0.36
rs1013209	C	0.029	4.5E-08	Opposite	0.74	-0.011	Opposite	0.94	Opposite	0.74
rs751543	T	0.029	4.5E-08	Same	0.95	0.002	Opposite	0.02	Opposite	0.32
rs17081935	T	0.031	4.8E-08	Opposite	0.75	-0.011	Same	0.27	Same	0.85
rs4821083	T	0.033	4.8E-08	Same	0.07	0.063	Same	0.54	Same	0.06
rs12534093	T	0.030	5.6E-08	Same	0.59	0.018	Opposite	0.97	Same	0.64

SNP	GIANT meta-analysis			FHS (family-based test)			ERF (family-based test)		Meta-analysis FHS+ERF (family-based test)	
	Height Increasing allele	BETA	*P*-value	Direction of effect relative to GIANT	*P*-value	BETA relative to GIANT	Direction of effect relative to GIANT	*P*-value	Direction of effect relative to GIANT	*P*-value
rs2072153	C	0.026	6.7E-08	Same	0.41	0.026	Same	0.42	Same	0.27
rs7567288	C	0.031	6.7E-08	Opposite	0.93	-0.003	Same	0.90	Opposite	0.98
rs2247341	A	0.025	6.8E-08	Same	0.42	0.022	Same	0.12	Same	0.16
rs7926971	G	0.024	7.3E-08	Same	1.6E-03	0.082	Opposite	0.04	Same	0.05
rs7332115	G	0.025	7.6E-08	Same	0.24	0.033	Same	0.15	Same	0.09
rs1047014	C	0.029	1.1E-07	Same	0.41	0.028	Opposite	0.49	Same	0.66
rs17806888	T	0.040	1.1E-07	Opposite	0.04	0.077	Same	0.42	Same	0.03
rs2597513	C	0.039	1.1E-07	Same	0.08	0.078	Same	0.45	Same	0.06
rs7971536	T	0.025	1.1E-07	Same	0.17	0.036	Same	0.72	Same	0.17
rs8181166	C	0.025	1.1E-07	Opposite	0.35	-0.025	Opposite	0.82	Opposite	0.35
rs822552	G	0.030	1.3E-07	Opposite	0.44	-0.025	Opposite	0.95	Opposite	0.47
rs12694997	G	0.027	1.8E-07	Same	0.05	0.063	Opposite	0.20	Same	0.22
rs4640244	A	0.028	2.0E-07	Opposite	0.67	0.013	Same	0.05	Same	0.21
rs7178424	C	0.024	2.2E-07	Same	0.02	0.067	Opposite	0.29	Same	0.10
rs7507204	C	0.028	2.3E-07	Same	0.05	0.071	Same	0.51	Same	0.04
rs11648796	G	0.031	2.4E-07	NA	1.00	NA	Same	0.65	Same	0.65
rs2279008	T	0.031	2.4E-07	Same	0.44	0.027	Same	0.15	Same	0.18
rs961764	G	0.023	2.4E-07	Same	0.16	0.038	Same	0.48	Same	0.11
rs4072910	G	0.029	2.5E-07	NA	1.00	NA	Same	0.49	Same	0.49
rs13088462	C	0.054	3.1E-07	Same	0.96	0.003	Opposite	0.66	Opposite	0.88
rs2778031	T	0.027	3.6E-07	Same	0.04	0.066	Same	0.59	Same	0.04
rs1351164	T	0.028	3.7E-07	Same	0.78	0.010	Same	0.96	Same	0.78
rs1330	T	0.024	4.4E-07	Opposite	0.49	-0.018	Same	0.58	Opposite	0.70
rs9456307	T	0.050	4.6E-07	Opposite	0.56	-0.032	Same	0.94	Opposite	0.62
rs11867479	T	0.024	4.9E-07	Same	0.07	0.051	Same	0.95	Same	0.10
rs7864648	T	0.025	4.9E-07	Opposite	0.67	-0.013	Same	0.44	Opposite	0.97
rs17391694	T	0.040	5.9E-07	Opposite	0.43	-0.042	Same	0.51	Opposite	0.67
rs10863936	G	0.022	6.2E-07	Same	0.02	0.060	Opposite	0.90	Same	0.05
rs654723	A	0.024	6.7E-07	Same	0.38	0.024	Opposite	0.86	Same	0.48
rs7567851	C	0.041	7.5E-07	Same	0.32	0.046	Opposite	0.93	Same	0.40
rs11599750	C	0.023	7.6E-07	Same	0.38	0.025	Same	0.18	Same	0.17
rs7112925	C	0.023	8.5E-07	Same	0.23	0.034	Same	0.08	Same	0.06
rs1046943	A	0.022	8.6E-07	Same	0.42	0.023	Same	0.28	Same	0.23
rs9835332	G	0.022	8.7E-07	Same	0.13	0.038	Same	0.29	Same	0.07
rs4605213	C	0.023	9.3E-07	Opposite	0.73	-0.011	Same	0.49	Opposite	0.99
rs12474201	A	0.023	1.0E-06	Same	0.38	0.025	Opposite	0.37	Same	0.69
rs862034	G	0.023	1.1E-06	Same	0.05	0.059	Same	0.43	Same	0.03
rs1043515	G	0.022	1.3E-06	Same	0.15	0.039	Same	0.05	Same	0.03
rs7697556	T	0.022	1.3E-06	Same	0.02	0.063	Opposite	0.62	Same	0.07
rs7909670	C	0.022	1.3E-06	Opposite	0.77	-0.008	Same	0.71	Opposite	0.92

SNP	GIANT meta-analysis			FHS (family-based test)			ERF (family-based test)		Meta-analysis FHS+ERF (family-based test)	
	Height Increasing allele	BETA	*P*-value	Direction of effect relative to GIANT	*P*-value	BETA relative to GIANT	Direction of effect relative to GIANT	*P*-value	Direction of effect relative to GIANT	*P*-value
rs1468758	C	0.026	1.5E-06	Same	0.76	0.009	Opposite	0.88	Same	0.84
rs3110496	G	0.023	1.6E-06	Same	0.01	0.078	Same	0.12	Same	0.00
rs10874746	C	0.022	1.7E-06	Opposite	0.29	-0.030	Same	0.03	Opposite	0.98
rs12902421	C	0.069	1.7E-06	Same	0.11	0.145	Opposite	0.45	Same	0.27
rs425277	T	0.024	1.7E-06	Same	0.09	0.052	Same	0.99	Same	0.13
rs6699417	T	0.022	1.7E-06	Same	0.85	0.006	Opposite	0.51	Opposite	0.91
rs891088	G	0.025	1.7E-06	Opposite	0.70	-0.012	Same	0.48	Opposite	0.96
rs1738475	C	0.022	1.9E-06	Same	0.24	0.030	Opposite	0.90	Same	0.32
rs4601530	C	0.024	2.0E-06	Opposite	0.79	-0.008	Same	0.69	Opposite	0.95
rs6714546	G	0.025	2.2E-06	Same	0.16	0.045	Opposite	0.78	Same	0.25
rs955748	G	0.024	2.2E-06	Same	0.57	0.018	Opposite	0.59	Same	0.78
rs10010325	A	0.021	2.3E-06	Same	0.45	0.019	Same	0.33	Same	0.27
rs1257763	A	0.069	2.5E-06	Same	0.02	0.150	Opposite	0.71	Same	0.05
rs16964211	G	0.051	2.5E-06	Same	0.94	0.005	Opposite	0.14	Opposite	0.57
rs1814175	T	0.023	2.6E-06	Same	0.43	0.023	Same	0.01	Same	0.07
rs6959212	C	0.023	2.8E-06	Same	0.60	0.014	Same	0.19	Same	0.30
rs1659127	A	0.024	2.9E-06	Opposite	0.41	-0.023	Opposite	0.16	Opposite	0.17
rs7853377	G	0.026	3.1E-06	Same	0.90	0.004	Opposite	0.92	Same	0.94
rs7532866	A	0.022	3.3E-06	Same	0.24	0.033	Opposite	0.78	Same	0.35
rs17782313	C	0.025	3.5E-06	Opposite	0.60	-0.017	Same	0.28	Same	1.00
rs13177718	C	0.041	4.1E-06	Opposite	0.51	-0.033	Opposite	0.70	Opposite	0.45
rs5017948	A	0.027	4.7E-06	Same	8.9E-04	0.126	Same	0.07	Same	1.6E-04
rs1570106	C	0.026	4.9E-06	Same	0.59	0.019	Opposite	0.14	Opposite	0.87
rs494459	T	0.021	4.9E-06	Opposite	0.14	-0.040	Same	0.10	Opposite	0.56

Supplementary Table 4. Estimated number of height loci for each of the effect sizes observed in Stage 2 given the power to detect the association in Stage 1

	SNP	MAF	Mean Difference	Standardized Effect size	Power	Estimated number of loci[†]
1	rs1325598	0.435	-0.016	1.18E-04	0.0151	74.5
2	rs9472414	0.217	-0.019	1.21E-04	0.0169	63.4
3	rs7155279	0.356	-0.016	1.22E-04	0.0171	62.3
4	rs1741344	0.375	0.016	1.23E-04	0.0178	59.3
5	rs1013209	0.252	-0.019	1.30E-04	0.0226	47.6
6	rs12470505	0.095	-0.028	1.35E-04	0.0263	41.5
7	rs6684205	0.294	0.019	1.45E-04	0.0350	30.9
8	rs2341459	0.279	0.020	1.53E-04	0.0434	24.6
9	rs4470914	0.178	0.023	1.53E-04	0.0436	24.5
10	rs6457821	0.018	-0.068	1.65E-04	0.0587	17.7
11	rs751543	0.275	-0.021	1.68E-04	0.0619	16.9
12	rs10838801	0.307	0.020	1.70E-04	0.0655	15.9
13	rs7319045	0.403	0.019	1.72E-04	0.0681	15.2
14	rs1582931	0.480	-0.019	1.82E-04	0.0848	12.2
15	rs4821083	0.151	-0.027	1.91E-04	0.1018	10.1
16	rs10152591	0.091	-0.034	1.93E-04	0.1044	9.8
17	rs310405	0.478	-0.020	2.00E-04	0.1185	8.7
18	rs6473015	0.274	0.023	2.10E-04	0.1426	7.3
19	rs9360921	0.113	0.033	2.15E-04	0.1529	6.7
20	rs12153391	0.250	-0.024	2.18E-04	0.1611	6.3
21	rs4665736	0.455	-0.021	2.21E-04	0.1681	6.0
22	rs7027110	0.230	0.025	2.21E-04	0.1692	6.0
23	rs2154319	0.244	0.025	2.27E-04	0.1839	5.5
24	rs17081935	0.203	0.028	2.48E-04	0.2444	4.2
25	rs11118346	0.477	-0.023	2.57E-04	0.2721	3.7
26	rs7849585	0.333	0.024	2.58E-04	0.2750	3.7
27	rs2629046	0.440	-0.023	2.63E-04	0.2906	3.5
28	rs422421	0.216	-0.028	2.64E-04	0.2927	3.5
29	rs2834442	0.343	-0.024	2.68E-04	0.3079	3.3
30	rs12680655	0.413	-0.024	2.75E-04	0.3286	3.1
31	rs7466269	0.370	-0.024	2.78E-04	0.3381	3.0
32	rs2638953	0.318	-0.026	2.82E-04	0.3529	2.9
33	rs11958779	0.306	0.026	2.90E-04	0.3783	2.7
34	rs634552	0.146	0.035	2.99E-04	0.4087	2.5
35	rs11144688	0.106	-0.040	3.03E-04	0.4230	2.4
36	rs720390	0.387	0.026	3.28E-04	0.5092	2.0
37	rs526896	0.279	-0.029	3.29E-04	0.5119	2.0
38	rs2110001	0.319	0.028	3.31E-04	0.5180	2.0
39	rs12982744	0.389	0.027	3.41E-04	0.5519	1.8
40	rs473902	0.079	-0.050	3.62E-04	0.6161	1.6
41	rs3782089	0.060	-0.057	3.67E-04	0.6317	1.6
42	rs9863706	0.216	-0.033	3.69E-04	0.6374	1.6
43	rs572169	0.311	0.030	3.73E-04	0.6494	1.5
44	rs2145998	0.499	0.027	3.75E-04	0.6564	1.5
45	rs2856321	0.358	0.029	3.76E-04	0.6587	1.5
46	rs2336725	0.450	0.028	3.85E-04	0.6842	1.5
47	rs10799445	0.235	-0.033	3.91E-04	0.6998	1.4
48	rs11684404	0.349	0.029	3.93E-04	0.7038	1.4
49	rs6439167	0.204	-0.035	3.97E-04	0.7163	1.4
50	rs1490384	0.499	0.028	3.98E-04	0.7169	1.4
51	rs11830103	0.213	0.035	4.01E-04	0.7253	1.4
52	rs2093210	0.405	0.029	4.08E-04	0.7431	1.3

	SNP	MAF	Mean Difference	Standardized Effect size	Power	Estimated number of loci[†]
53	rs2066807	0.070	0.058	4.43E-04	0.8183	1.2
54	rs2237886	0.099	0.050	4.53E-04	0.8359	1.2
55	rs4282339	0.203	-0.038	4.57E-04	0.8426	1.2
56	rs889014	0.360	-0.032	4.72E-04	0.8669	1.2
57	rs5742915	0.451	0.031	4.73E-04	0.8682	1.2
58	rs274546	0.406	-0.032	4.88E-04	0.8890	1.1
59	rs3764419	0.388	-0.032	4.89E-04	0.8910	1.1
60	rs1173727	0.407	0.032	4.94E-04	0.8974	1.1
61	rs227724	0.355	0.034	5.29E-04	0.9332	1.1
62	rs9969804	0.447	0.033	5.52E-04	0.9500	1.1
63	rs17511102	0.084	0.061	5.64E-04	0.9576	1.1
64	rs10770705	0.326	0.036	5.66E-04	0.9589	1.0
65	rs1950500	0.287	0.038	5.79E-04	0.9655	1.0
66	rs1708299	0.300	0.038	5.91E-04	0.9709	1.0
67	rs3812163	0.448	0.035	6.13E-04	0.9788	1.0
68	rs17318596	0.347	0.037	6.27E-04	0.9828	1.0
69	rs4986172	0.349	-0.037	6.35E-04	0.9848	1.0
70	rs7274811	0.240	-0.042	6.50E-04	0.9878	1.0
71	rs543650	0.415	-0.037	6.76E-04	0.9919	1.0
72	rs2079795	0.322	0.040	6.88E-04	0.9933	1.0
73	rs6457620	0.482	0.037	6.98E-04	0.9944	1.0
74	rs2145272	0.346	0.040	7.06E-04	0.9950	1.0
75	rs9967417	0.409	0.039	7.16E-04	0.9958	1.0
76	rs798489	0.301	-0.042	7.43E-04	0.9973	1.0
77	rs2780226	0.081	0.072	7.62E-04	0.9981	1.0
78	rs26868	0.455	0.040	7.74E-04	0.9984	1.0
79	rs2871865	0.115	-0.062	7.81E-04	0.9986	1.0
80	rs17346452	0.269	0.045	7.83E-04	0.9987	1.0
81	rs2580816	0.183	-0.051	7.91E-04	0.9988	1.0
82	rs10037512	0.449	-0.040	7.96E-04	0.9989	1.0
83	rs1046934	0.363	0.042	7.96E-04	0.9989	1.0
84	rs6569648	0.231	0.047	7.99E-04	0.9990	1.0
85	rs3129109	0.379	-0.041	8.06E-04	0.9991	1.0
86	rs10748128	0.351	0.042	8.07E-04	0.9991	1.0
87	rs9428104	0.241	-0.048	8.39E-04	0.9995	1.0
88	rs16942341	0.029	-0.124	8.52E-04	0.9996	1.0
89	rs11107116	0.228	0.050	8.68E-04	0.9997	1.0
90	rs7460090	0.127	-0.064	9.18E-04	0.9999	1.0
91	rs237743	0.214	0.053	9.26E-04	0.9999	1.0
92	rs6470764	0.189	-0.056	9.72E-04	1.0000	1.0
93	rs4800452	0.214	-0.056	1.05E-03	1.0000	1.0
94	rs788867	0.320	0.050	1.07E-03	1.0000	1.0
95	rs2665838	0.268	0.052	1.07E-03	1.0000	1.0
96	rs7759938	0.309	0.051	1.10E-03	1.0000	1.0
97	rs806794	0.315	-0.051	1.10E-03	1.0000	1.0
98	rs11259936	0.481	-0.047	1.12E-03	1.0000	1.0
99	rs11205277	0.416	0.048	1.13E-03	1.0000	1.0
100	rs2284746	0.482	-0.049	1.20E-03	1.0000	1.0
101	rs7763064	0.291	-0.055	1.23E-03	1.0000	1.0
102	rs3791675	0.236	-0.059	1.25E-03	1.0000	1.0
103	rs2256183	0.450	0.051	1.29E-03	1.0000	1.0
104	rs42235	0.308	0.062	1.62E-03	1.0000	1.0
105	rs6449353	0.149	-0.081	1.65E-03	1.0000	1.0
106	rs3118905	0.289	-0.063	1.65E-03	1.0000	1.0
107	rs7689420	0.165	-0.080	1.76E-03	1.0000	1.0

	SNP	MAF	Mean Difference	Standardized Effect size	Power	Estimated number of loci[†]
108	rs143384	0.435	0.061	1.83E-03	1.0000	1.0
109	rs1351394	0.496	0.073	2.63E-03	1.0000	1.0
110	rs724016	0.443	0.075	2.78E-03	1.0000	1.0
Estimated # of total loci						697.3
Total phenotypic variance explained (%)						15.7
Total genetic variance explained (%)						19.6

[†] Projections are made only for effect sizes for SNPs that reached $P<5x10^{-8}$ in Stage 1 and had at least 1% power.

Supplementary Table 5. Dominant, recessive and dominance deviation results for nominally significant (dominance deviation $P<0.05$) lead SNPs at the 207 loci with $P<5\times10^{-6}$ in Stage 1. The effect allele is the height increasing allele from Stage 1. Only SNPs with a dominance deviation $P<0.05$ are presented. The analysis is based on a subset of 103,034 individuals from Stage 1. None of the results remain significant at $P<0.05$ after correcting for the number of tests performed.

Marker	Effect allele	Other Allele	Additive beta (SE)	Additive P	Dominant beta (SE)	Dominant P	Recessive beta (SE)	Recessive P	Dom Dev beta (SE)	Dom Dev P
rs1047014	C	T	0.031 (0.006)	2.2×10^{-08}	0.041 (0.006)	9.3×10^{-11}	0.017 (0.013)	0.1991	0.026 (0.008)	0.002
rs17122670	A	G	0.032 (0.007)	8.8×10^{-06}	0.038 (0.008)	3.6×10^{-07}	-0.015 (0.027)	0.5645	0.044 (0.015)	0.003
rs425277	T	C	0.027 (0.005)	7.5×10^{-08}	0.023 (0.006)	2.0×10^{-04}	0.064 (0.012)	3.0×10^{-08}	-0.021 (0.008)	0.005
rs12982744	G	C	0.033 (0.005)	2.0×10^{-12}	0.049 (0.007)	9.1×10^{-14}	0.029 (0.009)	6.8×10^{-04}	0.018 (0.006)	0.006
rs1257763	A	G	0.077 (0.014)	4.0×10^{-08}	0.054 (0.012)	1.3×10^{-05}	0.358 (0.094)	1.3×10^{-04}	-0.132 (0.049)	0.007
rs2408058	G	A	0.035 (0.006)	8.4×10^{-09}	0.102 (0.02)	2.5×10^{-07}	0.033 (0.007)	2.5×10^{-06}	0.031 (0.012)	0.008
rs1708299	A	G	0.046 (0.005)	3.2×10^{-22}	0.048 (0.006)	2.0×10^{-14}	0.087 (0.01)	6.0×10^{-17}	-0.019 (0.007)	0.009
rs13177718	C	T	0.046 (0.009)	1.8×10^{-07}	0.164 (0.04)	4.3×10^{-05}	0.038 (0.009)	1.6×10^{-05}	0.055 (0.022)	0.012
rs9456307	T	A	0.056 (0.01)	1.7×10^{-08}	0.221 (0.053)	3.3×10^{-05}	0.05 (0.01)	8.5×10^{-07}	0.071 (0.028)	0.013
rs7601531	T	C	0.022 (0.005)	2.8×10^{-06}	0.041 (0.008)	6.5×10^{-07}	0.018 (0.007)	7.0×10^{-03}	0.015 (0.006)	0.019
rs2341459	T	C	0.031 (0.005)	7.1×10^{-10}	0.041 (0.006)	5.3×10^{-11}	0.028 (0.012)	1.9×10^{-02}	0.017 (0.008)	0.028
rs34651	C	T	0.057 (0.009)	4.0×10^{-11}	0.058 (0.009)	1.5×10^{-11}	0.017 (0.038)	0.65	0.044 (0.021)	0.032
rs1351394	T	C	0.059 (0.004)	3.1×10^{-40}	0.069 (0.007)	8.6×10^{-22}	0.085 (0.007)	1.7×10^{-32}	-0.013 (0.006)	0.032
rs17318596	A	G	0.032 (0.005)	3.5×10^{-11}	0.043 (0.006)	1.7×10^{-11}	0.029 (0.009)	8.4×10^{-04}	0.014 (0.007)	0.036
rs4072910	G	C	0.033 (0.006)	6.0×10^{-09}	0.051 (0.009)	1.2×10^{-08}	0.028 (0.008)	5.1×10^{-04}	0.015 (0.007)	0.036
rs42235	T	C	0.065 (0.005)	2.5×10^{-38}	0.067 (0.006)	2.5×10^{-26}	0.108 (0.011)	3.7×10^{-24}	-0.015 (0.007)	0.037
rs11648796	G	A	0.028 (0.006)	2.3×10^{-06}	0.034 (0.007)	3.6×10^{-07}	0.019 (0.014)	0.1882	0.019 (0.009)	0.040
rs10799445	A	C	0.028 (0.005)	1.0×10^{-07}	0.023 (0.014)	9.9×10^{-02}	0.037 (0.006)	7.8×10^{-09}	-0.018 (0.009)	0.043
rs822552	G	C	0.037 (0.006)	8.1×10^{-11}	0.043 (0.006)	1.6×10^{-11}	0.034 (0.013)	9.8×10^{-03}	0.017 (0.008)	0.044

Supplementary Table 6. Nominally significant (P<0.001) gene x gene interaction results for all pairwise tests between the lead SNPs at 207 loci with $P<5x10^{-6}$ in Stage 1. The betas refer to the height increasing alleles from Stage 1. The additive effect results for each individual SNP is based on the Stage 1 meta-analysis. The results for the pairwise interaction analysis are based on a subset of 103,034 individuals from Stage 1.

Markers (SNP1/SNP2)	Additive effect SNP1	Additive effect SNP1 P	Additive effect SNP2	Additive effect SNP2 P	Pairwise interaction beta (SE)	Interaction P
rs2145998 rs6470764	0.025	$2.7x10^{-08}$	0.047	$5.9x10^{-17}$	0.036 (0.008)	$7.7x10^{-06}$
rs1741344 rs4800452	0.026	$3.5x10^{-08}$	0.048	$2.4x10^{-17}$	-0.035 (0.009)	$3.8x10^{-05}$
rs7853377 rs955748	0.026	$3.1x10^{-06}$	0.024	$2.2x10^{-06}$	0.035 (0.009)	$6.1x10^{-05}$
rs494459 rs6470764	0.021	$4.9x10^{-06}$	0.047	$5.9x10^{-17}$	-0.032 (0.008)	0.000104
rs3110496 rs7759938	0.023	$1.6x10^{-06}$	0.042	$8.7x10^{-18}$	-0.028 (0.007)	0.000146
rs1814175 rs9428104	0.023	$2.6x10^{-06}$	0.038	$8.9x10^{-13}$	-0.030 (0.008)	0.000163
rs3110496 rs7697556	0.023	$1.6x10^{-06}$	0.022	$1.3x10^{-06}$	0.025 (0.007)	0.000218
rs143384 rs17346452	0.064	$4.9x10^{-39}$	0.038	$3.3x10^{-14}$	-0.028 (0.008)	0.000231
rs1351164 rs6684205	0.028	$3.7x10^{-07}$	0.033	$2.0x10^{-11}$	-0.031 (0.009)	0.000356
rs1013209 rs16942341	0.029	$4.5x10^{-08}$	0.134	$1.3x10^{-17}$	0.095 (0.027)	0.000357
rs16942341 rs5017948	0.134	$1.3x10^{-17}$	0.027	$4.7x10^{-06}$	0.107 (0.030)	0.00042
rs2408058 rs6879260	0.035	$2.2x10^{-08}$	0.028	$5.6x10^{-10}$	-0.031 (0.009)	0.000507
rs806794 rs9428104	0.053	$5.5x10^{-26}$	0.038	$8.9x10^{-13}$	-0.029 (0.008)	0.000535
rs16892729 rs2154319	0.025	$1.3x10^{-06}$	0.034	$4.3x10^{-10}$	-0.031 (0.009)	0.000591
rs17081935 rs2110001	0.031	$4.8x10^{-08}$	0.033	$9.8x10^{-10}$	0.032 (0.009)	0.00062
rs4640244 rs9428104	0.028	$2.0x10^{-07}$	0.038	$8.9x10^{-13}$	-0.030 (0.009)	0.000658
rs1173727 rs2580816	0.036	$4.0x10^{-15}$	0.041	$1.8x10^{-12}$	0.029 (0.009)	0.000713
rs1046934 rs17017854	0.046	$6.4x10^{-22}$	0.028	$4.0x10^{-06}$	0.030 (0.009)	0.000817
rs2154319 rs6772112	0.034	$4.3x10^{-10}$	0.046	$1.6x10^{-06}$	0.054 (0.016)	0.00088
rs3791675 rs6684205	0.050	$2.4x10^{-20}$	0.033	$2.0x10^{-11}$	0.028 (0.008)	0.000935
rs3791675 rs7759938	0.050	$2.4x10^{-20}$	0.042	$8.7x10^{-18}$	0.027 (0.008)	0.000972

Supplementary Table 7. Significant associations between height SNPs and cis gene expression (cis-eQTLs) in five different tissues.

Height SNP	Chr	Position	Nearby Gene	Height increasing allele	Tissue	Gene	Effect[a]	*P*	P_{adj} [b]	Peak SNP [c]	r^2 [d]	*P*	P_{adj} [e]	High correlation (r^2>0.8) with Peak SNP
Lymphocyte														
rs1043515	17	34175722	*PIP4K2B*	G	Lymphocyte	*CCDC49*	-	2.43E-09	0.77	rs11653487	0.66	1.70E-12	0.07	
					Lymphocyte	*PSMB3*	-	5.17E-06	0.03	rs8071479	0.21	2.14E-06	0.01	
					Lymphocyte	*RPL23*	-	4.79E-06	0.16	rs1239177	0.18	5.26E-15	2.89E-10	
rs1046943	6	109890634	*ZBTB24*	A	Lymphocyte	*AKD1*	+	9.91E-09	NA	rs10872046	NA	2.34E-10	NA	
					Lymphocyte	*MICAL1*	+	2.18E-06	0.42	rs6916579	0.63	4.20E-13	1.56E-04	
					Lymphocyte	*ZBTB24*	+	4.27E-13	0.93	rs3799842	0.90	6.47E-14	0.53	YES
rs10799445	1	225978506	*JMJD4*	A	Lymphocyte	*ZNF678*	-	1.41E-19	0.42	rs6426470	0.74	2.51E-25	0.03	
rs10863936	1	210304421	*DTL*	G	Lymphocyte	*INTS7*	-	1.91E-33	1.00	rs10863936	1.00	1.91E-33	1.00	YES
rs11599750	10	101795432	*CPN1*	C	Lymphocyte	*DNMBP*	+	2.97E-05	0.22	rs4148397	0.08	1.81E-15	7.47E-11	
rs11648796	16	732191	*NARFL*	G	Lymphocyte	*FAM173A*	+	9.45E-07	0.99	rs1406814	0.88	1.95E-07	0.52	YES
					Lymphocyte	*METRN*	+	3.08E-11	0.83	rs3169403	0.79	2.34E-12	0.35	
rs11830103	12	122389499	*SBNO1*	G	Lymphocyte	*ARL6IP4*	-	1.06E-11	0.55	rs11057276	0.46	1.84E-14	0.02	
					Lymphocyte	*CDK2AP1*	-	2.90E-17	0.93	rs1060105	0.89	2.44E-20	0.09	YES
					Lymphocyte	*MPHOSPH9*	-	2.44E-14	0.75	rs883263	0.74	1.54E-16	0.13	
					Lymphocyte	*SBNO1*	-	2.06E-11	0.12	rs10773000	0.32	2.57E-12	0.05	
					Lymphocyte	*SETD8*	-	2.02E-07	0.44	rs1727295	0.50	2.67E-08	0.15	
rs11958779	5	55037656	*SLC38A9*	G	Lymphocyte	*SLC38A9*	+	8.41E-13	0.95	rs4865615	0.79	6.51E-15	0.19	
rs12474201	2	46774789	*SOCS5*	A	Lymphocyte	*CRIPT*	+	1.20E-05	0.56	rs3087822	0.01	1.55E-22	1.30E-16	
rs12534093	7	23469499	*IGF2BP3*	T	Lymphocyte	*CCDC126*	-	3.49E-06	0.25	rs13227748	0.16	8.41E-36	1.76E-31	
					Lymphocyte	*TRA2A*	-	1.33E-05	0.02	rs4722238	0.10	3.48E-16	6.44E-13	
rs12694997	2	241911659	*SEPT2*	G	Lymphocyte	*FARP2*	-	6.12E-08	0.02	rs3755325	0.22	5.23E-10	4.22E-04	
					Lymphocyte	*SEPT2*	+	1.41E-20	0.96	rs11679955	0.96	1.14E-20	0.93	YES
rs1330	11	17272605	*NUCB2*	T	Lymphocyte	*NUCB2*	-	5.31E-08	0.75	rs214097	0.39	2.44E-19	5.86E-10	
rs143384	20	33489170	*GDF5*	G	Lymphocyte	*CPNE1*	-	9.60E-08	0.40	rs6060535	0.13	5.59E-38	1.52E-30	
					Lymphocyte	*RBM39*	+	3.43E-06	0.37	rs1204656	0.54	1.30E-06	0.22	
					Lymphocyte	*UQCC*	-	8.33E-08	0.89	rs6060402	0.74	1.44E-08	0.51	
rs1582931	5	122685098	*CEP120*	G	Lymphocyte	*CCDC100*	+	3.15E-06	4.43E-05	rs1465291	0.00	5.31E-07	6.48E-06	
					Lymphocyte	*CSNK1G3*	+	1.28E-05	NA	rs11743543	NA	1.00E-12	NA	
rs1708299	7	28156471	*JAZF1*	A	Lymphocyte	*JAZF1*	+	1.11E-06	0.28	rs1635853	0.69	2.45E-08	0.01	
rs17318596	19	46628935	*ATP5SL*	A	Lymphocyte	*ATP5SL*	-	3.98E-05	NA	rs12495167	NA	2.30E-06	NA	
rs17346452	1	170319910	*DNM3*	C	Lymphocyte	*DNM3*	-	3.21E-07	0.93	rs17277008	0.83	7.98E-08	0.47	YES
rs17780086	17	27367395	*LRRC37B*	A	Lymphocyte	*C17orf79*	-	1.81E-08	0.52	rs2074101	0.66	6.70E-11	0.02	
rs2066807	12	55026949	*STAT2*	G	Lymphocyte	*SPRYD4*	+	1.38E-06	0.87	rs2657880	0.08	1.15E-29	4.17E-22	
					Lymphocyte	*TMEM4*	-	1.37E-20	0.98	rs1274493	1.00	7.44E-23	0.13	YES

rs2072153	17	44745013	*ZNF652*	C	Lymphocyte	*243495_s_at*	+	5.64E-07	0.90	rs11657381	0.09	4.31E-36	2.67E-29	
					Lymphocyte	*ZNF652*	+	1.72E-05	NA	rs12273855	NA	2.44E-07	NA	
rs2247341	4	1671115	*SLBP/FGFR3*	A	Lymphocyte	*FAM53A*	-	3.40E-06	0.09	rs744658	0.09	6.72E-18	1.39E-13	
					Lymphocyte	*SLBP*	-	5.01E-06	0.98	rs1530588	1.00	3.48E-06	0.87	YES
rs2256183	6	31488508	*MICA*	A	Lymphocyte	*1557242_at*	+	2.35E-07	0.12	rs2844521	0.40	6.72E-24	7.31E-12	
					Lymphocyte	*HLA-B*	+	2.06E-05	0.05	rs3871248	0.12	1.00E-17	2.40E-13	
					Lymphocyte	*HLA-C*	+	4.39E-05	4.77E-07	rs9263875	0.01	6.09E-26	5.04E-27	
					Lymphocyte	*LOC285835*	+	8.89E-12	0.95	rs2428486	0.40	1.10E-27	6.00E-13	
rs2336725	3	53093779	*RTF1*	C	Lymphocyte	*RFT1*	+	7.81E-13	0.88	rs2163167	0.78	3.41E-14	0.37	
					Lymphocyte	*SFMBT1*	-	9.13E-07	0.79	rs2336723	0.79	7.22E-07	0.74	
rs237743	20	47336426	*ZNFX1*	A	Lymphocyte	*ARFGEF2*	+	4.22E-12	0.96	rs730544	0.43	4.59E-30	4.64E-16	
					Lymphocyte	*C20orf199*	-	2.12E-16	1.00	rs237743	1.00	2.12E-16	1.00	YES
rs2638953	12	28425682	*CCDC91*	C	Lymphocyte	*CCDC91*	+	8.99E-10	0.79	rs7307078	0.76	1.15E-12	0.06	
rs2665838	17	59320197	*CSH1/GH1*	G	Lymphocyte	*FTSJ3*	+	3.83E-15	0.005	rs2727276	0.28	2.47E-33	1.98E-20	
					Lymphocyte	*PSMC5*	+	1.16E-05	NA	rs1405489	NA	1.26E-06	NA	
rs3110496	17	24941897	*ANKRD13B*	G	Lymphocyte	*ABHD15*	-	6.10E-05	NA	rs12892137	NA	3.36E-06	NA	
rs3764419	17	26188149	*ATAD5 /RNF135*	C	Lymphocyte	*235803_at*	-	4.79E-15	0.38	rs1808255	0.51	8.56E-22	4.46E-05	
					Lymphocyte	*C17orf42*	-	1.39E-12	0.78	rs3760318	0.90	2.81E-14	0.35	YES
					Lymphocyte	*SUZ12P*	-	1.76E-05	0.31	rs11652289	0.13	8.90E-29	2.40E-26	
rs42235	7	92086012	*CDK6*	T	Lymphocyte	*CDK6*	-	4.39E-20	1.00	rs42235	1.00	4.39E-20	1.00	YES
rs4601530	1	24916698	*CLIC4*	C	Lymphocyte	*CLIC4*	+	5.00E-05	NA	rs13412931	NA	9.06E-08	NA	
rs4605213	17	46599746	*NME2*	C	Lymphocyte	*NME1-NME2*	-	1.44E-14	0.24	rs8069453	0.49	3.38E-25	4.73E-09	
rs4665736	2	25041103	*DNAJC27*	T	Lymphocyte	*ADCY3*	+	3.66E-17	0.88	rs6737082	0.61	1.79E-21	1.13E-14	
rs494459	11	118079885	*TREH*	T	Lymphocyte	*DDX6*	+	4.01E-09	0.99	rs603486	0.35	5.12E-18	1.17E-17	
rs4986172	17	40571807	*ACBD4*	C	Lymphocyte	*NMT1*	-	8.13E-07	0.21	rs2301597	0.32	6.70E-10	9.38E-04	
rs6439167	3	130533446	*C3orf47*	C	Lymphocyte	*H1FX*	+	3.27E-10	0.78	rs6765930	0.94	1.27E-11	0.44	YES
rs6449353	4	17642586	*LCORL*	T	Lymphocyte	*DCAF16*	+	1.12E-06	NA	rs2287291	NA	1.32E-08	NA	
rs6457620	6	32771977	*HLA locus*	G	Lymphocyte	*HLA-DQB1*	-	2.38E-14	0.72	rs5000634	0.64	6.63E-18	0.02	
rs6699417	1	88896031	*PKN2*	T	Lymphocyte	*CCBL2*	+	5.38E-19	0.77	rs10801690	0.46	6.97E-35	7.92E-12	
					Lymphocyte	*KAT3*	-	9.68E-17	0.31	rs10801690	0.46	1.36E-26	1.00E-08	
rs7178424	15	60167551	*C2CD4A*	C	Lymphocyte	*VPS13C*	+	2.40E-06	0.003	rs17303915	0.05	1.77E-16	2.47E-13	
rs7332115	13	32045548	*PDS5B /BRCA2*	G	Lymphocyte	*PDS5B*	-	9.88E-29	6.60E-06	rs2051570	0.33	4.52E-41	8.37E-18	
					Lymphocyte	*PFAAP5*	+	3.75E-39	0.85	rs9315167	0.93	1.18E-42	0.05	YES
rs798489	7	2768329	*GNA12*	C	Lymphocyte	*C9orf47*	-	2.69E-09	0.04	rs4719646	0.44	2.56E-10	0.007	
					Lymphocyte	*GNA12*	-	2.99E-27	0.76	rs1636264	0.88	3.55E-31	0.06	YES
rs9360921	6	76322362	*SENP6*	G	Lymphocyte	*SENP6*	+	4.43E-05	0.64	rs7385	0.40	1.23E-13	2.04E-07	
rs9472414	6	45054484	*SUPT3H /RUNX2*	T	Lymphocyte	*SUPT3H*	-	6.58E-06	0.19	rs1329716	0.17	2.25E-13	5.57E-08	
rs9835332	3	56642722	*C3orf63*	G	Lymphocyte	*ARHGEF3*	+	5.93E-08	0.82	rs2317247	0.29	2.24E-17	1.83E-08	
					Lymphocyte	*CCDC66*	-	1.34E-05	0.11	rs17216685	0.19	2.58E-08	7.56E-04	
					Lymphocyte	*RAP140*	+	4.19E-05	NA	rs213011	NA	4.07E-07	NA	

rs9863706	3	72520103	*RYBP*	C	Lymphocyte	*RYBP*	-	1.27E-05	0.16	rs753319	0.38	7.09E-18	6.67E-09	
rs9967417	18	45213498	*DYM*	G	Lymphocyte	*C18orf32*	+	7.79E-06	0.73	rs8091253	0.21	9.30E-21	1.39E-14	
rs9969804	9	94468941	*IPPK*	A	Lymphocyte	*BICD2*	-	1.04E-06	0.06	rs12685791	0.10	4.91E-11	9.09E-06	
					Lymphocyte	*IARS*	+	2.10E-05	0.30	rs10120915	0.45	1.88E-07	0.01	
					Lymphocyte	*NOL8*	+	4.58E-05	0.31	rs10820956	0.29	2.15E-10	5.51E-06	
Other tissues														
rs10010325	4	106325802	*TET2*	A	Omentum	*PPA2*	+	2.80E-06	1.00	rs10010325	1.00	2.80E-06	1.00	YES
rs1043515	17	34175722	*PIP4K2B*	G	Subcutaneous fat	*PIP5K2B*	+	1.53E-34	1.00	rs1043515	1.00	1.53E-34	1.00	YES
					Omentum	*PIP5K2B*	+	1.24E-17	1.00	rs1043515	1.00	1.24E-17	1.00	YES
					Osteoblast	*PSMB3*	-	5.72E-05	0.92	rs2338115	0.93	4.54E-05	0.77	YES
rs1046934	1	182290152	*TSEN15*	C	Omentum	*TSEN15*	+	1.55E-17	1.00	rs1046934	1.00	1.55E-17	1.00	YES
					Subcutaneous fat	*TSEN15*	+	1.28E-10	1.00	rs1327124	0.99	9.81E-11	0.99	YES
rs1046943	6	109890634	*ZBTB24*	A	Omentum	*AKD1*	+	4.75E-08	0.97	rs13201430	0.91	1.46E-08	0.87	YES
					Subcutaneous fat	*BC030091*	-	1.58E-31	0.99	rs3757235	0.97	4.75E-32	0.94	YES
					Omentum	*BC030091*	-	5.76E-25	0.94	rs6920372	0.97	2.84E-26	0.80	YES
					Liver	*BC030091*	-	3.84E-11	1.00	rs1046943	1.00	3.84E-11	1.00	YES
					Omentum	*HSS00017874*	+	3.36E-06	0.83	rs9480936	0.96	8.96E-07	0.84	YES
					Omentum	*PPIL6*	-	3.99E-07	0.17	rs17534632	0.71	1.14E-14	0.002	
					Subcutaneous fat	*SMPD2*	-	4.16E-22	0.27	rs2236582	0.71	3.24E-28	0.006	
					Omentum	*SMPD2*	-	4.97E-22	0.69	rs12197114	0.71	1.07E-29	0.005	
					Liver	*SMPD2*	-	5.64E-06	0.83	rs1048203	0.76	2.31E-09	0.13	
					Osteoblast	*SMPD2*	-	2.05E-05	0.51	rs1322818	0.45	3.84E-07	0.03	
					Omentum	*ZBTB24*	+	2.22E-11	0.94	rs1074766	0.96	5.17E-12	0.93	YES
					Subcutaneous fat	*ZBTB24*	+	6.13E-08	0.005	rs6899915	0.21	2.06E-08	0.002	
rs1047014	6	19949472	*ID4*	C	Omentum	*ID4*	-	7.98E-12	1.00	rs1047014	1.00	7.98E-12	1.00	YES
rs10799445	1	225978506	*JMJD4*	A	Osteoblast	*JMJD4*	-	3.93E-07	0.62	rs6664307	0.96	1.50E-07	0.52	YES
					Liver	*SNAP47*	+	8.63E-10	1.00	rs10799445	1.00	8.63E-10	1.00	YES
rs10863936	1	210304421	*DTL*	G	Subcutaneous fat	*INTS7*	+	1.00E-10	0.73	rs4951561	0.79	1.87E-11	0.59	
					Omentum	*INTS7*	+	1.65E-10	1.00	rs10863936	1.00	1.65E-10	1.00	YES
rs11107116	12	92502635	*SOCS2*	T	Omentum	*AL161980*	-	2.35E-42	1.00	rs11107116	1.00	2.35E-42	1.00	YES
					Subcutaneous fat	*AL161980*	-	1.77E-34	1.00	rs11107116	1.00	1.77E-34	1.00	YES
					Osteoblast	*MRPL42*	+	3.37E-04	0.001	rs10859513	0.001	7.96E-06	3.50E-05	
rs11259936	15	82371586	*ADAMTSL3*	C	Omentum	*DNM1P41*	+	3.99E-12	0.41	rs4125566	0.11	1.81E-106	2.88E-82	
					Subcutaneous fat	*DNM1P41*	+	3.80E-10	0.06	rs4125566	0.08	3.80E-78	1.14E-62	
					Subcutaneous fat	*GOLGA6L5*	+	3.14E-07	0.004	rs150968	0.08	4.47E-19	6.70E-14	
					Omentum	*LOC727849*	+	5.15E-06	0.24	rs12906983	0.17	2.24E-19	2.65E-12	

					Subcutaneous fat	*LOC90396*	-	1.95E-09	0.79	rs11631096	0.16	5.64E-65	8.41E-46	
rs11599750	10	101795432	*CPN1*	C	Omentum	*CWF19L1*	-	2.19E-19	1.00	rs11599750	1.00	2.19E-19	1.00	YES
					Subcutaneous fat	*CWF19L1*	-	2.38E-13	1.00	rs11599750	1.00	2.38E-13	1.00	YES
					Liver	*CWF19L1*	-	2.19E-09	0.63	rs12784396	0.36	8.48E-31	3.24E-14	
rs11648796	16	732191	*NARFL*	G	Omentum	*HAGHL*	+	4.25E-37	1.00	rs11648796	1.00	4.25E-37	1.00	YES
					Subcutaneous fat	*HAGHL*	+	1.44E-07	1.00	rs11648796	1.00	1.44E-07	1.00	YES
					Osteoblast	*HAGHL*	+	9.76E-05	0.52	rs763206	0.76	4.59E-05	0.31	
					Omentum	*RHBDL1*	+	4.53E-06	0.18	rs3752493	0.13	8.69E-20	2.11E-13	
rs11958779	5	55037656	*SLC38A9*	G	Subcutaneous fat	*AL117656*	-	3.12E-10	0.86	rs6867834	0.88	5.55E-12	0.54	YES
					Omentum	*AL117656*	-	2.67E-08	0.52	rs7721054	0.87	1.73E-10	0.31	YES
					Subcutaneous fat	*Contig47865*	-	1.18E-07	0.006	rs1109967	0.06	2.43E-31	6.25E-25	
					Omentum	*PPAP2A*	-	1.25E-18	0.87	rs11955759	0.89	1.37E-19	0.73	YES
					Subcutaneous fat	*PPAP2A*	-	8.81E-08	0.55	rs10940473	0.63	1.98E-08	0.27	
rs12470505	2	219616613	*CCDC108 /IHH*	T	Omentum	*AL050185*	-	6.74E-17	0.14	rs6735637	0.17	5.83E-85	4.97E-56	
					Subcutaneous fat	*AL050185*	-	8.50E-14	0.44	rs1402508	0.18	9.94E-65	5.31E-41	
					Liver	*Contig41005_RC*	-	1.90E-06	1.00	rs12470505	1.00	1.90E-06	1.00	YES
					Omentum	*SLC23A3*	-	3.55E-10	0.98	rs6719931	0.91	2.81E-11	0.77	YES
rs12474201	2	46774789	*SOCS5*	A	Omentum	*ATP6V1E2*	-	6.80E-10	0.04	rs4952833	0.08	2.27E-64	1.29E-51	
					Subcutaneous fat	*ATP6V1E2*	-	2.81E-07	1.00	rs12474201	1.00	2.81E-07	1.00	YES
					Omentum	*SOCS5*	-	8.85E-105	0.95	rs11695058	0.89	2.02E-123	0.009	YES
					Subcutaneous fat	*SOCS5*	-	2.66E-98	1.00	rs12474201	1.00	2.66E-98	1.00	YES
					Liver	*SOCS5*	-	7.19E-16	0.98	rs4953419	0.90	2.60E-17	0.63	YES
rs12694997	2	241911659	*SEPT2*	G	Omentum	*FARP2*	-	2.51E-14	0.75	rs11674695	0.81	1.31E-15	0.44	YES
					Subcutaneous fat	*FARP2*	-	2.78E-07	0.07	rs3755325	0.26	2.35E-10	4.43E-04	
					Omentum	*HSS00174467*	-	2.50E-06	1.00	rs12694997	1.00	2.50E-06	1.00	YES
rs143384	20	33489170	*GDF5*	G	Subcutaneous fat	*CEP250*	-	3.06E-16	0.67	rs224371	0.61	3.37E-33	9.86E-08	
					Omentum	*CEP250*	-	4.82E-14	0.33	rs10359	0.61	6.09E-29	7.81E-08	
					Omentum	*ERGIC3*	-	8.17E-12	0.81	rs224440	0.51	1.87E-17	0.002	
					Subcutaneous fat	*ERGIC3*	-	7.84E-09	0.94	rs10359	0.62	5.95E-15	0.003	
					Omentum	*UQCC*	-	1.19E-19	0.98	rs2425060	0.79	3.93E-25	0.04	
					Subcutaneous fat	*UQCC*	-	2.64E-12	0.92	rs6060371	0.77	1.32E-15	0.02	

					Liver	*UQCC*	-	1.59E-09	0.47	rs6060371	0.76	5.23E-12	0.005	
					Osteoblast	*UQCC*	-	4.44E-07	0.96	rs6142358	0.74	4.32E-09	0.08	
rs1490384	6	126892853	*C6orf173*	T	Subcutaneous fat	*CENPW*	+	8.87E-07	0.86	rs1361108	0.78	1.54E-09	0.19	
rs1582931	5	122685098	*CEP120*	G	Omentum	*CCDC100*	+	1.71E-06	0.98	rs12520233	0.84	1.21E-07	0.64	YES
rs1738475	1	23409478	*HTR1D*	C	Omentum	*LUZP1*	-	3.18E-48	7.84E-07	rs11578046	0.58	3.68E-62	3.19E-09	
					Subcutaneous fat	*LUZP1*	-	8.19E-38	0.69	rs1208932	0.80	2.51E-42	0.09	YES
					Liver	*LUZP1*	-	7.08E-12	0.61	rs1208932	0.80	6.81E-14	0.29	YES
rs17780086	17	27367395	*LRRC37B*	A	Omentum	*LRRC37B*	-	1.06E-08	1.00	rs9903408	1.00	1.06E-08	1.00	YES
rs1814175	11	49515748	*FOLH1*	T	Subcutaneous fat	*FOLH1*	+	3.74E-08	1.00	rs1814175	1.00	3.74E-08	1.00	YES
rs1950500	14	23900690	*NFATC4*	T	Omentum	*ADCY4*	+	3.98E-08	0.18	rs12436417	0.34	5.65E-15	4.37E-06	
					Subcutaneous fat	*DHRS1*	+	2.47E-06	0.59	rs7146665	0.16	2.50E-31	9.75E-22	
rs2066807	12	55026949	*STAT2*	G	Liver	*STAT2*	+	1.52E-11	0.89	rs2291361	0.88	1.35E-11	0.88	YES
					Subcutaneous fat	*STAT2*	-	4.12E-10	1.00	rs2066807	1.00	4.12E-10	1.00	YES
					Omentum	*STAT2*	-	6.56E-08	1.00	rs2066807	1.00	6.56E-08	1.00	YES
					Osteoblast	*USP52*	+	3.99E-04	0.91	rs2066819	1.00	1.88E-04	0.57	YES
rs2072153	17	44745013	*ZNF652*	C	Omentum	*ZNF652*	-	1.00E-28	0.58	rs8064621	0.65	4.82E-39	2.10E-04	
					Subcutaneous fat	*ZNF652*	-	7.54E-20	0.12	rs8064621	0.63	1.69E-33	8.54E-07	
rs2079795	17	56851431	*TBX2*	T	Subcutaneous fat	*C17orf82*	-	6.14E-08	0.91	rs740755	0.86	2.70E-08	0.61	YES
					Subcutaneous fat	*Contig40232_RC*	+	1.91E-08	1.00	rs9892365	1.00	1.91E-08	1.00	YES
					Liver	*Contig40232_RC*	+	2.14E-06	0.91	rs2240736	0.58	2.51E-10	0.02	
rs2110001	7	150147955	*TMEM176A*	G	Liver	*ABP1*	-	8.45E-45	0.58	rs10452848	0.37	9.93E-211	7.06E-84	
					Omentum	*ABP1*	+	1.44E-36	2.01E-09	rs17173637	0.24	2.49E-54	1.73E-22	
					Subcutaneous fat	*ABP1*	+	1.67E-10	0.002	rs17173637	0.19	2.24E-13	9.61E-06	
					Subcutaneous fat	*TMEM176A*	+	1.68E-06	0.93	rs13223879	0.48	9.90E-13	2.90E-04	
rs2145998	10	80791702	*PPIF*	T	Liver	*PPIF*	+	1.87E-11	6.93E-05	rs10824743	0.08	6.25E-23	3.06E-15	
rs2247341	4	1671115	*SLBP /FGFR3*	A	Liver	*TACC3*	-	1.85E-07	0.07	rs17802841	0.13	2.74E-21	7.66E-14	
rs2256183	6	31488508	*MICA*	A	Omentum	*ATP6V1G2*	+	7.75E-07	0.39	rs2239705	0.06	3.88E-89	1.99E-77	
					Omentum	*Contig31905_RC*	-	1.98E-62	0.13	rs2523467	0.48	6.21E-160	1.06E-48	
					Liver	*Contig31905_RC*	-	2.26E-53	0.06	rs9348866	0.50	1.03E-112	1.41E-31	
					Subcutaneous fat	*Contig31905_RC*	-	2.31E-38	0.36	rs2428486	0.46	5.44E-117	1.42E-42	
					Subcutaneous fat	*CREBL1*	+	6.24E-08	0.05	rs1058026	0.20	2.58E-14	3.50E-07	
					Omentum	*D83543*	-	4.26E-24	5.35E-04	rs3869132	0.27	1.66E-41	3.48E-16	
					Liver	*D83543*	-	8.24E-21	0.93	rs2844513	0.67	1.58E-34	4.02E-05	

					Subcutaneous fat	*D83543*	-	1.49E-11	0.20	rs3869132	0.25	1.01E-31	3.70E-16	
					Omentum	*hCT1834354.1*	-	2.47E-61	1.06E-27	rs9295986	0.19	2.46E-63	1.14E-29	
					Subcutaneous fat	*hCT1834354.1*	-	5.81E-51	8.15E-26	rs9295986	0.16	3.21E-51	1.49E-26	
					Liver	*hCT1834354.1*	-	1.17E-33	6.12E-13	rs9295986	0.19	4.58E-38	2.21E-16	
					Liver	*HLA-B*	+	1.30E-07	1.00	rs2256183	1.00	1.30E-07	1.00	YES
					Omentum	*HLA-B*	+	2.60E-07	0.04	rs1058026	0.19	2.31E-17	5.28E-10	
					Omentum	*HLA-DRB5*	-	3.75E-06	0.29	rs3135391	0.07	5.00E-217	6.80E-188	
rs2279008	19	17144303	*MYO9B*	T	Omentum	*OCEL1*	-	3.08E-06	4.57E-05	rs7258100	0.02	2.56E-08	4.29E-07	
rs2284746	1	17179262	*MFAP2*	G	Omentum	*MFAP2*	+	3.81E-33	1.00	rs2284746	1.00	3.81E-33	1.00	YES
					Osteoblast	*MFAP2*	+	1.01E-06	0.04	rs9435732	0.30	5.56E-09	0.001	
					Liver	*MSTP9*	-	4.63E-11	1.00	rs2284746	1.00	4.63E-11	1.00	YES
					Omentum	*MSTP9*	-	6.98E-11	0.16	rs6691985	0.43	1.09E-13	0.004	
					Subcutaneous fat	*MSTP9*	-	8.28E-10	0.78	rs7513616	0.69	8.93E-12	0.21	
rs2336725	3	53093779	*RTF1*	C	Omentum	*Contig33975_RC*	+	1.47E-06	0.05	rs1134546	0.11	8.80E-15	4.09E-09	
rs237743	20	47336426	*ZNFX1*	A	Subcutaneous fat	*ARFGEF2*	+	3.69E-12	0.008	rs1569750	0.09	3.16E-17	2.41E-07	
					Subcutaneous fat	*DDX27*	-	5.22E-06	1.00	rs237743	1.00	5.22E-06	1.00	YES
rs2597513	3	13530836	*HDAC11*	C	Omentum	*FBLN2*	-	2.27E-06	1.00	rs2597513	1.00	2.27E-06	1.00	YES
rs2638953	12	28425682	*CCDC91*	C	Subcutaneous fat	*AK092571*	-	2.00E-16	1.00	rs2638953	1.00	2.00E-16	1.00	YES
					Omentum	*AK092571*	-	4.21E-07	0.13	rs7978086	0.23	3.73E-12	1.75E-05	
rs2665838	17	59320197	*CSH1/GH1*	G	Omentum	*FTSJ3*	+	1.54E-34	0.57	rs1043127	0.63	1.50E-91	2.81E-37	
					Subcutaneous fat	*FTSJ3*	+	3.08E-20	0.28	rs1043127	0.62	4.31E-55	1.96E-22	
					Liver	*FTSJ3*	+	5.75E-15	0.27	rs2584608	0.66	1.01E-44	2.45E-21	
					Osteoblast	*FTSJ3*	+	1.08E-04	0.02	rs2665797	0.28	2.24E-09	9.52E-07	
					Omentum	*PSMC5*	+	1.75E-14	0.15	rs2727331	0.44	2.37E-21	8.12E-06	
					Subcutaneous fat	*PSMC5*	+	2.06E-08	0.33	rs721575	0.56	1.70E-13	7.00E-06	
					Subcutaneous fat	*TCAM1*	-	4.12E-11	0.65	rs6504179	0.62	1.27E-19	1.48E-07	
					Omentum	*TCAM1*	-	3.98E-06	0.77	rs3760252	0.63	5.23E-12	3.56E-06	
rs26868	16	2189377	*CASKIN1*	A	Omentum	*C16orf79*	-	2.16E-07	0.36	rs1126	0.52	6.27E-09	0.09	
					Omentum	*MLST8*	+	7.66E-11	0.31	rs26862	0.62	8.75E-16	0.006	
rs274546	5	131727766	*SLC22A5*	G	Subcutaneous fat	*PDLIM4*	-	3.04E-10	0.71	rs162890	0.40	1.47E-20	3.81E-07	
					Omentum	*PDLIM4*	-	8.25E-07	0.82	rs7727038	0.68	1.23E-09	0.11	
					Omentum	*SLC22A4*	-	1.30E-20	0.73	rs273901	0.74	9.99E-24	0.12	
					Liver	*SLC22A4*	-	8.56E-09	1.00	rs274546	1.00	8.56E-09	1.00	YES
					Subcutaneous fat	*SLC22A4*	-	5.08E-06	0.96	rs272886	0.98	1.85E-06	0.95	YES

rs2856321	12	11747040	*ETV6*	G	Omentum	*AK025217*	+	1.16E-06	0.31	rs2856327	0.19	4.57E-36	1.19E-24	
					Omentum	*Contig21370_RC*	-	1.20E-09	0.86	rs10845408	0.92	2.16E-10	0.77	YES
rs3110496	17	24941897	*ANKRD13B*	G	Subcutaneous fat	*ANKRD13B*	-	2.26E-09	1.00	rs3110496	1.00	2.26E-09	1.00	YES
					Omentum	*TP53I13*	+	1.36E-12	1.00	rs3110496	1.00	1.36E-12	1.00	YES
					Subcutaneous fat	*TP53I13*	+	3.30E-06	1.00	rs3110496	1.00	3.30E-06	1.00	YES
rs3129109	6	29192211	*OR2J3*	C	Liver	*hCT2282382*	+	3.73E-06	1.33E-04	rs2844827	0.02	4.38E-38	6.34E-36	
					Subcutaneous fat	*HSS00128987*	-	1.37E-28	0.41	rs1476016	0.59	1.18E-47	1.12E-08	
					Omentum	*HSS00128987*	-	5.35E-24	0.76	rs1476016	0.61	5.36E-43	5.81E-08	
					Omentum	*PGBD1*	-	1.44E-06	0.32	rs6917759	0.11	1.17E-33	3.02E-25	
					Subcutaneous fat	*PGBD1*	-	2.94E-06	0.59	rs16893937	0.13	1.21E-33	2.23E-24	
					Omentum	*ZNF323*	-	4.67E-11	0.18	rs853684	0.14	7.58E-54	3.16E-37	
					Subcutaneous fat	*ZNF323*	-	3.66E-06	0.61	rs213238	0.10	1.66E-55	6.84E-45	
rs3764419	17	26188149	*ATAD5 /RNF135*	C	Omentum	*C17orf42*	+	3.62E-40	1.00	rs3764419	1.00	3.62E-40	1.00	YES
					Subcutaneous fat	*C17orf42*	+	1.66E-32	1.00	rs9898858	0.99	7.28E-33	0.99	YES
					Liver	*C17orf42*	+	3.81E-13	1.00	rs3764419	1.00	3.81E-13	1.00	YES
					Omentum	*SUZ12P*	+	1.09E-70	0.98	rs1061342	0.75	6.70E-98	5.67E-07	
					Subcutaneous fat	*SUZ12P*	+	2.36E-52	0.34	rs1061342	0.77	1.86E-67	4.17E-05	
					Liver	*SUZ12P*	+	4.52E-11	0.64	rs7503542	0.75	5.40E-18	0.01	
					Liver	*UTP6*	-	6.53E-09	1.00	rs3764419	1.00	6.53E-09	1.00	YES
rs3782089	11	65093395	*SSSCA1*	C	Omentum	*NEAT1*	-	5.83E-08	0.29	rs4244811	0.19	3.84E-26	8.75E-16	
rs42235	7	92086012	*CDK6*	T	Omentum	*CDK6*	+	1.73E-23	0.08	rs17688839	0.50	2.53E-31	1.02E-05	
					Subcutaneous fat	*CDK6*	+	3.06E-11	0.46	rs42039	0.70	2.02E-12	0.22	
					Liver	*CDK6*	+	2.21E-06	0.67	rs42039	0.71	1.28E-09	0.04	
rs425277	1	2059032	*PRKCZ*	T	Omentum	*C1orf86*	+	4.65E-39	0.22	rs12082939	0.76	9.34E-60	1.61E-06	
					Liver	*C1orf86*	+	1.47E-26	0.28	rs262672	0.76	3.81E-32	0.04	
					Subcutaneous fat	*C1orf86*	+	2.72E-25	0.49	rs2257182	0.78	1.32E-39	1.55E-05	
					Omentum	*FLJ10346*	+	1.20E-08	0.99	rs427811	0.76	2.38E-11	0.22	
rs494459	11	118079885	*TREH*	T	Omentum	*AK021715*	+	3.84E-39	3.77E-04	rs603486	0.45	7.25E-48	5.13E-09	
					Subcutaneous fat	*AK021715*	+	2.32E-13	5.03E-08	rs492471	0.05	4.05E-22	2.72E-16	
					Liver	*AK021715*	+	1.39E-10	0.003	rs4499035	0.19	6.01E-15	1.19E-06	
					Subcutaneous fat	*PHLDB1*	+	6.42E-08	0.69	rs488141	0.71	8.92E-11	0.10	
					Omentum	*PHLDB1*	+	1.17E-06	0.93	rs638805	0.63	9.57E-11	0.03	
					Liver	*TREH*	+	8.72E-30	5.94E-11	rs11216943	0.16	1.87E-59	2.08E-35	
rs5742915	15	72123686	*PML*	C	Omentum	*PML*	-	2.52E-23	1.00	rs5742915	1.00	2.52E-23	1.00	YES

					Subcutaneous fat	*PML*	-	9.87E-13	1.00	rs5742915	1.00	9.87E-13	1.00	YES
rs6439167	3	130533446	*C3orf47*	C	Omentum	*COPG*	-	3.88E-06	0.54	rs7636293	0.51	1.30E-08	0.04	
rs6449353	4	17642586	*LCORL*	T	Omentum	*LCORL*	+	1.23E-06	0.002	rs2286534	0.07	1.06E-10	2.97E-07	
rs6457620	6	32771977	*HLA locus*	G	Omentum	*HLA-DQA1*	+	1.04E-11	0.48	rs9272346	0.09	3.13E-186	7.13E-151	
					Subcutaneous fat	*HLA-DQA1*	+	8.15E-11	0.36	rs9272346	0.09	1.78E-159	5.56E-129	
					Liver	*HLA-DQA1*	+	9.62E-11	0.06	rs9272346	0.09	1.50E-94	3.25E-76	
					Omentum	*HLA-DQA2*	-	1.97E-15	0.98	rs660895	0.23	1.49E-81	3.80E-49	
					Subcutaneous fat	*HLA-DQA2*	-	1.20E-10	0.34	rs660895	0.23	5.86E-75	8.50E-48	
					Subcutaneous fat	*HLA-DQB1*	-	5.15E-34	0.009	rs9272775	0.57	3.91E-36	5.84E-04	
					Omentum	*HLA-DQB1*	-	6.12E-34	0.004	rs9272775	0.56	3.95E-34	0.003	
					Liver	*HLA-DQB1*	-	1.04E-06	0.64	rs3891175	0.32	6.80E-29	1.28E-16	
					Omentum	*HLA-DRB1*	-	3.30E-15	0.45	rs4530903	0.14	4.01E-103	6.40E-72	
					Subcutaneous fat	*HLA-DRB1*	-	5.73E-12	0.41	rs4530903	0.15	4.67E-79	1.87E-55	
					Liver	*HLA-DRB1*	-	1.28E-08	0.79	rs4530903	0.14	3.13E-61	9.12E-45	
					Omentum	*HLA-DRB5*	+	8.73E-19	0.06	rs3135391	0.16	5.00E-217	4.31E-149	
					Subcutaneous fat	*HLA-DRB5*	+	9.00E-15	0.58	rs3135391	0.14	6.73E-195	3.25E-136	
					Liver	*HLA-DRB5*	+	1.73E-09	0.006	rs3135391	0.15	3.77E-154	2.33E-111	
rs6684205	1	216676325	*TGFB2*	G	Omentum	*Contig43791_RC*	-	3.36E-22	0.99	rs1418556	0.95	1.22E-23	0.32	YES
rs7155279	14	91555634	*TRIP11*	G	Omentum	*AK021920*	+	2.84E-06	0.49	rs17734627	0.07	3.68E-73	6.10E-62	
					Liver	*BC033643*	-	7.33E-09	0.24	rs7149561	0.51	5.53E-22	2.17E-07	
					Subcutaneous fat	*BC033643*	-	3.51E-06	0.08	rs2235978	0.52	5.53E-19	1.42E-07	
					Omentum	*MTAC2D1*	-	1.52E-06	4.19E-04	rs11625233	0.02	7.57E-70	7.40E-66	
rs7332115	13	32045548	*PDS5B /BRCA2*	G	Omentum	*N4BP2L2*	+	5.51E-107	0.96	rs1123462	0.94	1.95E-115	0.29	YES
					Subcutaneous fat	*N4BP2L2*	+	1.42E-84	1.00	rs11840502	0.99	2.31E-85	0.97	YES
					Liver	*N4BP2L2*	+	9.40E-31	0.99	rs9315167	0.85	1.85E-37	0.10	YES
					Osteoblast	*PFAAP5*	+	2.39E-17	1.00	rs9595908	1.00	2.38E-17	1.00	YES
rs7849585	9	138251691	*QSOX2*	T	Omentum	*QSCN6L1*	+	9.99E-15	1.00	rs7849585	1.00	9.99E-15	1.00	YES
					Subcutaneous fat	*QSCN6L1*	+	3.97E-14	0.92	rs12338076	0.93	1.45E-15	0.46	YES
rs798489	7	2768329	*GNA12*	C	Omentum	*CN265316*	+	7.18E-28	0.44	rs1713920	0.51	8.85E-73	2.86E-21	
					Subcutaneous fat	*CN265316*	+	2.26E-15	0.10	rs1713920	0.49	5.41E-49	1.31E-17	
					Liver	*CN265316*	+	2.40E-12	0.54	rs2527687	0.59	2.55E-20	3.91E-04	
rs806794	6	26308656	*Histone cluster*	A	Liver	*HIST1H2BD*	+	3.03E-06	0.48	rs9379829	0.69	1.84E-07	0.24	
					Omentum	*HIST1H4F*	-	4.63E-06	0.001	rs198834	0.06	2.83E-08	1.13E-05	

rs9360921	6	76322362	*SENP6*	G	Subcutaneous fat	*HSS00085450*	-	1.02E-12	1.00	rs9360921	1.00	1.02E-12	1.00	YES
					Osteoblast	*SENP6*	+	3.93E-04	0.24	rs3969287	0.40	3.50E-04	0.21	
rs9835332	3	56642722	*C3orf63*	G	Subcutaneous fat	*C3orf63*	+	4.20E-07	1.00	rs6445814	0.99	1.95E-07	0.98	YES
					Osteoblast	*CCDC66*	-	1.93E-07	0.85	rs7637449	0.93	1.96E-08	0.47	YES
rs9863706	3	72520103	*RYBP*	C	Omentum	*RYBP*	-	1.13E-07	1.00	rs9863706	1.00	1.13E-07	1.00	YES
rs9969804	9	94468941	*IPPK*	A	Omentum	*ANKRD19*	-	9.01E-11	0.94	rs9775485	0.12	1.11E-118	1.39E-90	
					Subcutaneous fat	*ANKRD19*	-	4.98E-07	0.93	rs10821027	0.09	1.08E-83	9.83E-68	
					Osteoblast	*BICD2*	+	2.80E-04	0.89	rs7863890	0.22	2.51E-14	1.47E-10	
					Omentum	*CENPP*	+	1.32E-44	0.004	rs10820995	0.44	4.06E-88	1.32E-29	
					Subcutaneous fat	*CENPP*	+	4.83E-30	0.16	rs10820995	0.41	8.06E-67	1.25E-23	
					Liver	*CENPP*	+	1.68E-28	0.05	rs10992265	0.39	1.79E-57	9.93E-21	

[a] Direction of effect of the height increasing allele
[b] P-value of the height SNP after conditioning on the peak SNP associated with the transcript
[c] SNP with the strongest association with the transcript in the region
[d] Correlation between the height SNP and peak SNP associated with the transcript
[e] P-value of the peak SNP after conditioning on the height SNP

Supplementary Table 8. Height SNPs in linkage disequilibrium ($r^2 \geq 0.8$) with non-synonymous SNPs, using the HapM phase II CEU data. For each gene, we annotated all reported isoforms.

Chr	Position	GIANT height SNP	Non-synonymous SNP	r^2	Amino acid change	Gene name	Gene isoform
1	148173037	rs11205277	rs11205303	0.889741	ATG (Met) => GTG (Val) [exon6]	*MTMR11*	NM_0011458
1	148173037	rs11205277	rs11205303	0.889741	ATG (Met) => GTG (Val) [exon5]	*MTMR11*	NM_181873
1	182287568	rs1046934	rs2274432	1	GGC (Gly) => GAC (Asp) [exon1]	*TSEN15*	NM_052965
1	182287568	rs1046934	rs2274432	1	GGC (Gly) => GAC (Asp) [exon1]	*TSEN15*	NM_0011273
1	182290152	rs1046934	rs1046934	1	CAA (Gln) => CAC (His) [exon2]	*TSEN15*	NM_052965
1	182290152	rs1046934	rs1046934	1	CAA (Gln) => CAC (His) [exon2]	*TSEN15*	NM_0011273
2	88656006	rs11684404	rs1805165	0.86857	GCT (Ala) => TCT (Ser) [exon13]	*EIF2AK3*	NM_004836
2	88676238	rs11684404	rs13045	1	CAA (Gln) => CGA (Arg) [exon3]	*EIF2AK3*	NM_004836
2	88694388	rs11684404	rs867529	0.86857	TCC (Ser) => TGC (Cys) [exon2]	*EIF2AK3*	NM_004836
2	241841521	rs12694997	rs7578199	0.88044	AAT (Asn) => AGT (Ser) [exon10]	*HDLBP*	NM_005336
2	241841521	rs12694997	rs7578199	0.88044	AAT (Asn) => AGT (Ser) [exon10]	*HDLBP*	NM_203346
3	56603071	rs9835332	rs7637449	0.918614	CGA (Arg) => CAA (Gln) [exon10]	*CCDC66*	NM_0011419
3	56603071	rs9835332	rs7637449	0.918614	CGA (Arg) => CAA (Gln) [exon10]	*CCDC66*	NM_0010125
3	56642722	rs9835332	rs9835332	1	ACA (Thr) => AGA (Arg) [exon11]	*C3orf63*	NM_015224
3	56642722	rs9835332	rs9835332	1	ACA (Thr) => AGA (Arg) [exon18]	*C3orf63*	NM_0011127
3	56691962	rs9835332	rs958755	1	CAA (Gln) => CCA (Pro) [exon1]	*C3orf63*	NM_0011127
4	57492171	rs17081935	rs3796529	1	CCA (Pro) => CTA (Leu) [exon4]	*REST*	NM_005612
5	131690961	rs274546	rs272893	1	ATA (Ile) => ACA (Thr) [exon5]	*SLC22A4*	NM_003059
5	176450403	rs422421	rs376618	0.868301	CCC (Pro) => CTC (Leu) [exon3]	*FGFR4*	NM_022963
5	176450403	rs422421	rs376618	0.868301	CCC (Pro) => CTC (Leu) [exon4]	*FGFR4*	NM_002011
5	176450403	rs422421	rs376618	0.868301	CCC (Pro) => CTC (Leu) [exon4]	*FGFR4*	NM_213647
6	29071227	rs3129109	rs6456880	0.90559	AAG (Lys) => CAG (Gln) [exon7]	*ZNF311*	NM_0010108
6	34322300	rs2780226	rs1150781	1	GGG (Gly) => GCG (Ala) [exon5]	*C6orf1*	NM_178508
6	34322300	rs2780226	rs1150781	1	GGG (Gly) => GCG (Ala) [exon5]	*C6orf1*	NM_0010087
6	34322300	rs2780226	rs1150781	1	GGG (Gly) => GCG (Ala) [exon5]	*C6orf1*	NM_0010087
6	35531864	rs6457821	rs7761870	1	TCA (Ser) => TTA (Leu) [exon2]	*FANCE*	NM_021922
6	35873021	rs6457821	rs2766597	1	CTG (Leu) => CCG (Pro) [exon1]	*CLPS*	NM_001832
6	109871228	rs1046943	rs1476387	0.95582	AGG (Arg) => AGT (Ser) [exon9]	*SMPD2*	NM_003080
6	109934409	rs1046943	rs2277114	0.871525	GTA (Val) => ATA (Ile) [exon35]	*AKD1*	NM_0011451
9	85807085	rs7853377	rs1982151	0.844041	AAT (Asn) => AGT (Ser) [exon3]	*RMI1*	NM_024945
9	94324803	rs9969804	rs10120210	0.930959	CAG (Gln) => CCG (Pro) [exon2]	*ECM2*	NM_001393
12	28303639	rs2638953	rs11049488	0.905427	GCA (Ala) => ACA (Thr) [exon2]	*CCDC91*	NM_018318
12	55026949	rs2066807	rs2066807	1	ATG (Met) => ATC (Ile) [exon20]	*STAT2*	NM_005419
15	60046929	rs7178424	rs3784634	0.80562	AGG (Arg) => AAG (Lys) [exon27]	*VPS13C*	NM_017684
15	60046929	rs7178424	rs3784634	0.80562	AGG (Arg) => AAG (Lys) [exon29]	*VPS13C*	NM_020821
15	60046929	rs7178424	rs3784634	0.80562	AGG (Arg) => AAG (Lys) [exon27]	*VPS13C*	NM_018080
15	60046929	rs7178424	rs3784634	0.80562	AGG (Arg) => AAG (Lys) [exon29]	*VPS13C*	NM_0010180
15	72123686	rs5742915	rs5742915	1	TTC (Phe) => CTC (Leu) [exon9]	*PML*	NM_033238
15	82373128	rs11259936	rs4842838	1	GTG (Val) => TTG (Leu) [exon16]	*ADAMTSL3*	NM_207517
19	46595060	rs17318596	rs10853751	0.804656	ACG (Thr) => ATG (Met) [exon1]	*EXOSC5*	NM_020158
19	46624115	rs17318596	rs284662	0.804656	AGC (Ser) => GGC (Gly) [exon3]	*B3GNT8*	NM_198540
20	47275067	rs237743	rs11908296	0.971236	GGA (Gly) => GTA (Val) [exon6]	*DDX27*	NM_017895
20	47299191	rs237743	rs6512577	1	ATG (Met) => ATA (Ile) [exon14]	*ZNFX1*	NM_021035

Supplementary Table 9. GIANT height variants associated with other traits and diseases reported in the NHGRI catalog of published GWAS at genome-wide level of significance (P<5x10^{-8}), based on a 1 megabase maximum distance and linkage disequilibrium (r^2>0.1) between the SNPs. Highlighted rows are those for which the GIANT height SNP and the NHGRI SNP showed a strong correlation (r^2>0.8).

GIANT height SNP	Chr	Position	Nearest or OMIM gene	GWAS SNP from NHGRI catalogue	GIANT height P-value for NHGRI SNP	Disease/Trait	r^2 between GIANT height and NHGRI SNP	D' between GIANT height and NHGRI SNP	Distance (kb) between GIANT height and NHGRI SNP	Height-increasing allele	Effect relative to height-increasing allele	Reference
rs11118346	1	217810342	***LYPLAL1***	rs2605100	1.42E-03	WHR (women)	0.17	0.69	99.495	A	lower WHR	Lindgren et al., PLoS Genet 2009
rs720390	3	187031377	***IGF2BP2***	rs4402960	6.30E-01	Type 2 diabetes	0.48	0.86	36.996	T	higher T2D risk	Saxena et al., Science 2007
				rs4402960	6.30E-01	Type 2 diabetes	0.48	0.86	36.996	T	higher T2D risk	Scott et al., Science 2007
				rs6769511	6.45E-01	Type 2 diabetes	0.48	0.86	18.393	C	higher T2D risk	Unoki et al., Nat Genet 2008
				rs4402960	6.30E-01	Type 2 diabetes	0.48	0.86	36.996	T	higher T2D risk	Zeggini et al., Science 2007
rs10010325	4	106325802	***TET2***	rs7679673	2.12E-01	Prostate cancer	0.12	0.37	44.819	A	higher cancer risk	Eeles et al., Nat Genet 2009
rs10037512	5	88390431	***MEF2C***	rs1366594	4.98E-09	BMD (hip)	0.97	1	21.386	A	lower BMD	Rivadeneira et al., Nat Genet 2009
rs274546	5	131727766	***SLC22A5***	rs2188962	5.46E-07	Crohn's disease	0.42	1	70.938	T	higher Crohn's risk	Barrett et al., Nat Genet 2008
				rs2522056	6.55E-04	Fibrinogen	0.21	0.81	101.859	G	lower fibrinogen	Dehghan et al., Circ Cardiovasc Genet 2009
				rs1016988	1.34E-03	Fibrinogen	0.17	0.87	44.707	T	lower fibrinogen	Danik et al., Circ Cardiovasc Genet 2009
				rs4143832	1.40E-01	Plasma eosinophil count	0.12	0.61	163.11	G	higher eosinophil count	Gudbjartsson et al., Nat Genet 2009
rs2256183	6	31488508	***MICA***	rs2844479	9.64E-10	Weight	0.12	0.46	192.427	A	increased weight	Thorleifsson et al., Nat Genet 2008
rs6457620	6	32771977	**HLA locus**	rs2187668	8.87E-03	Celiac disease	0.10	1	58.115	T	higher Celiac risk	van Heel et al., Nat Genet 2007
				rs9271366	7.17E-06	Multiple sclerosis	0.35	1	77.145	G	higher MS risk	Bahlo et al., Nat Genet 2009
				rs6457617	6.89E-08	Rheumatoid arthritis	1	1	0.148	C	lower RA risk	Julia et al., Arthritis Rheum 2008
				rs6457617	6.89E-08	Rheumatoid arthritis	1	1	0.148	C	lower RA risk	WTCCC, Nature 2007
				same SNP	3.65E-08	Rheumatoid arthritis	-	-	-	G	n/a	Raychaudhuri et al., Nat Genet 2008
				rs660895	4.65E-01	Rheumatoid arthritis	0.40	1	86.619	A	lower RA risk	Plenge et al., N Engl J Med 2007
				rs2187668	8.87E-03	SLE	0.10	1	58.115	T	higher SLE risk	Hom et al., N Engl J Med 2008
				rs9272346	6.12E-01	Type 1 diabetes	0.18	0.47	59.627	G	higher T1D risk	WTCCC, Nature 2007
				rs9272346	6.12E-01	Type 1 diabetes	0.18	0.47	59.627	G	higher T1D risk	Cooper et al., Nat Genet 2008
				rs2395185	6.38E-01	Ulcerative colitis	0.22	0.59	230.832	T	lower UC risk	Silverberg et al., Nat Genet 2009
				rs9268877	2.80E-01	Ulcerative colitis	0.12	0.39	232.852	G	lower UC risk	Franke et al., Nat Genet 2008
				rs2395185	6.38E-01	Ulcerative colitis	0.22	0.59	230.832	T	lower UC risk	Asano et al., Nat Genet 2009
				rs9268877	2.80E-01	Ulcerative colitis	0.12	0.39	232.852	G	n/a	Barrett et al., Nat Genet 2009
rs7759938	6	105485647	***LIN28B***	rs314276	1.03E-16	Menarche (age at onset)	0.96	1	29.045	A	later menarche	Ong et al., Nat Genet 2009
				rs314280	1.35E-10	Menarche (age at onset)	0.52	1	21.883	A	later menarche	Sulem et al., Nat Genet 2009
				same SNP	8.69E-18	Menarche (age at onset)	-	-	-	C	later menarche	Perry et al., Nat Genet 2009
				rs314277	3.65E-12	Menarche (age at onset)	0.25	1	28.708	A	later menarche	He et al., Nat Genet 2009
rs1490384	6	126892853	***C6orf173***	rs9388489	1.03E-13	Type 1 diabetes	0.84	1	152.441	G	higher T1D risk	Barrett et al., Nat Genet 2009
rs7763064	6	142838982	***GPR126***	rs3817928	1.97E-11	Pulmonary function	0.59	0.89	46.773	A	reduced pulmonary function	Hancock et al., Nat Genet 2009
rs1708299	7	28156471	***JAZF1***	rs864745	1.31E-12	Type 2 diabetes	0.40	0.94	9.39	T	higher T2D risk	Zeggini et al., Nat Genet 2008
rs6959212	7	38094851	***STARD3NL***	rs1524058	9.39E-05	BMD (spine)	0.73	1	7.951	C	lower BMD	Rivadeneira et al., Nat Genet 2009
rs2110001	7	150147955	***KCNH2***	rs2968863	1.33E-04	QT interval	0.10	0.85	106.115	C	longer QT interval	Pfeufer et al., Nat Genet 2009
				rs3807375	4.30E-05	QT interval	0.14	1.00	40.278	T	longer QT interval	Holm et al., Nat Genet 2010
rs11599750	10	101795432	***CPN1***	rs11597390	1.54E-04	Liver enzymes levels	0.51	0.82	55.993	G	lower enzyme levels	Yuan et al., Am J Hum Genet 2008
rs1330	11	17272605	***KCNJ11***	rs5215	6.70E-02	Type 2 diabetes	0.26	0.53	92.601	C	higher T2D risk	Zeggini et al., Science 2007
rs494459	11	118079885	***DDX6***	rs4639966	2.77E-01	SLE	0.22	1	1.156	T	lower SLE risk	Han et al., Nat Genet 2009

GIANT height SNP	Chr	Position	Nearest or OMIM gene	GWAS SNP from NHGRI catalogue	GIANT height P-value for NHGRI SNP	Disease/Trait	r^2 between GIANT height and NHGRI SNP	D' between GIANT height and NHGRI SNP	Distance (kb) between GIANT height and NHGRI SNP	Height-increasing allele	Effect relative to height-increasing allele	Reference
rs2066807	12	55026949	***STAT2***	rs2066808	2.75E-08	Psoriasis	1	1	2.709	G	lower psoriasis risk	Nair et al., Nat Genet 2009
rs3110496	17	24941897	***ANKRD13B***	rs2138852	5.11E-01	Mean platelet volume	0.10	0.45	214.422	T	higher platelet volume	Soranzo et al., Nat Genet 2009
				rs2138852	5.11E-01	Mean platelet volume	0.10	0.45	214.422	T	lower platelet volume	Meisinger et al., Am J Hum Genet 2008
rs4986172	17	40571807	***ACBD4***	rs12946454	3.23E-07	Systolic blood pressure	0.76	0.94	8.16	A	lower systolic b.p.	Newton-Cheh et al., Nat Genet 2009
rs2072153	17	44745013	***ZNF652***	rs16948048	4.22E-04	Diastolic blood pressure	0.32	1.00	50.452	A	lower diastolic b.p.	Newton-Cheh et al., Nat Genet 2009
rs17782313	18	56002077	***MC4R***	rs12970134	5.52E-04	Body mass index	0.81	0.96	33.653	A	higher BMI	Thorleifsson et al., Nat Genet 2008
				same SNP	3.48E-06	Body mass index	-	-	-	C	higher BMI	Willer et al., Nat Genet 2008
				same SNP	3.48E-06	Body mass index	-	-	-	C	higher BMI	Loos et al., Nat Genet 2008
				same SNP	3.48E-06	Obesity	-	-	-	C	higher obesity risk	Meyre et al., Nat Genet 2009
				rs12970134	5.52E-04	Waist circumference	0.81	0.96	33.653	A	lower WC	Chambers et al., Nat Genet 2008
				rs12970134	5.52E-04	Weight	0.81	0.96	33.653	A	increased weight	Thorleifsson et al., Nat Genet 2008
rs2834442	21	34612656	***KCNE2***	rs9982601	4.66E-01	MI (early onset)	0.17	0.66	91.658	C	lower MI risk	Kathiresan et al., Nat Genet 2009

Supplementary Table 10. List of 241 abnormal skeletal/growth genes identified in the OMIM database (http://www.ncbi.nlm.nih.gov/omim) using the following keywords: short stature, overgrowth, skeletal dysplasia, brachydactyly, and manually curating the list blind to GIANT height results.

ACAN	*COL9A3*	*GJA1*	*NEU1*	*SIL1*
ADAMTS10	*COMP*	*GLB1*	*NF1*	*SLC26A2*
ADAMTS2	*CRTAP*	*GLI3*	*NIPBL*	*SLC29A3*
ADAMTSL2	*CTDP1*	*GNAS*	*NOG*	*SLC2A2*
AGPS	*CTSK*	*GNPAT*	*NPR2*	*SLC34A3*
ALG12	*CUL4B*	*GNPTAB*	*NSD1*	*SLC35C1*
ALMS1	*CUL7*	*GPC3*	*OCRL*	*SLC35D1*
ALPL	*CYP11B1*	*GUSB*	*OFD1*	*SLC37A4*
ANKH	*CYP19A1*	*HCCS*	*PAPSS2*	*SLC39A13*
ARL6	*CYP21A2*	*HESX1*	*PAX3*	*SLC4A4*
ARSB	*CYP27B1*	*HMGA2*	*PAX8*	*SLC6A8*
ARSE	*DHCR7*	*HOXD13*	*PCNT*	*SMARCAL1*
ATP6V0A2	*DYM*	*HPRT1*	*PEX7*	*SMC1A*
ATP7A	*EBP*	*HRAS*	*PHEX*	*SMC3*
ATP8B1	*EFNB1*	*HSPG2*	*PHF6*	*SMPD1*
ATR	*EIF2AK3*	*HYAL1*	*PITX2*	*SMS*
ATRX	*ERCC2*	*ICK*	*POU1F1*	*SOS1*
B3GALTL	*ERCC3*	*IDUA*	*PQBP1*	*SOST*
B4GALT7	*ESCO2*	*IFT80*	*PROP1*	*SOX3*
BBS1	*EVC*	*IGBP1*	*PTCH1*	*SPG20*
BBS10	*EVC2*	*IGF1*	*PTCH2*	*SRY*
BBS12	*EXT1*	*IGF1R*	*PTEN*	*STAT5B*
BBS2	*EXT2*	*IGF2*	*PTH1R*	*TAZ*
BBS4	*FANCA*	*IHH*	*PTPN11*	*TBCE*
BBS5	*FANCB*	*IKBKG*	*RAB23*	*TBX1*
BBS7	*FANCC*	*JAG1*	*RAB3GAP1*	*TBX15*
BBS9	*FANCD2*	*KCNJ2*	*RAB3GAP2*	*TCF4*
BMPR1B	*FANCE*	*KDM5C*	*RAF1*	*TGFBR1*
BRAF	*FANCF*	*KIAA1279*	*RAI1*	*TGFBR2*
BRCA2	*FANCG*	*KRAS*	*RBM28*	*THRB*
BTK	*FANCI*	*LBR*	*RECQL4*	*TNFRSF11B*
BUB1B	*FANCL*	*LEMD3*	*RMRP*	*TP63*
C7orf11	*FANCM*	*LEPRE1*	*RNF135*	*TRAPPC2*
CA2	*FBN1*	*LHX4*	*ROR2*	*TRIM32*
CCDC28B	*FBN2*	*LIFR*	*RPL11*	*TRIM37*
CEP290	*FGD1*	*LIG4*	*RPL35A*	*TRPS1*
CHD7	*FGF23*	*LMNA*	*RPL5*	*TRPV4*
CHRNG	*FGFR2*	*LRP5*	*RPS17*	*UBR1*
CHST3	*FGFR3*	*MAP2K1*	*RPS19*	*WNT7A*
CLCN5	*FLNA*	*MAP2K2*	*RPS24*	*WRN*
COL10A1	*FLNB*	*MATN3*	*RPS6KA3*	*ZBTB16*
COL11A1	*FOXC1*	*MC4R*	*RPS7*	
COL11A2	*FUCA1*	*MECP2*	*RUNX2*	
COL1A1	*G6PC*	*MGP*	*SBDS*	
COL1A2	*GALNS*	*MKKS*	*SDHA*	
COL2A1	*GDF5*	*MKS1*	*SECISBP2*	
COL5A1	*GH1*	*MMP13*	*SEMA3E*	
COL5A2	*GHR*	*MRPS16*	*SHH*	
COL9A1	*GHRHR*	*MYCN*	*SHOX*	
COL9A2	*GHSR*	*NBN*	*SHROOM4*	

Supplementary Table 11. Height SNPs found to be located near or in the abnormal skeletal/growth genes identified in the OMIM database and listed in Supplementary Table 10.

SNP	Abnormal skeletal/growth gene (OMIM)	The closest gene to the height SNP is the abnormal skeletal/growth gene	The height SNP is in the abnormal skeletal/growth gene
rs16942341	*ACAN*	yes	yes
rs4072910	*ADAMTS10*	yes	no
rs16964211	*CYP19A1*	yes	yes
rs9967417	*DYM*	yes	yes
rs11684404	*EIF2AK3*	yes	yes
rs6457821	*FANCE*	no	no
rs143384	*GDF5*	yes	yes
rs2665838	*GH1*	no	no
rs572169	*GHSR*	yes	yes
rs7971536	*GNPTAB*	no	no
rs1351394	*HMGA2*	yes	yes
rs2871865	*IGF1R*	yes	yes
rs12470505	*IHH*	yes	no
rs17782313	*MC4R*	yes	no
rs227724	*NOG*	yes	no
rs422421	*NSD1*	no	no
rs473902	*PTCH1*	yes	yes
rs3764419	*RNF135*	no	no
rs10874746	*RPL5*	no	no
rs9472414	*RUNX2*	no	no
rs10838801	*SLC39A13*	no	no

Supplementary Table 12. Nominally significant biological pathways following gene set enrichment analysis of height meta-analysis.

Database	Biological pathway or gene set	Original # genes in gene set	# genes in gene set analyzed by GSEA§	Nominal GSEA *P*-value	False discovery rate (FDR)	Expected # genes above 95th percentlie cutoff	Observed # genes above 95th percentlie cutoff	# genes in gene set 300 kb or less from validated height SNPs	Genes 300 kb or less from validated height SNPs	Number of OMIM genes (Supp. Table 10)
KEGG	Hedgehog signaling pathway	54	50	0.0009	0.0777*	3	9	9	BMP6, IHH, PTCH1, WNT6, WNT9A, FBXW11, HHIP, WNT10A, WNT3A	7
KEGG	Gamma-hexachlorocyclohexane degradation	26	21	0.0028	0.0568*	1	5	2	DHRS1, LOC283871	1
KEGG	MAPK signaling pathway	269	243	0.0040	0.2796	12	22	23	ARRB1, CACNB1, CHUK, FGFR3, FGFR4, GNA12, MKNK2, MEF2C, MAP3K3, MOS, GADD45B, NF1, NFATC4, PPM1A, MAPK9, MAP2K3, RASA2, RPS6KA1, TGFB1, TGFB2, TNF, MAP3K14, RASGRP3	16
KEGG	Antigen processing and presentation	77	52	0.0132	0.3014	3	7	16	HLA-B, HLA-C, HLA-DMA, HLA-DMB, HLA-DOB, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, LTA, PSME1, PSME2, TAP1, TAP2	0
KEGG	TGF-beta signaling pathway	83	80	0.0167	0.3131	4	9	10	AMH, BMP6, ID4, LTBP1, TGFB1, TGFB2, TNF, GDF5, CUL1, NOG	7
KEGG	Type II diabetes mellitus	45	43	0.0172	0.2934	2	6	9	INSR, KCNJ11, PKM2, PRKCD, PRKCZ, MAPK9, ABCC8, TNF, SOCS2	1
KEGG	FC epsilon RI signaling pathway	79	73	0.0282	0.3237	4	8	8	CSF2, IL5, IL13, LYN, PRKCD, MAPK9, MAP2K3, TNF	2
KEGG	Folate biosynthesis	37	36	0.0305	0.3549	2	5	1	ATP13A2	2
KEGG	Citrate cycle TCA cycle	27	26	0.0417	0.3464	1	4	5	CS, PC, PCK2, SDHB, SUCLG2	1
Ingenuity	Hepatic Cholestasis	61	57	0.0237	1	3	7	12	ABCC2, CYP27A1, ESR1, FGFR4, INSR, SLC4A2, TAP1, TAP2, TNF, MAP3K14, SLCO1B3, SLCO1C1	0
Ingenuity	VDR/RXR Activation	63	62	0.0341	0.6864	3	7	6	CSF2, GTF2B, PPARD, PSMC5, TGFB2, NCOA1	2
Ingenuity	Role of BRCA1 in DNA Damage Response	29	29	0.0507	0.4980	1	4	4	BRCA2, FANCC, FANCE, RAD50	9
Ingenuity	Fc Epsilon RI Signaling	20	17	0.0531	0.8701	1	3	5	CSF2, IL5, IL13, LYN, TNF	2
PANTHER	TGF-beta signaling pathway	64	59	0.0025	0.1844*	3	9	8	AMH, BMP3, BMP6, SKI, TGFB1, TGFB2, GDF5, DCP1A	7
PANTHER	Hedgehog signaling pathway	14	14	0.0042	0.2033*	1	4	3	IHH, PTCH1, FBXW11	7
PANTHER	Apoptosis signaling pathway	53	49	0.0109	0.2250*	2	7	10	BOK, CMA1, CTSG, GZMH, GZMB, LTA, LTB, TNFSF10, MAP3K14, RIPK3	0
PANTHER	Endothelin signaling pathway	19	19	0.0144	0.2319*	1	4	4	ADCY3, EDN2, PRKG2, ADCY4	1

PANTHER	Parkinson disease	43	41	0.0171	0.2348*	2	6	5	LYN, SEPT2, PSMB3, CUL1, STUB1	0
PANTHER	B cell activation	24	22	0.0223	0.2368*	1	4	4	CD79B, NFKBIL1, PRKCD, PRKCZ	0
PANTHER	Nicotinic acetylcholine receptor signaling pathway	42	39	0.0453	0.3888	2	5	3	MYO1F, MYO6, MYO9B	2
PANTHER, MF	Histone	86	31	0.0001†	0.0028*	2	9	29	HIST1H1C, HIST1H1D, HIST1H1E, HIST1H1T, HIST1H2AE, HIST1H2AD, HIST1H1A, HIST1H2AC, HIST1H2AB, HIST2H2AC, HIST1H3A, HIST1H3D, HIST1H3C, HIST1H3E, HIST1H3G, HIST1H3B, HIST1H4A, HIST1H4D, HIST1H4F, HIST1H4C, HIST1H4H, HIST1H4B, HIST1H4E, HIST1H4G, HIST1H3F, H1FX, H1FOO, HIST2H2AB, HIST2H3D	0
PANTHER, MF	Extracellular matrix glycoprotein	111	85	0.0015	0.1157*	4	12	16	ACAN, FBLN2, EFEMP1, GPC5, GP9, LTBP1, LTBP2, LTBP3, MFAP2, MSLN, FBLN5, EFEMP2, ADAMTSL3, HAPLN3, SCUBE3, MPFL	6
PANTHER, MF	Annexin	71	64	0.0038	0.1821*	3	9	13	AIF1, FBLN2, EFEMP1, LETM1, LTBP1, LTBP2, LTBP3, NUCB2, PRKCD, PKN2, PRKCZ, FBLN5, EFEMP2	1
PANTHER, MF	Transcription factor	198	127	0.0041	0.2089*	6	14	13	NR2F6, ESR1, NFIC, PPARD, BAT2, YEATS4, NCOA1, SCMH1, SFMBT1, MBTD1, GATAD1, L3MBTL3, VGLL2	6
PANTHER, MF	Exoribonuclease	35	25	0.0069	0.2009*	1	5	7	ISG20, PAN2, EXOSC2, EXOSC5, CNOT6, ISG20L1, PNPT1,	0
PANTHER, MF	Other transcription factor	349	298	0.0117	0.3260	15	24	30	RUNX3, E2F1, E2F2, ETS1, ETV5, ETV6, FLI1, ID4, IRF1, MEF2C, ATXN3, NFATC4, NRL, PA2G4, RELA, SKI, SNAPC4, STAT2, TEAD1, TEAD3, TBX4, CREB5, IRF9, FEV, UTP6, GNPTAB, LIN28, RFXDC1, FOXR1, LIN28B	6
PANTHER, MF	Metalloprotease	158	133	0.0158	0.4290	7	13	10	CPN1, PAPPA, ADAM7, ADAMTS3, ADAM28, MMP24, PMPCA, ADAMDEC1, PAPPA2, ADAMTS10	4
PANTHER, MF	Ligase	69	57	0.0206	0.3908	3	7	5	CTPS, DCI, SUCLG2, ZMIZ1, GDPD5	1
PANTHER, MF	ATP-binding cassette (ABC) transporter	46	34	0.0240	0.4536	2	5	7	ABCA3, ABCC2, TAP1, TAP2, ABCB6, RAD50, ABCB8	0
PANTHER, MF	Other phosphatase	82	71	0.0260	0.3693	4	8	8	PPAP2A, FIG4, MTMR11, NUDT4, NUDT3, INPP5E, ACPL2, LOC283871	2
PANTHER, MF	Damaged DNA-binding protein	27	25	0.0327	0.3545	1	4	3	BRCA2, RAD50, UTP6	0
PANTHER, MF	Other RNA-binding protein	192	151	0.0382	0.4413	8	13	14	CARS, STAU1, SLBP, FUBP1, FUBP3, IGF2BP3, IGF2BP2, CPSF6, HNRPUL1, ANKZF1, BRUNOL5,	1

									RBM45, ZFAND2B, C14orf21	
PANTHER, MF	Major histocompatibility complex antigen	46	26	0.0386	0.3567	1	4	14	HFE, HLA-B, HLA-C, HLA-DMA, HLA-DMB, HLA-DOB,HLA-DQA1, HLA-DQA2,HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, MICA, MICB	0
PANTHER, MF	Kinase	30	29	0.0518	0.4439	1	4	2	DGKE, DCAKD	0
GO:0005694	Chromosome	147	111	5e-5†	0.0905*	6	16	29	HIST1H1C, HIST1H1D, HIST1H1E, HIST1H1T, HIST1H2AD, HIST1H2BD, HIST1H2BB, HIST1H1A, HMGA1, HMGA2, HIST1H2AC, HIST1H2AB, HIST2H2AC, HIST1H2BH, HIST1H2BC, HIST2H2BE, HIST1H4G, HIST1H3F, H1FX, RAD50, TINF2, CENPO, H1FOO, HIST2H2AB, C6orf173, SETD8, CENPP, HIST2H2BF, HIST2H3D	4
GO:0060389	Pathway-restricted SMAD protein phosphorylation	14	14	0.0001	0.0984*	1	5	3	BMP6, TGFB1, TGFB2	0
GO:0000786	Nucleosome	64	34	0.0002	0.0650*	2	8	21	HIST1H1C, HIST1H1D, HIST1H1E, HIST1H1T, HIST1H2AD, HIST1H2BD, HIST1H2BB, HIST1H1A, HIST1H2AC, HIST1H2AB, HIST2H2AC, HIST1H2BH, HIST1H2BC, HIST2H2BE, HIST1H4G, HIST1H3F, H1FX, H1FOO, HIST2H2AB, HIST2H2BF, HIST2H3D	0
GO:0006334	Nucleosome assembly	80	47	0.0003	0.0966*	2	9	22	HIST1H1C, HIST1H1D, HIST1H1E, HIST1H1T, HIST1H2AD, HIST1H2BD, HIST1H2BB, HIST1H1A, NAP1L4, HIST1H2AC, HIST1H2AB, HIST2H2AC, HIST1H2BH, HIST1H2BC, HIST2H2BE, HIST1H4G, HIST1H3F, H1FX, H1FOO, HIST2H2AB, HIST2H2BF, HIST2H3D	0
GO:0050680	Negative regulation of epithelial cell proliferation	22	21	0.0006	0.0705*	1	6	9	RUNX3, CDK6, CDKN1C, PPARD, PTCH1, TGFB1, TGFB2, TSC2, TINF2	0
GO:0009653	Anatomical structure morphogenesis	103	94	0.0007	0.1567*	5	13	15	CHUK, RPL10A, NEDD8, PITX1, PKD1, POU5F1, PTCH1, WHSC1, LST1, IGF2BP3, IGF2BP2, RCAN3, SCMH1, SIX4, WNT3A	1
GO:0032147	Activation of protein kinase activity	10	10	0.0008	0.0994*	1	4	3	INSR, TGFB2, LYK5	0
GO:0002474	Antigen processing and presentation of	11	10	0.0010	0.0764*	1	4	3	HFE, HLA-B, HLA-C	0

	peptide antigen via MHC class I									
GO:0000175	3'-5'-exoribonuclease activity	10	10	0.0013	0.0679*	1	4	4	ISG20, EXOSC2, EXOSC5, PNPT1	0
GO:0007259	JAK-STAT cascade	27	26	0.0016	0.1300*	1	6	7	FGFR3, GH1, IL6ST, PKD1, STAT2, SOCS2, IL31RA	2
GO:0003007	Heart morphogenesis	29	28	0.0021	0.1520*	1	6	4	INSR, PTCH1, TGFB2, ZMIZ	4
GO:0030879	Mammary gland development	29	29	0.0023	0.1692*	1	6	5	BRCA2, IGF1R, PTCH1, TGFB1, WNT3A	2
GO:0043560	Insulin receptor substrate binding	12	12	0.0024	0.0888*	1	4	4	IGF1R, INSR, PRKCD, PRKCZ	1
GO:0000421	Autophagic vacuole membrane	13	12	0.0026	0.0907*	1	4	3	TM9SF1, ATG9A, ATG9B	0
GO:0005578	Proteinaceous extracellular matrix	225	198	0.0026	0.2502*	10	20	25	ACAN, ECM2, FBLN2, EFEMP1, GPC5, LOXL1, LTBP1, LTBP2, MFAP2, NTN2L, OMD, OGN, TGFB1, WNT6, WNT9A, ADAMTS3, FBLN5, MMP24, ANGPTL4, ASPN, ADAMTSL3, WNT10A, ADAMTS10, WNT3A, HAPLN3	6
GO:0007405	Neuroblast proliferation	14	14	0.0035	0.1436*	1	4	3	ID4, FRS2, HHIP	0
GO:0000080	G1 phase of mitotic cell cycle	10	7	0.0041	0.0909*	0	3	4	CDK6, CDKN1C, E2F1, MAP3K11	0
GO:0032355	Response to estradiol stimulus	53	53	0.0041	0.2674	3	8	7	GH1, IHH, INSR, NOS3, PTCH1, TGFB1, SOCS2	3
GO:0031965	Nuclear membrane	86	81	0.0058	0.3132	4	10	12	ABL1, MYO6, PML, TRIM27, NUPL2, NUP210, TMEM176B, DTL, INTS2, SENP2, QSOX2, LASS3	0
GO:0005743	Mitochondrial inner membrane	254	222	0.0059	0.3414	11	20	19	CYP27A1, DCI, LETM1, NDUFA7, NDUFB1, NDUFB10, PC, PHB, SDHB, SLC3A1, PPIF, ACAA2, ATP5L, ABCB8, PMPCA, C4orf14, COQ10A, DHRS1, SLC25A45	2
GO:0010628	Positive regulation of gene expression	27	25	0.0059	0.2293*	1	5	3	CSF2, MAPK9, TGFB1	0
GO:0000398	Nuclear mRNA splicing, via spliceosome	45	45	0.0061	0.2757	2	7	7	HNRPM, SFRS10, BAT1, SF3A2, SF3B4, TRA2A, LSM7	**Number of OMIM genes (Supp. Table 10)**
GO:0005242	Inward rectifier potassium channel activity	18	16	0.0061	0.1952*	1	4	5	KCNH2, KCNJ1, KCNJ2, KCNJ5, KCNJ12	7
GO:0017148	Negative regulation of translation	16	16	0.0063	0.1969*	1	4	3	EIF2AK3, IGF2BP3, IGF2BP2	1

GO:0016604	Nuclear body	16	16	0.0067	0.1936*	1	4	3	SKI, PCGF2, BTBD14A	16
GO:0042612	MHC class I protein complex	22	16	0.0076	0.2048*	1	4	6	HFE, HLA-B, HLA-C, MICA, MICB, PROCR	0
GO:0007067	Mitosis	192	180	0.0081	0.3591	9	17	16	CCNF, E4F1, SEPT2, YEATS4, HMGA2, TIMELESS, STAG1, SSSCA1, RGS14, PDS5B, FZR1, NCAPG, NUP37, FAM44B, NY-SAR-48, SETD8	7
GO:0007569	Cell aging	27	26	0.0083	0.2728	1	5	3	BRCA2, PML, ZMIZ1	1
GO:0060395	SMAD protein signal transduction	10	9	0.0085	0.1814*	0	3	2	BMP6, SKI	2
GO:0001763	Morphogenesis of a branching structure	10	9	0.0087	0.1781*	0	3	2	IHH, TGFB1	2
GO:0001501	Skeletal system development	126	113	0.0088	0.3536	6	12	11	ACAN, BMP3, BMP6, FGFR3, IHH, LTBP3, NPR3, PITX1, NOG, EIF2AK3, LOC283871	1

Nominal gene set enrichment analysis (GSEA) *p*-values and false discovery rates were computed for biological gene sets taken from four different resources using MAGENTA (Segrè *et al*., PLoS Genetics, *in press*, 2010). Results are presented for the nominally significant pathways ($p<0.01$ for Gene Ontology (GO) and $p<0.05$ for the other databases). The Bonferroni corrected cutoffs for the different databases are: KEGG (135 pathways): $p<0.0004$, Ingenuity (81 pathways): $p<0.0006$, PANTHER (94 pathways): $p<0.0005$, PANTHER, MF (Molecular Function classification; 216 gene sets): $p<0.0002$, and Gene Ontology (GO) biological process and molecular function terms (1,785 gene sets): $p<0.00003$. (†) specifies a gene set that passes or is close to the Bonferroni cutoff. Since Bonferroni correction is stringent due to considerable gene overlap between pathways within each database, we also evaluated the statistical significance of each gene set using a false discovery rate (FDR), calculated for each database separately. An asterisk (*) refers to pathways with an FDR<0.25 (i.e. one in four gene sets more significant than the given gene set is likely to be false). [§] The number of genes per gene set analyzed by MAGENTA refers to the gene set size after removing genes with no SNPs in their gene region, all but one gene in each subset of genes that were assigned the same best local SNP due to physically proximity in the genome, and genes that were absent from our human gene list. Gene set size was restricted to 10 to 1,000 genes. All genes within 300 kb of the validated height SNPs are listed, including those removed due to physical clustering adjustment or due to lack of SNPs in their region. Underlined genes are those that came up as one of the 21 relevant OMIM height genes captured by the 180 associated signals (i.e. those listed in Supplementary Table 11)

Supplementary Table 13. Biological evidence for genes at the 180 height associated loci. The list of genes is based on genes listed in Supplementary Table 12 (i.e. within a nominally associated pathway and less than 300kb away from one of the 180 height-associated signals), genes with expression evidence where the associated signal had an $r^2 > 0.8$ with the peak SNP in the region in any of the tissues listed in Supplementary Table 7, and genes listed in Supplementary Table 8, where the associated signal was in high LD with a nsSNP. OMIM Evidence is based on genes obtained from the OMIM database (http://www.ncbi.nlm.nih.gov/omim) and listed in Supplementary Table 11. Jackson Lab Evidence was obtained by matching Gene column entries to Jackson Lab database (http://www.informatics.jax.org/) on genes reported to have either "growth/size", "limb/tail/digit"or "skeleton" phenotype.

Gene	Expression Evidence	Missense SNP in LD r2>=0.8 (amino acid change, Polyphen2 prediction)	OMIM Evidence	Gene nearest to height signal	Jackson Lab Evidence	Biological Pathways	Number of lines of evidence
ACAN		rs938608 (S930I, possibly damaging) rs938609 (S939T, probably damaging) rs2882676 (E1508A, benign)	yes	yes	growth/size limbs/digit/tail skeleton	Extracellular matrix glycoprotein	5
CDK6	Lymphocyte			yes	growth/size	Negative regulation of epithelial cell proliferation	4
EIF2AK3		rs1805165 (A704S, benign) rs13045 (Q166R, benign) rs867529 (S136C, benign)	yes	yes	growth/size limbs/digit/tail skeleton		4
FGFR4		rs376618 (P136L, benign)		yes	growth/size	MAPK signaling pathway	4
GDF5			yes	yes	growth/size limbs/digit/tail skeleton	TGFbeta signaling pathway	4
HMGA2			yes	yes	growth/size limbs/digit/tail	Chromosome	4
ID4	Omentum			yes	growth/size	TGFbeta signaling pathway	4
IGF1R			yes	yes	growth/size limbs/digit/tail skeleton	Mammary gland development	4
NOG			yes	yes	growth/size limbs/digit/tail skeleton	TGFbeta signaling pathway	4
PML	Omentum Subcutaneous fat	rs5742915 (F645L, benign)		yes		Nuclear membrane	4
PTCH1			yes	yes	growth/size limbs/digit/tail skeleton	Hedgehog signaling pathway	4

STAT2	Liver Omentum Subcutaneous fat	rs2066807 (M594I, benign)		yes		Other transcription factor	4
ADAMTS10			yes	yes		Metalloprotease	3
ADAMTSL3		rs4842838 (V661L, benign)		yes		Extracellular matrix glycoprotein	3
BMP2				yes	growth/size limbs/digit/tail skeleton	Hedgehog signaling pathway	3
BMP6				yes	growth/size skeleton	Hedgehog signaling pathway	3
CYP19A1			yes	yes	growth/size skeleton		3
C3orf63	Subcutaneous fat	rs9835332 (T609R, benign) rs958755 (Q38P, benign)		yes			3
DYM			yes	yes	growth/size limbs/digit/tail skeleton		3
EFEMP1				yes	growth/size skeleton	Extracellular matrix glycoprotein	3
ESR1				yes	growth/size limbs/digit/tail skeleton	Transcription factor	3
ETV6				yes	growth/size	Other transcription factor	3
FANCE		rs7761870 (S204L, benign)	yes			Role of BRCA1 in DNA damage response	3
FLI1				yes	growth/size	Other transcription factor	3
FRS2				yes	growth/size limbs/digit/tail	Neuroblast proliferation	3
GH1			yes		growth/size	JAK-STAT cascade	3
GHSR			yes	yes	growth/size skeleton		3
GNA12	Lymphocyte			yes		MAPK signaling pathway	3
HHIP				yes	growth/size	Hedgehog signaling pathway	3
HMGA1				yes	growth/size	Chromosome	3
IHH			yes		growth/size limbs/digit/tail skeleton	Hedgehog signaling pathway	3
INSR				yes	growth/size	Type-2 diabetes	3
LTBP1				yes	skeleton	TGFbeta signaling pathway	3

MC4R			yes	yes	growth/size skeleton		3
MEF2C				yes	growth/size limbs/digit/tail skeleton	MAPK signaling pathway	3
MFAP2	Omentum			yes		Extracellular matrix glycoprotein	3
NFATC4				yes	growth/size skeleton	MAPK signaling pathway	3
PAPPA				yes	growth/size skeleton	Metalloprotease	3
PITX1				yes	limbs/digit/tail skeleton	Anatomical structure morphogenesis	3
PPARD				yes	growth/size	VDR/RXR activation	3
PPARD				yes	growth/size	VDR/RXR activation	3
PRKG2				yes	growth/size limbs/digit/tail skeleton	Endothelin signaling pathway	3
RUNX2			yes		growth/size, limbs/digit/tail, skeleton	TGFbeta signaling pathway	3
RYBP	Omentum			yes	growth/size		3
SCMH1				yes	skeleton	Transcription factor	3
SLBP	Lymphocyte			yes		Other RNA-binding protein	3
SOCS2				yes	growth/size limbs/digit/tail skeleton	Type-2 diabetes	3
STK36		rs1344642 (R583Q, probably damaging) rs1863704 (G1003D, benign)			growth/size skeleton	Hedgehog signaling pathway	3
TBX2				yes	limbs/digit/tail	Other transcription factor	3
TEAD1				yes	growth/size	Other transcription factor	3
TGFB2				yes	growth/size limbs/digit/tail skeleton	TGFbeta signaling pathway	3
TSEN15	Omentum Subcutaneous fat	rs2274432 (G19D, probably damaging)		yes			3
SEPT2	Lymphocyte			yes			2
ADAM28				yes		Metalloprotease	2
ADAMTS17				yes		Metalloprotease	2

ADAMTS3				yes		Metalloprotease	2
AKD1	Omentum	rs2277114 (V1555I, benign)					2
ANKRD13B	Subcutaneous fat			yes			2
BNC2				yes	growth/size skeleton		2
C6orf173				yes		chromosome	2
CCDC108				yes			2
CCDC66	Osteoblast	rs7637449 (R460Q, probably damaging)					2
CCDC91		rs11049488 (A36T, benign)		yes			2
CLIC4				yes	growth/size		2
CLPS		rs2766597 (L8P, possibly damaging)			growth/size		2
CPN1				yes		Metalloprotease	2
DDX27	Subcutaneous fat	rs11553387 (G206V, benign)					2
DNM3	Lymphocyte			yes			2
DTL				yes		Nuclear membrane	2
ECM2		rs10120210 (Q56P, probably damaging)				Proteinaceous extracellular matrix	2
EXOSC5		rs10853751 (T5M, benign)				Exoribonuclease	2
FBLN2	Omentum					Extracellular matrix glycoprotein	2
FBXW11				yes		Hedgehog signaling pathway	2
FOLH1	Subcutaneous fat			yes			2
FUBP3				yes		Other RNA-binding protein	2
GNPTAB			yes			Other transcription factor	2
GPC5				yes		Extracellular matrix glycoprotein	2
H1FX	Lymphocyte					Histone	2
HLA-B	Liver					Antigen processing and presentation	2
IGF2BP2				yes		Other RNA-binding protein	2
IGF2BP3				yes		Other RNA-binding protein	2
ITPR3		rs2229642 (L2436V, benign)			growth/size		2
KCNQ1				yes	growth/size		2
L3MBTL3				yes		Transcription factor	2
LIN28				yes		Other transcription factor	2
LIN28B				yes		Other transcription factor	2
LPAR1				yes	growth/size		2
LRRC37B	Omentum			yes			2
LTBP2				yes		Extracellular matrix glycoprotein	2

LUZP1	Liver Subcutaneous fat				growth/size		2
MICA				yes		Major histocompatibility complex antigen	2
MKL2				yes		Other transcription factor	2
MTMR11		rs11205303 (M159V, benign)				Other phosphatase	2
MYO9B				yes		Nicotinic acetylcholine receptor signaling pathway	2
NFIC				yes		Transcription factor	2
NME2				yes	growth/size		2
NPPC				yes	growth/size limbs/digit/tail skeleton		2
NPR3				yes	growth/size limbs/digit/tail skeleton		2
NUCB2				yes		Annexin	2
PAPPA2				yes		Metalloprotease	2
PCSK5				yes	growth/size limbs/digit/tail skeleton		2
PDS5B				yes	growth/size limbs/digit/tail skeleton		2
PEX2				yes	growth/size skeleton		2
PIP4K2B				yes	growth/size limbs/digit/tail skeleton		2
PKN2				yes		Annexin	2
PPAP2A	Omentum					Other phosphatase	2
PPIF				yes		Mitochondrial inner membrane	2
PRKCZ				yes		Type-2 diabetes	2
PSMB3	Osteoblast					Parkinson disease	2
PTPRJ				yes	growth/size		2
QSOX2				yes		Nuclear membrane	2
REST		rs3796529 (P797L, probably damaging)			growth/size		2
RPL5			yes	yes			2

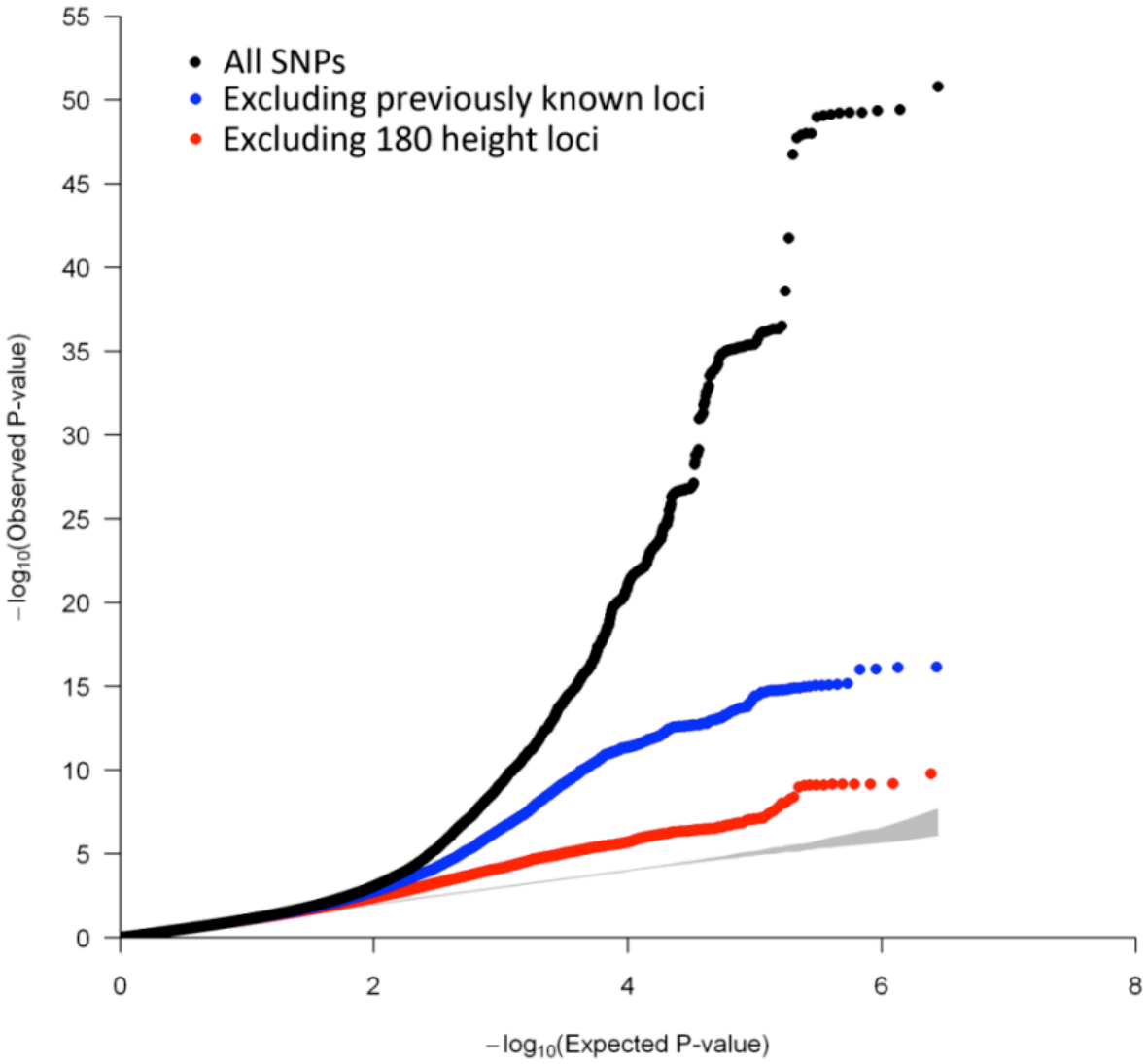
SLC22A4	Liver Subcutaneous fat	rs272893 (I306T, benign)					2
SLC22A5				yes	growth/size		2
SLC39A13			yes		growth/size limbs/digit/tail skeleton		2
SLIT3				yes	growth/size		2
SOCS5	Liver Omentum Subcutaneous fat			yes			2
TNS1				yes		Other phosphatase	2
TRIP11				yes	growth/size		2
UTP6	Liver					Other transcription factor	2
VGLL2				yes		Transcription factor	2
ZBTB24	Lymphocyte Omentum			yes			2
ZNFX1		rs6512577 (M1259I, benign)		yes			2
AK092571	Subcutaneous fat						1
AL117656	Omentum Subcutaneous fat						1
AL161980	Omentum Subcutaneous fat						1
ATP6V1E2	Subcutaneous fat						1
B3GNT8		rs284662 (S137G, benign)					1
BC030091	Liver Omentum Subcutaneous fat						1
C17orf42	Liver Lymphocyte Omentum Subcutaneous fat						1
C17orf82	Subcutaneous fat						1
C20orf199	Lymphocyte						1
C6orf1		rs1150781 (G150A, unknown)					1
CCDC100	Omentum						1
CDK2AP1	Lymphocyte						1
Contig21370_ RC	Omentum						1

Contig40232_RC	Subcutaneous fat						1
Contig41005_RC	Liver						1
Contig43791_RC	Omentum						1
CWF19L1	Omentum Subcutaneous fat						1
FAM173A	Lymphocyte						1
FARP2	Omentum						1
FNDC3B		rs7652177 (T179S, benign)					1
HAGHL	Omentum Subcutaneous fat						1
HDLBP		rs7578199 (N418S, benign)					1
HSS00017874	Omentum						1
HSS00085450	Subcutaneous fat						1
HSS00174467	Omentum						1
INTS7	Lymphocyte Omentum						1
JMJD4	Osteoblast						1
MSTP9	Liver						1
N4BP2L2	Liver Omentum Subcutaneous fat						1
NSD1			yes				1
PFAAP5	Lymphocyte Osteoblast						1
PIP5K2B	Omentum Subcutaneous fat						1
PPA2	Omentum						1
QSCN6L1	Omentum Subcutaneous fat						1
RMI1		rs1982151 (N455S, benign)					1
RNF135			yes				1
SLC23A3	Omentum						1
SMPD2		rs1476387 (R265S, benign)					1
SNAP47	Liver						1
TCF19		rs2073721 (M211V, benign)					1

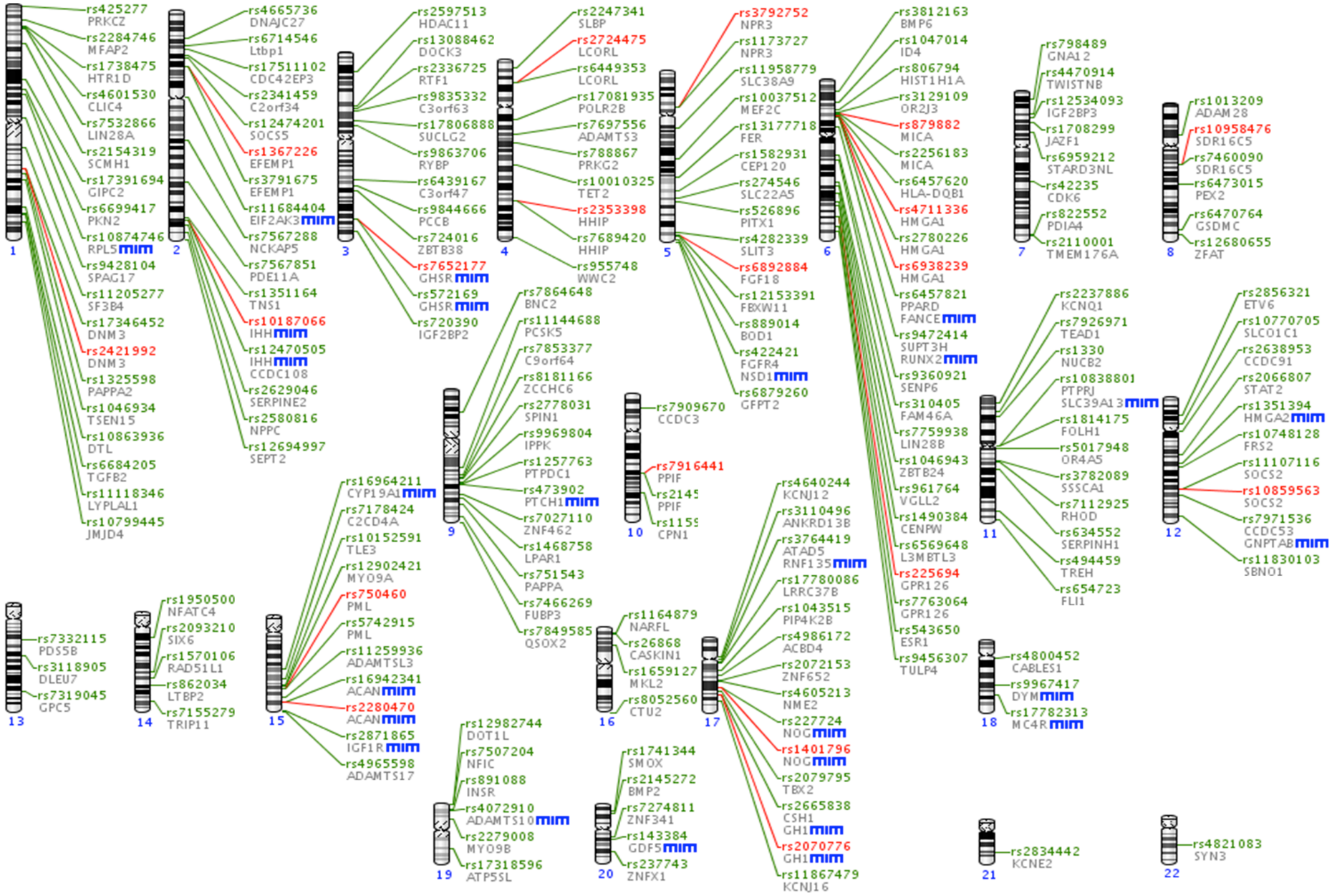
TMEM4	Lymphocyte						1
TP53I13	Omentum Subcutaneous fat						1
USP52	Osteoblast						1
VPS13C		rs3784634 (R931K, benign)					1
ZNF142		rs3770213 (L956H, benign) rs3770214 (S751G, benign)					1
ZNF311		rs6456880 (K511Q, benign)					1

Supplementary Figures

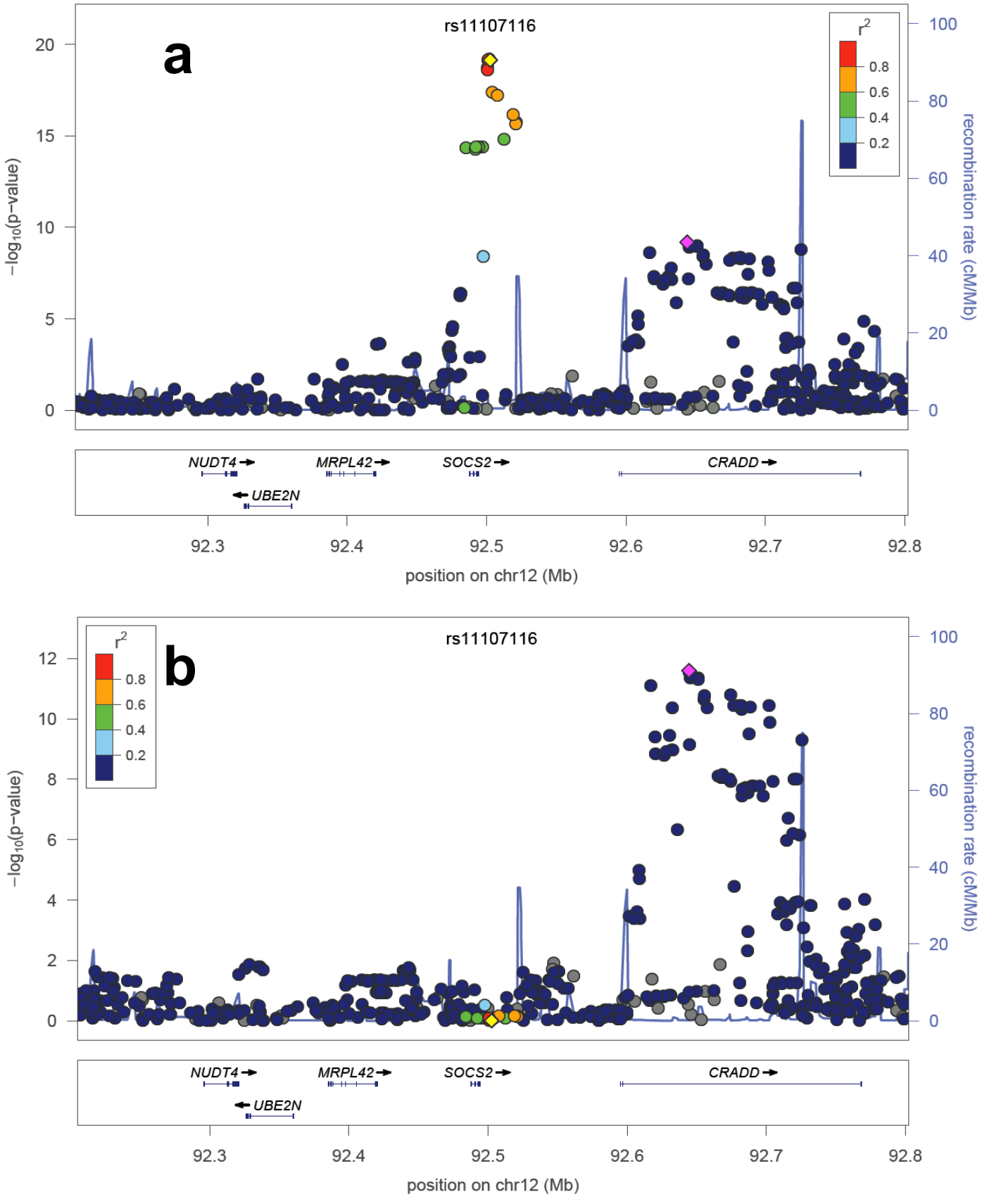
Supplementary Figure 1. Quantile-quantile plot of SNPs after Stage 1 GIANT GC-corrected meta-analysis (black), after removal of SNPs near 47 loci previously shown to associated with height in Caucasians (blue), and after removal of SNPs near 180 loci shown to associate with height in this study (red). All SNPs near (2Mb window) or in linkage disequilibrium (r^2 ≥0.01) with the 47 or 180 index height SNPs were excluded to draw the blue and red distributions, respectively.



Supplementary Figure 2. 199 loci associated with adult height variation. Karyogram displaying the genome location of the 180 height SNPs identified from the primary meta-analysis (green) and the 19 secondary signals (red) discovered in the conditional analysis to be associated with height. The closest genes to the SNPs (gray) are followed by a MIM (blue) label if the gene underlies a skeletal growth-related Mendelian disorder described in OMIM. The plot was created using Affyrmation (http://genepipe.ngc.sinica.edu.tw/affyrmation/).



Supplementary Figure 3. A second example regional association plot of a locus with a secondary signal before (a) and after (b) conditioning. The plots are centered on the conditioned SNP (yellow diamond) at the locus. The secondary signal SNP is highlighted as the pink diamond. r^2 is based on the CEU HapMap II samples. The blue line and right hand Y axis represent CEU HapMap II based recombination rates. Created by LocusZoom (http://csg.sph.umich.edu/locuszoom/).



Supplementary Methods Tables

Supplementary Methods Table 1. Study design, number of individuals and sample quality control for genome-wide association study cohorts.

Study		Study design	Total sample size (N)	Sample QC		Samples in analyses (N)	Anthropometric assessment method	References
Short name	Full name			Call rate*	other exclusions			
Stage 1 (GWA studies)								
ADVANCE	Atherosclerotic Disease, VAscular FunctioN, and GenetiC Epidemiology	Population-based case-control (multi ethnic)	599 (Europeans)	>98.5%	1) duplicates 2) missing weight or height	584: 275 case, 309 ctrls	measured	Assimes T.L. et al. Susceptibility locus for clinical and subclinical coronary artery disease at chromosome 9p21 in the multi-ethnic ADVANCE study. Hum Mol Genet. (2008) 17(15):2320-8.
AGES	Age, Gene/Environment Susceptibility-Reykjavik Study	Population-based	3219	≥ 97%	1) mismatch with previous genotypes; 2) remove A/T & G/C SNPs; 3) remove SNPs not in HapMap	3219	measured	Harris T.B. et al. Age, Gene/Environment Susceptibility-Reykjavik Study: multidisciplinary applied phenomics. American Journal of Epidemiology (2007) 165 (9): 1076-87
Amish HAPI Heart Study	Amish Heredity and Phenotype Intervention Heart Study	Founder population	918	≥ 93%	1) Misidentified pedigree relationships 2) Misidentified sex	907	measured	Mitchell B.D. et al. The genetic response to short-term interventions affecting cardiovascular function: Rationale and design of the Heredity and Phenotype Intervention (HAPI) Heart Study. Am Heart J (2008) 823:828,
ARIC	Atherosclerosis Risk in Communities Study	Population-based	8861 (whites)	≥ 90%	1) True sex/gender mismatch 2) Discordant genotype with earlier TaqMan genotyping. If >10/47 genotypes discordant -> exclude 3) First-degree relative 4) PC>8SD in Eigenstrat run (10 iterations with 10 PCs) 5) Outlier based on average IBS 6) missing height or other covariate	8110	measured	(1) The ARIC Investigators. Atherosclerosis Risk in Communities (ARIC) Study: design and objectives. Am. J. Epidemiol. (1989) 129: 687-702. (2) Heard-Costa N.L. et al. NRXN3 is a novel locus for waist circumference: a genome-wide association study from the CHARGE Consortium. Plos Genet. (2009) 5(6): e1000539.
B58C-T1DGC	British 1958 birth cohort (Type 1 Diabetes Genetic Consortium controls)	Population-based	2592	≥ 98%	1) contamination; 2) non-European identity; 3) Missing body height.	2591	measured	(1) Strachan D.P. et al. Lifecourse influences on health among British adults: effects of region of residence in childhood and adulthood. Int J Epidemiol (2007) 36:522-531 (2) Barrett J.C. et al. The Type 1 Diabetes Genetics Consortium. Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. Nat Genet (2009) 41:703-707
B58C-WTCCC	British 1958 birth cohort (Wellcome Trust Case Control Consortium controls)	Population-based birth cohort	1502	≥97%	1) contamination; 2) non-European identity and relatedness; 3) Missing body height.	1479	measured	The Wellcome Trust Case Control Consortium Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature (2007) 447: 661-678

BRIGHT	British Genetic of Hypertension (BRIGHT) study	Hypertension cases	2000	≥ 97%	1) heterozygosity <23% or >30%; 2) external discordance; 3) non-European ancestry; 4) duplicate/first/second degree relatives.	1806	measured	Caulfield M. et al. Genome-wide mapping of human loci for essential hypertension. Lancet.(2003) 361:2118-23.
CAPS1 cases	Cancer Prostate in Sweden 1	Case-control	505	> 95%	1) related individuals and duplicates; 2) ethnic outliers; 3) missing body weight and height.	489	self-reported	Duggan D. et al. Two genome-wide association studies of aggressive prostate cancer implicate putative prostate tumor suppressor gene DAB2IP. J Natl Cancer Inst (2007) 99:1836-44
CAPS1 controls	Cancer Prostate in Sweden 1	Case-control	506	> 95%	1) related individuals and duplicates; 2) ethnic outliers; 3) missing body weight and height.	491	self-reported	Duggan D. et al. Two genome-wide association studies of aggressive prostate cancer implicate putative prostate tumor suppressor gene DAB2IP. J Natl Cancer Inst (2007) 99:1836-44
CAPS2 cases	Cancer Prostate in Sweden 2	Case-control	1483	> 95%	1) related individuals and duplicates; 2) ethnic outliers; 3) missing body weight and height.	1483	self-reported	Duggan D. et al. Two genome-wide association studies of aggressive prostate cancer implicate putative prostate tumor suppressor gene DAB2IP. J Natl Cancer Inst (2007) 99:1836-44.
CAPS2 controls	Cancer Prostate in Sweden 2	Case-control	519	> 95%	1) related individuals and duplicates; 2) ethnic outliers; 3) missing body weight and height.	519	self-reported	Duggan D. et al. Two genome-wide association studies of aggressive prostate cancer implicate putative prostate tumor suppressor gene DAB2IP. J Natl Cancer Inst (2007) 99:1836-44
CAD-WTCCC	WTCCC Coronary Arteryt Disease cases	Case series	2000	≥ 97%	1) heterozygosity <23% or >30%; 2) discrepancy with external identifying information; 3) ethnic outliers; 4) related individuals and duplicates;	1879	self reported	The Wellcome Trust Case Control Consortium Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature (2007) 447: 661-678
CHS	Cardiovascular Health Study	Population-based	3232	>95%	1) Prevalent clinical CVD 2) African-americans 3) Sex discordant 4) Missing body weight and height	3228	measured	Fried L.P. et al. The Cardiovascular Health Study: design and rationale. Ann Epidemiol. (1991) 1: 263-276.
CoLaus	Cohorte Lausannoise	Population-based	6188	>90%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing height	5409	measured	Firmann M. et al. The CoLaus study: a population-based study to investigate the epidemiology and genetic determinants of cardiovascular risk factors and metabolic syndrome BMC Cardiovascular Disorders (2008) 8:6
deCODE	deCODE genetics sample set	Population-based	38446	≥ 96%	Missing body weight and height.	26799	measured	Thorleifsson G. et al. Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nat Genet. (2009) 41, 18-24.
DGI cases	Diabetes Genetics Initiative	Case-control	1464	≥ 95%	1) Related individuals and duplicates 2) Sex mismatch 3) Phenotype missing	1317	measured	Saxena R. et al. Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. Science (2007) 316:1331-6.
DGI controls	Diabetes Genetics Initiative	Case-control	1467	≥ 95%	1) Related individuals and duplicates 2) Sex mismatch 3) Phenotype missing	1090	measured	Saxena R. et al. Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. Science (2007) 316:1331-6..
EGCUT	Estonian Genome Center, University of Tartu	Population-based	1428	≥ 95%	1) Related individuals and duplicates 2) Sex mismatch 3) Phenotype missing	1417	measured	(1) Nelis M. et al. Genetic Structure of Europeans: A View from the North–East. PLoS ONE (2009) 4(5): e5472. (2) Metspalu A. et al. The Estonian Genome Project. Drug Development Research (2004) 62, 97-101.

EPIC-Obesity Study	European Prospective Investigation into Cancer and Nutrition - Obesity Study	Population-based	3821	≥ 94%	1) heterozygosity <23% or >30%; 2) >5.0% discordance in SNP pairs with r2= 1 in HapMap; 3) ethnic outliers; 4) related individuals and duplicates; 5) Missing body weight and height.	3552	measured	(1) Day N.E. et al. EPIC-Norfolk: study design and characteristics of the cohort. European Prospective Investigation of Cancer. British Journal of Cancer (1999) 80: 95-103. (2) Loos R.J. et al. Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nat Genet (2008) 40: 768-775.
ERF (EUROSPAN)	Erasmus Rucphen Family	Family based	2300	> 95%	1)excess heterozygosity based on FDR 2)ehtnic outliers 3)sex mismatch 4)missing phenotype	2060	measured	(1) Aulchenko Y.S. et al. Linkage disequilibrium in young genetically isolated Dutch population. Eur J Hum Genet (2004) 12: 527-534 (2) Axenovich T.I. et al. Linkage analysis of adult height in a large pedigree from a Dutch genetically isolated population. Hum Genet. (2010) 126: 457-71.
Fenland	Fenland Study	Population-based	1500	≥ 95%	1) heterozygosity <27.3% or >28.8%; 2) duplicate check; 3) relatedness check	1402	measured	Willer C.J. et al. Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nat Genet. (2009) 41:25-34
FHS controls	Family Heart Study	Case-control	434	≥ 98%	1) technical errors 2) discrepancies between reported sex and sex-diagnostic markers	415	measured	Higgins M. et al. NHLBI Family Heart Study: objectives and design, Am J Epidemiol (1996) 143, 1219–1228.
FHS cases	Family Heart Study	Case-control	463	≥ 98%	1) technical errors 2) discrepancies between reported sex and sex-diagnostic markers	441	measured	Higgins M. et al. NHLBI Family Heart Study: objectives and design, Am J Epidemiol (1996) 143, 1219–1228.
FRAM	Framingham Heart Study	Population-based, multi-generational	9274	≥ 97%	1) pHWE<1e-6call rate<97% 2) mishap p<1e-9 3) MAF<0.01 4) Mendelian errors>100 5) SNPs not in Hapmap or strandedness issues merging with Hapmap	8089	measured	(1) Dawber T.R. et al. An approach to longitudinal studies in a community: the Framingham Study. Ann N Y Acad Sci. (1963)107:539-556. (2) Feinleib M. et al. The Framingham Offspring Study. Design and preliminary data. Prev Med. (1975) 4:518-525. (3) Splansky G.L. et al. The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. Am J Epidemiol. (2007) 165:1328-1335.
FTC	Finnish Twin Cohort	Monozygotic twins	152 pairs	≥ 95%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body weight and body mass index.	125	measured	(1) Aulchenko Y.S. et al. Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nat Genet. (2009) 41:47-55.
FUSION controls	Finland-United States Investigation of NIDDM Genetics	Case-control	1174	> 97.5%	related individuals; missing BMI or height	1167	measured	Scott L.J. et al. A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. Science (2007) 316:1341-1345.
FUSION cases	Finland-United States Investigation of NIDDM Genetics	Case-control	1161	> 97.5%	related individuals; missing BMI or height	1082	measured	Scott L.J. et al. A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. Science (2007) 316:1341-1345.
GENMETS controls	Health 2000 / GENMETS substudy of Metabolic syndrome	Case-control	948	≥ 95%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body weight and body mass index.	823	height calculated using BMI and weight	http://www.terveys2000.fi/indexe.html
GENMETS cases	Health 2000 / GENMETS substudy of Metabolic syndrome	Case-control	932	≥ 95%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body weight and body mass index.	824	height calculated using BMI and weight	http://www.terveys2000.fi/indexe.html

GerMiFSI (cases only)	German Myocard Infarct Family Study I	Case-control	875	> 97%	1) related individuals and duplicates; 2)missin phenotypes 3) heterozygosity mean +- 3*sd outlier	600	measured	Samani N.J. et al. Genomewide association analysis of coronary artery disease. N Engl J Med.(2007) 357:443-453.
GerMiFSII (cases only)	German Myocard Infarct Family Study II	Case-control	1222	> 97%	1) related individuals and duplicates; 2)missin phenotypes 3) heterozygosity mean +- 3*sd outlier	1124	measured	Erdmann J. et al. New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nat Genet. (2009) 41:280-282.
KORA S3	Cooperative Health Research in the Region of Augsburg, KOoperative Gesundheitsforschung in der Region Augsburg	Population-based	1644	≥ 93%	1) german passport; 2) missing height.	1643	measured	Wichmann H.E. et al. KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen (2005) 67 Suppl 1, S26-30.
KORA S4	Cooperative Health Research in the Region of Augsburg, KOoperative Gesundheitsforschung in der Region Augsburg	Population-based	1814	≥ 93%	1) german passport; 2) missing height.	1811	measured	Wichmann H.E. et al. KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen (2005) 67 Suppl 1, S26-30.
MICROS	MICROS (EUROSPAN)	Population-based	1098	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	1079	measured	Pattaro C. et al. The genetic study of three population microisolates in South Tyrol (MICROS): study design and epidemiological perspectives. BMC Med Genet (2007) 8:29
MIGEN	Myocardial Infarction Genetics Consortium	Case-control	6042	≥ 95%	1) Related individuals and duplicates 2) Sex mismatch 3) Phenotype missing	2652	measured	Kathiresan S. et al. Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nat Genet. (2009) 41:334-41.
NBS-WTCCC	WTCCC National Blood Service donors	Population-based	1500	≥ 97%	1) heterozygosity <23% or >30%; 2) discrepancy with external identifying information; 3) ethnic outliers; 4) related individuals and duplicates;	1441	self reported	The Wellcome Trust Case Control Consortium. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature (2007) 447, 661-678
NFBC1966	Northern Finland Birth Cohort 1966	Population-based	5654	≥ 95%	1) gender discrepancy with genetic data from X-linked markers; 2) withdrawn consent; 3) duplicates and first and second degree relatives; 4) contaminated samples	4499	measured	(1) Sabatti C. et al. Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. Nat Genet (2008) 41: 35-46. (2) Sovio U. et al. Genetic determinants of height growth assessed longitudinally from infancy to adulthood in the northern Finland birth cohort 1966. PLoS Genet (2009) 5(3): e1000409
NHS	The Nurses' Health Study	Nested case-control	2368	>90%	1) Low genotying completion (<90%); 2) Unclear identity and admixed origin; 3) Missing height.	2265	self-reported	Hunter D. et al. A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nat Genet. (2007) 39: 870-874.

NSPHS	Northern Sweden Population Health Study (EUROSPAN)	Population-based	720	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	652	measured	(1) Johansson A. et al. Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Hum Mol Genet (2009) 18: 373-80. (2) Hicks A.A. et al. Genetic determinants of circulating sphingolipid concentrations in European populations. PLoS Genet. (2009) 5(10):e1000672
NTRNESDA	Netherlands Twin Register & the Netherlands Study of Depression and Anxiety	Case-control	3720	≥ 95%	1) evidence of sample contamination (heterozygosity); 2) ethnic outliers; 3) related individuals and duplicates; 5) missing body height.	3522	questionnaire and measured	(1) Boomsma D.I. et al. Netherlands Twin Register: from twins to twin families. Twin Res Hum Genet (2006) 9: 849–857. (2) Penninx B. et al. The Netherlands Study of Depression and Anxiety (NESDA): rationales, objectives and methods. Int J Methods Psychiatr Res (2008) 17: 121-140. (3) Boomsma D.I. et al. Genome-wide association of major depression: Description of samples for the GAIN major depressive disorder study: NTR and NESDA Biobank Projects. Eur J Hum Genet (2008) 16: 335–342.
ORCADES	Orkney Complex Disease Study (part of EUROSPAN)	Population-based	719	≥ 97%	1) ethnic outliers; 2) duplicates; 3) missing height.	695	measured	(1) Johansson A. et al. Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Hum Mol Genet. (2009) 18: 373-380. (2) Hicks A.A. et al. Genetic determinants of circulating sphingolipid concentrations in European populations. PLoS Genet. (2009) 5(10):e1000672
PLCO	The Prostate, Lung Colorectal and Ovarian Cancer Screening Trial	Case-control	2298	≥ 94%	1) Gender discordance 2) Non-European ancestry 3) Related individuals and duplicates; 4) Missing height.	2244	self-reported	Yeager M. et al. Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nat Genet (2007) 39: 645-649.
PROCARDIS	Precocious Coronary Artery Disease	Case-control	2573	> 95%	none	2312	measured	Broadbent H.M. et al. Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. Hum Mol Genet (2008) 17: 806-814.
RS-I	Rotterdam Study I	Population-based	7983	≥ 97.5%	1) gender mismatch with typed X-linked markers; 2) excess autosomal heterozygosity > 0.336~FDR>0.1%; 3) duplicates and/or 1st or 2nd degree relatives using IBS probabilities >97% from PLINK; 4) ethnic outliers using IBS distances > 3SD from PLINK; 5) Missing body weight and height.	5744	measured	(1) Estrada K. et al. A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. Hum Mol Genet (2009) 18:3516-3524 (2) Estrada K. et al. GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data. Bioinformatics (2009) 25:2750-2752 (3) Hofman A. et al. The Rotterdam Study: 2010 objectives and design update. Eur J Epidemiol (2009) 24: 553-572 (4) Hofman A. et al. Determinants of disease and disability in the elderly: the Rotterdam Elderly Study. Eur J Epidemiol (1991) 7: 403-422
RUNMC	Nijmegen Bladder Cancer Study (NBCS) & Nijmegen Biomedical Study (NBS), Radboud University Nijmegen Medical Centre	Population-based	3081	≥ 96%	Missing body weight and height.	2873	self-assessed and reported by questionnaire	(1) Wetzels J.F. et al. Age- and gender-specific reference values of estimated GFR in Caucasians: the Nijmegen Biomedical Study. Kidney Int (2007) 72, 632-637. (2) Kiemeney L.A. et al. Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nat Genet (2008) 40: 1307-1312.
SardiNIA	SARDINIA	Population-based	6148	≥ 90%	1) Morquio syndrome 2) Missing height	4298	measured	Pilia G. et al. Heritability of cardiovascular and personality traits in 6,148 Sardinians. PLoS Genet (2006) 2: e132

SASBAC cases	Swedish And Singapore Breast Association Consortium	Case-control	803	≥ 96%	1) related individuals and duplicates; 2) ethnic outliers; 3) missing body weight and height.	794	self-reported	(1) Magnusson C. et al. Breast-cancer risk following long-term oestrogen- and oestrogen-progestin-replacement therapy. Int J Cancer (1999) 81: 339-344. (2) Einarsdóttir K. et al. Comprehensive analysis of the ATM, CHEK2 and ERBB2 genes in relation to breast tumour characteristics and survival: a population-based case-control and follow-up study. Breast Cancer Res (2006) 8: R67.
SASBAC controls	Swedish And Singapore Breast Association Consortium	Case-control	764	≥ 96%	1) related individuals and duplicates; 2) ethnic outliers; 3) missing body weight and height.	758	self-reported	(1) Magnusson C. et al. Breast-cancer risk following long-term oestrogen- and oestrogen-progestin-replacement therapy. Int J Cancer (1999) 81: 339-344. (2) Einarsdóttir K. et al. Comprehensive analysis of the ATM, CHEK2 and ERBB2 genes in relation to breast tumour characteristics and survival: a population-based case-control and follow-up study. Breast Cancer Res (2006) 8: R67.
SEARCH / UKOPS	Studies of Epidemiology and Risk factors in Cancer Heredity / UK Ovarian Cancer Population Study	Population-based	1710	≥ 80%	1) ethnic outliers 2) duplicates 3) Missing height	1592	self-assessed	Song H. et al. A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nat Genet (2009) 41: 996-1000.
SHIP	Study of Health in Pomerania	Population-based	4310	≥ 92%	1) missing genotype or phenotype data	4092	measured	John U. et al. Study of health in Pomerania (SHIP): a health examination survey in an east German region: objectives and design. Soz-Präventivmed (2001) 46: 186-194.
T2D-WTCCC	WTCCC Type 2 Diabetes cases	case series	1999	≥ 97%	1) heterozygosity <23% or >30%; 2) discrepancy with external identifying information; 3) ethnic outliers; 4) related individuals and duplicates;	1903	measured	The Wellcome Trust Case Control Consortium Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature (2007) 447: 661-678
TwinsUK	TwinsUK	Twins pairs	2226	≥ 95%	1) heterozygosity <33% or >37%; 2) ethnic outliers; 3) related individuals and duplicates; 4) Missing body weight and height.	1479	measured	(1) Spector T.D., Williams F.M. The UK Adult Twin Registry (TwinsUK). Twin Res Hum Genet (2006) 9: 899-906. (2) Spector T.D., MacGregor A.J. The St. Thomas' UK Adult Twin Registry. Twin Res (2002) 5: 440-443.
VIS	VIS (EUROSPAN) and KORCULA	Population-based	795	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	784	measured	(1) Johansson A. et al. Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Hum Mol Genet. (2009) 18: 373-380. (2) Hicks A.A. et al. Genetic determinants of circulating sphingolipid concentrations in European populations. PLoS Genet. (2009) 5(10):e1000672
Stage 2 (in-silico replication studies)								
BHS	Busselton Health Study	Population-based	1366	≥ 75%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body waist and hip.	1328	measured	(1) James A.L. et al. Decline in lung function in the Busselton Health Study: the effects of asthma and cigarette smoking. Am J Respir Crit Care Med (2005) 171:109-114. (2) Hui J. et al. A genome-wide association scan for asthma in a general Australian population. Hum Genet (2008) 123:297-306

Corogene	Genetic Predisposition of Coronary Heart Disease in Patients Verified with Coronary Angiogram	Population-based	4130	≥ 95%	1) missing gender 2) related individuals and duplicates 3) (For this specific analysis) Missing body height	3758	measured	Soranzo, N. et al. A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nat. Genet (2009). 41: 1182-1190.
EGCUT	Estonian Genome Center, University of Tartu	Population-based	345	≥ 95%	1) Related individuals and duplicates 2) Sex mismatch 3) Phenotype missing	345	measured	(1) Nelis M. et al. Genetic Structure of Europeans: A View from the North–East. PLoS ONE (2009) 4(5): e5472. (2) Metspalu A. The Estonian Genome Project. Drug Development Research (2004) 62: 97-101.
FHS	Family Heart Study	Case-control	1808	≥ 98%	1) technical errors 2) discrepancies between reported sex and sex-diagnostic markers	1463	measured	Higgins M. et al. NHLBI Family Heart Study: objectives and design, Am J Epidemiol (1996) 143: 1219-1228.
FINGESTURE cases	Finnish Genetic Study of Arrhythmic Events	Disease cohort (MI cases only)	1103	≥ 97%	1) PLINK heterozygosity F-value <-0.05 or >0.05; 2) ethnic outliers; 3) related individuals and duplicates; 4) Missing body weight and height.	943	measured	Kaikkonen K.S. et al. Family history and the risk of sudden cardiac death as a manifestation of an acute coronary event. Circulation (2006) 114, 1462-7
GOOD	Gothenburg Osteoporosis and Obesity Determinants Study	Population-based	1056	≥ 97.5%	1) heterozygosity > 33%; 2) ethnic outliers; 3) related individuals and duplicates.	938	measured	Lorentzon M. et al. Free testosterone is a positive whereas free estradiol is a negative predictor of cortical bone size in young Swedish men-The GOOD Study. J Bone Miner Res (2005) 20: 1334-1341.
HBCS	Helsinki Birth Cohort Study	Birth cohort study	1872	≥ 95%	1) related individuals and duplicates 2) (From this specific analysis) Missing body height	1726	measured	Ylihärsilä H. et al. Body mass index during childhood and adult body composition in men and women aged 56-70 y. Am J Clin Nutr. (2008) 87:1769-1775. Kajantie E. et al. Size at birth as a predictor of mortality in adulthood: a follow-up of 350 000 person-years. Int J Epidemiol (2005) 34:655-663.
HYPERGENES controls	HYPERGENES	Case-control	1934	>90%	1) ethnic outliers 2) Missing body weight and height.	1838	measured	http://www.hypergenes.eu/
HYPERGENES cases	HYPERGENES	Case-control	2124	>90%	1) ethnic outliers 2) Missing body weight and height.	1787	measured	http://www.hypergenes.eu/
MGS	Molecular Genetics of Schizophrenia/NIMH Repository Control Sample	Population-based (survey research method)	2681	99.7%	1) call rate < 97% for samples,95% for SNPs 2) heterozygosity <26% or >28.5%; 3) excess duplicate discordancies or mendelian errors (SNPs); 4) ethnic outliers (principal component scores); 5) related individuals and duplicates; 6) Missing body weight or height.	2597	self-reported	(1) Shi J. et al. Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature. (2009) 460: 753-757. (2) Sanders A.R. et al. No significant association of 14 candidate genes with schizophrenia in a large European ancestry sample: implications for psychiatric genetics. Am J Psychiatry. (2008) 165: 497-506.
NHS	The Nurses' Health Study	Nested case-control	3221	>98%	1) Low genotying completion (<98%); 2) Unclear identity and admixed origin; 3) related individuals and duplicates; 4) DNA contamination; 5) Missing height;	3217	self-reported	Qi L. et al. Genetic variants in ABO blood group region, plasma soluble E-selectin levels, and risk of type 2 diabetes. Hum Mol Genet. (2010) Feb 10, doi:10.1093/hmg/ddq057

RS-II	Rotterdam Study II	Population-based	3011	≥ 97.5%	1) gender mismatch with typed X-linked markers; 2) excess autosomal heterozygosity (F<-0.055); 3) duplicates and/or 1st degree relatives using IBD PiHAT >40% from PLINK; 4) ethnic outliers IBS distances > 4SD mean HaMAP CEU cluster from PLINK; 5) Missing body weight and height.	2124	measured	(1) Estrada K. et al. A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. Hum Mol Genet (2009) 18:3516-3524 (2) Estrada K. et al. GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data. Bioinformatics (2009) 25:2750-2752 (3) Hofman A. et al. The Rotterdam Study: 2010 objectives and design update. Eur J Epidemiol (2009) 24: 553-572 (4) Hofman A. et al. Determinants of disease and disability in the elderly: the Rotterdam Elderly Study. Eur J Epidemiol (1991) 7: 403-422
RS-III	Rotterdam Study III	Population-based	3932	≥ 97.5%	1) gender mismatch with typed X-linked markers; 2) excess autosomal heterozygosity (F<-0.055); 3) duplicates and/or 1st degree relatives using IBD PiHAT >40% from PLINK; 4) ethnic outliers IBS distances > 4SD mean HaMAP CEU cluster from PLINK; 5) Missing body weight and height.	2009	measured	(1) Estrada K. et al. A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. Hum Mol Genet (2009) 18:3516-3524 (2) Estrada K. et al. GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data. Bioinformatics (2009) 25:2750-2752 (3) Hofman A. et al. The Rotterdam Study: 2010 objectives and design update. Eur J Epidemiol (2009) 24: 553-572 (4) Hofman A. et al. Determinants of disease and disability in the elderly: the Rotterdam Elderly Study. Eur J Epidemiol (1991) 7: 403-422
Sorbs	Sorbs are self-contained population from Eastern Germany, European Descent	Population-based	1097	≥ 94%	1) gender mismatch; 2) ethnic outliers; 3) duplicates; 4) Missing body weight and height.	907	measured	Tönjes A. et al. Association of FTO variants with BMI and fat mass in the self-contained population of Sorbs in Germany. Eur J Hum Genet. (2010) 18:104-10.
WGHS	Women's Genome Health Study	Population-based	23,294	>98%	1) includes only WGHS participants with confirmed, self-reported European ancestry; 2) all SNPs have HWE p>10E-6; 3) all SNPs have genotype for >90% samples 4) only samples with biometric measures included in analysis	23099	self-report	Ridker P.M. et al. Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy American women. Clin Chem. (2008) 54:249-55. .
YFS	The Cardiovascular Risk in Young Finns Study	Population-based cohort	2,443	≥ 95%	1) missing gender 2) related individuals and duplicates 3) (From this specific analysis) Missing body height	1995	measured	Raitakari O.T. et al. Cohort profile: The cardiovascular risk in Young Finns Study. Int J Epidemiol. (2008) 37:1220-6
Polygene analysis study								
QIMR	Twin studies at the Queensland Instutite of Medical Research	Population-based	2,654	≥ 95%	1) close relatives based on pedigree information; 2) ethnic outliers; 3) Missing height.	1475	measured or self-report	Medland et al. Common Variants in the Trichohyalin Gene Are Associated with Straight Hair in Europeans. Amer J Hum Genet (2009) 85:750-5.
* Sample genotyping success rate; i.e. minimum percentage of successfully genotyped SNPs of GWAs per sample								

Supplementary Methods Table 2. Information on genotyping methods, quality control of SNPs, imputation, and statistical analysis.

Cohort	Genotyping						Imputation			Association analyses				
	Platform	Genotype calling algorithm	Inclusion criteria			SNPs that met QC criteria	Imputation software	Inclusion criteria		SNPs in meta-analysis (after MAFxN>3 filter)	I_{GC}			Analyses software
			MAF	Call rate*	p for HWE			MAF	Imputation quality		all	men	women	
Stage 1 (GWA studies)														
ADVANCE cases	Illumina 550k	BeadStudio	none	≥98.5%	$>10^{-3}$	543,985	BIMBAM	>0%	none	2,193,902	NA	1.047	1.022	SNPTEST
ADVANCE controls	Illumina 550k	BeadStudio	none	≥98.5%	$>10^{-3}$	543,985	BIMBAM	>0%	none	2,206,332	NA	1.046	0.996	SNPTEST
AGES	Illumina Human370CNV	BeadStudio	≥1%	≥95%	$>10^{-6}$	308,340	MACH	>0%	r2-hat≥0.30	2,458,927	NA	1.075	1.082	ProbABEL
Amish HAPI Heart Study	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥1%	≥95%	$>10^{-6}$	338,598	MACH	>0%	r2-hat≥0.30	2,291,092	1.057	0.938	1.045	MMAP
ARIC	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	>1%	≥95%	$>10^{-5}$	685,812	MACH	>0%	r2-hat≥0.30	2,511,301	NA	1.021	1.039	ProbABEL
B58C-T1DGC	Illumina HumanHap 550 V.1	ILLUMINUS	>0%	none	none	539,458	MACH	>0%	r2-hat≥0.30	2,507,988	NA	1.024	1.014	ProbABEL
B58C-WTCCC	Affymetrix GeneChip Human Mapping 500K	CHIAMO	>5%	none	none	392,575	IMPUTE	>0%	proper-info≥0.40	2,448,428	NA	0.999	1.003	SNPTEST
BRIGHT	Affymetrix GeneChip Human Mapping 500K	CHIAMO	≥5%	≥95%	$>10^{-6}$	387,666	IMPUTE	>0%	proper-info≥0.40	2,429,136	NA	1.015	0.995	SNPTEST
CAPS1 cases	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥1%	≥95%	$>10^{-7}$	330,124	IMPUTE	>0%	proper-info≥0.40	2,387,578	NA	0.993	NA	SNPTEST
CAPS1 controls	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥1%	≥95%	$>10^{-7}$	330,124	IMPUTE	>0%	proper-info≥0.40	2,390,475	NA	0.995	NA	SNPTEST
CAPS2 cases	Affymetrix GeneChip Human Mapping 5.0K	BLRMM-P	≥1%	≥95%	$>10^{-7}$	348,163	IMPUTE	>0%	proper-info≥0.40	2,416,296	NA	1.044	NA	SNPTEST
CAPS2 controls	Affymetrix GeneChip Human Mapping 5.0K	BLRMM-P	≥1%	≥95%	$>10^{-7}$	348,163	IMPUTE	>0%	proper-info≥0.40	2,391,556	NA	1.041	NA	SNPTEST
CAD-WTCCC	Affymetrix GeneChip Human Mapping 500K	CHIAMO	>5%	≥95%	$>10^{-6}$	387,667	IMPUTE	>0%	proper-info≥0.40	2,430,482	NA	1.025	1.009	SNPTEST
CHS	Illumina 370-CNV	BeadStudio		>97%	$>10^{-5}$	306,655	BimBam	>0%	r2-hat ≥0.30	2,191,645	NA	1.11	1.15	R
CoLaus	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥1%	≥70%	$>10^{-7}$	390,631	IMPUTE	>0%	proper-info ≥0.40	2,479,491	NA	1.013	1.034	QUICKTEST
deCODE	Illumina HumanHap300 or HumanHapCNV370	BeadStudio	≥1%	≥96%	$>10^{-6}$	290,447	IMPUTE	>0%	proper-info≥0.40	2,456,118	0.948	0.977	0.986	SNPTEST
DGI cases	Affymetrix 500K	BRLMM	≥1%	≥95%	$>10^{-6}$	386,731	MACH	>0%	r2-hat≥0.30	2,410,247	1.029	0.977	1.049	MACH2QTL

DGI controls	Affymetrix 500K	BRLMM	≥1%	≥95%	$>10^{-6}$	386,731	MACH	>0%	r2-hat≥0.30	2,408,993	1.029	1.045	0.995	MACH2QTL
EGCUT	Illumina Beadarray Human370CNV	BeadStudio	≥1%	≥98%	$>10^{-6}$	299,484	IMPUTE	>0%	proper-info≥0.40	2,429,620	NA	1.032	1.013	SNPTEST
EPIC-Obesity Study	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥1%	≥90%	$>10^{-6}$	397,438	IMPUTE	>0%	proper-info≥0.40	2,420,624	NA	1.018	1.027	SNPTEST
ERF (EUROSPAN)	Illumina 318K, 370K, Affymetrix 250K	BRLMM, BeadStudio	>0.5%	>95%	$>10^{-6}$	NA	MACH	>0%	r2-hat≥0.30	2,463,846	1.031	1.012	1.019	ProbABEL
Fenland	Affymetrix SNP5.0	BRLMM	≥1%	≥90%	$>10^{-6}$	362,055	IMPUTE	>0%	proper-info≥0.40	2,406,753	NA	1.039	1.04	SNPTEST
FHS (cases + controls)	Illumina 1Million GeneChip	BeadStudio	≥1%	≥98%	$>10^{-6}$	874,830	MACH	>0%	r2-hat≥0.30	2,375,010	1.066	1.06	1.064	SAS
FRAM	Affymetrix 500K Affymetrix 50K supplemental	BRLMM	≥1%	≥97%	$>10^{-6}$	378,163	MACH	>0%	r2-hat≥0.30	2,455,455	1.071	1.027	1.062	R
FTC	Illumina HumanHap 318K	BeadStudio	≥1%	≥90%	$>10^{-6}$	304,582	MACH	>0%	r2-hat≥0.30	2,268,674	NA	NA	1.005	ProbABEL
FUSION controls	Illumina Infinium™ II HumanHap300 BeadChip	BeadStudio	>1%	≥90%	$\geq 10^{-6}$	315,635	MACH	>0%	r2-hat≥0.30	2,466,546	1.112	1.056	1.074	MACH2QTL
FUSION cases	Illumina Infinium™ II HumanHap300 BeadChip	BeadStudio	>1%	≥90%	$\geq 10^{-6}$	315,635	MACH	>0%	r2-hat≥0.30	2,466,546	1.08	1.077	1.027	MACH2QTL
GENMETS controls	Illumina HumanHap 610K	Illuminus	≥1%	≥95%	$>10^{-6}$	555,388	MACH	>0%	r2-hat≥0.30	2,345,066	NA	1.043	1.006	ProbABEL
GENMETS cases	Illumina HumanHap 610K	Illuminus	≥1%	≥95%	$>10^{-6}$	555,388	MACH	>0%	r2-hat≥0.30	2,343,751	NA	1.016	1.007	ProbABEL
GerMiFSI	Affymetrix NSP/STY	BRLMM	>1%	>97%	$>10^{-5}$	282,215	MACH	>0%	r2-hat≥0.30	2,333,219	NA	1.014	1.026	GenABEL
GerMiFSII	Affymetrix 6.0	Birdseed	>1%	>97%	$>10^{-5}$	653,149	MACH	>0%	r2-hat≥0.30	2,492,325	NA	1.07	1.015	GenABEL
KORA S3	Affymetrix 500K	BRLMM	none	none	none	490,032	MACH	>0%	r2-hat≥0.30	2,415,072	NA	1.018	1.016	MACH2QTL
KORA S4	Affymetrix 6.0	Birdseed	none	none	none	909,622	IMPUTE	>0%	proper-info≥0.40	2,109,266	NA	1.009	1.036	SNPTEST
MICROS	ILLUMINA318K	BeadStudio	≥1%	≥98%	$>10^{-6}$	318,237	MACH	>0%	r2-hat ≥0.30	2,435,539	1.004	1	0.994	ProbABEL
MIGEN	Affymetrix 6.0	Birdseed	≥1%	≥95%	$>10^{-6}$	727,496	MACH	>0%	r2-hat ≥0.30	2,288,269.4 (average)	NA	1.002 (average)	1.0015 (average)	MACH2QTL
NBS-WTCCC	Affymetrix GeneChip Human Mapping 500K	CHIAMO	>5%	≥95%	$>10^{-6}$	387,667	IMPUTE	>0%	proper-info ≥0.40	2,415,926	NA	1.002	1.008	SNPTEST
NFBC1966	Illumina HumanCNV-370DUO Analysis BeadChip	Standard Illumina BeadStudio	≥5%	≥95%	$>10^{-4}$	328,007	IMPUTE	>0%	proper-info ≥0.40	2,460,379	NA	1.037	1.053	SNPTEST
NHS	Illumina HumanHap550	Standard Illumina BeadStudio	≥1%	≥90%	none	510,073	MACH	>0%	r2-hat ≥0.30	2,520,546	NA	NA	1.005	MACH2QTL
NSPHS	ILLUMINA318K	BeadStudio	≥1%	≥98%	$>10^{-6}$	318,236	MACH	>0%	r2-hat≥0.30	2,382,373	1.023	1.03	1.015	ProbABEL

NTRNESDA	Perlegen - Affymetrix gene chip 600K	Proprietary Perlegen	>1%	≥95%	none	435,291	IMPUTE	>0%	proper-info≥0.40	2,493,317	NA	1.028	1.062	SNPTEST
ORCADES	ILLUMINA318K	BeadStudio	≥ 1%	≥98%	$>10^{-6}$	318,235	MACH	>0%	r2-hat≥0.30	2,433,999	1.004	0.966	1.042	ProbABEL
PLCO	Illumina HumanHap300 and Illumina HumanHap240	Illumina Bead Studio	none	≥90%	none	523,231	MACH	>0%	r2-hat≥0.30	2,527,780	NA	1.006	NA	MACH2QTL
PROCARDIS	HumanHap300 BeadChips	Illumina Beadstudio 2.0 software	>5%	≥95%	$>5x10^{-7}$	~820k	IMPUTE	>0%	proper-info≥0.40	2,580,770	NA	1.084	1.014	SNPTEST
RS-I	Illumina /HumanHap 550K V.3 ADHumanHap 550 V.3 DUO;	BeadStudio Genecall	≥1%	≥97.5%	$>10^{-6}$	512,349	MACH	>0%	(O/E)σ2 ratio≥0.1 r2-hat≥0.30	2,488,215	NA	1.045	1.064	MACH2QTL
RUNMC	Illumina HumanHapCNV370	BeadStudio	≥1%	≥96%	$>10^{-6}$	312,199	IMPUTE	>0%	proper-info≥0.40	2,465,662	0.996	0.996	0.996	SNPTEST
SardiNIA	Affymetrix 500K and Affymetrix 10K	BRLMM	≥5%	≥90%	$>10^{-6}$	356,359	MACH	>0%	r2-hat≥0.30	2,251,689	1.313	1.171	1.213	Merlin
SASBAC cases	Illumina HumanHap300+240S	Standard Illumina BeadStudio (GenCall)	≥3%	≥90%	$>10^{-7}$	510,578	IMPUTE	>0%	proper-info≥0.40	2,491,965	NA	NA	1.009	SNPTEST
SASBAC controls	Illumina HumanHap550	Standard Illumina BeadStudio (GenCall)	≥3%	≥90%	$>10^{-7}$	512,223	IMPUTE	>0%	proper-info≥0.40	2,474,508	NA	NA	1.012	SNPTEST
SEARCH / UKOPS	Illumina HumanHap 610 Quad	Illuminus	≥1%	≥95%	$>10^{-4}$	495,229	In-house method similar to IMPUTE	>0%	r2-hat≥0.30	2,486,650	NA	NA	1.02	Regression analysis on dosages
SHIP	Affymetrix Human SNP Array 6.0	Birdseed V2	≥0%	≥0%	≥0	869,224	IMPUTE	>0%	proper-info≥0.40	2,609,015	NA	1.034	1.046	SNPTEST v1.1.5 InforSense
T2D-WTCCC	Affymetrix GeneChip Human Mapping 500K	CHIAMO	>5%	≥95%	$>10^{-6}$	387,667	IMPUTE	>0%	proper-info≥0.40	2,425,374	NA	1.008	1.011	SNPTEST
TWINSUK	Illumina / HumanHap 300 & 550	Illuminus	≥1%	≥95%	$>10^{-6}$	295,702	IMPUTE	>0%	proper-info≥0.40	2,460,943	NA	NA	1.022	SNPTEST
VIS	Illumina HumanHap300v1	BeadStudio	≥1%	≥98%	$>10^{-6}$	317,465	MACH	>0%	r2-hat≥0.30	2,423,083	0.989	1.002	0.991	ProbABEL
Stage 2 (in-silico replication studies)														
BHS	Illumina Human 610-Quad	Illuminus	≥1%	≥95%	$>5.7x10^{-7}$	549,294	MACH	≥1%	r2-hat≥0.30	664	-	-	-	R
Corogene	Illumina BeadChip Human 610-Quad	Illuminus	≥1%	≥95%	$>10^{-6}$	554,988	MACH	≥1%	r2-hat≥0.30	663	-	1.079	1.084	PLINK
EGCUT	Illumina Beadarray Human370CNV	BeadStudio	≥1%	≥98%	$>10^{-6}$	316,924	IMPUTE	≥1%	proper-info≥0.30	662	-	1.034	1.025	SNPtest

FHS	Illumina 1Million GeneChip	BeadStudio	≥1%	≥98%	$>10^{-6}$	874,830	MACH	≥1%	r2-hat≥0.30	665	-	-	-	SAS
FINGESTURE cases	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	≥5%	≥95%	$>10^{-6}$	606,717	MACH	>0%	r2-hat≥0.30	663	-	-	-	MACH2QTL
GOOD	Illumina Infinium HumanHap 610K	BeadStudio	≥1%	≥98%	$>10^{-6}$	521,160	MACH	>0%	r2-hat≥0.30	664	-	-	-	MACH2QTL
HBCS	Illumina custom made BeadChip Human 670-Quad	Illuminus	≥1%	≥95%	$>10^{-6}$	533491	MACH	≥1%	r2-hat≥0.30	663	-	1.000	1.002	PLINK
HYPERGENES controls	Illumina Human1M-Duov3_B	GenCall, BeadStudio	≥1%	≥90%	$>10^{-7}$	Center I: 861759, Center II: 872576	MACH	>0%	r2-hat≥0.30	642	-	-	-	Matlab
HYPERGENES cases	Illumina Human1M-Duov3_B	GenCall, BeadStudio	≥1%	≥90%	$>10^{-7}$	Center I: 861759, Center II: 872576	MACH	>0%	r2-hat≥0.30	642	-	-	-	Matlab
MGS	Affymetrix Genome-Wide Human SNP Array 6.0	Birdsuite 2.0	≥1%	≥95%	$>10^{-6}$	696,492	MACH	≥1%	r2-hat≥0.30	662	-	-	-	PLINK and local software
NHS	Affymetrix Genome-Wide Human 6.0 array	Birdseed calling algorithm v2	≥2%	≥98%	$>10^{-4}$	704,409	MACH	≥2%	r2-hat≥0.30	392	-	-	-	ProbABEL
RS-II	Illumina / HumanHap 550 V.3 DUO; Illumina / HumanHap 610 QUAD	Genomestudio Genecall	≥1%	≥97.5%	$>10^{-6}$	466,389	MACH	≥1%	(O/E)σ2 ratio≥0.1 r2-hat ≥0.30	664	-	1.004	1.012	MACH2QTL
RS-III	Illumina / HumanHap 610 QUAD	Genomestudio Genecall	≥1%	≥97.5%	$>10^{-6}$	514,073	MACH	≥1%	(O/E)σ2 ratio≥0.1 r2-hat ≥0.30	664	-	1.004	1.018	MACH2QTL
Sorbs	500K Affymetrix GeneChip (250K Sty and 250K Nsp arrays) and Affymetrix Genome-Wide Human SNP Array 6.0	BRLMM algorithm for 500K and Birdseed Algorithm for SNP Array 6.0	≥1%	≥95%	$>10^{-4}$	378,513	IMPUTE	>1%	proper-info>0.40	650	-	-	-	SNPTEST
WGHS	Illumina HumanHap300 Duo "+"	Beadstudio v 3.3	NA	≥90%	$>10^{-6}$	339,596	MACH	>0%	r2-hat≥0.30	663	-	-	-	R
YFS	Illumina custom made BeadChip Human 670-Quad	Illuminus	≥1%	≥95%	$>10^{-6}$	546,674	MACH	≥1%	r2-hat≥0.30	663	-	1.017	1.043	PLINK
Polygene analysis study														
QIMR	Illumina HumanHap 610 Quad	BeadStudio	≥1%	≥95%	$>10^{-6}$	493,578								

* SNP genotyping success rate; i.e. minimum percentage of successfully genotyped samples per SNP

Supplementary Methods Table 3: Study-specific descriptive statistics

		Men								Women							
Study	Trait	n	mean	SD	median	min	max	correlation with BMI	correlation with height	n	mean	SD	median	min	max	correlation with BMI	correlation with height
Stage 1 (GWA studies)																	
ADVANCE cases	Age (yrs)	114	40.42	3.98	41.20	20.40	45.10	-0.10	-0.12	161	49.46	4.68	50.50	34.00	55.00	0.01	-0.15
	Height (m)	114	1.77	0.07	1.77	1.61	1.95	0.15	1.00	161	1.64	0.07	1.64	1.48	1.84	-0.14	1.00
	BMI (kg/m²)	114	31.39	5.77	30.89	19.48	54.32	1.00	0.15	161	31.40	8.17	30.65	17.30	61.08	1.00	-0.14
	Weight (kg)	114	99.03	21.16	97.59	64.05	181.44	0.92	0.49	161	83.98	21.78	81.74	48.58	153.00	0.95	0.16
ADVANCE controls	Age (yrs)	128	40.46	3.23	41.20	33.40	46.80	-0.03	0.15	183	48.69	4.45	49.80	34.80	55.40	0.09	-0.03
	Height (m)	128	1.79	0.07	1.78	1.58	1.96	0.02	1.00	181	1.66	0.06	1.66	1.45	1.80	-0.14	1.00
	BMI (kg/m²)	128	27.00	4.48	26.21	17.86	49.38	1.00	0.02	181	26.08	6.36	24.65	15.76	54.12	1.00	-0.14
	Weight (kg)	128	86.45	16.38	84.37	51.48	158.76	0.88	0.43	182	71.35	17.13	68.27	40.23	140.71	0.92	0.21
AGES Midlife	Age (yrs)	1352	49.69	5.87	50.00	34.00	75.00	0.05	-0.21	1867	52.00	6.54	52.00	34.00	77.00	0.15	-0.23
	Height (m)	1352	1.78	0.06	1.78	1.56	1.98	0.01	1.00	1867	1.64	0.05	1.64	1.45	1.83	-0.15	1.00
	BMI (kg/m²)	1351	25.62	3.09	25.48	16.94	38.61	1.00	0.01	1856	24.89	3.81	24.31	13.65	50.41	1.00	-0.15
	Weight (kg)	1351	81.32	11.41	80.40	51.00	139.00	0.87	0.51	1856	67.13	10.51	66.00	32.80	140.60	0.91	0.27
Amish HAPI Heart Study	Age (yrs)	471	46.2	16.9	43.0	20.0	99.0	0.25	-0.41	437	47.5	15.1	48.0	20.0	95.0	0.25	-0.40
	Height (m)	470	1.73	0.07	1.73	1.48	1.94	-0.05	1.00	437	1.61	0.06	1.61	1.39	1.75	-0.22	1.00
	BMI (kg/m²)	468	26.3	3.5	26.0	18.6	39.0	1.00	-0.05	437	28.5	5.7	28.3	16.9	47.1	1.00	-0.22
	Weight (kg)	468	78.6	11.7	77.0	49.4	112.8	0.86	0.45	437	73.5	14.4	71.9	37.8	114.3	0.93	0.16
ARIC	Age (yrs)	3823	54.69	5.70	55.00	44.00	66.00	-0.04	-0.16	4287	53.97	5.67	54.00	44.00	66.00	0.04	-0.15
	Height (m)	3823	1.76	0.06	1.76	1.49	1.99	-0.03	1.00	4287	1.62	0.06	1.62	1.37	1.87	-0.08	1.00
	BMI (kg/m²)	3822	27.48	4.01	26.97	17.21	56.26	1.00	-0.03	4286	26.63	5.52	25.45	14.38	55.20	1.00	-0.08
	Weight (kg)	3822	85.54	13.76	84.09	44.55	182.27	0.89	0.43	4286	70.00	14.99	66.82	36.36	141.82	0.94	0.26
B58C-T1DGC	Age (yrs)	1259	45.31	0.34	45.33	44.50	46.00	-0.02	-0.05	1328	45.27	0.34	45.25	44.50	46.00	0.00	-0.04
	Height (m)	1261	1.76	0.07	1.76	1.55	1.99	-0.03	1.00	1330	1.63	0.06	1.63	1.40	1.85	-0.07	1.00
	BMI (kg/m²)	1259	28.02	4.19	27.56	16.84	51.63	1.00	-0.03	1328	26.97	5.58	25.73	17.18	52.20	1.00	-0.07
	Weight (kg)	1259	87.05	14.41	86.00	50.80	177.10	0.89	0.43	1328	71.63	15.45	68.40	43.00	155.30	0.93	0.29
B58C-WTCCC	Age (yrs)	741	44.89	0.34	44.75	44.50	45.60	-0.01	-0.04	738	44.89	0.35	44.75	44.50	45.60	0.02	0.02
	Height (m)	741	1.76	0.07	1.76	1.52	2.02	-0.05	1.00	738	1.62	0.06	1.63	1.42	1.80	-0.10	1.00
	BMI (kg/m²)	741	27.84	4.29	27.23	15.93	48.41	1.00	-0.05	738	26.92	5.44	25.56	17.34	56.55	1.00	-0.10
	Weight (kg)	741	86.56	14.63	85.20	51.00	137.50	0.87	0.39	738	70.96	14.68	68.20	41.80	139.40	0.91	0.29
BRIGHT	Age (yrs)	719	56.29	11.15	57.00	21.00	84.00	-0.12	-0.24	1087	57.43	11.23	58.00	21.00	85.00	0.07	-0.24
	Height (m)	719	1.74	0.07	1.74	1.51	1.95	-0.06	1.00	1087	1.61	0.06	1.61	1.39	1.81	-0.08	1.00
	BMI (kg/m²)	719	27.74	3.28	27.68	17.20	38.26	1.00	-0.06	1087	27.36	4.04	27.03	16.85	41.66	1.00	-0.08
	Weight (kg)	719	84.22	11.90	83.45	51.00	121.00	0.80	0.54	1087	71.19	11.55	69.90	41.70	122.80	0.87	0.41
CAPS1 cases	Age (yrs)	505	68.15	7.38	67.90	49.50	81.10	-0.16	-0.19	NA	NA	NA	NA	NA	NA	NA	NA
	Height (m)	489	1.77	0.07	1.77	1.58	1.97	-0.04	1.00	NA	NA	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	484	26.42	3.48	26.01	18.36	41.77	1.00	-0.04	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	485	82.50	12.26	82.00	47.00	135.00	0.86	0.47	NA	NA	NA	NA	NA	NA	NA	NA
CAPS1 controls	Age (yrs)	506	66.36	7.50	65.90	44.90	79.80	-0.17	-0.25	NA	NA	NA	NA	NA	NA	NA	NA

	Height (m)	491	1.77	0.07	1.76	1.58	2.01	0.04	1.00	NA	NA	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	483	26.49	3.58	26.25	16.60	58.36	1.00	0.04	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	485	82.75	13.10	82.00	53.00	187.00	0.88	0.51	NA	NA	NA	NA	NA	NA	NA	NA
CAPS2 cases	Age (yrs)	1483	66.13	7.07	65.40	44.90	82.20	-0.09	-0.24	NA	NA	NA	NA	NA	NA	NA	NA
	Height (m)	1483	1.77	0.06	1.77	1.54	2.00	0.02	1.00	NA	NA	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	1423	26.34	3.37	25.95	15.74	55.24	1.00	0.02	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	1424	82.53	12.24	82.00	47.00	185.00	0.88	0.49	NA	NA	NA	NA	NA	NA	NA	NA
CAPS2 controls	Age (yrs)	519	67.24	7.35	66.90	49.10	80.10	-0.05	-0.09	NA	NA	NA	NA	NA	NA	NA	NA
	Height (m)	519	1.76	0.06	1.76	1.59	1.98	-0.07	1.00	NA	NA	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	500	26.03	3.32	25.75	17.56	45.20	1.00	-0.07	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	504	80.80	11.38	80.00	55.00	140.00	0.88	0.42	NA	NA	NA	NA	NA	NA	NA	NA
CAD-WTCCC	Age (yrs)	1491	59.96	7.98	61.00	35.00	82.00	-0.16	-0.10	388	60.28	8.47	61.00	36.00	81.00	-0.09	-0.12
	Height (m)	1491	1.74	0.07	1.74	1.40	1.98	-0.08	1.00	388	1.60	0.07	1.59	1.42	1.78	-0.09	1.00
	BMI (kg/m²)	1489	27.55	3.91	27.13	16.53	53.40	1.00	-0.08	387	27.84	5.23	27.18	12.81	51.73	1.00	-0.09
	Weight (kg)	1489	83.25	13.07	82.50	37.70	173.00	0.86	0.44	387	71.04	14.13	69.20	29.20	149.50	0.91	0.33
CHS	Age (yrs)	1281	73.00	5.66	72.00	65.00	95.00	-0.15	-0.22	1957	71.90	5.15	71.00	65.00	98.00	-0.14	-0.23
	Height (m)	1277	1.73	0.07	1.73	1.51	1.93	-0.04	1.00	1955	1.59	0.06	1.59	1.24	1.78	-0.04	1.00
	BMI (kg/m²)	1276	26.40	3.50	26.10	18.60	44.20	1.00	-0.04	1952	26.40	4.78	25.80	18.50	48.30	1.00	-0.05
	Weight (kg)	1276	79.70	11.90	79.00	50.00	145.00	0.86	0.46	1952	67.10	12.90	65.50	37.30	133.20	0.91	0.04
CoLaus	Age (yrs)	2547	52.92	10.77	52.20	34.90	75.10	0.18	-0.19	2862	53.88	10.72	53.70	35.00	75.40	0.16	-0.20
	Height (m)	2547	1.75	0.07	1.75	1.33	1.98	-0.15	1.00	2862	1.63	0.07	1.63	1.31	1.85	-0.21	1.00
	BMI (kg/m²)	2547	26.64	4.19	26.20	11.70	81.10	1.00	-0.15	2861	25.15	4.91	24.20	8.10	59.20	1.00	-0.21
	Weight (kg)	2547	81.54	13.41	79.90	36.50	175.40	0.85	0.38	2861	66.43	12.98	64.00	21.40	171.00	0.91	0.22
deCODE	Age (yrs)	9213	64.74	15.93	78.00	18.00	103.00	-0.15	-0.31	17586	57.94	18.46	43.00	11.50	108.00	0.08	-0.34
	Height (m)	9213	1.78	0.07	1.80	1.30	2.07	0.02	1.00	17586	1.65	0.06	1.69	1.34	1.99	-0.07	1.00
	BMI (kg/m²)	9213	27.71	4.70	45.99	14.52	72.14	1.00	0.02	17586	26.83	5.49	18.56	13.67	73.51	1.00	-0.07
	Weight (kg)	9213	87.89	16.57	149.00	40.00	216.00	0.88	0.44	17586	73.49	15.77	53.00	33.00	220.00	0.92	0.30
DGI cases	Age (yrs)	687	63.22	10.32	64.28	31.36	91.04	-0.19	-0.24	630	65.43	10.45	66.46	31.12	93.09	-0.26	-0.21
	Height (m)	687	1.74	0.06	1.74	1.43	2.00	-0.02	1.00	630	1.61	0.06	1.61	1.41	1.85	-0.08	1.00
	BMI (kg/m²)	687	28.15	3.87	27.97	18.05	46.71	1.00	-0.02	630	28.78	4.86	28.20	18.51	53.73	1.00	-0.08
	Weight (kg)	687	85.58	13.34	84.80	53.40	148.00	0.87	0.47	630	74.60	13.38	73.50	43.80	141.00	0.90	0.35
DGI controls	Age (yrs)	553	58.11	10.34	58.28	31.71	84.78	-0.01	-0.03	537	59.11	10.27	59.60	33.74	89.94	-0.02	-0.27
	Height (m)	553	1.76	0.06	1.76	1.57	2.00	-0.03	1.00	537	1.63	0.06	1.63	1.42	1.87	-0.10	1.00
	BMI (kg/m²)	553	26.62	3.20	26.37	16.95	43.89	1.00	-0.03	537	26.72	4.16	26.20	17.67	45.37	1.00	-0.10
	Weight (kg)	553	82.21	11.39	80.30	50.80	143.00	0.86	0.49	537	70.52	11.69	69.50	43.00	124.00	0.89	0.35
EGCUT	Age (yrs)	697	40.62	16.78	38.00	18.00	90.00	0.41	-0.39	720	42.88	15.93	42.00	18.00	92.00	0.35	-0.26
	Height (m)	697	1.79	0.07	1.79	1.58	2.03	-0.15	1.00	720	1.65	0.06	1.65	1.45	1.84	-0.14	1.00
	BMI (kg/m²)	697	26.05	4.61	25.39	15.82	54.00	1.00	-0.15	720	26.25	6.02	25.08	15.90	58.40	1.00	-0.14
	Weight (kg)	697	83.32	15.27	82.00	49.00	191.00	0.90	0.30	720	71.41	16.36	68.00	39.00	160.00	0.94	0.20
EPIC-Obesity Study	Age (yrs)	1621	59.8	9.0	60.0	39.0	77.0	0.03	-0.25	1931	58.8	8.9	59.0	39.0	77.0	0.08	-0.26
	Height (m)	1621	1.74	0.07	1.74	1.49	1.97	-0.05	1.00	1931	1.61	0.06	1.61	1.25	1.83	-0.13	1.00
	BMI (kg/m²)	1621	28.3	3.9	28.2	16.9	43.6	1.00	-0.05	1931	28.6	5.2	28.4	16.1	47.6	1.00	-0.13
	Weight (kg)	1621	85.5	13.3	85.0	42.8	137.6	0.87	0.45	1931	74.0	14.1	72.8	44.6	126.6	0.92	0.27
ERF (EUROSPAN)	Age (yrs)	890	50.14	14.98	50.67	18.00	88.60	0.14	-0.49	1170	49.30	15.34	49.52	18.03	92.10	0.27	-0.42

	Height (m)	890	1.75	0.07	1.75	1.52	1.96	-0.08	1.00	1170	1.61	0.07	1.62	1.41	1.83	-0.11	1.00
	BMI (kg/m²)	890	27.14	3.98	26.78	15.85	42.44	1.00	-0.08	1170	26.36	4.77	25.64	15.54	45.37	1.00	-0.11
	Weight (kg)	890	82.70	13.52	81.40	48.00	133.30	0.86	0.43	1170	68.96	13.14	67.00	42.10	133.90	0.90	0.32
Fenland	Age (yrs)	615	44.48	7.32	45.00	30.00	57.00	0.08	-0.09	787	45.34	7.18	46.00	30.00	57.00	0.09	-0.11
	Height (m)	615	1.77	0.07	1.77	1.59	2.01	-0.01	1.00	787	1.64	0.06	1.64	1.43	1.90	-0.07	1.00
	BMI (kg/m²)	615	27.62	4.07	27.27	18.62	56.66	1.00	-0.01	787	26.68	5.46	25.44	17.27	55.39	1.00	-0.07
	Weight (kg)	615	86.76	13.87	85.50	49.40	155.70	0.83	0.46	787	71.48	15.25	68.30	42.40	142.50	0.93	0.28
FHS controls	Age (yrs)	218	52.09	12.20	54.19	26.99	76.86	0.10	-0.18	216	58.25	8.57	59.10	27.33	81.09	-0.06	-0.11
	Height (m)	208	1.77	0.07	1.78	1.55	1.98	-0.07	1.00	207	1.62	0.06	1.63	1.46	1.81	0.04	1.00
	BMI (kg/m²)	208	27.74	3.59	27.10	19.56	42.51	1.00	-0.07	207	26.64	4.66	25.61	17.48	43.39	1.00	0.04
	Weight (kg)	208	87.22	13.09	84.80	57.61	131.09	0.83	0.50	207	70.34	13.59	67.59	43.09	122.05	0.93	0.41
FHS cases	Age (yrs)	220	54.20	11.87	55.75	26.38	74.14	0.02	-0.27	243	57.43	10.08	58.42	26.48	84.00	-0.04	-0.32
	Height (m)	208	1.77	0.07	1.77	1.58	1.96	-0.18	1.00	233	1.62	0.06	1.62	1.42	1.79	-0.02	1.00
	BMI (kg/m²)	208	28.51	4.68	28.15	15.96	45.72	1.00	-0.18	233	28.27	6.51	26.75	18.43	50.18	1.00	-0.02
	Weight (kg)	208	89.04	15.03	87.77	51.71	146.51	0.89	0.27	233	73.87	17.94	69.40	45.36	1.00	0.95	0.29
FRAM	Age (yrs)	3700	38.72	8.73	38.00	21.00	72.00	0.16	-0.05	4389	38.23	8.63	38.00	21.00	70.00	0.27	-0.08
	Height (m)	3700	1.77	0.07	1.77	1.52	2.00	-0.04	1.00	4389	1.63	0.06	1.63	1.40	1.85	-0.07	1.00
	BMI (kg/m²)	3700	27.07	4.18	26.61	16.91	56.54	1.00	-0.04	4384	24.88	5.25	23.57	14.96	60.58	1.00	-0.07
	Weight (kg)	3700	84.43	14.43	82.56	44.00	177.36	0.86	0.44	4384	65.84	14.64	62.60	38.10	170.10	0.89	0.35
FTC	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	126	63.49	12.08	66.28	26.52	75.94	0.27	-0.22
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	125	1.61	0.06	1.61	1.47	1.78	-0.18	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	125	25.07	3.41	24.65	18.69	35.04	1.00	-0.18
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	126	65.53	9.68	64.25	46.50	100.50	0.86	0.30
FUSION controls	Age (yrs)	572	63.41	7.62	64.00	46.00	90.91	-0.05	-0.24	599	63.71	7.27	64.75	42.60	89.15	0.05	-0.29
	Height (m)	569	1.74	0.06	1.74	1.56	1.91	-0.05	1.00	598	1.60	0.06	1.60	1.44	1.79	-0.12	1.00
	BMI (kg/m²)	572	27.02	3.53	26.78	19.22	51.07	1.00	-0.05	599	27.24	4.15	26.80	17.50	45.90	1.00	-0.12
	Weight (kg)	572	81.40	11.98	80.65	52.10	151.10	0.84	0.46	599	69.99	11.44	68.80	45.70	127.10	0.88	0.33
FUSION cases	Age (yrs)	623	62.06	7.33	62.41	40.77	77.81	-0.21	-0.18	469	63.66	7.75	64.01	45.00	83.19	-0.21	-0.22
	Height (m)	617	1.73	0.06	1.73	1.52	1.97	0.00	1.00	465	1.60	0.06	1.59	1.40	1.76	0.02	1.00
	BMI (kg/m²)	623	29.44	4.02	29.14	18.19	43.14	1.00	0.00	469	31.20	5.25	30.71	16.00	47.59	1.00	0.02
	Weight (kg)	623	88.43	13.58	88.00	50.90	144.00	0.89	0.42	469	79.51	14.70	76.90	35.00	125.50	0.91	0.39
GENMETS controls	Age (yrs)	401	48.91	10.15	49.00	30.00	74.00	0.03	-0.27	422	48.60	10.18	49.00	30.00	74.00	0.04	-0.26
	Height (m)	401	1.75	0.07	1.75	1.55	1.80	-0.16	1.00	422	1.75	0.07	1.75	1.55	1.96	-0.16	1.00
	BMI (kg/m²)	401	25.41	3.08	24.94	17.09	39.04	1.00	-0.16	422	25.34	3.15	24.92	17.09	39.04	1.00	-0.16
	Weight (kg)	401	78.03	10.33	77.00	54.00	116.00	0.82	0.43	422	77.62	10.60	77.00	51.00	113.00	0.81	0.45
GENMETS cases	Age (yrs)	410	49.11	10.55	49.00	30.00	75.00	-0.07	-0.24	414	52.25	11.62	51.00	30.00	75.00	-0.07	-0.27
	Height (m)	410	1.76	0.07	1.76	1.58	1.97	-0.13	1.00	414	1.61	0.07	1.61	1.35	1.82	-0.13	1.00
	BMI (kg/m²)	410	29.45	3.62	28.84	23.19	47.07	1.00	-0.13	414	29.62	4.88	28.68	20.58	45.78	1.00	-0.13
	Weight (kg)	410	91.16	12.56	89.00	65.00	151.00	0.81	0.47	414	76.60	13.40	75.00	49.00	123.00	0.87	0.36
GerMiFSI	Age (yrs)	394	57.27	8.57	59.00	32.00	82.00	-0.08	-0.17	206	60.39	8.67	61.00	36.00	82.00	0.04	-0.02
	Height (m)	394	1.75	0.06	1.75	1.59	1.97	-0.05	1.00	206	1.63	0.06	1.63	1.44	1.79	0.00	1.00
	BMI (kg/m²)	394	27.36	3.30	26.83	18.42	46.24	1.00	-0.05	206	27.17	4.17	26.91	19.05	40.75	1.00	0.00
	Weight (kg)	394	83.92	11.67	83.00	60.00	140.00	0.86	0.46	206	72.29	12.24	71.00	48.00	115.00	0.90	0.42
GerMiFSII	Age (yrs)	901	60.14	12.17	59.00	29.00	88.00	-0.01	-0.01	223	62.80	12.76	61.00	34.00	90.00	-0.17	0.17

	Height (m)	901	1.74	0.07	1.74	1.52	2.00	0.02	1.00	223	1.62	0.06	1.61	1.50	1.79	-0.20	1.00
	BMI (kg/m²)	901	27.82	3.54	27.41	18.44	54.08	1.00	-0.02	223	28.06	4.76	27.69	16.90	46.30	1.00	-0.20
	Weight (kg)	901	83.00	12.49	83.00	50.20	160.00	0.85	0.50	223	73.55	12.62	72.10	47.00	130.00	0.90	0.23
KORA S3	Age (yrs)	813	52.96	10.09	54.00	25.00	69.00	0.22	-0.33	831	52.09	10.08	53.00	25.00	69.00	0.33	-0.32
	Height (m)	813	1.74	0.07	1.74	1.51	1.96	-0.14	1.00	830	1.61	0.06	1.61	1.44	1.80	-0.25	1.00
	BMI (kg/m²)	813	27.69	3.45	27.29	18.73	40.67	1.00	-0.14	829	26.98	4.64	26.40	16.71	45.43	1.00	-0.25
	Weight (kg)	813	83.58	11.46	83.30	59.00	132.50	0.79	0.44	829	69.87	11.88	68.30	42.50	121.80	0.88	0.19
KORA S4	Age (yrs)	884	54.22	8.92	54.00	28.00	72.00	0.13	-0.31	930	53.62	8.80	53.00	25.00	74.00	0.32	-0.27
	Height (m)	883	1.74	0.07	1.74	1.56	1.95	-0.13	1.00	928	1.61	0.06	1.61	1.44	1.83	-0.18	1.00
	BMI (kg/m²)	883	27.99	3.91	27.59	18.31	55.11	1.00	-0.13	928	27.49	5.07	26.78	18.21	51.22	1.00	-0.18
	Weight (kg)	883	85.13	12.93	84.00	54.20	192.70	0.83	0.40	929	71.46	13.30	69.60	43.90	142.00	0.90	0.23
MICROS	Age (yrs)	475	45.09	15.67	41.97	18.19	87.85	0.28	-0.45	622	45.38	16.41	42.55	18.00	83.88	0.40	-0.52
	Height (m)	467	1.73	0.07	1.73	1.53	1.95	-0.07	1.00	612	1.61	0.07	1.61	1.40	1.79	-0.28	1.00
	BMI (kg/m²)	475	26.07	3.96	25.62	18.13	42.75	1.00	-0.07	622	25.28	5.32	24.27	14.03	71.26	1.00	-0.28
	Weight (kg)	468	78.38	13.32	76.90	47.00	127.50	0.86	0.43	612	65.16	13.19	63.00	36.60	169.00	0.91	0.13
MIGEN	Age (yrs)	1622	45.40	6.97	45.70	19.40	92.00	0.03	-0.08	1030	49.39	7.40	51.00	18.71	61.00	0.09	-0.14
	Height (m)	1622	1.76	0.08	1.75	1.53	2.08	0.02	1.00	1030	163.10	0.08	1.63	1.10	1.96	-0.06	1.00
	BMI (kg/m²)	1622	27.93	4.57	27.40	17.49	54.30	1.00	0.02	1030	27.96	7.03	26.35	14.78	78.41	1.00	-0.06
	Weight (kg)	1622	86.57	16.30	84.00	52.00	181.60	0.88	0.47	1030	74.42	19.71	70.00	43.09	205.02	0.94	0.27
NBS-WTCCC	Age (yrs)	696	45.41	11.77	47.00	17.00	69.00	0.06	-0.15	745	41.44	12.58	42.00	17.00	69.00	0.15	-0.19
	Height (m)	696	1.78	0.07	1.78	1.50	2.00	-0.07	1.00	745	1.65	0.07	1.65	1.48	1.83	-0.20	1.00
	BMI (kg/m²)	694	26.76	4.12	26.30	18.13	53.19	1.00	-0.07	743	25.75	4.46	24.86	18.08	47.22	1.00	-0.20
	Weight (kg)	694	85.03	14.35	82.73	54.09	173.00	0.88	0.41	743	69.74	12.21	66.82	50.00	127.27	0.89	0.25
NFBC1966	Age (yrs)	2250	31.00	0.00	31.00	31.00	31.00	NA	NA	2249	31.00	0.00	31.00	31.00	31.00	NA	NA
	Height (m)	2250	1.78	0.06	1.78	1.52	2.03	-0.04	1.00	2249	1.65	0.06	1.65	1.05	1.87	-0.10	1.00
	BMI (kg/m²)	2250	25.18	3.62	24.86	15.32	47.58	1.00	-0.04	2247	24.16	4.68	23.13	15.43	54.35	1.00	-0.10
	Weight (kg)	2250	80.15	12.72	78.70	49.40	150.40	0.89	0.42	2247	65.52	13.24	63.00	29.20	165.40	0.92	0.28
NHS	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	2265	54.32	6.67	55.00	21.00	66.00	0.05	-0.02
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	2265	1.64	0.06	1.63	1.45	1.98	-0.10	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	2265	25.13	4.53	24.13	16.40	53.14	1.00	-0.10
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	2265	149.16	27.78	144.00	84.00	310.00	0.92	0.29
NSPHS	Age (yrs)	309	47.56	20.83	48.00	15.00	87.00	0.31	-0.32	347	46.47	20.60	45.00	14.00	91.00	0.49	-0.40
	Height (m)	308	1.71	0.07	1.72	1.48	1.89	-0.04	1.00	344	1.58	0.07	1.59	1.40	1.75	-0.16	1.00
	BMI (kg/m²)	307	26.75	4.54	26.23	17.78	46.49	1.00	-0.04	340	25.97	5.07	24.98	16.44	46.68	1.00	-0.16
	Weight (kg)	307	78.42	14.66	77.00	51.00	138.00	0.88	0.42	342	64.99	13.11	63.00	38.00	121.00	0.89	0.29
NTRNESDA	Age (yrs)	1211	46.08	13.43	48.00	18.00	81.00	0.26	-0.29	2311	42.64	13.23	42.00	18.00	78.00	0.23	-0.23
	Height (m)	1211	1.82	0.07	1.82	1.59	2.07	-0.14	1.00	2311	1.69	0.06	1.69	1.50	1.96	-0.15	1.00
	BMI (kg/m²)	1210	26.05	3.92	25.62	15.95	50.21	1.00	-0.14	2306	25.15	4.82	24.19	14.61	53.27	1.00	-0.15
	Weight (kg)	1210	85.89	13.80	84.15	50.10	170.00	0.87	0.36	2306	71.83	14.06	69.20	44.00	167.00	0.92	0.24
ORCADES	Age (yrs)	332	54.27	15.73	54.66	17.29	93.75	0.29	-0.38	384	53.01	15.68	54.27	17.71	97.62	0.25	-0.38
	Height (m)	324	1.75	0.07	1.75	1.59	1.99	-0.22	1.00	371	1.61	0.06	1.61	1.38	1.78	-0.17	1.00
	BMI (kg/m²)	332	28.08	4.27	27.67	16.97	47.10	1.00	-0.22	384	27.48	5.18	26.60	18.47	47.63	1.00	-0.17
	Weight (kg)	324	85.76	13.21	84.25	44.40	148.40	0.87	0.28	371	71.06	13.69	69.10	45.60	123.10	0.92	0.22
PLCO	Age (yrs)	2244	64.2	5.1	64.0	55.0	74.0	-0.11	-0.11	NA	NA	NA	NA	NA	NA	NA	NA

	Height (m)	2244	1.78	0.07	1.78	1.55	2.03	-0.04	1.00	NA	NA	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	2236	27.5	3.8	27.1	13.3	48.2	1.00	-0.04	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	2236	87.4	13.6	86.2	38.6	176.9	0.88	0.44	NA	NA	NA	NA	NA	NA	NA	NA
PROCARDIS	Age (yrs)	1700	59.29	7.08	60.00	34.00	82.00	-0.07	-0.14	612	61.21	6.72	62.00	33.00	81.00	0.03	-0.21
	Height (m)	1700	1.75	0.07	1.75	1.51	2.06	-0.10	1.00	612	1.63	0.07	1.64	1.44	1.85	-0.22	1.00
	BMI (kg/m²)	1700	27.60	3.80	27.14	18.34	48.23	1.00	-0.10	612	26.71	5.00	25.94	15.43	51.37	1.00	-0.22
	Weight (kg)	1700	84.51	12.91	83.50	51.00	159.00	0.84	0.44	612	71.21	13.30	69.00	42.00	145.00	0.89	0.23
RS-I	Age (yrs)	2427	68.13	8.16	67.05	55.01	97.81	-0.08	-0.31	3547	70.32	9.60	69.40	55.00	99.22	0.05	-0.38
	Height (m)	2372	1.75	0.07	1.75	1.51	1.98	-0.05	1.00	3375	1.61	0.07	1.62	1.01	1.92	-0.15	1.00
	BMI (kg/m²)	2372	25.68	2.99	25.61	14.19	38.19	1.00	-0.05	3372	26.74	4.10	26.31	15.43	59.50	1.00	-0.15
	Weight (kg)	2375	78.58	10.74	77.80	41.00	122.30	0.82	0.53	3383	69.59	11.29	68.70	40.10	146.50	0.85	0.37
RUNMC	Age (yrs)	1839	63.47	8.34	64.00	24.00	91.00	-0.02	-0.12	1132	55.41	11.14	64.00	25.00	91.00	0.17	-0.23
	Height (m)	1777	1.77	0.07	1.85	1.55	2.00	-0.10	1.00	1096	1.66	0.06	1.75	1.38	1.85	-0.15	1.00
	BMI (kg/m²)	1777	25.98	3.66	21.90	16.10	61.30	1.00	-0.10	1096	25.44	4.26	24.50	17.30	52.70	1.00	-0.15
	Weight (kg)	1777	81.49	12.33	75.00	46.00	185.00	0.87	0.40	1096	70.30	12.16	75.00	46.00	150.00	0.90	0.29
SardiNIA	Age (yrs)	1886	44.08	18.10	42.90	14.00	93.90	0.51	-0.46	2419	43.19	17.30	42.10	14.00	101.30	0.55	-0.50
	Height (m)	1883	1.66	0.07	1.66	1.44	1.96	-0.22	1.00	2415	1.55	0.06	1.55	1.31	1.78	-0.31	1.00
	BMI (kg/m²)	1885	26.15	4.11	25.90	14.90	42.90	1.00	-0.22	2416	24.75	5.03	23.80	13.90	53.30	1.00	-0.31
	Weight (kg)	1883	72.27	11.71	72.00	34.00	135.00	0.84	0.33	2415	59.17	11.40	57.00	32.00	145.00	0.90	0.11
SASBAC cases	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	795	62.64	6.26	63.00	50.00	75.00	0.11	-0.08
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	794	1.64	0.06	1.65	1.47	1.82	-0.16	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	793	25.79	4.00	25.21	16.22	46.67	1.00	-0.16
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	794	69.68	11.18	68.00	40.00	117.00	0.86	0.30
SASBAC controls	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	764	62.77	6.34	63.00	49.00	75.00	0.02	-0.05
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	758	1.64	0.05	1.64	1.28	1.81	-0.06	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	755	25.52	4.10	25.22	16.94	59.52	1.00	-0.06
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	760	68.67	11.69	67.00	42.00	168.00	0.89	0.33
SEARCH/UKOPS	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	1710	57.15	10.20	58.00	20.00	91.00	-0.09	-0.13
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	1592	1.63	0.07	1.63	1.35	1.83	-0.14	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	1556	26.99	5.20	25.99	17.47	53.67	1.00	-0.14
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	1581	71.32	13.99	69.00	44.00	135.17	0.91	0.27
SHIP	Age (yrs)	2019	50.88	16.43	52.00	20.00	80.00	0.25	-0.48	2073	48.58	16.02	48.00	20.00	81.00	0.41	-0.48
	Height (m)	2019	1.75	0.07	1.75	1.48	1.98	-0.12	1.00	2073	1.63	0.07	1.63	1.42	1.94	-0.26	1.00
	BMI (kg/m²)	2019	27.68	4.04	27.41	18.06	48.07	1.00	-0.12	2073	26.92	5.31	26.16	16.10	52.40	1.00	-0.26
	Weight (kg)	2019	85.06	13.56	83.80	49.90	156.40	0.83	0.40	2073	71.20	13.74	69.20	41.30	133.30	0.89	0.16
T2D-WTCCC	Age (yrs)	1105	58.95	9.91	59.00	29.00	96.00	-0.31	-0.17	798	57.94	10.45	59.00	27.00	85.00	-0.30	-0.16
	Height (m)	1105	1.75	0.07	1.75	1.50	1.98	-0.02	1.00	798	1.61	0.07	1.61	1.37	1.83	0.01	1.00
	BMI (kg/m²)	1105	30.29	5.36	29.71	18.02	55.91	1.00	-0.02	798	32.56	6.87	31.52	17.91	62.37	1.00	0.01
	Weight (kg)	1105	93.37	17.86	91.17	47.63	161.94	0.91	0.40	798	85.04	19.29	82.56	43.00	155.70	0.93	0.37
TwinsUK	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	1479	46.19	12.31	47.55	16.62	76.54	0.15	-0.20
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	1479	1.62	0.06	1.63	1.42	1.80	-0.12	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	1477	25.02	4.80	24.06	13.22	52.71	1.00	-0.12
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	1477	66.03	12.97	64.00	35.10	140.90	0.92	0.27
VIS	Age (yrs)	328	55.95	14.94	57.00	18.00	88.00	0.23	-0.40	467	56.97	15.64	57.00	18.00	93.00	0.30	-0.45

	Height (m)	325	1.76	0.07	1.76	1.58	2.04	-0.10	1.00	459	1.62	0.07	1.62	1.43	1.91	-0.20	1.00
	BMI (kg/m²)	328	27.55	3.69	27.49	18.36	40.69	1.00	-0.10	467	27.18	4.50	27.08	17.01	52.02	1.00	-0.20
	Weight (kg)	325	85.56	13.01	84.80	50.90	136.50	0.83	0.47	445	70.99	12.45	69.80	46.60	153.00	0.89	0.26
Stage 2 (in-silico replication studies)																	
BHS	Age (yrs)	558	53.47	17.15	53.65	17.60	91.40	0.15	-0.38	770	53.71	17.07	53.05	17.30	90.50	0.11	-0.43
	Height (m)	558	1.75	0.07	1.75	1.53	1.99	-0.09	1.00	770	1.62	0.06	1.62	1.35	1.90	-0.15	1.00
	BMI (kg/m²)	558	26.62	3.57	26.25	15.77	40.12	1.00	-0.09	769	25.49	4.42	24.66	16.82	40.77	1.00	-0.15
	Weight (kg)	558	81.80	12.31	80.25	46.40	127.00	0.83	0.47	769	67.06	12.02	65.00	34.80	109.00	0.90	0.29
Corogene	Age (yrs)	2266	59.66	12.83	61.00	25.00	92.00	-0.03	-0.26	1490	62.61	13.47	65.00	25.00	94.00	0.09	-0.30
	Height (m)	2267	1.76	0.07	1.76	1.34	2.03	-0.04	1.00	1491	1.62	0.07	1.62	1.05	1.85	-0.14	1.00
	BMI (kg/m²)	2265	27.39	4.23	26.79	15.95	54.88	1.00	-0.04	1491	26.87	5.21	26.07	13.63	57.68	1.00	-0.14
	Weight (kg)	2265	85.00	14.42	83.50	44.00	170.00	0.89	0.41	1491	70.14	13.88	68.30	36.00	144.00	0.90	0.28
EGCUT	Age (yrs)	135	40.93	17.81	36.50	18.00	80.00	0.33	-0.55	210	41.03	16.46	39.00	18.00	87.00	0.41	-0.37
	Height (m)	135	1.79	0.07	1.80	1.58	2.04	-0.14	1.00	210	1.66	0.07	1.66	1.44	1.84	-0.25	1.00
	BMI (kg/m²)	135	26.03	4.95	25.11	17.30	43.65	1.00	-0.14	210	25.63	6.09	24.02	17.00	48.24	1.00	-0.25
	Weight (kg)	135	83.68	16.41	80.50	50.00	143.00	0.91	0.27	210	70.46	16.22	66.50	40.00	136.00	0.93	0.10
FHS	Age (yrs)	662	48.20	13.70	46.30	25.60	85.70	0.15	-0.24	880	47.50	13.00	45.00	25.70	85.80	0.19	-0.26
	Height (m)	632	1.77	0.07	1.77	1.57	2.03	-0.09	1.00	831	1.63	0.06	1.63	1.41	1.96	-0.12	1.00
	BMI (kg/m²)	632	27.80	4.30	27.20	18.40	46.20	1.00	-0.09	831	27.10	6.10	26.10	16.50	55.00	1.00	-0.12
	Weight (kg)	632	87.10	14.60	85.30	55.30	140.60	0.88	0.39	831	72.30	16.60	68.90	41.70	144.20	0.94	0.22
FINGESTURE cases	Age (yrs)	745	61.19	10.58	62.00	34.00	85.00	-0.13	-0.33	198	67.44	10.33	68.00	31.00	85.00	-0.05	-0.28
	Height (m)	745	1.74	0.07	1.74	1.55	1.97	0.10	1.00	198	1.60	0.06	1.60	1.46	1.76	-0.02	1.00
	BMI (kg/m²)	739	27.22	3.93	27.02	16.20	44.80	1.00	0.10	196	28.14	5.17	27.98	16.67	46.09	1.00	-0.02
	Weight (kg)	743	82.32	14.09	81.00	42.00	150.00	0.89	0.53	197	71.91	14.06	71.60	37.50	112.00	0.92	0.38
GOOD	Age (yrs)	938	18.90	0.60	18.80	18.00	20.10	0.03	0.01	NA	NA	NA	NA	NA	NA	NA	NA
	Height (m)	938	1.82	0.07	1.82	1.61	2.03	-0.05	1.00	NA	NA	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	938	22.40	3.20	21.90	16.10	41.60	1.00	-0.05	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	938	73.90	11.60	72.00	51.30	127.00	0.88	0.42	NA	NA	NA	NA	NA	NA	NA	NA
HBCS	Age (yrs)	737	61.41	2.75	60.80	57.00	69.30	-0.03	-0.15	991	61.55	3.05	60.90	56.70	69.80	-0.10	0.03
	Height (m)	736	1.77	0.06	1.77	1.59	1.97	-0.03	1.00	990	1.63	0.06	1.63	1.46	1.83	-0.09	1.00
	BMI (kg/m²)	736	27.56	4.30	27.01	18.75	68.39	1.00	-0.03	990	27.75	5.06	26.98	14.79	50.10	1.00	-0.09
	Weight (kg)	737	86.33	14.51	84.50	56.20	213.30	0.92	0.36	990	73.90	13.89	71.70	37.30	133.80	0.93	0.28
HYPERGENES - controls	Age (yrs)	1072	62.27	10.71	59.81	28.00	98.00	-0.09	-0.12	766	64.30	11.28	61.00	44.93	113.00	-0.15	-0.14
	Height (m)	1072	1.71	0.07	1.70	1.50	1.96	-0.14	1.00	766	1.60	0.06	1.60	1.40	1.81	-0.16	1.00
	BMI (kg/m²)	1072	25.95	3.27	25.59	10.15	40.77	1.00	-0.14	766	24.98	3.73	24.60	16.53	41.35	1.00	-0.16
	Weight (kg)	1072	76.10	10.59	75.00	29.00	118.00	0.81	0.46	766	64.25	10.13	63.00	41.00	110.00	0.87	0.34
HYPERGENES - cases	Age (yrs)	1189	49.41	10.42	50.00	17.63	84.00	0.04	-0.33	598	48.45	9.57	49.00	18.38	93.00	0.10	-0.19
	Height (m)	1189	1.72	0.07	1.72	1.48	1.96	-0.08	1.00	598	1.60	0.07	1.60	1.40	1.97	-0.10	1.00
	BMI (kg/m²)	1189	27.42	3.52	27.13	16.00	47.43	1.00	-0.08	598	26.88	4.96	26.21	17.45	52.35	1.00	-0.10
	Weight (kg)	1189	81.33	12.06	80.00	49.00	139.50	0.82	0.51	598	68.59	13.66	67.00	44.00	164.00	0.89	0.36
MGS	Age (yrs)	1247	52.67	16.01	52.00	18.00	90.00	0.02	-0.13	1350	48.48	16.29	48.00	18.00	90.00	0.03	-0.20
	Height (m)	1247	1.79	0.07	1.78	1.58	2.06	0.04	1.00	1350	1.64	0.07	1.65	1.35	2.01	-0.04	1.00
	BMI (kg/m²)	1247	30.85	6.45	29.84	15.83	72.56	1.00	0.04	1350	31.92	8.55	30.32	16.34	69.09	1.00	-0.04
	Weight (kg)	1247	98.77	22.67	95.25	53.98	249.48	0.93	0.38	1350	86.13	24.22	81.65	47.63	201.85	0.95	0.26

NHS	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	3217	53.22	6.96	54.00	22.00	65.00	-0.02	-0.07
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	3217	1.64	0.08	1.63	1.35	1.83	-0.04	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	2988	27.13	5.63	26.00	17.01	54.87	1.00	-0.04
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	2988	160.87	35.21	155.00	90.00	340.00	0.94	0.30
RS-II	Age (yrs)	973	64.48	7.59	61.89	55.14	93.95	-0.13	-0.22	1156	65.04	8.33	62.03	55.12	95.33	-0.03	-0.31
	Height (m)	971	1.76	0.06	1.76	1.57	2.03	-0.10	1.00	1153	1.63	0.06	1.63	1.42	1.90	-0.06	1.00
	BMI (kg/m²)	971	26.92	3.36	26.72	16.78	40.52	1.00	-0.10	1151	27.52	4.45	26.89	16.66	50.12	1.00	-0.06
	Weight (kg)	972	83.32	11.58	82.20	54.00	126.80	0.85	0.44	1151	72.77	12.74	71.10	36.20	150.00	0.90	0.38
RS-III	Age (yrs)	879	55.94	5.43	56.12	45.46	84.15	0.09	-0.24	1130	56.20	6.03	56.42	45.75	97.22	0.07	-0.23
	Height (m)	879	1.79	0.07	1.79	1.61	2.00	-0.07	1.00	1130	1.65	0.06	1.65	1.47	1.85	-0.10	1.00
	BMI (kg/m²)	879	28.03	4.07	27.31	18.42	46.68	1.00	-0.07	1130	27.48	5.06	26.55	14.02	56.87	1.00	-0.10
	Weight (kg)	879	89.75	14.32	87.70	58.30	153.50	0.88	0.41	1130	74.89	14.28	72.80	35.00	158.60	0.92	0.29
Sorbs	Age (yrs)	371	48.10	16.70	48.10	18.10	82.10	0.39	-0.43	536	48.00	15.90	48.60	18.00	88.40	0.49	-0.54
	Height (m)	371	1.77	0.07	1.77	1.58	1.95	-0.24	1.00	536	1.64	0.07	1.64	1.44	1.82	-0.32	1.00
	BMI (kg/m²)	371	27.20	4.00	26.80	19.00	43.90	1.00	-0.24	536	26.90	5.50	26.20	15.40	47.40	1.00	-0.32
	Weight (kg)	371	85.40	12.70	84.00	58.00	139.00	0.85	0.30	536	72.10	14.00	70.00	43.00	126.00	0.92	0.07
WGHS	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	23294	54.70	7.12	52.90	38.71	89.89	-0.02	-0.07
	Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	23099	1.64	0.06	1.65	1.30	2.01	-0.06	1.00
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	22888	25.91	4.96	24.89	14.23	59.58	1.00	-0.06
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	23046	70.00	14.18	68.04	38.56	175.09	0.92	0.32
YFS	Age (yrs)	1123	37.55	5.06	39.00	30.00	45.00	0.13	-0.12	1320	37.57	5.01	39.00	30.00	45.00	0.11	-0.06
	Height (m)	911	1.80	0.07	1.80	1.57	2.03	0.04	1.00	1084	1.66	0.06	1.66	1.45	1.89	-0.06	1.00
	BMI (kg/m²)	908	26.76	4.29	26.11	17.54	49.35	1.00	0.04	1081	25.32	5.03	24.34	16.56	58.82	1.00	-0.06
	Weight (kg)	908	86.56	15.65	85.00	54.00	166.00	0.91	0.45	1083	69.82	14.55	67.00	42.00	166.00	0.94	0.29
Polygene analysis study																	
QIMR	Age (yrs)	527	23.20	12.00	16.33	15.40	74.00	NA	0.15	948	29.86	14.95	26.00	15.70	84.00	NA	-0.15
	Height (m)	527	1.77	0.07	1.77	1.58	1.99	NA	1.00	948	1.64	0.07	1.64	1.44	1.93	NA	1.00

Supplementary Note

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Polygene analyses
Nilanjan Chatterjee (lead), Karol Estrada (lead), Timothy M Frayling, Michael E Goddard, Andrew C Heath, Joel N Hirschhorn, Erik Ingelsson, Guillaume Lettre, Reedik Mägi , Massimo Mangino, Nicholas G Martin, Mark I McCarthy (chair), Grant W Montgomery, Dale R Nyholt, Jeffrey R O'Connell, Ju-Hyun Park, Shaun Purcell, Albert Vernon Smith, Peter M Visscher (lead), Michael N Weedon, Cristen J Willer, Jian Yang

Secondary signals (conditional) analyses
Sonja I Berndt, Ingrid B Borecki, Mary F Feitosa, Teresa Ferreira (lead), Timothy M Frayling, Erik Ingelsson, Hana Lango Allen (lead), Cecilia M Lindgren (chair), Reedik Mägi, Karen L Mohlke, Joshua C Randall, Elizabeth K Speliotes, Michael N Weedon (chair), Robert Weyant (lead), Eleanor Wheeler, Cristen J Willer (chair)

Gene expression (eQTL) analyses
Sonja I Berndt (chair), Anna Dixon, Elin Grundberg, Ke Hao, Joel N Hirschhorn, Lee Kaplan, Tony Kwan, Liming Liang (lead), Tomi Pastinen (lead), Eric E Schadt (lead), Elizabeth K Speliotes, Dominique J Verlaan

Gene-by-gene interaction analyses
Tushar Bhangale, Timothy M Frayling, Cecilia M Lindgren, John RB Perry, Michael N Weedon (chair), Cristen J Willer, Andrew R Wood (lead)

Family-based and population stratification analyses
Elizabeth L Altmaier, Najaf Amin, Joel N Hirschhorn, Hana Lango Allen, Fernando Rivadeneira (chair), Cornelia M van Duijn, Sailaja Vedantam, Michael N Weedon

Imputation and signal validation by direct genotyping analyses

WTCCC-T2D cohort (imputation validation): Timothy M Frayling, Hana Lango Allen, Michael N Weedon (chair); GCI cohort (signal validation): Kristin G Ardlie, Joel N Hirschhorn (chair), Guillaume Lettre, Rany M Salem, Michael C Turchin

Cohort-specific contributions

Stage 1 – Genome-wide association cohorts

Cohort	Author	Overseeing (PI)	Geno-typing	Pheno-typing	Data analysis
ADVANCE	Devin Absher		X	X	X
	Themistocles L Assimes		X	X	X
	Carlos Iribarren	X			
	Joshua W Knowles		X	X	X
	Thomas Quertermous	X			
AGES	Thor Aspelund				X
	Gudny Eiriksdottir	X			
	Vilmundur Gudnason	X			
	Tamara B Harris	X			
	Lenore J Launer	X			
	Albert Vernon Smith				X
Amish	Quince Gibson				X
	Shen Haiqing		X	X	
	Jeffrey R O'Connell				X
	Alan R Shuldiner	X			
ARIC	Eric Boerwinkle	X	X	X	
	Keri L Monda				X
	Tom H Mosley, Jr	X			
	Kari E North	X			X
B58C-T1DGC and B58C-WTCCC	Wendy L McArdle		X		
	David P Strachan	X		X	X
BRIGHT	Mark J Caulfield	X			
	Anna Dominiczak			X	
	Martin Farrall			X	
	Toby Johnson				X
	Patricia B Munroe	X			
CAD-WTCCC	Anthony J Balmforth			X	
	Alistair S Hall	X			
	Suzanne Rafelt				X
	Nilesh J Samani	X			
	John R Thompson				X
CAPS	Henrik Grönberg	X		X	
	Erik Ingelsson	X			X
	Fredrik Wiklund			X	X
	Jianfeng Xu			X	X
CHS	Alice Arnold	X		X	
	Nicole L Glazer				X
	Talin Haritunians		X		
	Robert Kaplan	X		X	
	Barbara McKnight				X
	Jerome I Rotter		X		
CoLaus	Jacques S Beckmann	X			
	Sven Bergmann	X			
	Toby Johnson				X
	Zoltán Kutalik				X
	Vincent Mooser	X	X		
	Dawn Waterworth	X	X		
deCODE	Daniel Gudbjartsson				X
	Kari Stefansson	X			
	Valgerdur Steinthorsdottir				X
	Gudmar Thorleifsson				X
	Unnur Thorsteinsdottir	X			
	G. Bragi Walters			X	

Cohort	Author	Overseeing (PI)	Geno-typing	Pheno-typing	Data analysis
DGI	Peter Almgren			X	
	Leif C Groop	X		X	
	Joel N Hirschhorn				
	Guillaume Lettre				X
	Martin Ridderstråle			X	
	Elizabeth K Speliotes				X
	Sailaja Vedantam				X
EGCUT	Helene Alavere			X	
	Tõnu Esko				X
	Andres Metspalu	X			
	Mari Nelis		X		
	Mari-Liis Tammesoo				X
EPIC	Inês Barroso		X		
	Ruth JF Loos		X		X
	Nicholas J Wareham	X			
	Eleanor Wheeler		X		X
	Jing Hua Zhao				
ERF (EUROSPAN)	Najaf Amin				X
	Yurii S Aulchenko				X
	Ben Oostra	X			
	Cornelia M van Duijn	X		X	X
	M. Carola Zillikens				X
Family Heart Study	Ingrid B Borecki	X	X	X	
	Mary F Feitosa			X	X
	Shamika Ketkar			X	X
	Michael A Province	X			
FENLAND	Ruth JF Loos	X		X	
	Jian'an Luan		X		X
	Nicholas J Wareham	X			
FRAM	Larry D Atwood	X	X		
	Adrienne L Cupples	X			X
	Nancy L Heard-Costa				X
	Julius Suh Ngwa				X
	Charles White				X
FTC	Jaakko Kaprio	X			
	Kirsi Pietiläinen			X	
	Samuli Ripatti				X
	Aila Rissanen	X			
	Ida Surakka				X
FUSION	Richard N Bergman	X			
	Michael Boehnke	X			
	Francis S Collins	X			
	Anne U Jackson				X
	Karen L Mohlke	X			
	Heather M Stringham			X	
	Jaakko Tuomilehto	X			
	Cristen J Willer				X
Genmets	Antti Jula			X	
	Seppo Koskinen			X	
	Leena Peltonen	X	X		
	Samuli Ripatti				X
	Veikko Salomaa	X		X	
	Ida Surakka				X
GerMIFSI and GerMIFSIII	Jeanette Erdmann	X			
	Christian Hengstenberg	X		X	
	Inke R König				X
	Michael Preuss				X
	Stefan Schreiber	X		X	
	Heribert Schunkert	X			
	H.-Erich Wichmann			X	
	Andreas Ziegler				X
KORA S3	Christian Gieger	X			X

Cohort	Author	Overseeing (PI)	Geno-typing	Pheno-typing	Data analysis
	Iris M Heid				X
	Thomas Meitinger		X		
	Martina Müller				X
KORA S4	Eva Albrecht				X
	Thomas Illig		X		
	H.-Erich Wichmann	X		X	
	Thomas Winkler				X
MICROS (EUROSPAN)	Alessandro De Grandi		X	X	
	Andrew A Hicks		X		
	Åsa Johansson				X
	Irene Pichler			X	
	Peter P Pramstaller	X			
MIGEN	Roberto Elosua				
	Aki S Havulinna			X	
	Sekar Kathiresan	X			
	Olle Melander	X			
	Christopher J O'Donnell	X			
	David S Siscovick	X			
	Elizabeth K Speliotes				X
	Benjamin F Voight	X			
NFBC1966	Lachlan Coin				X
	Paul Elliott		X	X	
	Nelson Freimer		X		
	Anna-Liisa Hartikainen		X	X	
	Marjo-Riitta Jarvelin	X	X	X	
	Markku Koiranen			X	
	Jaana Laitinen			X	
	Mark I McCarthy		X		
	Leena Peltonen		X		
	Anneli Pouta			X	
	Ulla Sovio				X
	Paavo Zitting		X	X	
NBS-WTCCC	Willem H Ouwehand	X			
	Jennifer G Sambrook			X	
NHS	Frank B Hu	X	X	X	
	David J Hunter	X	X	X	
	Peter Kraft		X		X
	Lu Qi		X	X	X
NSPHS (EUROSPAN)	Ulf Gyllensten	X			
	Wilmar Igl		X		
	Åsa Johansson		X	X	X
NTRNESDA	Dorret I Boomsma	X			
	Eco JC Geus		X		
	Jouke-Jan Hottenga		X		X
	Brenda W Penninx	X			
	Jan H Smit			X	
	Gonneke Willemsen			X	
ORCADES (EUROSPAN)	Harry Campbell		X		
	Åsa Johansson				X
	Veronique Vitart				X
	Sarah H Wild			X	
	James F Wilson	X			
	Alan F Wright	X		X	
PLCO	Sonja I Berndt	X		X	X
	Stephen J Chanock	X	X		
	Richard B Hayes	X			
	Kevin B Jacobs		X		X
PROCARDIS	Martin Farrall				
	Anders Hamsten	X			
	Mark Lathrop	X	X		
	John F Peden			X	
	Hugh Watkins	X			

Cohort	Author	Overseeing (PI)	Geno-typing	Pheno-typing	Data analysis
RS-I	Yurii S Aulchenko				X
	Karol Estrada		X		X
	Albert Hofman	X		X	
	Manfred Kayser	X			
	Marjolein J Peters		X		
	Fernando Rivadeneira	X	X	X	X
	André G Uitterlinden	X	X	X	X
	Cornelia M van Duijn	X		X	X
	Joyce B J van Meurs		X		
	M. Carola Zillikens				X
RUNMC	Katja K Aben	X			
	Martin den Heijer	X			
	Lambertus Kiemeney	X			
SardiNIA	Goncalo R Abecasis	X			X
	Andrea Maschio		X		
	Antonella Mulas		X		
	Serena Sanna				X
	David Schlessinger	X			
	Manuela Uda	X		X	
SASBAC	Per Hall	X		X	
	Erik Ingelsson	X			X
	Jianjun Liu			X	
SEARCH/UKOPS	Jonathan Patrick Tyrer				X
SHIP	Florian Ernst		X		X
	Wolfgang Hoffmann	X		X	
	Thomas Kocher	X			
	Astrid Petersmann		X		
	Carsten Oliver Schmidt			X	
	Henry Völzke	X			
T2D-WTCCC	Teresa Ferreira				X
	Timothy M Frayling	X		X	
	Andrew T Hattersley	X		X	
	Hana Lango Allen				X
	Cecilia M Lindgren	X	X		X
	Reedik Mägi				X
	Mark I McCarthy	X	X	X	
	Andrew P Morris				X
	John RB Perry				X
	Inga Prokopenko				X
	Joshua C Randall				X
	Nigel W Rayner		X		X
	Neil R Robertson		X		X
	Michael N Weedon				X
	Andrew R Wood				X
TwinsUK	Massimo Mangino		X	X	X
	Nicole Soranzo	X	X		X
	Tim D Spector	X		X	
VIS (EUROSPAN) and KORCULA	Caroline Hayward		X		X
	Åsa Johansson				X
	Ivana Kolcic			X	
	Ana Marusic			X	
	Ozren Polasek			X	X
	Igor Rudan	X		X	
	Lina Zgaga			X	

Stage 2 – in silico replication cohorts

Cohort	Author	Overseeing (PI)	Geno-typing	Pheno-typing	Data analysis
BHS	John P Beilby	X		X	
	Matthew N Cooper				X
	Jennie Hui		X		
	Robert Lawrence				X
	Arthur W Musk	X		X	
	Lyle J Palmer	X			
Corogene	Marja-Liisa Lokki		X		
	Markku S Nieminen	X			
	Niina Pellikka				X
	Leena Peltonen	X	X		
	Markus Perola				X
	Juha Sinisalo			X	
EGCUT	Helene Alavere			X	
	Tõnu Esko				X
	Andres Metspalu	X			
	Mari Nelis		X		
	Mari-Liis Tammesoo				X
Family Heart Study	Ingrid B Borecki	X	X	X	
	Mary F Feitosa			X	X
	Shamika Ketkar			X	X
	Michael A Province	X			
FINGESTURE	Gabrielle Boucher				X
	Heikki V Huikuri	X		X	X
	Juhani Junttila			X	X
	John D Rioux	X			X
GOOD	Mattias Lorentzon		X	X	X
	Claes Ohlsson	X	X	X	X
	Liesbeth Vandenput			X	X
HBCS	Johan Eriksson	X		X	
	Eero Kajantie			X	
	Markus Perola		X		X
	Samuli Ripatti		X		X
	Elisabeth Widen		X		
HYPERGENES	Lorena Citterio			X	
	Daniele Cusi	X			
	Nicola Glorioso		X	X	
	Carlo Rivolta	X	X		
	Erika Salvi				X
	Laura Zagato			X	
MGS	Jubao Duan		X		
	Pablo V Gejman	X	X	X	
	Douglas F Levinson	X			X
	Alan R Sanders		X	X	
	Jianxin Shi				X
NHS	Frank B Hu	X	X	X	
	David J Hunter	X	X	X	
	Peter Kraft		X		X
	Lu Qi		X	X	X
RS-II and RS-III	Yurii S Aulchenko				X
	Karol Estrada		X		X
	Albert Hofman	X		X	
	Manfred Kayser	X			
	Marjolein J Peters		X		
	Fernando Rivadeneira	X	X	X	X
	André G Uitterlinden	X	X	X	X
	Cornelia M van Duijn	X		X	X
	Joyce B J van Meurs		X		
	M. Carola Zillikens				X
Sorbs	Peter Kovacs		X	X	
	Reedik Mägi				X

	Inga Prokopenko				X
	Michael Stumvoll	X			
	Anke Tönjes	X		X	
WGHS	Daniel I Chasman		X		X
	Guillaume Paré		X		
	Alex N Parker		X		
	Paul M Ridker	X			
YFS	Mika Kähönen	X		X	
	Johannes Kettunen		X		X
	Terho Lehtimäki	X		X	
	Niina Pellikka		X		X
	Olli Raitakari	X		X	
	Jorma Viikari	X		X	

Additional analyses cohorts

Cohort	Author	Overseeing (PI)	Geno-typing	Pheno-typing	Data analysis
GCI height extremes (additional genotyping)	Kristin G Ardlie	X			
	Joel N Hirschhorn	X			
	Guillaume Lettre			X	X
	Rany M Salem				X
	Michael C Turchin		X		X
QIMR (polygene analysis)	Andrew C Heath	X		X	
	Nick G Martin	X	X	X	
	Grant W Montgomery	X	X		
	Dale R Nyholt	X	X		X
	Peter M Visscher		X		X

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