**S1 Text** *Cohort information***ABCD study**The Amsterdam Born Children and their Development (ABCD) cohort study is a large, community-based birth cohort, which started in 2003 with the inclusion of 8,000 pregnant women living in Amsterdam and its main aim is to study factors in early life (during pregnancy and infancy) that explain health later in life. Detailed information on life style habits, psychosocial determinants, obstetric complications, blood pressure course during pregnancy, as well as childhood growth patterns has been gathered. Data for this study comes from ABCD-Genetic Enrichment (ABCD-GE) study, a sub-study of 1192 ethnic Dutch children. The blood was collected from a simple finger prick during the 5-year health check-up of the children (2008-2010). DNA was extracted from the dried blood spots. The ABCD study protocol was approved by the Central Committee on Research Involving Human Subjects in The Netherlands, the medical ethics review committees of the participating hospitals and the Registration Committee of the Municipality of Amsterdam. All ABCD participants gave written informed consent for data collection of the phenotypes. Regarding the DNA collection and analysis, an opt-out procedure was used (METC approval 2002\_039#B2013531).

**Avon Longitudinal Study of Parents and Children (ALSPAC)**

Pregnant women resident in Avon, UK with expected dates of delivery 1st April 1991 to 31st December 1992 were invited to take part in the study[1,2]. The initial number of pregnancies enrolled is 14,541 (for these at least one questionnaire has been returned or a “Children in Focus” clinic had been attended by 19/07/99). Of these initial pregnancies, there was a total of 14,676 foetuses, resulting in 14,062 live births and 13,988 children who were alive at 1 year of age.

When the oldest children were approximately 7 years of age, an attempt was made to bolster the initial sample with eligible cases who had failed to join the study originally. As a result, when considering variables collected from the age of seven onwards (and potentially abstracted from obstetric notes) there are data available for more than the 14,541 pregnancies mentioned above. The number of new pregnancies not in the initial sample (known as Phase I enrolment) that are currently represented on the built files and reflecting enrolment status at the age of 24 is 913 (456, 262 and 195 recruited during Phases II, III and IV respectively), resulting in an additional 913 children being enrolled. The phases of enrolment are described in more detail in the cohort profile paper and its update (see footnote 4 below). The total sample size for analyses using any data collected after the age of seven is therefore 15,454 pregnancies, resulting in 15,589 foetuses. Of these 14,901 were alive at 1 year of age.

A 10% sample of the ALSPAC cohort, known as the Children in Focus (CiF) group, attended clinics at the University of Bristol at various time intervals between 4 to 61 months of age. The CiF group were chosen at random from the last 6 months of ALSPAC births (1432 families attended at least one clinic). Excluded were those mothers who had moved out of the area or were lost to follow-up, and those partaking in another study of infant development in Avon.

Please note that the study website contains details of all the data that is available through a fully searchable data dictionary and variable search tool: http://www.bristol.ac.uk/alspac/researchers/our-data/

Ethical approval was obtained from the ALSPAC Ethics and Law Committee and the Local Research Ethics Committees.

*ALSPAC GWAS data*

A total of 9,912 participants were genotyped using the Illumina HumanHap550 quad genome-wide SNP genotyping platform by the Wellcome Trust Sanger Institute, Cambridge, UK and the Laboratory Corporation of America, Burlington, NC, USA using support from 23andMe. Details on the QC procedure have been published previously[3]. Individuals were excluded from further analysis on the basis of having incorrect sex assignments; extreme heterozygosity (<0.320 and >0.345 for the Sanger data and <0.310 and >0.330 for the LabCorp data); high levels of individual missingness (>3%); evidence of cryptic relatedness (>10% IBD) and being of non-European ancestry (as detected by a multidimensional scaling analysis seeded with HapMap 2 individuals). EIGENSTRAT analysis revealed no additional obvious population stratification and genome-wide analyses with other phenotypes indicate a low lambda. The resulting data set consisted of 8,365 individuals. SNPs with a minor allele frequency of <1% and call rate of <95% were removed. Only SNPs which passed an exact test of Hardy–Weinberg equilibrium (HWE) (*P-*value  >5 × 10-7) were considered for analysis. Known autosomal variants were imputed with IMPUTE2, using 1000G V1 CEPH. After imputation, SNPs with a minor allele frequency <0.01 and an r2 imputation quality score <0.3 were excluded and this resulted in 18486880 SNPs available for analysis. Association analyses were performed using SNPTEST.   
  
**BMDCS**

The multi-center, longitudinal Bone Mineral Density in Childhood Study enrolled children 5 to 19 years of age in five locations in the United States; Children’s Hospital of Los Angeles (Los Angeles, CA), Cincinnati Children’s Hospital Medical Center (Cincinnati, OH), Creighton University (Omaha, NE), Children’s Hospital of Philadelphia (Philadelphia, PA), and Columbia University (New York, NY). As described previously, females 6-15 years and males 6-16 years of age were enrolled in 2002-2003, and measured annually for six years (up to seven visits)[4,5]. Additional study participants, 5 and 19 years of age were enrolled in 2006-2007 and evaluated annually for two years (up to three visits). In 2010 and 2011, additional 507 children of European ethnic origin aged 5 to 18 year old were enrolled for a one-time visit in the Creighton and Cincinnati centers. Criteria for study entry targeted normal development and healthy bones. Key criteria included term birth (≥37 wk gestation); birth weight >2.3 kg; no evidence of precocious or delayed puberty, and height, weight or BMI within the 3rd to the 97th percentile for age. Exclusion criteria included multiple fractures (more than two fractures if age <10 years or more than three fractures if age >10 years), current or previous medication use or medical condition known to affect bone health, and extended bed rest. Opposite sex siblings were not excluded from study participation; for the purpose of this analysis the older sibling was excluded. A blood or saliva sample was collected at the final study visit. Written informed consent was obtained the parent or guardian for study participants less than 18 years of age and from the study participant if age 18 years and older. Assent was obtained from participants less than age 18 years. The protocol was approved by the Institutional Review Board of each Clinical Center.

Measurements were obtained by trained personnel with the research participant wearing light clothing with shoes and hair adornments removed. Height was measured with a stadiometer to the nearest 0.1cm and weight was measured with a digital electronic scale to the nearest 0.1kg.

**BRain dEvelopment and Air polluTion ultrafine particles in scHool childrEn Project (BREATHE)**

This is a population-based study that aims to investigate the impact of air pollution on the cognitive development of children. Children from second, third and fourth levels of 39 primary schools in Barcelona and surroundings were visited four times during 2012 and 2013. Children were born in 2001-2004 and were 7-11 years old during the visits. Informed consent was obtained from all participants and the study was approved by the Research Center Ethics Committee.

Weight and height were measured with calibrated scales and a portable stadiometer, respectively, with the children standing in light clothing and barefoot, by trained field workers. BMI was calculated as weight in kilograms divided by the square of height in meters. Sex- and age-adjusted standard deviation scores (SDS) were constructed using LMS growth (Pan H, Cole TJ, 2012. http://www.healthforallchildren.co.uk).

DNA samples from 2,492 BREATHE children were obtained from saliva collected in Oragene DNA OG‐500kit (DNA Genotek) following manufacturer’s instructions with minor modifications. All DNA samples were quantified using Quant-iT™ PicoGreen® dsDNA Assay Kit (Life Technologies). A subset of 1,778 children was selected for genome-wide genotyping. Genome-wide genotyping was performed using the HumanCore BeadChip WG-330-1101 (Illumina) at the Spanish National Genotyping Center (CEGEN) at the Spanish National Cancer Research Centre (CNIO). Genotype calling was done using the GeneTrain2.0 algorithm (with a default threshold of 0.15) based on HapMap clusters implemented in the GenomeStudio software. Twenty CEU HapMap duplicates and twenty BREATHE duplicates were included in the study and gave consistent results.

PLINK was used for the genetic data quality control. Five samples were initially excluded because they were filtered from the epidemiological database. We applied the following sample quality control thresholds: sample call rate>97% (N=3 exclusions) and heterozigosity 4 SD (N=5 exclusions). Then, we checked sex discordances (N=18 exclusions, 1%), relatedness (N=80 exclusions: one twin, 32 siblings, 39 cousins, eight incongruent sibling's couples). In total we excluded 106 subjects (6%). Genetic variants were filtered by SNP call rate>95%, MAF>1% and HWE *P*-value>1.10 x 10-6 (N=58,827 exclusions, 19.7%). The final genetic data set consisted of 1,633 subjects and 240,103 SNPs coded in b37 and + strand.  Imputation of genetic variants was done using IMPUTE V2 and the cosmopolitan 1000 genome panel (release March 2012).

**British 1958 Birth Cohort (1958BC-WTCCC and 1958BC-T1DGC)**   
The 1958 British Birth Cohort (1958BC) consists of all born during one week in March 1958 in England, Scotland, and Wales (n=17,638)[6]. The cohort has been followed-up from birth with contact at ages 7, 11,  16, 23, 33, 42, 45, 46 and 50 years. Measurements of height and weight were obtained at all childhood contacts and in this study; information from 7 years was used to calculate BMI defining centiles from within the study. At age 45 years, 11,971 cohort members who had not died or emigrated, were invited to a biomedical assessment. In total 9,377 participants provided data, including several clinical assessments and DNA collection. Ethical approval for the 45y survey was obtained from South East Multi-centre Research Ethics Committee (ref. 01/1/44)  and the Joint UCL/UCLH Committees on the Ethics of Human Research (Committee A) Ref: 08/H0714/40.

Genome-wide data for the 1958BC has been obtained through two sub-studies, both using the 1958BC members as a control population. First, 3000 DNA samples were randomly selected as part of the Wellcome Trust Case Control Consortium (WTCCC2) and genotyped on the Affymetrix SNP 6.0 platform[7]. Samples were genotyped through the JDRF/WT Diabetes and Inflammation Laboratory (DIL) using the Illumina Infinium 550K chip[8]. Imputation was done in IMPUTE after quality control. For B58C-WTCCC2 quality control included SNP exclusions (Minor allele frequency (MAF) < 0.01, HWE *P*-value <1 x 10-20, call rate < 0.98, genotype plate association <1 x 10-5), and sample exclusions (heterozgygosity, call rate, relatedness, non-European ancestry and sex discrepancy). For B58C-T1DGC, criteria for SNP exclusions were MAF < 0.01, HWE *P*-value <1 x 10-7, or SNP call rate < 0.95, and sample exclusions were made for heterozygosity, call rate, non-European ancestry and potential sex discrepancy.

**Cardiovascular Risk in Young Finns Study (YFS)**

YFS is a large prospective population-based multicentre study aimed at examining the risk factors and their determinants in children and adolescents of risk factors for atherosclerosis[9]. The baseline cross-sectional study was carried out in 1980, including 3596 subjects at ages 3, 6, 9, 12, 15, and 18. Between 1980 and 1992, these subjects were followed up at 3-year intervals, and then as adults in 2001, 2007 and 2010-2012. The main aim of the YFS is to determine the contribution made by childhood lifestyle, biological and psychological measures to the risk of cardiovascular diseases in adulthood.

Genotyping was performed with the Illumina 670K SNP chip at the Wellcome Trust Sanger Centre. Quality control measures were taken prior to imputation (excluding genotypes with call rate <0.95, MAF <0.01, HWE *P*-value <1 x 10-6). Genotype imputation was performed using IMPUTE2[10,11] and a reference panel from the 1000 Genomes. All subjects gave their written informed consent in 2007 and the study was approved by local ethics committees of the participating universities.

**Children’s Hospital of Philadelphia (CHOP)**

All subjects were consecutively recruited from the Greater Philadelphia area from 2006 to 2014 at the Children's Hospital of Philadelphia. Our study cohort consisted of children of European ancestry. All of these participants had their blood drawn in to an 8ml EDTA blood collection tube and were subsequently DNA extracted for genotyping. All subjects were biologically unrelated and were aged between 2 and 18 years old. This study was approved by the Institutional Review Board of the Children's Hospital of Philadelphia. Parental informed consent was given for each study participant for both the blood collection and subsequent genotyping. BMI was determined from height and weight measurements in the clinical record.

We performed high throughput genome-wide SNP genotyping, using the Illumina Infinium™ II HumanHap550 BeadChip technology (Illumina, San Diego), at the Center for Applied Genomics at CHOP. We used 750ng of genomic DNA to genotype each sample, according to the manufacturer’s guidelines.

Samples were genotyped on a combination of the HumanHap 550 version 1, HumanHap 550 Version 3 and 610 Quad SNP chips. The 535,931 SNPs in common with the three different chip versions used were the basis for all further analyses. 1,878 SNPs were excluded for having a HWE *P*-value less than 1 x 10-6. 321 SNPs were thrown out for missing more than 5 percent of genotypes and 20,902 SNPs were thrown out for having a minor allele frequency less than 1 percent. Impute2 was used to impute ~37 million SNPs using the 1000 Genomes Project Phase 1 reference haplotypes.

**CHOP (Europe)**

The CHOP study (European Childhood Obesity Project) is an ongoing European multicenter randomized prospective nutritional intervention study in 1678 healthy term newborns recruited between October 1, 2002 and July 31, 2004. Currently, infants are followed up until the age of 11 years. Main objective of the CHOP study is to assess the effect of early and later nutrition on children’s weight development, growth, body composition and risk of obesity and the role of genetic variation and epigenetic and metabolic programming plays in this context. A detailed description of the study design and the comprehensive prospective measurements can be found in recent publications[12-16]. The local ethics committees of each study center approved all study procedures: Belgium (Comitè d’Ethique de L’Hopital Universitaire des Enfants Reine Fabiola; no. CEH 14/02), Germany (Bayerische Landesärztekammer Ethik-Kommission; no. 02070), Italy (Azienda Ospedaliera San Paolo Comitato Etico; no. 14/2002), Poland (Instytut Pomnik–Centrum Zdrowia Dziecka Komitet Etyczny; no 243/KE/2001), and Spain (Comité ético de investigación clinica del Hospital Universitario de Tarragona Joan XXIII). Written informed parental consent was obtained for each participating infant and from children of age 8 years onwards.

*Genotyping , Quality Control and Imputation*

For this genome-wide-association analysis (GWAS) genetic data on n=374 children were available from the CHOP study. Buffy coats were collected from children of age 5.5 years during physical exam. Samples were genotyped from buffy coats with Illumina HumanOmniExpress-24 v1.0 arrays by Dr Eva Reischl and team at the Genome Analysis Center of Helmholtz Zentrum Muenchen, Germany by standard procedures according to manufactures instructions (Illumina Inc., San Diego, USA).

Quality control on genotyped data were performed at Helmholtz Zentrum Muenchen and in even more detail by Dr Linda Broer and team at the Department of Internal Medicine, Genetic Laboratory, Erasmus Medical Center, Rotterdam, The Netherlands. QC tests using mainly PLINK comprised SNP missingness test (GENO>0.05), frequency test (MAF<0.001), HWE-test (p<=1 × 10-7), Sample call rate >95% and SNP call rate >80% and Sample call rate >97.5% and SNP call rate >95%, test for evidence of heterozygosity or excess homozygosity, test for gender mismatch, test for Caucasian samples and test for familiar relationships (IBD). From the originally n=382 samples with 701,281 SNPs 264 SNPS failed the HWE-test (p<=1 × 10-7) and 14,627 SNPs failed the MAF test (<0.1%) leaving 686,390 SNPs. For 8 samples there was evidence of excess heterogeneity (F-value < mean –(4×SD)) and these samples were removed leaving n=374 samples with 686,390 SNPs. No gender mismatches were identified. However, 10 of the 374 samples were identified as potentially non-European by IBS/IBD distance analysis in PLINK but kept in the data set. This issue was accounted for by including 10 pruned principal components from multidimensional scaling procedure in the GWAS analysis as adjustment factors (see below). Overall, quality controlled genotyped data from 374 children with 686,390 SNPs were available.

Imputation of these quality controlled genotyped data with reference to the 1000G reference panel (phase1\_v3) were performed by Dr Linda Broer and team at the Department of Internal Medicine, Genetic Laboratory, Erasmus Medical Center, Rotterdam, The Netherlands. Imputation was done using a two steps procedure using MINIMAC3 and MACH for phasing and imputation respectively for the 374 children and by using the Michigan Imputation server (<https://imputationserver.sph.umich.edu/index.html>). The final number of SNPs with MAF>1% and r2 >0.3 after the imputation process is 9,642,852. MACH R² when excluding variants MAF < 1% is 0.88 (median = 0.97, SD = 0.20).

*Conducted analysis and description of covariates*

Statistical analysis is based on all genotyped and imputed data (9,642,852 SNPs over 22 chromosomes) for n=374 children. However due to missing data in phenotype (standardized BMI) analysis is based on n=369 children only. Weight and height were measured with calibrated scales and stadiometer, respectively, with the children standing in light clothing and barefoot, by trained field workers. BMI was calculated as weight in kilograms divided by the square of height in meters. Sex- and age-adjusted standard deviation scores (SDS) were constructed using LMS growth (Pan H, Cole TJ, 2012. [http://www.healthforallchildren.co.uk](http://www.healthforallchildren.co.uk/) ).

The following additive linear model described in the analysis plan was conducted by statistical software rvtest (<https://github.com/zhanxw/rvtests>[17] and accounting for imputation of SNPs by analysing dosage data and by adjusting for the 10 pruned principal components derived from MDS analysis of genotyped data (see QC above).

*BMI\_SDS ~ SNP + 10 pruned principal MDS-components*

**Copenhagen Study on Asthma in Childhood 2000 birth cohort (COPSAC2000)**

The COPSAC2000 birth cohort study is a prospective clinical study of a birth cohort of 411 infants born to mothers with a history of asthma. The newborns were enrolled at the age of 1 month, the recruitment of which was previously described in detail[18]. The study was conducted in accordance with the guiding principles of the Declaration of Helsinki and was approved by the Local Ethics Committee (KF 01-289/96), and the Danish Data Protection Agency (2008-41-1754). Both parents gave written informed consent before enrolment.

The families used doctors employed at the clinical research unit, and not the family practitioner, for diagnosis and treatment of any respiratory or skin-related symptoms. Participants were assessed at the COPSAC clinical research unit at six monthly intervals; additional visits were arranged immediately upon the onset of symptoms. All growth parameters were measured and obtained by the COPSAC physicians at each scheduled six monthly visit until age 7 and history were obtained using structured questions and closed response categories. At every visit weight was measured using calibrated digital weight scales and length by infantometer, Kiddimetre® (Raven Equipment Limited, Essex England). From 2.5 years, height was measured using a stadiometer (Harpenden; Holtain Ltd, Crymych, Dyfed, Wales)[19].

High throughput genome-wide SNP genotyping were performed using the Illumina Infinium™ II High throughput genome-wide SNP genotyping were performed using the Illumina HumanOmniExpressExome BeadChip (Illumina, San Diego), at AROS Applied Biotechnology[20]. Imputation was performed using IMPUTE2 and 1000 genomes (phase I v3 ALL) as reference panel. Statistical analysis was carried out using R project, assuming an additive model and taking genotype uncertainty into account.

**Copenhagen Study on Asthma in Childhood 2010 birth cohort (COPSAC2010)**

The COPSAC2010 birth cohort study is a prospective clinical study of a 700 unselected newborns, previously described in detail[19]. The study was conducted in accordance with the guiding principles of the Declaration of Helsinki and was approved by the Local Ethics Committee (H-B-2008-093), and the Danish Data Protection Agency (2008-41-2599). Both parents gave written informed consent before enrolment.

The families used doctors employed at the clinical research unit, and not the family practitioner, for diagnosis and treatment of any respiratory or skin-related symptoms. Participants were assessed at the COPSAC clinical research unit at six monthly intervals; additional visits were arranged immediately upon the onset of symptoms. All growth parameters were measured and obtained by the COPSAC physicians at each scheduled six monthly visit until age 3 and history were obtained using structured questions and closed response categories. At every visit weight was measured using calibrated digital weight scales and length by infantometer, Kiddimetre® (Raven Equipment Limited, Essex England). From 2.5 years, height was measured using a stadiometer (Harpenden; Holtain Ltd, Crymych, Dyfed, Wales)[19].

High throughput genome-wide SNP genotyping were performed using the Illumina HumanOmniExpressExome BeadChip (Illumina, San Diego), at AROS Applied Biotechnlogy[20]. Imputation was performed using IMPUTE2 and 1000 genomes (phase I v3 ALL) as reference panel. Statistical analysis was carried out using R project, assuming an additive model and taking genotype uncertainty into account.

**Danish National Birth Cohort (DNBC) - GOYA offspring**

The Danish National Birth cohort (DNBC) was established in 1996-2002 enrolling a total of 100,417 pregnancies among 92,274 women from all over Denmark[21]. From this cohort, the nested genome-wide association study GOYA (Genomics of extremely Overweight young Adults) sampled and genotyped 1960 mothers with the highest BMI and 1948 randomly selected mothers[22]. The GOYA offspring sample consists of 407 children born to the obese mothers and 481 children born to the randomly selected mothers, all with available cord blood. A questionnaire follow-up was conducted when the children were 7 years old including self-reported information on the child’s weight and height.

The children were genotyped using the Illumina Infinium HumanCoreExome Beadchip (Illumina, San Diego, CA, USA) and genotypes were called using the Genotyping module, version 1.9.4 of GenomeStudio software, Version 2011.1 (Illumina). During genotype quality control, we excluded closely related individuals and samples with extreme inbreeding coefficients, mislabeled gender or call rate < 95% as well as duplicates and individuals identified as ethnic outliers. We applied a > 95% genotype call rate filer for the inclusion of SNPs. Genotype imputations were performed to the 1000 Genome reference panel (phase 1) with SHAPEIT and IMPUTE2. Written informed consent was obtained at recruitment from all participating mothers on behalf of themselves and their children.

**DNBC-PTB**

The DNBC-PTB is a nested study within the DNBC focused on the genetics of preterm birth. GWAS genotyping of the DNBC-PTB samples was done using the Illumina 660 Quad chip. Prior to imputation, we required participants to have a genotype call rate >96%, and we

excluded SNPs based on a missing rate >2%, deviation from Hardy-Weinberg equilibrium (P<10-6), and a minor allele frequency <1%. We also excluded samples based on heterozygosity (>3SD from the mean), non-European ancestry (>6SD from the mean in any of the first 5 principal components), potential sex discrepancy, and Mendelian inconsistency. The GWAS data were imputed with SHAPEIT and IMPUTE2 using the 1000 Genomes phase I data as reference set. SNPTEST was used for association analysis. The BMI analysis was based on 1007 children (524 boys, 483 girls) and SNPTEST was used for association analysis.

**EDEN**

The EDEN Mother-Child Cohort Study EDEN is a population-based, prospective, mother-child cohort study on prenatal and early postnatal nutritional, environmental, and social determinants of the children’s development and health. The study was approved by the Ethics Committee of Kremlin Bicêtre (France) and by the Data Protection Authority Comission Nationale de l’Informatique et des Libertés. All mothers provided written informed consent for themselves and their child. Recruitment of pregnant women expecting singletons took place between 2003 and 2006 at the University Hospitals in Poitiers and Nancy, France. At birth, infants were weighed using electronic scales (Seca Ltd), and length was measured using a wooden somatometer (Testut). At age 1 year, the infants’ weight was obtained by subtraction of the weigh tof the mother alone (Terraillon SL-351) fromwhen holding their infant wearing light clothes; infant length was measured using a somatometer (NMMedical). At age 5 years, children were weighed with electronic scales (Seca Ltd), and standing height was measured with a wall-mounted stadiometer (Seca Ltd).

DNA was extracted from cord blood samples collected at birth. Genotypes at the SLC39A8 (rs13107325) locus was measured at the Medical Research Council Epidemiology Unit, Cambridge (iPLEX platform;Sequenom). The variant passed genotyping quality control criteria (call rate>95%; Hardy-Weinberg equilibrium, P > .01)

**EFSOCH**

The Exeter Family Study Of Childhood Health (EFSOCH) recruited 1017 families from a postcode-defined area of central Exeter, UK[23]. Detailed anthropometric measurements were taken from both parents at 28 weeks of gestation, and from their children at birth, 12 weeks, 1 year and 2 years of age. Fasting blood samples were taken from the parents at 28 weeks of gestation, and an umbilical cord blood sample at delivery. These were used for biochemical analysis and DNA extraction. Measurements taken on the offspring at birth, 12 weeks of age, and 1 and 2 years of age include length (to nearest 0.1 cm using the Harpenden stadiometer) and weight (to nearest 0.1 kg using Soehnle scales)[24]. The measurements at 2 years were analysed for the current study.  
 Genotyping of the whole EFSOCH sample (2768 mothers, fathers and children) was performed using the Illumina Infinium HumanCoreExome-24 array (n=551,839 SNPs/indels). The genotyping has been described previously[25]. Included samples were of European ancestry (assessed using flashPCA[26]) had genotype call rate >98%. Genotype data was used to validate phenotypic sex. Kinship was validated using King[27]. SNPs were removed if they had call rates <95% , showed evidence of deviation from Hardy-Weinberg equilibrium (P<1x10-6), or had a minor allele frequency (MAF) <1%. Imputation was performed using the Michigan imputation server and samples were imputed to the Haplotype Reference Consortium HRC v1.1 reference panel.

**FAMILY**

The Family Atherosclerosis Monitoring In earLY life (FAMILY) study was designed to longitudinally examine the fetal and early childhood determinants for the development of adiposity, cardiovascular diseases and atherosclerosis in children and has been described in detail previously[28]. Briefly, 857 families including 901 newborns, 857 mothers and 530 fathers were enrolled from three hospitals in the greater Hamilton region (Ontario, Canada) from 2004 to 2009 and were followed for up to 5 years, with a planned follow-up for 10 years or more. We selected singletons (n=816 families) into our study because twins or triplets have a strong impact on birthweight and postnatal growth velocity. Genomic DNA was extracted from buffy coats and genotyping was conducted using the Illumina Cardio-Metabochip (San Diego, CA, USA). Standard procedures were conducted to assess the quality of genotyping. We found that 26 individuals had SNP missingness rates >10%, 16 individuals were from 5 families having non-biological fathers, and 11 individuals had sex-discordance between reported and SNP-identified sex; all of these were excluded from the analysis. Six pairs of individuals had cryptic relatedness (2nd degree relatives) and one of each pair was randomly selected for analysis. The self-reported ethnicity was verified by principal component analysis (PCA) across array-wide SNPs (~200K) using EIGENSTRAT and the first 10 axes were used to adjust for population stratification. The majority of the FAMILY participants were white Caucasians (92.8% mothers, 89.3% fathers and 91.1% children). Considering the inclusion criteria of the present study, 543 children were included in the final analysis. Informed consent was obtained from all the adult participants, and the parents provided consent for their children. All experiments were performed in accordance with relevant guidelines and regulations. The research ethics boards at Hamilton Health Sciences and St Joseph’s Health Center in Hamilton, and Joseph Brant Memorial Hospital in Burlington, Ontario, Canada approved the FAMILY study.

**French Young**

We studied 670 French obese children, recruited through a multi-media campaign by the CNRS UMR8199 unit in Lille, in the Department of Pediatric Endocrinology of Jeanne de Flandres Hospital or in the Toulouse Children’s Hospital[29]. Obese children, recruited by the CNRS UMR8199 unit and by the Jeanne de Flandres hospital between 1997 and 2007, are issued from pedigrees having at least one obese child with a BMI ≥ 97th percentile for sex and age and both parents. Additional obese children were recruited in Toulouse Children’s Hospital between 1997 and 2001 during pediatric obesity consultation and all harbor a BMI ≥ 97th percentile for sex and age. The 349 lean French children were selected from the STANISLAS family study[30]30 or from the Fleurbaix Laventie Ville Santé II study, both being family-based recruitments[31]. The Fleurbaix Laventie Ville Santé II Study includes 224 nuclear families recruited in 1999 and representative of the Northern France general population. The STANISLAS cohort includes 1006 families consisting of the two biological parents with at least two children, recruited in the Nancy area between September 1993 and August 1995 and representative of the Eastern France general population. Cases and controls were genotyped using the Illumina Human CNV370-Duo array. Imputation was performed using SHAPEIT (for the pre-phasing step) and IMPUTE 2 (for the actual imputation) based on the 1,000 Genomes reference panel (release date: March 2012). Cases and controls were imputed separately. Prior to imputation, a quality control filter on genotyped SNPs was applied: i) call rate >= 95%, ii) *P*-value of the HWE test > 0.0001.  
 **Generation R Study (Generation R)**

The Generation R Study is a population-based prospective cohort study from fetal life until young adulthood. All children were born between April 2002 and January 2006. This study is designed to identify early environmental and genetic determinants of growth, development and health from fetal life until young adulthood and has been described previously in detail[32]. Detailed measurements were performed using ultrasound and physical examinations, biological samples and advanced imaging techniques. The study has been approved by the Medical Ethics Committee of the Erasmus Medical Center, Rotterdam. Written informed consent was obtained from all participants.

Analysis were restricted to individuals of European ethnic origin with genome-wide data and at least one BMI measurement available between 2 and 6 years of age. Length was measured to the nearest millimeter and weight was recorded by well-trained staff in community health centers using standardized procedures[32].

Cord blood for DNA isolation was available in 58% of all live-born participating children. Sex-mismatch rate between genome based sex and midwife-record based sex was low (<0.5%), indicating that possible contamination of maternal DNA was extremely low. Missing cord blood samples were mainly due to logistical constraints at the delivery. Genome-wide association scans (GWAs) were run using the Illumina 610 Quad and 660 platforms[32]. MACH (version 1.0.15) software was used to impute genotypes to the 1000 Genomes (March 2010 release) cosmopolitan panel[33,34]. Before imputation, SNPs were excluded if they had high levels of missing data (SNP call rate <98%), strong departures from Hardy-Weinberg equilibrium (*P*-value <1 x10-6), or low MAF (<1%) (20).   
  
**German Infant Study on the influence of Nutrition Intervention PLUS environmental and genetic influences on allergy development & Influence of life-style factors on the development of the immune system and allergies in East and West Germany (GINIplus&LISA)**

The influence of Life-style factors on the development of the Immune System and Allergies in East and West Germany (LISA) Study is a population based birth cohort study. A total of 3097 healthy, mature (gestational age over 37 weeks) neonates with a birth weight over 2500g were recruited between 1997 and 1999 in Munich, Leipzig, Wesel and Bad Honnef.

A total of 5991 mothers and their newborns were recruited into the German Infant study on the influence of Nutrition Intervention PLUS environmental and genetic influences on allergy development (GINIplus) between September 1995 and June 1998 in Munich and Wesel. Detailed descriptions of the LISA and GINIplus studies have been published elsewhere[35,36].

Weight and height were measured in both studies at age 2, 4, and 5 years by the family physician and at age 10 years by the physician of the study or by the parents. Sex- and age-adjusted standard deviation scores (SDS) were calculated using LMSGrowth ([http://www.healthforallchildren.co.uk](http://www.healthforallchildren.co.uk/), reference British1990). For both studies, approval by the local Ethics Committees and written consent from participant’s families were obtained.

In the discovery analysis, 1471 children from the GINIplus&LISA study from Munich with genome-wide data were included. DNA was analyzed using the Affymetrix Human SNP Array 5.0 or 6.0 for each individual. Genome-wide data was called using BRLMM-P algorithm (Affy 5.0) or BIRDSEEDv2 (Affy 6.0) and imputed after quality control (MAF>1%, HWE *P*-value >1 x 10-6, call rate per SNP and person >95%) in IMPUTE. Genome-wide association analysis of BMI was carried out in SNPTEST V2.

**GOYA (Male)**

The cohort was derived from a draft board examination cohort for men, constituted by young Danish adults with negligible admixture of other ethnicities. These men also had measurements of height and weight in school and the data were extracted from the school health records. BMI in the current study was calculated from yearly measurements of height and weight at ages between 7 and 10 years. Cases are defined as having at least one BMI above the age specific 95% percentile and controls as having all BMI below the 50th percentile. The controls were used during the discovery stage and both cases and controls in the replication phase.

The study was approved by the regional scientific ethics committee and by the Danish Data Protection Board. Genome-wide genotyping on the Illumina610 quad BeadChip was carried out at the Centre National de Génotypage (CNG), Evry, France.

Pre imputation quality control involved:

1. SNP exclusions based on a. Call Rate <95%, b. Hardy Weinberg Equilibrium (HWE) *p*<1e-07,  and c. Minor allele frequency (MAF) < 1%, and

2. Individual based exclusions: a. Call Rate <95%, b. gender mismatch, c. heterozygosity (HET<0.302 or HET>0.35 were removed), d. Relatedness (IBD>0.2 removed), and e. Non CEU ancestry individuals removed through MDS based clustering.

We carried out Phasing using mach-1.0.16 and imputation using minimac-omp based on the GIANT reference panel: 1000 Genomes Phase 1 Release version 3. Link: ALL GIANT.phase1\_release\_v3.20101123.snps\_indels\_svs.genotypes.refpanel.ALL.vcf.gz.tgz

**Helsinki Birth Cohort Study (HBCS)**The Helsinki Birth Cohort Study (HBCS) is a population-based prospective cohort of singletons born at the Helsinki University Central Hospital between the years 1934 and 1944. Birth records on 4630 men and 4130 women who lived in Finland in 1971 were taken, including measurements of weight and length. Serial measurements of height and weight were extracted from child welfare clinic and school health clinic records, with an average of ten measurements between birth and 2 years, and eight measurements between 2 and 11 years of age. Between 2000 and 2002, a representative subset of 928 males and 1075 females returned for clinical examinations. At this visit, blood was taken for DNA extraction. Genotyping was performed on a custom Illumina 670 Quad platform at the Wellcome Trust Sanger Centre. Quality control was performed before imputation (excluding genotypes with call rate <0.95, MAF <0.01, HWE *P*-value <1 x 10-6) with MACH. The current analysis includes 1575 males and females (43% male) with BMI adjusted to their exact birthday at age 10. Informed consent was collected from all study participants. The study design was approved by the local ethics committee.

**INfancia y Medio Ambiente [Environment and Childhood] (INMA) Project**Population-based birth cohorts were established as part of the INMA – INfancia y Medio Ambiente [Environment and Childhood] Project in several regions of Spain following a common protocol. This project aims to study the associations between pre- and postnatal environmental exposures and growth, health, and development from early foetal life until adolescence and has been described previously in detail[37]. Pregnant women were enrolled during the 1st trimester of pregnancy at public primary health care centers or public hospitals. Detailed measurements were performed using ultrasound and physical examinations and biological samples were collected. Informed consent was obtained from all participants and the study was approved by the Hospital Ethics Committees in each participating region.

This particular analysis uses the INMA cohorts of Menorca (MEN), Valencia (VAL), Sabadell (SAB) in the discovery phase, and of Gipuzkoa (GIP) in the replication phase. Analyses were restricted to individuals of European ethnic origin with genome-wide data and a BMI measurement available between 2 and 10 years of age. Weight and height were measured with calibrated scales and a wall-mounted stadiometer, respectively, with the children standing in light clothing and barefoot, by trained field workers. BMI was calculated as weight in kilograms divided by the square of height in meters. Sex- and age-adjusted standard deviation scores (SDS) were constructed using LMS growth (Pan H, Cole TJ, 2012. http://www.healthforallchildren.co.uk).

DNA was obtained from cord blood, whole blood collected at 4y or saliva using the Chemagen protocol at the Spanish National Genotyping Centre (CEGEN). Children whose parents reported to be white and to be born in Spain or in European countries and that were not lost during the follow-up were selected for genotyping. Genome-wide genotyping was performed using the HumanOmni1-Quad Beadchip (Illumina) at CEGEN (MEN, SAB, VAL subcohorts) and GSA Beadchip (Illumina) at the Human Genotyping Facility (HuGeF), Dept Internal Medicine, Erasmus MC, The Netherlands (GIP subcohort). Genotype calling was done using the GeneTrain2.0 algorithm based on HapMap clusters implemented in the GenomeStudio software. Quality control was done using PLINK and following standard criteria. First of all, SNPs were flipped to the human genome + strand. We applied the following initial quality control thresholds: sample call rate>98% and/or LRR SD<0.3. Then, we checked sex, relatedness, heterozygosity and population stratification. Genetic variants were filtered for SNP call rate>95%, MAF>1% and HWE *P*-value> 1.10E-06. Imputation of genetic variants was done using IMPUTE V2 and the cosmopolitan 1000 genome panel (release March 2012) (MEN, SAB, VAL) and the Michigan imputation server using the Haplotype Reference Consortium HRC v1.1 reference panel (GIP).  
  
**LIFE-Child**

LIFE Child (NCT02550236) is an ongoing regional population-based study with comprehensive phenotyping including anthropometric and clinical data, laboratory data, genetic data and psychoscocial assessment in children and parents conducted in the city of Leipzig, Germany[38,39]. As a part of LIFE, the Leipzig Research Center for Civilization Diseases, it aims to monitor healthy child development from birth to adulthood and to understand the development of civilization diseases such as obesity. LEIPZIG childhood obesity cohort/LIFE Child Obesity is an obesity enriched subset with additional metabolic and cardiovascular phenotyping including OGTT. All procedures are performed in accordance with the ethical standards of the institutional and/or national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards. All legal guardians gave written informed consent, and the study has been approved by Ethics Committee of the University of Leipzig.

**MAAS**

The Manchester Asthma and Allergy Study is an unselected (i.a. population-based), birth cohort study[40-44]. The setting is the maternity catchment area of Wythenshawe and Stepping Hill Hospitals, comprising of 50 square miles of South Manchester and Cheshire, UK, a stable mixed urban-rural population. Study was approved by the Local Research Ethics Committee. Informed consent was obtained from all parents.

*Screening & Recruitment*

All pregnant women were screened for eligibility at antenatal visits (8th-10th week of pregnancy). The study was explained to the parents, and informed consent for initial questionnaires and skin prick testing was obtained. Both parents completed a questionnaire about their and their partner’s history of asthma and allergic diseases and smoking habits. If the pregnant woman’s partner was not present at the antenatal clinic visit, an invitation was sent for him to attend an open-access evening clinic for skin prick testing and questionnaire. Once both parents had completed questionnaires and skin prick testing, a full explanation of the proposed future follow-up for the child was given. Of the 1499 couples who met the inclusion criteria (<10 weeks of pregnancy, maternal age >18 years, questionnaire and skin test data available for both parents), 288 declined to take part in the study. A total of 1185 participants had at least some evaluable data.

*Follow-up*

The children have been followed prospectively, and attended review clinics at ages 1, 3, 5, 8 and 11 years.

*Phenotyping*

BMI was measured as outlined in Wang *et al*[45]. Briefly we measured weight, without shoes or outer clothing (to nearest 0.01kg), using a weighing scale, and height (to nearest 0.1cm) using a stadiometer.

*Genotyping*

DNA samples were genotyping on an illumina 610 quad chip. The illumina genotypes were called using the Illumina GenCall application following the manufacturer’s instructions. Quality control criteria for samples included: 97% call rate, exclusion of samples with an outlier autosomal heterozygosity (scree-plot visualisation) gender validation and sequenome genotype concordance. Quality control criteria for SNPs included a 95% call rate, HWE *P*-value > 5.9 x 10-7, MAF > 0.005. Genotypes were prephased with SHAPIT shapeit.v2.644 and imputed with IMPUTE version 2.2.2 with 1March2012 release of the 1000 genomes Phase I integrated variant set release (v3; updated 26 Aug 2012) reference genotypes. Association analysis was carried out using SNPTEST version 2.4.1 using frequentist with the score method.

**Northern Finnish Birth Cohort Study 1966 (NFBC1966)**

The Northern Finland Birth Cohort study 1966 (NFBC1966) (http://www.oulu.fi/nfbc/) includes 12,058 live born individuals, of European descent, with expected dates of birth during 1966 in the two northernmost provinces of Finland, Oulu and Lapland [46]. The University of Oulu Ethics Committee and the Ethical Committee of Northern Ostrobothnia Hospital District have approved the study. The data on all cohort members were prospectively collected since pregnancy and supplemented at the ages of 1, 14, 31 and 46 years. Growth measurements were obtained from communal child health clinics or from clinical examinations [47]. All those living in northern Finland or in the capital area were invited to a clinical examination and blood sampling at age 31 years [48]. BMI used in this analysis was calculated from the measurements of height and weight obtained throughout the childhood from child clinics. For this analysis a total of 52,486 BMI measures obtained at ages 2-18 years were used. Blood samples were drawn and DNA was extracted when individuals were 31 years old. Participants provided written informed consent.

DNA was successfully extracted for 5,753 participants from fasted blood samples. Illumina’s HumanCNV370-Duo Analysis BeadChip was used for genome-wide genotyping. After SNP filtering (SNPs with MAF < 0.05, HWE p<5.7x10-7 or call rate < 0.95 removed) and sample filtering (sample call rate < 0.95, mean heterozygosity < 0.29, MDS outliers, duplicates, contaminated samples, IBS pairwise sharing < 0.20, consent withdrawal or gender mismatch excluded), imputation was done for 1000G Phase 1 reference panel using 364,590 SNPs for 5402 participants.

**Northern Finland Birth Cohort Study 1986 (NFBC1986)**

The NFBC1986 includes 9,432 live born children with expected dates of birth between 1st July 1985 and 30th June 1986 in the two northernmost provinces of Finland, Oulu and Lapland. The University of Oulu Ethics Committee and the Ethical Committee of Northern Ostrobothnia Hospital District have approved the study. The cohort has been followed up since early pregnancy until young adulthood. Growth measurements were obtained from communal child health clinics or from clinical measurements. All those alive with known address were invited to a clinical examination at the age of 15 to 16 years, when blood samples were drawn. Participants provided written informed consent. BMI was calculated from the measurements height and weight obtained at ages 2-18 years. A total of 65,034 BMI measures were used in this analysis. DNA was extracted for 6,266 subjects using standard methods. A total of 3,834 samples were genotyped using Illumina HumanOmniExpressExome-8v1.2 platform and Beadstudio calling algorithm. After SNP filtering (SNPs with HWE p<1x10-4, call rate < 0.99 removed) and samples filtering (call rate < 0.95, mean heterozygosity < 0.305, IBS pairwise sharing < 0.2, gender mismatch, duplicate samples or consent withdrawal), genotype data was available for 3,743 adolescents. This includes a selected set of 372 individuals exposed to gestational diabetes, gestational hypertensive disorders and preterm birth, and the rest is a random sample. Imputation was done based on 889,119 SNPs for 1000G Phase 3 imputation panel. For the current BMI analyses, full data with growth and GWAS information were available for 1,506 individuals.

**Norwegian Mother, Father and Child (MoBa) Cohort Study (Two contributing projects; Pål R. Njølstad (6828 samples in replication) & Bo Jacobsson (522 samples in discovery))**

The Norwegian Mother, Father and Child (MoBa) Cohort Study ([www.fhi.no/moba](http://www.fhi.no/moba)) is a prospective population-based pregnancy cohort study conducted by the Norwegian Institute of Public Health[49-52]. Participants were recruited from all over Norway from 1999-2008. The women consented to participation in 40.6% of the pregnancies. The cohort now includes 114.500 children, 95.200 mothers and 75.200 fathers.

Blood samples were obtained from both parents during pregnancy and from mothers and children (umbilical cord) at birth. MoBa has obtained a licence from the Norwegian Data Inspectorate. Measurements of height and weight were performed at health stations by health personnel during routine health station follow-ups.  
 The establishment of MoBa and initial data collection was based on a license from the Norwegian Data protection agency and approval from The Regional Committee for Medical Research Ethics. The MoBa cohort is currently regulated by the Norwegian Health Registry Act. The current study was approved by The Regional Committee for Medical Research Ethics.

Pål R. Njølstad: Study was approved by the Regional Committee for Medical and Health Research Ethics in Norway (2012/67) on version 9 of the quality assured data files. 11.000 samples were genotyped using the Illumina HumanCoreExome-12 v.1.1 and HumanCoreExome-24 v.1.0 chips. Genotypes were called using Illumina Genome Studio using only samples with call rate >=0.98 and GenCall score >= 0.15 for defining cluster positions. We excluded variants with low call rates, signal intensity, quality scores, heterozygote excess and deviation from Hardy-Weinberg equilibrium based on the following QC parameters: call rate <98%, cluster separation <0.4, 10% GC-score <0.3, AA T Dev > 0.025, HWE P-value <1 x 10-6. As 214 samples had a duplicate available, we also removed SNPs with more than three discordant genotypes (where both samples had a non-missing genotype). Samples were excluded based on call rate <98% and heterozygosity excess >4SD. Study participants with non-Norwegian ancestry were excluded after merging with samples from the HapMap project (ver. 3) to remove ethnic outliers. Sample pairs with PI\_HAT > 0.1 in identical-by-descent (IBD) calculations were resolved by removing the sample with the highest missing-phenotype value, or by random in case of ties. Of the 9256 samples with Norwegian ancestry 6828 were eligible for analyses in the current study.

Bo Jacobsson: Study is based on version 6 of the quality-assured data files released for research in 2011, and was approved by The Regional Committee for Medical Research Ethics. This sub-study included only 522 samples. BMI was calculated based on self-reported height and weight in questionnaire.

**The Netherlands Twin Register** **(NTR)**

*Phenotyping*

The Netherlands Twin Register (NTR) collects data on development and growth in twins who are registered at birth by their parents[53,54]. In the NTR, data on BMI were available from the surveys sent out at ages 2, 3, 5, 7 and 10 years. At age 2 and 3, parents were asked to fill out all the dates and measures of height and weight as measured by the Dutch Community Health Services at regular intervals. At age 5, parents were asked to fill out the height and weight of the twins with the dates of measurement since the 3th birthday. At age 7 and 10, parents were asked to fill out the current height and weight of the twins with the date of assessment. In addition, laboratory measures were available for a group of individuals that participated in smaller subprojects55. Improbable data points were checked for data entry errors and corrected or excluded where necessary. Sex- and age adjusted standardized BMI scores were calculated with the 1990 British growth reference charts using the program LMSGrowth (available from http://www.healthforallchildren.co.uk). The measurement point between 24 and 120 months closest to 120 months was selected.

*Genotyping and Imputation*

Genotyping was done on the Affymetrix 6.0 platform[56]. SNPs were lifted over to build 37 (HG19) and strand aligned to 1000 Genomes phase I Interim release ALL panel (23 Nov 2010 sequence and June 2011 haplotypes). SNPs were excluded if alleles did not match or differed in frequency (>0.20) with the imputation reference set, if MAF was <1%, HWE p-value was < 0.00001 or call rate was <95%. Sample were excluded if sex did not match between genotyped and expected, if Plink F-value (heterozygosity) was > 0.10 or < -0.10 or if genotype call rate was < 90%. One individual from each monozygotic (MZ) twin pair was excluded. For imputation this dataset was merged with other NTR data, genotyped on different genotyping platforms, namely Affymetrix Perlegen 5.0, Illumina 370, Illumina 660 and Illumina Omni Express 1M.  The same QC steps were applied to each dataset. Samples additionally were checked for IBD within the merged dataset and were excluded if IBD did not match expected family relationships. Samples genotyped on different platforms have concordance rate > 99.0% or were removed otherwise. Same HWE, MAF filters as well as allele frequency comparison with reference set were applied to the merged dataset. Finally SNPs with MAF within range if 0.35 to 0.50 and allele combinations C/G and A/T were removed to avoid strand issues during imputation. The data were phased using Mach and imputed using Minimac. After imputation SNPs were removed, if they showed association with genotyping platform (p < 0.00001), if HWE p-value for the full dataset was < 0.000001, if Mendelian error rate was > 2%, if MAF was < 0.004, or if imputation quality R2 was < 0.30.

*Statistical Analysis*

Children with non-Dutch / non-European ancestry were excluded from the analyses. The final sample size for the analysis of BMI was 1,767 individuals. Analyses were performed in Plink in a linear regression framework; age and sex adjusted standard deviation scores were regressed on genome-wide SNP data and 3 genotyping chips. Data included one twin of each monozygotic twin pair, and both dizygotic twins. Standard errors were adjusted for family clustering using the --family option in Plink.  

**The Physical Activity and Nutrition in Children (PANIC) Study**   
The Physical Activity and Nutrition in Children (PANIC) Study is an 8-year controlled physical activity and dietary intervention study in a population sample of children from the city of Kuopio, Finland (<http://www.panicstudy.fi/en/panic-study-briefly>)[57]. The main aims of the study are to investigate behavioral, biological, environmental, and genetic risk factors for overweight, type 2 diabetes, atherosclerotic cardiovascular diseases, musculoskeletal diseases, psychic problems, dementia, and oral health problems and the effects of a long-term physical activity and dietary intervention on risk factors for these chronic diseases and conditions. Altogether 512 children 6-9 years of age participated in the baseline examinations in 2007-2009. Six children were excluded from the study at baseline because of physical disabilities that could hamper participation in the intervention or no time or motivation to attend in the study. The remaining 506 children were divided in the physical activity and dietary intervention group and the control group. The intervention included six physical activity and dietary counseling sessions for the children and their parents or caregivers during the 2-year follow-up (0.5, 1.5, 3, 6, 12, and 18 months after baseline) (<http://www.panicstudy.fi/en/intervention>). The control group received general advice on health improving physical activity and diet according to the Finnish recommendations at baseline but no active intervention. Altogether 440 (87%) of the 506 children participated in the 2-year follow-up examinations in 2009-2011. The intervention was continued between 2-year and 8-year follow-up examinations and included seven physical activity and dietary counseling sessions (24, 36, 48, 60, 72, 84, and 96 months after baseline). Altogether 277 adolescents participated in the 8-year follow-up examinations in 2016-2017. A large number of behavioral, biological, environmental, and genetic risk factors for obesity, type 2 diabetes, atherosclerotic cardiovascular diseases, musculoskeletal diseases, psychic problems, dementia, and oral health problems were assessed between fetal period and adolescence (<http://www.panicstudy.fi/en/assessments1>). Most of the assessments were performed at baseline in 2007-2009, at 2-year follow-up in 2009-2011, and at 8-year follow-up in 2016-2017. The most important assessments will also be repeated at 14-year follow-up in 2021-2023. The PANIC study protocol was approved by the Research Ethics Committee of the Hospital District of Northern Savo. A written informed consent was acquired from the parents or caregivers of the children, and the children also provided their assent to participation.

The present analyses were carried out among children of European ethnic origin with genome-wide data and BMI measured at the latest time point between 6 and 10 years of age. The analyses included 374 children (193 boys, 181 girls)  in the discovery phase. Body weight and height were measured without shoes and in light clothing in the PANIC study laboratory (72%) or were obtained from the health registers of the city of Kuopio (28%). Body weight was measured the children having fasted for 12 hours, having emptied the bladder, and standing in light underwear using a calibrated InBody®720 bioelectrical impedance device (Biospace Co. Ltd., Seoul, South Korea) to accuracy of 0.1 kg. Body height was measured using a wall-mounted stadiometer to accuracy of 0.1 cm. Sex- and age-adjusted weight, height, and BMI standard deviation scores (SDS) were computed using the LMSgrowth software ([http://www.healthforallchildren.co.uk](http://www.healthforallchildren.co.uk/)) using the British 1990 growth references. Genomic DNA was isolated from the blood mononuclear cells using the QIAamp DNA Blood kit (Qiagen, Hilden, Germany). Genotyping was performed using the Illumina Custom Infinium CardioMetabo BeadChip (Illumina, San Diego, CA, USA) in the discovery phase and the Illumina Infinium HumanCoreExome BeadChip in the replication phase (Illumina, San Diego, CA, USA).  
  
**Prevention and incidence of asthma and mite allergy birth cohort study - (PIAMA)**   
PIAMA is a birth cohort study consisting of two parts: a placebo controlled intervention study in which the effect of mite impermeable mattress covers on the development of asthma and allergy was studied and a natural history study in which no intervention took place. Details of the study design have been published previously[58]. Recruitment took place in 1996-1997 through prenatal clinics. A screening questionnaire was distributed to pregnant women visiting one of 52 prenatal clinics at three regions in the Netherlands. A total of 10,232 pregnant women completed a validated screening questionnaire. Mothers reporting a history of asthma, current hay fever or allergy to pets or house dust mite were defined as allergic. Based on this screening, 7,862 women were invited to participate, of whom 4,146 women (1,327 allergic and 2,819 non-allergic) gave written informed consent. Follow-up of the children took place at 3 months of age and yearly from 1 to 8 years of age. The Medical Ethical Committees of the participating institutes approved the study, and all participants gave written informed consent. DNA was collected from 2,162 children, and height and weight measures were obtained in 2,440 children during medical examinations at age 4 and/or 8 years. Genome-wide genotyping was performed in two phases. The first phase was performed within the framework of the GABRIEL Consortium using an Illumina Human 610K quad array[59]. Genotypes were available from 172 children with asthma and from 187 controls after quality control. A second group of 268 children who were more extensively examined during follow up was genotyped with an Illumina HumanOmniExpress array. A final group of 1377 children was genotyped with the Illumina Human Omni Express Exome Array.  The current replication analysis was restricted to individuals of European ethnic origin with genome-wide data and phenotype information (n=1958 children).  
  
**SCOOP**  
The Severe Childhood Onset Obesity Project (SCOOP) cohort comprised of ~4,800 British individuals of European ancestry is a sub-cohort of the Genetics of Obesity Study (GOOS)[60] (https://www.goos.org.uk/), which has recruited 7,000 individuals with severe early-onset obesity (BMI standard deviation score (SDS) > 3; onset of obesity before the age of 10 years). SCOOP individuals with congenital leptin deficiency or mutations in the melanocortin 4 receptor gene (MC4R) were excluded by prior Sanger sequencing. The current replication analysis includes 685 children aged 2-10 years genotyped on the Illumina HumanCoreExome-12v1-1 Beadchip imputed to the UK10K and 1000G Phase 3 reference panel[61] as described previously[62].  
  
**SKOT I**   
The Småbørns Kost Og Trivsel I (SKOT I) study is a population-based prospective cohort and recruitment and inclusion criteria have been described in detail elsewhere[63]. In short, the 329 children included in SKOT I were healthy singletons randomly recruited from the National Civil Registry and living in Copenhagen and Frederiksberg municipality (Denmark). The included children were born at term and had Danish-speaking parents. Prior to participation, written informed consent was obtained from all parents of the children. The Committees on Biomedical Research Ethics for the Capital Region of Denmark approved the study protocol (H-KF-2007-0003).The children were genotyped using the Illumina Infinium HumanCoreExome Beadchip (Illumina, San Diego, CA, USA) and genotypes were called using the Genotyping module, version 1.9.4 of GenomeStudio software, Version 2011.1 (Illumina). During genotype quality control, we excluded closely related individuals and samples with extreme inbreeding coefficients, mislabeled gender or call rate < 95% as well as duplicates and individuals identified as ethnic outliers. We applied a > 95% genotype call rate filer for the inclusion of SNPs. Additional genotypes were imputed into 1000 Genomes (phase 1) using IMPUTE2. Prior to participation, written informed consent was obtained from all parents of the children included in SKOT I. The Committees on Biomedical Research Ethics of the Capital Region of Denmark approved the study protocol of SKOT-I (H-KF-2007-0003).   
  
**Special Turku Coronary Risk Factor Intervention Project (STRIP)**

The STRIP study is a prospective randomised life-style intervention trial that began in infancy and continued through childhood and adolescence to early adulthood[64]. Altogether 1,062 children born in 1989-1991 were recruited at the age of 5 months by the well-baby clinics in Turku, and were randomised into an intervention group (n=540) or a control group (n=522). The life-style intervention continued until the participants reached the age of 20 years (n=~500). At the moment, the study participants are 27 to 29 years old (2018).

The purpose of the life-style intervention was to reduce exposure to cardiovascular disease risk factors with main focus on diet. Primary target of the dietary counselling was replacement of saturated fat with unsaturated fat in the child’s diet. The counselling also promoted intake of vegetables, fruits, and whole-grain products, and low intake of salt. In addition to investigating the efficiency of dietary counselling in improving risk factor levels, safety of the low-saturated fat diet was assessed in terms of growth and development. The main outcome measures comprise nutrient intake, serum lipid and lipoprotein concentrations, blood pressure, measures of somatic growth and development, and ultrasonic measures of arterial intima-media thickness, elasticity and endothelial function.

Weight was measured  in light clothing using an S10 electronic scale (Soehnle, Murrhardt, Germany) to the nearest 0.1 kg and height to the nearest 0.1 cm using a Harpender stadiometer (Holtain, Crymych, U.K.). BMI was calculated in kilograms/square of height in meters[65].

Altogether, 666 STRIP children were genotyped using the custom Illumina genotyping array, Metabochip, at the Center for Inherited Disease Research, the Johns Hopkins University, USA. Genotype imputation was performed using IMPUTE2[10,11] and a reference panel from the 1000 Genomes.

The study was approved by the Joint Commission on Ethics of the Turku University and the Turku University Central Hospital. Informed consent was obtained from all parents at the beginning of the trial and from the children at 15 and 18 years of age.  
  
**TEENS of Attica: Genes and Environment Study (TEENAGE)**  
The TEENAGE study is a cross-sectional study. The study target population comprised 857 adolescent students aged 13–15 years attending the first three classes of public secondary schools located in the wider Athens area of Attica. Prior to recruitment all study participants gave their verbal assent along with their parents’/guardians’ written consent forms. The study protocol was approved by the Institutional Review Board of Harokopio University and the Greek Ministry of Education, Lifelong Learning and Religious Affairs[66]. DNA samples of 707 study participants were genotyped using Illumina HumanOmniExpress BeadChips (Illumina, San Diego, CA, USA) at the Wellcome Trust Sanger Institute, Hinxton, UK. Genotyping and data quality control have been described previously[67]. Genotypes were called using Illuminus algorithm[68] and SNPs were imputed using the program IMPUTE[69]. Body weight and height at earlier time points from recruitment were collected retrospectively from participants’ medical health records and BMI was calculated as weight (kg) / height (m2). Analysis was restricted to individuals with available BMI measurement at ages between 2 and 6 years of age (N=252). Sex- and age-adjusted standard deviation scores (SDS) were constructed using LMS growth (http://www.healthforallchildren.co.uk)  
  
**TEDS**   
TEDS recruited over 15,000 families of twins born in England and Wales in 1994, 1995 and 1996 and the sample remains representative of the UK population. Ethical approval for TEDS has been provided by the Institute of Psychiatry ethics committee, reference number 05/Q0706/228.

Height and weight data were collected by postal questionnaire from the parents when their children were 3, 4, 7 and 10 years of age. Correlations with measured heights and weights in a sub-sample of these children at age 11 were 0.83 and 0.90. BMI was calculated from the height and weight data (BMI = weight (kg)/(height (m)^2)) and converted to BMI z-scores. BMI z-scores take into consideration the child's age and sex. They were based on 1990 UK growth reference curves and were calculated using the program LMSGrowth (available from http://homepage.mac.com/tjcole).

DNA for 8,743 individuals (including 3,722 dizygotic co-twin samples) was extracted from saliva and buccal cheek swab samples and hybridized to HumanOmniExpressExome-8v1.2 genotyping arrays at the Institute of Psychiatry, Psychology and Neuroscience Genomics & Biomarker Core Facility, London, UK. The raw image data from the array were normalized, pre-processed, and filtered in GenomeStudio according to Illumina Exome Chip SOP v1.4. (<http://confluence.brc.iop.kcl.ac.uk:8090/display/PUB/Production+Version%3A+Illumina+Exome+Chip+SOP+v1.4>). In addition, prior to genotype calling, 919 multi-mapping SNPs and 501 samples with callrate <0.95 were removed. The ZCALL program was used to augment the genotype calling for samples and SNPs that passed the initial QC.

DNA from 3,747 samples was extracted from buccal cheek swabs and genotyped at Affymetrix, Santa Clara, California, USA. From this sample, 3,665 samples were successfully hybridized to AffymetrixGeneChip 6.0 SNP genotyping arrays (<http://www.affymetrix.com/support/technical/datasheets/genomewide_snp6_datasheet.pdf>) using experimental protocols recommended by the manufacturer (Affymetrix Inc., Santa Clara, CA). The raw image data from the arrays were normalized and pre-processed at the Wellcome Trust Sanger Institute, Hinxton, UK for genotyping as part of the Wellcome Trust Case Control Consortium 2 (<https://www.wtccc.org.uk/ccc2/>) according to the manufacturer’s guidelines (http://www.affymetrix.com/support/downloads/manuals/genomewidesnp6\_manual.pdf). Genotypes for the Affymetrix arrays were called using CHIAMO (https://mathgen.stats.ox.ac.uk/genetics\_software/chiamo/chiamo.html).

After initial quality control and genotype calling, the same quality control was performed on the samples genotyped on the Illumina and Affymetrix platforms separately using PLINK[70-73]

Samples were removed from subsequent analyses on the basis of call rate (<0.98), suspected non-European ancestry, heterozygosity, and relatedness other than dizygotic twin status. SNPs were excluded if the minor allele frequency was smaller than 0.5%, if more than 2% of genotype data were missing, or if the Hardy Weinberg p-value was lower than 10-5. Non-autosomal markers and indels were removed. Association between SNP and the platform, batch, plate or well on which samples were genotyped was calculated; SNPs with an effect p-value < 10-4 were excluded. A total sample of 10,346 samples (including 3,320 dizygotic twin pairs and 7,026 unrelated individuals), with 7,289 individuals and 559,772 SNPs genotyped on Illumina and 3,057 individuals and 635,269 SNPs genotyped on Affymetrix.

Genotypes from the two platforms were separately phased using EAGLE2[74] and imputed into the 1000 Genomes reference panel (phase 3) using the Positional Burrows-Wheeler Transform method[75] through the Sanger Imputation Service[76] .

**TDCOB (cases and controls)**

The Danish Childhood Obesity Data and Biobank (ClinicalTrials.giv ID-no.: NCT00928473) includes children and adolescents with normal weight, overweight or obesity. Data material was collected between Januari 2009 and March 2015. A total of 1,069 children and adolescents, aged 6-18 years, with overweight or obesity (defined as BMI-SDS > 1.28 according to Danish national standards[77] were recruited through the Children’s Obesity Clinic, Department of Pediatrics, Copenhagen University Hospital Holbaek, Denmark. Between September 2010 and March 2013, a population-based control sample of Danish children and adolescents aged 6-18 years was recruited from schools across 11 municipalities in Denmark[78]. In the discovery stage of the present analysis, children that were between 2-10 years of age at the baseline examination were included. In the replication stage of the present analysis, we included children for which we were able to retrieve information on BMI in the age range 2-10 years based on self-report, school records and other registry data. There was no overlap between children included in the discovery stage and children included in the replication stage. The TDCOB cases and controls were genotyped using the Illumina Infinium HumanCoreExome Beadchip (Illumina, San Diego, CA, USA) and genotypes were called using the Genotyping module, version 1.9.4 of GenomeStudio software, Version 2011.1 (Illumina). Individuals identified as duplicates, ethnic outliers, or with extreme inbreeding coefficients, mislabeled gender or a call-rate <95% were excluded during genotyping quality control. Additional genotypes were imputed into the 1000 genomes phase 1 panel using IMPUTE2. Informed written and oral consent was obtained from all parents (participant < 18 years) or participants. This study was approved by the Ethics Committee of Region Zealand, Denmark, (ID No. SJ-104) and by the Danish Protection Agency.

**Tracking Adolescents' Individual Lives Survey (TRAILS)**

TRAILS (TRacking Adolescents' Individual Lives Survey) is a prospective cohort study of Dutch adolescents with bi- or triennial measurements from age 11 to, at this moment, age 26 and consists of a general population and a clinical cohort[79]. Data on infant and childhood growth, including birth weight and length, were extracted from records of wellchild clinics. These clinics are attended by 95% of the Dutch population. Children attend at ages 1, 2, 3, 4, 6, 9,11, 14, and 18 months and 2, 3, 4, 5, 10, and 13 years. During all visits, weight and length/height were measured by trained nurses[80].

DNA of 1335 samples was genotyped using the llumina Cyto SNP12 v2 chip (Illumina, San Diego, CA, USA) at the department of Genetics, University Medical Center Groningen. Genotype calling and quality control were carried out using Illumina GenomeStudio and PLINK[71], respectively. Impute v2[69] was used for imputation. Association analysis was performed using SNPtest v2.5[81].

**The Raine Study**

The Raine Study was started as a randomized controlled trial to evaluate the effects of repeated ultrasound in pregnant women in Perth, Western Australia[82]. In total, 2,900 pregnant women were recruited between 1989 and 1991 prior to 18 weeks gestation at the King Edward Memorial Hospital (Perth, Western Australia). Women were randomized to repeated ultrasound measurements at 18, 24, 28, 34 and 38 weeks gestation or to a single ultrasound assessment at 18‐weeks. The cohort individuals have been assessed at average ages of 1, 2, 3, 5, 8, 10, 14, 17, 20, and 22 and both height and weight were collected at each assessment.

DNA was collected at the year 14 and 17 follow-ups. The study was conducted with appropriate institutional ethics approval, and written informed consent was obtained from mothers at all follow‐ups and participants at the year 17 follow-up. DNA was collected using standardized procedures from 74% of all adolescents who attended the 14 year follow-up on and a further 5% at the 17 year follow-up measurements. We performed high throughput genome-wide SNP genotyping using the genome‐wide Illumina 660 Quad Array for each individual. Genotype data were imputed against 1000 Genomes (March 2012 release) using MACH and Minimac after quality control (MAF>1%, HWE *P*-value >5 x 10-7, call rate per SNP and person >95%). Genome-wide association analysis of the obesity phenotype was carried out in Probabel.

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