Contents of Supplementary Information

1. Supplementary Tables and Notes

These tables and notes are provided in this document.

2. Supplementary Data

These table (excel spreadsheet) and plots (pdf file) are provided in separate documents.

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- 60 regional plots for birth weight association

Supplementary Table 1. Description of studies contributing to trans-ancestry meta-analysis: ancestry group and country of origin, sample size, data collection methods, and birth weight summaries and exclusions.

(a) Component 1: European ancestry GWAS

Study	Ancestry group	Country of origin	Year(s) of birth	Sample size (M/F)	Data collection	Phenotype exclusions	Mean (SD) birth weight (grams)			Median (IQR) GA (week) at delivery
							Males	Females	Combined	
1958 British Birth Cohort	European	UK	1958	4,595 (2,320/2,275)	Measured by midwives; supplemented with obstetric records and interviews with mothers	Multiple births, GA <37 weeks	3439 (484)	3277 (468)	3359 (483)	40 (39-41)
ALSPAC[a,b]	European	UK	~1992	7,285 (3,722/3,563)	Identified from obstetric data, records from the ALSPAC measurers, and birth notification	Multiple births, GA <37 weeks, 5 SD winsorisation	3553 (491)	3423 (450)	3490 (476)	40 (40-41)
CHOP-Caucasian	European	USA	1988-present	9,405 (5,040/4,365)	Questionnaire and medical records	Multiple births, GA <37 weeks (when available)	3447 (582)	3343 (549)	3398 (569)	N/A
CoLaus	European	Switzerland	1928-1970	2,089 (892/1,197)	Self-reported as adults	N/A	3490 (668)	3250 (661)	3352 (675)	N/A
COPSAC-2000	European	Denmark	1998-2001	352 (173/179)	Medical records	Multiple births, GA <37 weeks	N/A	N/A	3555 (485)	40 (39-41)
COPSAC-2010	European	Denmark	2008-2011	589 (306/283)	Medical records	Multiple births, GA <37 weeks	3635 (483)	3536 (474)	3588 (481)	40 (39-41)
COPSAC-REGISTRY	European	Denmark	1987-1999	1,210 (804/406)	Medical Records	Multiple births, GA <37 weeks	3609 (498)	3443 (447)	3553 (488)	40 (39-41)
DNBC	European	Denmark	1996-2003	915 (475/440)	Danish Medical Birth Register	Multiple births, GA <37 weeks, congenital abnormalities	3767 (480)	3625 (443)	3699 (468)	40 (40-41)
ERF	European	Netherlands	Various	459 (187/272)	Interview	GA <37 weeks	3161 (680)	2955 (608)	3039 (644)	N/A
EPIC	European	UK	1993-1997	8,939 (3,448/5,491)	Self-reported	N/A	3505 (786)	3266 (750)	3358 (772)	N/A
Fenland (GA+)	European	UK	1950-1975	5,188 (2,088/3,100)	Self-reported as adults	GA described as "very pre-term" or "pre-term"	3433 (638)	3260 (594)	3394 (555)	N/A
Fenland (GA-)	European	UK	1950-1975	833 (509/324)	Self-reported as adults	None	3465 (593)	3154 (608)	3354 (624)	N/A
Generation R	European	Netherlands	2002-2006	2,701 (1,378/1,323)	Hospital records and community midwives	Multiple births, GA <37 weeks	3628 (494)	3518 (475)	3574 (488)	40 (39-41)
GINIplus & LISAplus (GA+)	European	Germany	1996-1999	656 (360/296)	Parental report of medical records	Multiple births, GA <37 weeks, <2500g	3498 (406)	3376 (417)	3443 (415)	40 (39-41)

Study	Ancestry group	Country of origin	Year(s) of birth	Sample size (M/F)	Data collection	Phenotype exclusions	Mean (SD) birth weight (grams)			Median (IQR) GA (week) at delivery
							Males	Females	Combined	
GINIplus & LISAplus (GA-)	European	Germany	1996-1999	790 (391/399)	Parental report of medical records	Multiple births, GA <37 weeks, <2500g	3499 (429)	3348 (423)	3423 (433)	N/A
GOYA	European	Denmark	1943-1952	149/0 (obese), 141/0 (control)	School health records	N/A	N/A	N/A	3553 (711)	N/A
HBCS	European	Finland	1934-1944	1472 (639/833)	Birth records	Multiple births, GA <37 weeks	3536 (460)	3375 (439)	3444 (454)	40 (39-41)
INMA	European	Spain	1997-2006	1,021 (527/494)	Well-trained midwives and nurses	None	3362 (406)	3188 (422)	3278 (423)	40 (39-41)
INTER99	European	Denmark	1939-1969	4,243 (1,981/2,262)	Measured by midwives and obtained from obstetric record registry	Multiple births, GA <37 weeks	3505 (493)	3370 (469)	3433 (485)	N/A
Leipzig	European	Germany	1985 - 2010	597 (304/293)	Questionnaire to mothers, documentation of medical screening examination if available	GA <37 weeks	3573 (531)	3480 (538)	3527 (536)	40 (39-40)
NEO	European	Netherlands	1943-1963	504 (exact; 200/304), 3215 (range; 1,450/1,765)	Questionnaire	N/A	3669 (1068)	3236 (973)	3514 (1271)	N/A
NFBC1966	European	Finland	1966	5,009 (2,393/2,616)	Measured in hospitals	Multiple births, GA <37 weeks or unknown	3607 (506)	3480 (466)	3541 (489)	40 (39-41)
NFBC1986	European	Finland	1986	4,680 (2,306/2,374)	Measured in hospitals	Multiple births, GA <37 weeks or unknown	3626 (543)	3519 (521)	3572 (535)	40 (39-40)
NTR	European	Netherlands	1926-1998	1,265 (447/818)	Parental report or self-reported	Multiple births, GA <37 weeks	3414 (619)	3544 (630)	3343 (601)	40 (40-40)
ORCADES	European	Scotland	1920-1991	960 (330/630)	Self-reported as adults	N/A	3401 (607)	3654 (685)	3488 (640)	N/A
PANIC	European	Finland	1999-2002	436 (231/205)	Medical records and parental questionnaire	Multiple births, GA <37 weeks	3646 (488)	3528 (444)	3588 (474)	40 (39-41)
RAINE	European	Australia	1989-1991	1,347 (693/654)	Recorded at delivery by study personnel or obtained from hospital reports	Multiple births, GA <37 weeks	3505 (471)	3390 (462)	3449 (470)	40 (39-41)
SORBS	European	Germany	1925-1988	298 (113/185)	Interview at recruitment	N/A	N/A	N/A	3393 (673)	N/A
STRIP	European	Finland	1989-1991	599 (311/288)	Medical records	Multiple births, GA <37 weeks	3696 (471)	3535 (443)	3619 (465)	40 (39-40)
TEENAGE (GA+)	European	Greece	1993-1998	279 (126/153)	Measured by midwives or paediatricians; supplemented with data from mothers' interviews	GA <37 weeks	3403 (467)	3280 (421)	3336 (445)	40 (38-40)
TEENAGE (GA-)	European	Greece	1993-1998	551 (234/317)	Measured by midwives or paediatricians; supplemented with data from mothers' interviews	N/A	3398 (459)	3298 (438)	3341 (449)	N/A
TDCOB-cases	European	Denmark	1987-2007	669	Measured by midwives and registered in	Multiple births	3682	3629	3660	40 (39-41)

				(391/278)	Danish Civil Registry		(536)	(545)	(540)	
TDCOB-controls	European	Denmark	1991-2006	560 (211/349)	Measured by midwives and registered in Danish Civil Registry	Multiple births	3627 (517)	3483 (485)	3540 (502)	40 (39-41)
YFS	European	Finland	1962-1977	1,915 (861/1,054)	Mothers' interview	Multiple births, GA >3 weeks pre-term	3648 (491)	3510 (451)	3572 (475)	N/A

(b) Component 2: UK BioBank

Study	**Ancestry group**	**Country of origin**	**Year(s) of birth**	**Sample size (M/F)**	**Data collection**	**Phenotype exclusions**	**Mean (SD) birth weight (grams)**			**Median (IQR) GA (weeks) at delivery**
							Males	**Females**	**Combined**	
UK BioBank	European	UK	2006-2010	67,786 (40,425/27,361)	Self-reported as adults	Multiple births, birth weight <2500g or >4000g	3452 (416)	3349 (417)	3391 (420)	N/A

(c) Component 3: Non-European ancestry GWAS

Study	**Ancestry group**	**Country of origin**	**Year(s) of birth**	**Sample size (M/F)**	**Data collection**	**Phenotype exclusions**	**Mean (SD) birth weight (grams)**			**Median (IQR) GA (weeks) at delivery**
							Males	**Females**	**Combined**	
CHOP-AA	African American	USA	1988-present	6,635 (3,343/3,292)	Questionnaire and medical records	Multiple births, GA <37 weeks (when available)	3276 (554)	3184 (535)	3231 (546)	N/A
CLHNS	Filipino	Philippines	1983-84	1,449 (755/694)	Local birth attendants	Multiple births, GA <37 weeks	3067 (401)	3018 (403)	3043 (403)	40 (38-40)
Generation R Turkish	Turkish	Netherlands	2002-2006	420 (215/205)	Hospital records and community midwives	Multiple births, GA <37 weeks	3477 (500)	3369 (415)	3424 (463)	40 (39-41)
Generation R Moroccan	Moroccan	Netherlands	2002-2006	365 (188/177)	Hospital records and community midwives	Multiple births, GA <37 weeks	3642 (447)	3417 (344)	3533 (416)	41 (40-41)
Generation R Surinamese	Surinamese	Netherlands	2002-2006	395 (215/180)	Hospital records and community midwives	Multiple births, GA <37 weeks	3288 (556)	3130 (490)	3216 (532)	40 (39-41)
SCORM	Chinese	Singapore	1992-1995	840 (420/420)	Documented medical record booklet	GA <37 weeks	3229 (422)	3182 (475)	3205 (450)	39 (38-40)

M, Males; F, Females; GA, gestational age; IQR, interquartile range; N/A, not applicable; SD, standard deviation.

[a] Boyd A, Golding J, Macleod J, Lawlor DA, Fraser A, et al. Cohort Profile: the 'children of the 90s'--the index offspring of the Avon Longitudinal Study of Parents and Children. *Int J Epidemiol* 42, 111-127 (2013).

[b] The study website contains details of all the data that is available through a fully searchable data dictionary (http://www.bris.ac.uk/alspac/researchers/data-access/data-dictionary/).

Supplementary Table 2. Description of studies contributing to trans-ancestry meta-analysis: genotyping, quality control, pre-phasing, imputation, and association analysis.

(a) Component 1: European ancestry GWAS

Study	Genotyping array(s)[a]	Sample quality control		SNP scaffold quality control			Prephasing software	Imputation		Association analysis		Lambda (M/F)
		Call rate	Additional filters	Call rate	HWE *P*-value	Frequency		Software	Reference panel	Software	Covariates or adjustment	
1958 British Birth Cohort	I550, I610	None	Relatedness, ancestry outliers, sex discrepancy, identity, channel contrast	95%	1x10^{-4}	MAF<1%	MaCH	Minimac	1000G Mar 2012	ProbABEL	GA	1.01/1.00
ALSPAC	I550	97%	Heterozygosity, relatedness, ancestry outliers	95%	5×10^{-7}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC7	1.02/1.01
CHOP-Caucasian	I550, I610	95%	Relatedness, ancestry outliers, sex discrepancy	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-3	0.96/0.96
CoLaus	A5	90%	Relatedness, ancestry outliers	90%	1x10^{-7}	MAF<1%	MaCH	Minimac	1000G Mar 2012	In-house	None	0.99/1.00
COPSAC-2000	I550	97.5%	Heterozygosity, relatedness, ancestry outliers	98%	1x10^{-6}	MAF<0.1%	MaCH	Minimac	1000G Mar 2012	mach2qtl	GA	1.00/1.01
COPSAC-2010	IOEE	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	QuickTest	GA, PC1-5	1.01/1.00
COPSAC-REGISTRY	IOEE	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	97.5%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	QuickTest	GA, PC1-5	1.00/1.00
DNBC	I660	96%	Heterozygosity, ancestry outliers, sex discrepancy	98%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	1.00/1.00
ERF	Various	98%	Relatedness, ancestry outliers, sex discrepancy	98%	5x10^{-8}	MAF<0.5%	MaCH	Minimac	1000G Mar 2012	ProbABEL	Kinship matrix	1.02/0.95
EPIC	AUKBB	97%	Heterozygosity, relatedness, sex discrepancy, singletons, channel contrast	95%	1x10^{-6}	MAC<1	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-10	1.00/1.01
Fenland (GA+)	AUKBB	95%	Sex discrepancy, identity	95%	1x10^{-6}	MAC<2	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1-10	1.00/1.01
Fenland (GA-)	AUKBB	95%	Sex discrepancy, identity	95%	1x10^{-6}	MAC<2	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-10	0.99/1.00
Generation R	I610, I660	97.5%	Heterozygosity, ancestry outliers, sex discrepancy	98%	1x10^{-6}	MAF<1%	MaCH	Minimac	1000G Mar 2012	mach2qtl	GA, PC1-4	1.03/1.01
GINIplus & LISAplus	A5, A6	95%	Heterozygosity, ancestry outliers, sex discrepancy	95%	1x10^{-5}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	0.99/1.00
GOYA	I610	95%	Heterozygosity, ancestry outliers, sex discrepancy	95%	1x10^{-7}	MAF<1%	MaCH	MaCH	1000G Mar 2012	QuickTest	None	1.00/0.99
HBCS	I670	95%	Heterozygosity, relatedness, ancestry outliers	95%	1x10^{-6}	MAF<1%	MaCH	MaCH	1000G Mar 2012	mach2qtl	GA	1.02/1.02

Study	Genotyping array(s)[a]	Sample quality control		SNP scaffold quality control			Prephasing software	Imputation		Association analysis		Lambda (M/F)
		Call rate	Additional filters	Call rate	HWE *p*-value	Frequency		Software	Reference panel	Software	Covariates or adjustment	
INMA	IOQ	98%	Heterozygosity, relatedness, ancestry outliers, duplicates	95%	1.1x10^{-6}	MAF<1%	IMPUTE2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	1.00/0.99
INTER99	ICM	95%	Relatedness, ancestry outliers, sex discrepancy	95%	1x10^{-4}	MAF<1%	IMPUTE2	IMPUTE2	1000G Mar 2012	SNPTEST	PC1	0.97/1.02
Leipzig	ICM	95%	Duplicates, ancestry outliers, sex discrepancy	95% (99% if MAF<5%)	1x10^{-4}	MAF<1%	IMPUTE2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	0.95/0.96
NEO	ICE	98%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	98%	1x10^{-6}	None	IMPUTE2	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-5	0.99/0.99
NFBC1966	I370	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy, duplicates, withdrawn consent	95% (99% if MAF<5%)	5.7x10^{-7}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1-3	1.00/0.99
NFBC1986	ICM	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy, duplicates, withdrawn consent	95% (99% if MAF<5%)	5.7x10^{-7} (1x10^{-4} if MAF<5%)	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1-3	1.00/1.10
NTR	A6, I370, I660, IOQ	90%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	95%	1x10^{-5}	MAF<1%	MaCH	Minimac	1000G Mar 2012	PLINK	GA, array, PC1-6 (global), PC1-3 (local)	1.08/1.04
ORCADES	I300, IOQ, IOE	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy, duplicates	95% (99% if MAF<5%)	1x10^{-6}	MAF<1%	SHAPEIT	IMPUTE2	1000G Mar 2012	ProbABEL	array, PC1-3	1.00/0.99
PANIC	ICM, ICE	90 %	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1-4	1.01/1.01
RAINE	I660	97%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy, chromosomal abnormalities	95%	5.7x10^{-7}	MAF<1%	MaCH	MaCH	1000G Mar 2012	ProbABEL	GA, PC1-2	1.01/0.99
SORBS	I660	94%	Relatedness, ancestry outliers, sex discrepancy, duplicates	95%	1x10^{-4}	MAF<1%	MaCH	Minimac	1000G Mar 2012	ProbABEL	Kinship matrix	1.01/1.01
STRIP	A5, A6	95%	Heterozygosity, ancestry outliers, twins	95%	1x10^{-6}	MAF<0.1%	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1-4	1.01/1.01
TEENAGE (GA+)	ICM	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	95% (99% if MAF<5%)	1x10^{-4}	MAF<1%	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	GA	1.02/1.00
TEENAGE (GA-)	IOE	95%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	95% (99% if MAF<5%)	1x10^{-4}	MAF<1%	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	None	1.02/0.98

TDCOB-cases	IOE	95%	Heterozygosity, relatedness, ancestry outliers	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1	1.02/1.01
TDCOB-controls	ICE	95%	Heterozygosity, relatedness, ancestry outliers	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1	1.02/1.05
YFS	I670	95%	Heterozygosity, relatedness, sex discrepancy, duplicates	95%	1x10^{-6}	MAF<1%	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-4	0.99/1.01

(b) Component 2: UK BioBank

Study	**Genotyping array(s)**[a]	**Sample quality control**		**SNP scaffold quality control**			**Prephasing software**	**Imputation**		**Association analysis**		**Lambda**
		Call rate	**Additional filters**	**Call rate**	**HWE *P*-value**	**Frequency**		**Software**	**Reference panel**	**Software**	**Covariates or adjustment**	
UK BioBank	AUKBB	98%	Heterozygosity, relatedness, ancestry outliers	95%	N/A	MAF<1%	SHAPEIT2	IMPUTE2	1000G Oct 2014 & UK10K	BOLT-LMM	Sex, genotype array	N/A

(c) Component 3: Non-European ancestry GWAS.

Study	**Genotyping array(s)**[a]	**Sample quality control**		**SNP scaffold quality control**			**Prephasing software**	**Imputation**		**Association analysis**		**Lambda (M/F)**
		Call rate	**Additional filters**	**Call rate**	**HWE *P*-value**	**Frequency**		**Software**	**Reference panel**	**Software**	**Covariates or adjustment**	
CHOP-AA	I550, I610	95%	Relatedness, ancestry outliers, sex discrepancy	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-3	0.98/0.98
CLHNS	ICM	98.6%	Relatedness, sex discrepancy	97%	1×10^{-6}	N/A	MaCH	MaCH	1000G Mar 2012	mach2qtl	GA	1.02/1.02
Generation R Turkish	I610, I660	97.5%	Heterozygosity, ancestry outliers, sex discrepancy	95%	1x10^{-7}	MAF<1%	MaCH	Minimac	1000G Mar 2012	mach2qtl	GA, PC1-4	1.01/1.02
Generation R Moroccan	I610, I660	97.5%	Heterozygosity, ancestry outliers, sex discrepancy	90%	1x10^{-7}	MAF<1%	MaCH	Minimac	1000G Mar 2012	mach2qtl	GA, PC1-4	1.01/0.98
Generation R Surinamese	I610, I660	97.5%	Heterozygosity, ancestry outliers, sex discrepancy	98%	1x10^{-7}	MAF<1%	MaCH	Minimac	1000G Mar 2012	mach2qtl	GA, PC1	0.99/0.95
SCORM	I550	95%	Heterozygosity, relatedness, sex discrepancy	95%	1x10^{-6}	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	0.98/0.99

HWE, Hardy-Weinberg equilibrium; MAF, minor allele frequency; MAC, minor allele count; GA, gestational age; PC, principal component.
[a] Genotype array codes: Affymetrix 5.0 (A5); Affymetrix 6.0 (A6); Affymetrix Axiom UK BiLEVE (AUKBL); Affymetrix Axiom UK BioBank (AUKBB); Illumina Human370CNV (I370); Illumina HumanHap550 (I550); Illumina HumanHap610 (I610); Illumina HumanHap660 (I660); Illumina HumanHap670 (I670); Illumina CardioMetabochip (ICM); Illumina OmniQuad (IOQ); Illumina OmniExpress (IOE); Illumina CoreExome (ICE); Illumina OmniExpressExome (IOEE).

Supplementary Table 3. BW association summary statistics for each component of the trans-ancestry meta-analysis of 153,781 individuals for lead SNPs at loci attaining genome-wide significance ($P<5\times10^{-8}$).

Locus: *WNT4-ZBTB40*. Lead SNP: rs2473248. Effect/other alleles: C/T.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.86	0.039	0.008	5.0×10^{-7}	71,642	0.66
Component 2: UKBB	0.88	0.025	0.008	0.0032	67,786	N/A
European ancestry meta-analysis	0.87	0.033	0.006	1.1×10^{-8}	139,428	0.21
Component 3: non-European ancestry	0.78	0.039	0.018	0.034	8,653	0.43
Trans-ancestry meta-analysis	0.87	0.033	0.005	1.1×10^{-9}	148,081	0.72

Locus: *ZBTB7B*. Lead SNP: rs3753639. Effect/other alleles: C/T.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.23	0.038	0.006	3.9×10^{-9}	70,376	0.60
Component 2: UKBB	0.25	0.024	0.006	0.00017	67,786	N/A
European ancestry meta-analysis	0.24	0.031	0.004	7.3×10^{-12}	138,162	0.12
Component 3: non-European ancestry	0.18	0.037	0.020	0.061	8,655	0.40
Trans-ancestry meta-analysis	0.23	0.031	0.004	1.3×10^{-12}	146,817	0.72

Locus: *FCGR2B*. Lead SNP: rs72480273. Effect/other alleles: C/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.16	0.029	0.007	8.7×10^{-5}	70,594	0.14
Component 2: UKBB	0.19	0.033	0.007	2.3×10^{-6}	67,786	N/A
European ancestry meta-analysis	0.17	0.031	0.005	8.0×10^{-10}	138,380	0.69
Component 3: non-European ancestry	0.15	0.005	0.023	0.84	8,655	0.71
Trans-ancestry meta-analysis	0.17	0.030	0.005	1.5×10^{-9}	147,035	0.86

Locus: *DTL*. Lead SNP: rs61830764. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.38	0.031	0.006	1.0×10^{-7}	70,372	0.12
Component 2: UKBB	0.38	0.013	0.006	0.019	67,786	N/A
European ancestry meta-analysis	0.38	0.022	0.004	5.6×10^{-8}	138,158	0.029
Component 3: non-European ancestry	0.15	0.016	0.024	0.50	8,655	0.30
Trans-ancestry meta-analysis	0.36	0.022	0.004	4.5×10^{-8}	146,813	0.18

Locus: *ATAD2B*. Lead SNP: rs7575873. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.88	0.040	0.008	4.9×10^{-7}	71,639	0.98
Component 2: UKBB	0.87	0.036	0.008	6.3×10^{-6}	67,786	N/A
European ancestry meta-analysis	0.88	0.038	0.006	1.3×10^{-11}	139,425	0.71
Component 3: non-European ancestry	0.93	-0.011	0.027	0.67	10,104	0.61
Trans-ancestry meta-analysis	0.88	0.036	0.006	6.2×10^{-11}	149,529	0.35

Locus: *EPAS1*. Lead SNP: rs1374204. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.70	0.050	0.006	1.0×10^{-16}	66,667	0.94
Component 2: UKBB	0.70	0.044	0.006	9.7×10^{-14}	67,786	N/A
European ancestry meta-analysis	0.70	0.047	0.004	6.2×10^{-29}	134,453	0.42
Component 3: non-European ancestry	0.63	0.031	0.016	0.049	8,654	0.14
Trans-ancestry meta-analysis	0.70	0.046	0.004	1.5×10^{-29}	143,107	0.82

Locus: *PTH1R*. Lead SNP: rs2242116. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.38	0.018	0.005	0.00048	75,884	0.48
Component 2: UKBB	0.38	0.025	0.006	5.5×10^{-6}	67,786	N/A
European ancestry meta-analysis	0.38	0.022	0.004	1.4×10^{-8}	143,670	0.37
Component 3: non-European ancestry	0.57	0.012	0.014	0.41	10,103	0.92
Trans-ancestry meta-analysis	0.39	0.021	0.004	1.2×10^{-8}	153,773	0.94

Locus: *ADCY5*. Lead SNP: rs11719201. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.22	0.052	0.006	5.2×10^{-18}	75,884	0.34
Component 2: UKBB	0.24	0.039	0.006	4.0×10^{-10}	67,786	N/A
European ancestry meta-analysis	0.23	0.046	0.004	2.4×10^{-26}	143,670	0.14
Component 3: non-European ancestry	0.13	0.037	0.022	0.095	9,264	0.18
Trans-ancestry meta-analysis	0.23	0.046	0.004	6.4×10^{-27}	152,934	0.35

Locus: *CPA3*. Lead SNP: rs10935733. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.42	0.023	0.005	2.2×10^{-5}	71,640	0.58
Component 2: UKBB	0.39	0.021	0.005	0.00012	67,786	N/A
European ancestry meta-analysis	0.41	0.022	0.004	9.2×10^{-9}	139,426	0.80
Component 3: non-European ancestry	0.60	0.038	0.015	0.013	10,103	0.62
Trans-ancestry meta-analysis	0.42	0.023	0.004	6.2×10^{-10}	149,529	0.33

Locus: *CCNL1-LEKR1*. Lead SNP: rs13322435. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.60	0.063	0.005	1.0×10^{-30}	71,640	0.0091
Component 2: UKBB	0.60	0.042	0.006	3.4×10^{-13}	67,786	N/A
European ancestry meta-analysis	0.60	0.053	0.004	3.7×10^{-41}	139,426	0.0080
Component 3: non-European ancestry	0.45	0.040	0.015	0.0066	10,103	0.66
Trans-ancestry meta-analysis	0.59	0.052	0.004	1.3×10^{-42}	149,529	0.14

Locus: *LCORL*. Lead SNP: rs925098. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.28	0.040	0.006	4.8×10^{-12}	71,640	0.46
Component 2: UKBB	0.26	0.027	0.006	9.0×10^{-6}	67,786	N/A
European ancestry meta-analysis	0.27	0.034	0.004	5.4×10^{-16}	139,426	0.11
Component 3: non-European ancestry	0.34	0.011	0.015	0.44	10,102	0.28
Trans-ancestry meta-analysis	0.28	0.032	0.004	1.3×10^{-15}	149,528	0.060

Locus: *HHIP*. Lead SNP: rs6537307. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.50	0.023	0.005	1.5×10^{-5}	71,645	0.35
Component 2: UKBB	0.49	0.029	0.005	1.1×10^{-7}	67,786	N/A
European ancestry meta-analysis	0.50	0.025	0.004	9.5×10^{-12}	139,431	0.41
Component 3: non-European ancestry	0.21	0.038	0.018	0.036	9,557	0.92
Trans-ancestry meta-analysis	0.48	0.026	0.004	1.3×10^{-12}	148,988	0.80

Locus: 5q11.2. Lead SNP: rs854037. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.81	0.038	0.007	7.8×10^{-9}	71,643	0.021
Component 2: UKBB	0.82	0.014	0.007	0.045	67,786	N/A
European ancestry meta-analysis	0.81	0.027	0.005	2.2×10^{-8}	139,429	0.011
Component 3: non-European ancestry	0.53	0.009	0.014	0.52	10,103	0.29
Trans-ancestry meta-analysis	0.80	0.025	0.005	3.5×10^{-8}	149,532	0.010

Locus: *EBF1*. Lead SNP: rs7729301. Effect/other alleles: A/G.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.72	0.021	0.006	0.00035	75,883	0.23
Component 2: UKBB	0.74	0.027	0.006	1.0×10^{-5}	67,786	N/A
European ancestry meta-analysis	0.73	0.024	0.004	1.6×10^{-8}	143,669	0.48
Component 3: non-European ancestry	0.58	0.033	0.014	0.022	10,104	0.64
Trans-ancestry meta-analysis	0.72	0.025	0.004	1.3×10^{-9}	153,773	0.78

Locus: *CDKAL1*. Lead SNP: rs35261542. Effect/other alleles: C/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.72	0.047	0.006	6.1×10^{-17}	75,881	0.94
Component 2: UKBB	0.74	0.041	0.006	1.4×10^{-11}	67,786	N/A
European ancestry meta-analysis	0.73	0.044	0.004	4.4×10^{-27}	143,667	0.49
Component 3: non-European ancestry	0.75	0.044	0.016	0.0059	10,102	0.35
Trans-ancestry meta-analysis	0.73	0.044	0.004	9.7×10^{-29}	153,769	0.42

Locus: *HIST1H2BE*. Lead SNP: rs9379832. Effect/other alleles: A/G.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.67	0.029	0.006	7.2×10^{-7}	70,375	1.0
Component 2: UKBB	0.73	0.016	0.006	0.011	67,786	N/A
European ancestry meta-analysis	0.70	0.023	0.004	6.6×10^{-8}	138,161	0.13
Component 3: non-European ancestry	0.77	0.044	0.021	0.038	10,103	0.70
Trans-ancestry meta-analysis	0.71	0.024	0.004	1.2×10^{-8}	148,264	0.42

Locus: *HMGA1*. Lead SNP: rs7742369. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.17	0.027	0.007	0.0011	69,259	0.90
Component 2: UKBB	0.18	0.030	0.007	2.4×10^{-5}	67,786	N/A
European ancestry meta-analysis	0.18	0.028	0.005	1.0×10^{-8}	137,045	0.77
Component 3: non-European ancestry	0.44	0.013	0.016	0.41	9,561	0.18
Trans-ancestry meta-analysis	0.19	0.027	0.005	1.1×10^{-8}	146,606	0.16

Locus: *L3MBTL3*. Lead SNP: rs1415701. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.75	0.025	0.006	2.3×10^{-5}	75,880	0.69
Component 2: UKBB	0.73	0.025	0.006	3.2×10^{-5}	67,786	N/A
European ancestry meta-analysis	0.74	0.025	0.004	2.6×10^{-9}	143,666	1.00
Component 3: non-European ancestry	0.63	0.048	0.015	0.0013	10,102	0.64
Trans-ancestry meta-analysis	0.73	0.027	0.004	4.0×10^{-11}	153,768	0.40

Locus: *ESR1*. Lead SNP: rs1101081. Effect/other alleles: C/T.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.72	0.044	0.006	5.4×10^{-14}	71,641	0.95
Component 2: UKBB	0.73	0.031	0.006	2.7×10^{-7}	67,786	N/A
European ancestry meta-analysis	0.72	0.038	0.004	1.6×10^{-19}	139,427	0.14
Component 3: non-European ancestry	0.79	0.027	0.017	0.13	10,103	0.47
Trans-ancestry meta-analysis	0.73	0.037	0.004	6.1×10^{-20}	149,530	0.28

Locus: *GNA12*. Lead SNP: rs798489. Effect/other alleles: C/T.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.73	0.020	0.006	0.00040	75,884	0.75
Component 2: UKBB	0.73	0.027	0.006	1.0×10^{-5}	67,786	N/A
European ancestry meta-analysis	0.73	0.023	0.004	2.0×10^{-8}	143,670	0.44
Component 3: non-European ancestry	0.92	0.053	0.027	0.048	9,708	0.14
Trans-ancestry meta-analysis	0.74	0.024	0.004	5.0×10^{-9}	153,378	0.84

Locus: *IGF2BP3*. Lead SNP: rs11765649. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.76	0.021	0.006	0.00049	71,642	0.80
Component 2: UKBB	0.74	0.032	0.006	1.3x10^{-7}	67,786	N/A
European ancestry meta-analysis	0.75	0.027	0.004	5.8x10^{-10}	139,428	0.19
Component 3: non-European ancestry	0.87	0.003	0.022	0.88	10,103	0.37
Trans-ancestry meta-analysis	0.76	0.026	0.004	1.0x10^{-9}	149,531	0.60

Locus: *TBX20*. Lead SNP: rs6959887. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.61	0.031	0.005	1.4x10^{-9}	75,873	0.58
Component 2: UKBB	0.61	0.013	0.006	0.021	67,786	N/A
European ancestry meta-analysis	0.61	0.023	0.004	1.5x10^{-9}	143,659	0.013
Component 3: non-European ancestry	0.63	-0.007	0.014	0.65	10,098	0.62
Trans-ancestry meta-analysis	0.61	0.021	0.004	1.0x10^{-8}	153,757	0.054

Locus: *YKT6-GCK*. Lead SNP: rs138715366. Effect/other alleles: C/T.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.9908	0.227	0.034	1.7x10^{-11}	64,557	0.86
Component 2: UKBB	0.9915	0.253	0.031	7.1x10^{-16}	67,786	N/A
European ancestry meta-analysis	0.9911	0.241	0.023	7.2x10^{-26}	132,343	0.57
Component 3: non-European ancestry	0.9977	0.855	0.333	0.010	3,292	1.00
Trans-ancestry meta-analysis	0.9913	0.244	0.023	1.4x10^{-26}	135,635	0.16

Locus: *MLXIPL*. Lead SNP: rs62466330. Effect/other alleles: C/T.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.06	0.052	0.011	1.9x10^{-6}	74,414	0.24
Component 2: UKBB	0.07	0.046	0.011	1.5x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.07	0.049	0.008	1.2x10^{-10}	142,200	0.70
Component 3: non-European ancestry	0.04	0.142	0.045	0.0015	7,815	0.52
Trans-ancestry meta-analysis	0.07	0.051	0.007	5.9x10^{-12}	150,015	0.23

Locus: *ANK1-NKX6-3*. Lead SNP: rs13266210. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.78	0.023	0.006	0.00034	71,643	0.19
Component 2: UKBB	0.79	0.040	0.007	1.5x10^{-9}	67,786	N/A
European ancestry meta-analysis	0.79	0.031	0.005	1.3x10^{-11}	139,429	0.054
Component 3: non-European ancestry	0.81	0.013	0.019	0.48	9,562	0.30
Trans-ancestry meta-analysis	0.79	0.030	0.004	1.6x10^{-11}	148,991	0.32

Locus: *TRIB1*. Lead SNP: rs6989280. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.73	0.026	0.006	5.6x10^{-6}	75,885	0.34
Component 2: UKBB	0.73	0.017	0.006	0.0069	67,786	N/A
European ancestry meta-analysis	0.73	0.022	0.004	2.2x10^{-7}	143,671	0.25
Component 3: non-European ancestry	0.32	0.027	0.016	0.085	10,104	0.85
Trans-ancestry meta-analysis	0.70	0.022	0.004	5.0x10^{-8}	153,775	0.92

Locus: *SLC45A4*. Lead SNP: rs12543725. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.59	0.023	0.005	1.1x10^{-5}	71,645	0.39
Component 2: UKBB	0.59	0.023	0.005	3.0x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.59	0.023	0.004	1.2x10^{-9}	139,431	0.94
Component 3: non-European ancestry	0.78	0.005	0.018	0.78	8,653	0.42
Trans-ancestry meta-analysis	0.60	0.022	0.004	1.9x10^{-9}	148,084	0.65

Locus: *PTCH1*. Lead SNP: rs28510415. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.09	0.041	0.009	1.4x10^{-5}	66,960	0.40
Component 2: UKBB	0.10	0.070	0.009	1.7x10^{-14}	67,786	N/A
European ancestry meta-analysis	0.09	0.056	0.007	1.5x10^{-17}	134,746	0.023
Component 3: non-European ancestry	0.03	-0.086	0.043	0.049	8,654	0.79
Trans-ancestry meta-analysis	0.09	0.053	0.006	4.0x10^{-16}	143,400	0.0055

Locus: *LPAR1*. Lead SNP: rs2150052. Effect/other alleles: T/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.50	0.021	0.005	8.6x10^{-5}	71,638	0.23
Component 2: UKBB	0.51	0.021	0.005	7.5x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.50	0.021	0.004	2.2x10^{-8}	139,424	0.95
Component 3: non-European ancestry	0.46	0.008	0.015	0.61	8,655	0.71
Trans-ancestry meta-analysis	0.50	0.020	0.004	2.8x10^{-8}	148,079	0.99

Locus: *PHF19*. Lead SNP: rs7847628. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.68	0.028	0.006	1.1x10^{-6}	71,638	0.47
Component 2: UKBB	0.68	0.018	0.006	0.0014	67,786	N/A
European ancestry meta-analysis	0.68	0.023	0.004	1.0x10^{-8}	139,424	0.23
Component 3: non-European ancestry	0.57	0.017	0.015	0.25	10,104	0.30
Trans-ancestry meta-analysis	0.67	0.023	0.004	5.4x10^{-9}	149,528	0.17

Locus: *STRBP*. Lead SNP: rs700059. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.15	0.027	0.007	0.00028	71,641	0.090
Component 2: UKBB	0.14	0.040	0.008	2.1x10^{-7}	67,786	N/A
European ancestry meta-analysis	0.14	0.033	0.005	4.7x10^{-10}	139,427	0.22
Component 3: non-European ancestry	0.43	0.059	0.016	0.00018	8,653	0.34
Trans-ancestry meta-analysis	0.16	0.036	0.005	1.2x10^{-12}	148,080	0.21

Locus: *HHEX-IDE*. Lead SNP: rs61862780. Effect/other alleles: T/C.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.51	0.027	0.005	9.2x10^{-8}	75,884	0.37
Component 2: UKBB	0.51	0.029	0.005	7.6x10^{-8}	67,786	N/A
European ancestry meta-analysis	0.51	0.028	0.004	3.0x10^{-14}	143,670	0.81
Component 3: non-European ancestry	0.77	0.025	0.017	0.13	10,103	0.12
Trans-ancestry meta-analysis	0.52	0.028	0.004	9.5x10^{-15}	153,773	0.80

Locus: *NT5C2*. Lead SNP: rs74233809. Effect/other alleles: C/T.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.08	0.032	0.009	0.00039	75,881	0.88
Component 2: UKBB	0.08	0.042	0.010	3.0x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.08	0.037	0.007	5.2x10^{-8}	143,667	0.49
Component 3: non-European ancestry	0.12	0.061	0.022	0.0057	10,104	0.39
Trans-ancestry meta-analysis	0.08	0.039	0.006	1.8x10^{-9}	153,771	0.14

Locus: *ADRB1*. Lead SNP: rs7076938. Effect/other alleles: T/C.

Analysis	**EAF**	**B**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.73	0.046	0.006	1.3x10^{-15}	75,885	0.79
Component 2: UKBB	0.73	0.025	0.006	4.5x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.73	0.036	0.004	4.7x10^{-18}	143,671	0.011
Component 3: non-European ancestry	0.64	0.018	0.015	0.22	10,103	0.56
Trans-ancestry meta-analysis	0.73	0.035	0.004	4.7x10^{-18}	153,774	0.19

Locus: *PLEKHA1*. Lead SNP: rs2421016. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.50	0.022	0.005	1.0x10^{-5}	75,873	0.25
Component 2: UKBB	0.47	0.019	0.005	0.00047	67,786	N/A
European ancestry meta-analysis	0.49	0.021	0.004	1.8x10^{-8}	143,659	0.62
Component 3: non-European ancestry	0.40	0.021	0.014	0.15	10,100	0.28
Trans-ancestry meta-analysis	0.48	0.021	0.004	6.1x10^{-9}	153,759	0.83

Locus: *INS-IGF2*. Lead SNP: rs72851023. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.07	0.055	0.011	6.7x10^{-7}	67,990	0.014
Component 2: UKBB	0.08	0.041	0.010	8.0x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.07	0.048	0.008	2.9x10^{-10}	135,776	0.35
Component 3: non-European ancestry	0.02	-0.048	0.064	0.45	7,815	1.00
Trans-ancestry meta-analysis	0.07	0.046	0.007	6.8x10^{-10}	143,591	0.64

Locus: *MTNR1B*. Lead SNP: rs10830963. Effect/other alleles: G/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.28	0.029	0.006	5.1x10^{-7}	75,877	0.20
Component 2: UKBB	0.28	0.017	0.006	0.0059	67,786	N/A
European ancestry meta-analysis	0.28	0.023	0.004	2.9x10^{-8}	143,663	0.12
Component 3: non-European ancestry	0.20	-0.013	0.021	0.54	10,102	0.76
Trans-ancestry meta-analysis	0.27	0.022	0.004	1.0x10^{-7}	153,765	0.23

Locus: *APOLD1*. Lead SNP: rs11055034. Effect/other alleles: C/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.74	0.028	0.006	2.1x10^{-6}	75,867	0.91
Component 2: UKBB	0.72	0.016	0.006	0.0099	67,786	N/A
European ancestry meta-analysis	0.73	0.022	0.004	1.8x10^{-7}	143,653	0.13
Component 3: non-European ancestry	0.81	0.046	0.020	0.019	9,942	0.67
Trans-ancestry meta-analysis	0.73	0.023	0.004	2.3x10^{-8}	153,595	0.32

Locus: *ABCC9*. Lead SNP: rs139975827. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.61	0.027	0.007	4.9x10^{-5}	55,417	0.72
Component 2: UKBB	0.63	0.023	0.006	5.8x10^{-5}	67,786	N/A
European ancestry meta-analysis	0.62	0.025	0.004	1.1x10^{-8}	123,203	0.72
Component 3: non-European ancestry	0.70	-0.018	0.018	0.32	8,655	0.68
Trans-ancestry meta-analysis	0.63	0.022	0.004	1.0x10^{-7}	131,858	0.22

Locus: *ITPR2*. Lead SNP: rs12823128. Effect/other alleles: T/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.54	0.017	0.005	0.00086	71,645	0.59
Component 2: UKBB	0.53	0.025	0.005	3.8x10^{-6}	67,786	N/A
European ancestry meta-analysis	0.54	0.021	0.004	1.9x10^{-8}	139,431	0.32
Component 3: non-European ancestry	0.86	0.000	0.021	1.0	10,103	0.054
Trans-ancestry meta-analysis	0.56	0.020	0.004	3.2x10^{-8}	149,534	0.65

Locus: *HMGA2*. Lead SNP: rs1351394. Effect/other alleles: T/C.

Analysis	EAF	B	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.50	0.048	0.005	7.6x10^{-21}	75,885	0.40
Component 2: UKBB	0.49	0.039	0.005	3.1x10^{-13}	67,786	N/A
European ancestry meta-analysis	0.49	0.044	0.004	1.9x10^{-32}	143,671	0.24
Component 3: non-European ancestry	0.34	0.033	0.015	0.028	10,102	0.75
Trans-ancestry meta-analysis	0.48	0.043	0.004	2.0x10^{-33}	153,773	0.72

Locus: *IGF1*. Lead SNP: rs7964361. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.08	0.038	0.009	$5.6x10^{-5}$	71,642	0.63
Component 2: UKBB	0.09	0.040	0.010	$2.3x10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.09	0.039	0.007	$4.7x10^{-9}$	139,428	0.86
Component 3: non-European ancestry	0.03	-0.010	0.040	0.81	9,264	0.21
Trans-ancestry meta-analysis	0.08	0.038	0.007	$9.7x10^{-9}$	148,692	0.20

Locus: *LINC00332*. Lead SNP: rs2324499. Effect/other alleles: G/C.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.68	0.026	0.006	$7.9x10^{-6}$	71,639	0.25
Component 2: UKBB	0.67	0.018	0.006	0.0019	67,786	N/A
European ancestry meta-analysis	0.68	0.022	0.004	$7.3x10^{-8}$	139,425	0.34
Component 3: non-European ancestry	0.60	0.034	0.016	0.027	8,655	0.41
Trans-ancestry meta-analysis	0.67	0.023	0.004	$8.3x10^{-9}$	148,080	0.64

Locus: *RB1*. Lead SNP: rs2854355. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.28	0.024	0.006	0.00012	69,775	0.036
Component 2: UKBB	0.26	0.023	0.006	0.00024	67,786	N/A
European ancestry meta-analysis	0.27	0.023	0.004	$9.8x10^{-8}$	137,561	0.91
Component 3: non-European ancestry	0.19	0.037	0.020	0.066	8,654	0.86
Trans-ancestry meta-analysis	0.26	0.024	0.004	$2.2x10^{-8}$	146,215	0.63

Locus: *RNF219-AS1*. Lead SNP: rs1819436. Effect/other alleles: C/T.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.86	0.041	0.008	$2.4x10^{-7}$	71,193	0.19
Component 2: UKBB	0.88	0.024	0.008	0.0030	67,786	N/A
European ancestry meta-analysis	0.87	0.033	0.006	$6.3x10^{-9}$	138,979	0.14
Component 3: non-European ancestry	0.84	0.033	0.021	0.12	8,654	0.96
Trans-ancestry meta-analysis	0.87	0.033	0.005	$1.8x10^{-9}$	147,633	0.80

Locus: *FES*. Lead SNP: rs12906125. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.69	0.020	0.006	0.00036	73,495	0.92
Component 2: UKBB	0.67	0.025	0.006	$1.1x10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.68	0.023	0.004	$1.7x10^{-8}$	141,281	0.55
Component 3: non-European ancestry	0.75	0.018	0.017	0.30	10,103	0.87
Trans-ancestry meta-analysis	0.69	0.023	0.004	$1.0x10^{-8}$	151,384	0.75

Locus: *IGF1R*. Lead SNP: rs7402982. Effect/other alleles: A/G.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.43	0.022	0.005	$4.9x10^{-5}$	71,637	0.24
Component 2: UKBB	0.41	0.024	0.006	$1.3x10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.43	0.023	0.004	$2.3x10^{-9}$	139,423	0.83
Component 3: non-European ancestry	0.35	0.020	0.017	0.23	10,103	0.61
Trans-ancestry meta-analysis	0.42	0.023	0.004	$1.1x10^{-9}$	149,526	0.61

Locus: *GPR139*. Lead SNP: rs1011939. Effect/other alleles: G/A.

Analysis	EAF	β	SE	*P*-value	*N*	*Q P*-value
Component 1: European ancestry	0.31	0.022	0.006	0.00013	75,818	0.93
Component 2: UKBB	0.28	0.022	0.006	0.00030	67,786	N/A
European ancestry meta-analysis	0.30	0.022	0.004	$1.3x10^{-7}$	143,604	0.97
Component 3: non-European ancestry	0.57	0.047	0.015	0.0013	10,098	0.52
Trans-ancestry meta-analysis	0.31	0.024	0.004	$2.7x10^{-9}$	153,702	0.66

Locus: *CLDN7*. Lead SNP: rs113086489. Effect/other alleles: T/C.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.57	0.033	0.005	7.1×10^{-10}	71,640	0.10
Component 2: UKBB	0.55	0.028	0.005	2.6×10^{-7}	67,786	N/A
European ancestry meta-analysis	0.56	0.031	0.004	9.1×10^{-16}	139,426	0.51
Component 3: non-European ancestry	0.40	0.012	0.015	0.40	10,104	0.29
Trans-ancestry meta-analysis	0.55	0.030	0.004	1.3×10^{-15}	149,530	0.77

Locus: *SUZ12P1-CRLF3*. Lead SNP: rs144843919. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.97	0.036	0.018	0.0048	53,571	0.13
Component 2: UKBB	0.96	0.087	0.015	1.0×10^{-8}	67,786	N/A
European ancestry meta-analysis	0.96	0.066	0.012	1.4×10^{-8}	121,357	0.033
Component 3: non-European ancestry	0.96	0.112	0.049	0.022	6,635	0.056
Trans-ancestry meta-analysis	0.96	0.068	0.011	1.5×10^{-9}	127,992	0.068

Locus: *SP6-SP2*. Lead SNP: rs12942207. Effect/other alleles: C/T.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.31	0.025	0.006	2.2×10^{-5}	71,635	0.85
Component 2: UKBB	0.30	0.020	0.006	0.00063	67,786	N/A
European ancestry meta-analysis	0.30	0.022	0.004	5.1×10^{-8}	139,421	0.59
Component 3: non-European ancestry	0.26	0.050	0.018	0.0053	8,654	0.98
Trans-ancestry meta-analysis	0.30	0.024	0.004	3.0×10^{-9}	148,075	0.75

Locus: *ACTL9*. Lead SNP: rs61154119. Effect/other alleles: T/G.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.84	0.030	0.007	6.4×10^{-5}	63,412	0.00014
Component 2: UKBB	0.85	0.026	0.007	0.00050	67,786	N/A
European ancestry meta-analysis	0.84	0.028	0.005	1.1×10^{-7}	131,198	0.70
Component 3: non-European ancestry	0.79	0.033	0.018	0.077	8,655	0.64
Trans-ancestry meta-analysis	0.84	0.028	0.005	2.3×10^{-8}	139,853	0.98

Locus: *PEPD*. Lead SNP: rs10402712. Effect/other alleles: A/G.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.25	0.021	0.006	0.00033	71,642	0.23
Component 2: UKBB	0.26	0.022	0.006	0.00042	67,786	N/A
European ancestry meta-analysis	0.26	0.022	0.004	4.4×10^{-7}	139,428	0.98
Component 3: non-European ancestry	0.40	0.038	0.014	0.0086	10,102	0.89
Trans-ancestry meta-analysis	0.27	0.023	0.004	2.3×10^{-8}	149,530	0.72

Locus: *JAG1*. Lead SNP: rs6040076. Effect/other alleles: C/G.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.48	0.023	0.005	3.1×10^{-5}	71,638	0.82
Component 2: UKBB	0.51	0.023	0.005	1.8×10^{-5}	67,786	N/A
European ancestry meta-analysis	0.49	0.023	0.004	2.0×10^{-9}	139,424	0.96
Component 3: non-European ancestry	0.69	-0.006	0.018	0.73	8,655	0.026
Trans-ancestry meta-analysis	0.51	0.022	0.004	7.2×10^{-9}	148,079	0.24

Locus: *C20orf203*. Lead SNP: rs28530618. Effect/other alleles: A/G.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.50	0.032	0.005	5.0×10^{-9}	70,376	0.45
Component 2: UKBB	0.47	0.020	0.005	0.00015	67,786	N/A
European ancestry meta-analysis	0.49	0.026	0.004	7.7×10^{-12}	138,162	0.14
Component 3: non-European ancestry	0.63	-0.011	0.016	0.50	10,102	0.25
Trans-ancestry meta-analysis	0.50	0.024	0.004	8.4×10^{-11}	148,264	0.18

Locus: *MAFB*. Lead SNP: rs6016377. Effect/other alleles: T/C.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.41	0.028	0.005	$3.8x10^{-7}$	71,639	0.10
Component 2: UKBB	0.45	0.020	0.006	0.00043	67,786	N/A
European ancestry meta-analysis	0.43	0.024	0.004	$9.5x10^{-10}$	139,425	0.29
Component 3: non-European ancestry	0.74	0.025	0.018	0.17	10,103	0.26
Trans-ancestry meta-analysis	0.45	0.024	0.004	$3.7x10^{-10}$	149,528	0.27

Locus: *NRIP1*. Lead SNP: rs2229742. Effect/other alleles: G/C.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.85	0.037	0.008	$6.6x10^{-6}$	75,886	0.66
Component 2: UKBB	0.90	0.034	0.009	$9.1x10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.87	0.036	0.006	$2.2x10^{-9}$	143,672	0.82
Component 3: non-European ancestry	0.82	-0.085	0.044	0.052	9,264	0.72
Trans-ancestry meta-analysis	0.87	0.034	0.006	$1.5x10^{-8}$	152,936	0.092

Locus: *KREMEN1*. Lead SNP: rs134594. Effect/other alleles: C/T.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.35	0.022	0.006	$8.9x10^{-5}$	69,554	0.36
Component 2: UKBB	0.35	0.023	0.006	$3.2x10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.35	0.023	0.004	$1.0x10^{-8}$	137,340	0.84
Component 3: non-European ancestry	0.33	0.002	0.016	0.90	8,655	0.59
Trans-ancestry meta-analysis	0.35	0.022	0.004	$2.2x10^{-8}$	145,995	0.25

Locus: *SREBF2*. Lead SNP: rs62240962. Effect/other alleles: C/T.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.91	0.054	0.010	$2.6x10^{-8}$	68,286	0.69
Component 2: UKBB	0.92	0.040	0.010	$6.0x10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.91	0.047	0.007	$9.7x10^{-12}$	136,072	0.30
Component 3: non-European ancestry	0.97	0.07	0.048	0.15	7,815	0.028
Trans-ancestry meta-analysis	0.92	0.047	0.007	$3.7x10^{-12}$	143,887	0.69

Locus: *PLAC1*. Lead SNP: rs11096402. Effect/other alleles: G/A.

Analysis	**EAF**	**β**	**SE**	***P*-value**	***N***	***Q P*-value**
Component 1: European ancestry	0.28	0.027	0.007	$2.0x10^{-4}$	37,417	0.73
Component 2: UKBB	0.24	0.028	0.006	$1.8x10^{-6}$	57,620	N/A
European ancestry meta-analysis	0.25	0.028	0.005	$1.3x10^{-9}$	95,037	0.31
Component 3: non-European ancestry	N/A	N/A	N/A	N/A	N/A	N/A
Trans-ancestry meta-analysis	N/A	N/A	N/A	N/A	N/A	N/A

PLAC1 result (on X chromosome) was not available in non-European ancestry studies.

EAF, effect allele frequency; SE, standard error.

Supplementary Table 4. Summary statistics for lead SNPs attaining genome-wide significant evidence ($P<5\times10^{-8}$) of association with BW in European ancestry meta-analysis of up to 143,677 individuals and/or trans-ancestry meta-analysis of up to 153,781 individuals.

Locus	SNP	Chr	Position (b37, bp)	Alleles		EAF	European ancestry		Trans-ancestry		Status[a]	EUR r^2 with lead TA	Present in HapMap?	Best proxy in HapMap	
				Effect	Other		β (SE)	*P*-value	β (SE)	*P*-value				SNP	EUR r^2
WNT4-ZBTB40	rs2473248	1	22,536,643	C	T	0.87	0.033 (0.006)	1.1×10^{-8}	0.033 (0.005)	1.1×10^{-9}	TA/EUR		No	rs2744726	0.99
ZBTB7B	rs3753639	1	154,986,091	C	T	0.24	0.031 (0.004)	7.3×10^{-12}	0.031 (0.004)	1.3×10^{-12}	TA/EUR		No	rs905938	0.77
FCGR2B	rs72480273	1	161,644,871	C	A	0.17	0.031 (0.005)	8.0×10^{-10}	0.030 (0.005)	1.5×10^{-9}	TA/EUR		No	rs17413015	0.97
DTL	rs61830764	1	212,289,976	A	G	0.38	0.022 (0.004)	5.6×10^{-8}	0.022 (0.004)	4.5×10^{-8}	TA		No	rs1387815	0.51
ATAD2B	rs7575873	2	23,962,647	A	G	0.88	0.038 (0.006)	1.3×10^{-11}	0.036 (0.006)	6.2×10^{-11}	TA		No	rs718139	0.98
	rs181211713	2	23,965,445	G	A	0.87	0.038 (0.006)	1.2×10^{-11}	0.036 (0.005)	7.3×10^{-11}	EUR	0.94	No		
EPAS1	rs1374204	2	46,484,205	T	C	0.70	0.047 (0.004)	6.2×10^{-29}	0.046 (0.004)	1.5×10^{-29}	TA		Yes		
	rs17034876	2	46,484,310	T	C	0.70	0.047 (0.004)	2.6×10^{-29}	0.046 (0.004)	1.9×10^{-29}	EUR	0.99	Yes		
PTH1R	rs2242116	3	46,941,116	A	G	0.38	0.022 (0.004)	1.4×10^{-8}	0.021 (0.004)	1.2×10^{-8}	TA		Yes		
	rs2168443	3	46,947,087	T	A	0.38	0.023 (0.004)	3.5×10^{-9}	0.021 (0.004)	1.3×10^{-8}	EUR	0.99	Yes		
ADCY5	rs11719201	3	123,068,744	T	C	0.23	0.046 (0.004)	2.4×10^{-26}	0.046 (0.004)	6.4×10^{-27}	TA/EUR		No	rs7613951	0.97
	rs9883204	3	123,096,820	T	C	0.25	0.041 (0.004)	8.4×10^{-22}	0.040 (0.004)	6.1×10^{-22}	Previous	0.85	Yes		
CPA3	rs10935733	3	148,622,968	T	C	0.41	0.022 (0.004)	9.2×10^{-9}	0.023 (0.004)	6.2×10^{-10}	TA/EUR		No	rs12496367	0.81
CCNL1-LEKR1	rs13322435	3	156,795,468	A	G	0.60	0.053 (0.004)	3.7×10^{-41}	0.052 (0.004)	1.3×10^{-42}	TA		Yes		
	rs900399	3	156,798,732	A	G	0.61	0.052 (0.004)	2.2×10^{-41}	0.051 (0.004)	2.9×10^{-41}	EUR	0.92	Yes		
	rs900400	3	156,798,775	T	C	0.61	0.053 (0.004)	1.1×10^{-40}	0.051 (0.004)	8.4×10^{-41}	Previous	0.92	Yes		
LCORL	rs925098	4	17,919,811	G	A	0.27	0.034 (0.004)	5.4×10^{-16}	0.032 (0.004)	1.3×10^{-15}	TA		Yes		
	rs2724475	4	17,946,432	T	C	0.27	0.034 (0.004)	5.3×10^{-16}	0.032 (0.004)	1.3×10^{-15}	EUR	0.97	Yes		
	rs724577	4	17,993,410	A	C	0.27	0.033 (0.004)	1.7×10^{-15}	0.031 (0.004)	1.5×10^{-14}	Previous	0.98	Yes		

Locus	**SNP**	**Chr**	**Position (b37, bp)**	**Alleles**		**EAF**	**European ancestry**		**Trans-ancestry**		**Status**[a]	**EUR r^2 with lead TA**	**Present in HapMap?**	**Best proxy in HapMap**	
				Effect	**Other**		**β (SE)**	***P*-value**	**β (SE)**	***P*-value**				**SNP**	**EUR r^2**
HHIP	rs6537307	4	145,601,863	G	A	0.50	0.025 (0.004)	9.5x10^{-12}	0.026 (0.004)	1.3x10^{-12}	TA		Yes		
	rs2131354	4	145,599,908	A	G	0.53	0.026 (0.004)	4.1x10^{-12}	0.026 (0.004)	2.3x10^{-12}	EUR	0.88	No		
5q11.2	rs854037	5	57,091,783	A	G	0.81	0.027 (0.005)	2.2x10^{-8}	0.025 (0.005)	3.5x10^{-8}	TA/EUR		Yes		
	rs4432842	5	57,172,078	T	C	0.70	0.021 (0.004)	3.4x10^{-7}	0.019 (0.004)	7.0x10^{-7}	Previous	0.47	Yes		
EBF1	rs7729301	5	157,886,953	A	G	0.73	0.024 (0.004)	1.6x10^{-8}	0.025 (0.004)	1.3x10^{-9}	TA		No	rs2946164	0.97
	rs2946179	5	157,886,627	C	T	0.73	0.024 (0.004)	1.3x10^{-8}	0.024 (0.004)	1.5x10^{-9}	EUR	0.98	No		
CDKAL1	rs35261542	6	20,675,792	C	A	0.73	0.044 (0.004)	4.4x10^{-27}	0.044 (0.004)	9.7x10^{-29}	TA/EUR		No	rs7756992	0.97
	rs6931514	6	20,703,952	A	G	0.73	0.043 (0.004)	6.2x10^{-26}	0.043 (0.004)	1.0x10^{-26}	Previous	0.94	Yes		
HIST1H2BE	rs9379832	6	26,186,200	A	G	0.70	0.023 (0.004)	6.6x10^{-8}	0.024 (0.004)	1.2x10^{-8}	TA		No	rs806794	0.62
HMGA1	rs7742369	6	34,165,721	G	A	0.18	0.028 (0.005)	1.0x10^{-8}	0.027 (0.005)	1.1x10^{-8}	TA		Yes		
	rs1187118	6	34,169,020	A	T	0.17	0.030 (0.005)	3.6x10^{-9}	0.027 (0.005)	1.4x10^{-8}	EUR	0.95	No		
L3MBTL3	rs1415701	6	130,345,835	G	A	0.74	0.025 (0.004)	2.6x10^{-9}	0.027 (0.004)	4.0x10^{-11}	TA/EUR		Yes		
ESR1	rs1101081	6	152,032,917	C	T	0.72	0.038 (0.004)	1.6x10^{-19}	0.037 (0.004)	6.1x10^{-20}	TA		No	rs851977	0.99
	rs10872678	6	152,039,964	T	C	0.72	0.038 (0.004)	6.9x10^{-20}	0.036 (0.004)	1.3x10^{-19}	EUR	0.98	Yes		
GNA12	rs798489	7	2,801,803	C	T	0.73	0.023 (0.004)	2.0x10^{-8}	0.024 (0.004)	5.0x10^{-9}	TA		Yes		
	rs798498	7	2,795,882	T	G	0.69	0.023 (0.004)	1.3x10^{-8}	0.022 (0.004)	3.8x10^{-8}	EUR	0.83	Yes		
IGF2BP3	rs11765649	7	23,479,013	T	C	0.75	0.027 (0.004)	5.8x10^{-10}	0.026 (0.004)	1.0x10^{-9}	TA/EUR		No	rs12540730	0.86
TBX20	rs6959887	7	35,295,365	A	G	0.61	0.023 (0.004)	1.5x10^{-9}	0.021 (0.004)	1.0x10^{-8}	TA/EUR		Yes		
YKT6-GCK	rs138715366	7	44,246,271	C	T	0.99	0.241 (0.023)	7.2x10^{-26}	0.244 (0.023)	1.4x10^{-26}	TA/EUR		No	rs2908277	0.096
MLXIPL	rs62466330	7	73,056,805	C	T	0.07	0.049 (0.008)	1.2x10^{-10}	0.051 (0.007)	5.9x10^{-12}	TA		No	rs17401675	1
	rs111778406	7	72,957,570	G	A	0.07	0.049 (0.008)	5.8x10^{-11}	0.050 (0.007)	1.3x10^{-11}	EUR	0.78	No		

Locus	SNP	Chr	Position	Alleles		EAF	European ancestry		Trans-ancestry		Status^a	EUR r^2 with lead TA	Present in HapMap?	Best proxy in HapMap	
			(b37, bp)	Effect	Other		β (SE)	*P*-value	β (SE)	*P*-value				SNP	EUR r^2
ANK1-NKX6.3	rs13266210	8	41,533,514	A	G	0.79	0.031 (0.005)	1.3x10^{-11}	0.030 (0.004)	1.6x10^{-11}	TA/EUR		Yes		
TRIB1	rs6989280	8	126,508,746	G	A	0.73	0.022 (0.004)	2.2x10^{-7}	0.022 (0.004)	5.0x10^{-8}	TA		Yes		
SLC45A4	rs12543725	8	142,247,979	G	A	0.59	0.023 (0.004)	1.2x10^{-9}	0.022 (0.004)	1.9x10^{-9}	TA/EUR		Yes		
PTCH1	rs28510415	9	98,245,026	G	A	0.09	0.056 (0.007)	1.5x10^{-17}	0.053 (0.006)	4.0x10^{-16}	TA		No	rs3824488	1
	rs3780573	9	98,239,503	A	G	0.10	0.055 (0.006)	7.0x10^{-18}	0.050 (0.006)	1.1x10^{-15}	EUR	1.00	No		
LPAR1	rs2150052	9	113,945,067	T	A	0.50	0.021 (0.004)	2.2x10^{-8}	0.020 (0.004)	2.8x10^{-8}	TA		Yes		
	rs1411424	9	113,892,963	A	G	0.52	0.021 (0.004)	2.2x10^{-8}	0.020 (0.004)	4.1x10^{-8}	EUR	0.86	Yes		
PHF19	rs7847628	9	123,631,225	G	A	0.68	0.023 (0.004)	1.0x10^{-8}	0.023 (0.004)	5.4x10^{-9}	TA		Yes	rs1056567	0.87
	rs4836833	9	123,632,829	C	G	0.67	0.023 (0.004)	8.6x10^{-9}	0.022 (0.004)	1.5x10^{-8}	EUR	0.88	Yes		
STRBP	rs700059	9	125,824,055	G	A	0.14	0.033 (0.005)	4.7x10^{-10}	0.036 (0.005)	1.2x10^{-12}	TA		Yes		
	rs10818797	9	126,020,405	C	T	0.14	0.035 (0.005)	1.2x10^{-10}	0.035 (0.005)	1.5x10^{-11}	EUR	0.91	Yes		
HHEX-IDE	rs61862780	10	94,468,643	T	C	0.51	0.028 (0.004)	3.0x10^{-14}	0.028 (0.004)	9.5x10^{-15}	TA		No	rs2497306	0.97
	rs2497304	10	94,492,716	C	T	0.52	0.028 (0.004)	2.6x10^{-14}	0.028 (0.004)	1.4x10^{-14}	EUR	0.90	Yes		
NT5C2	rs74233809	10	104,913,940	C	T	0.08	0.037 (0.007)	5.2x10^{-8}	0.039 (0.006)	1.8x10^{-9}	TA		No	rs11191582	1
	rs79237883	10	104,940,946	C	T	0.08	0.037 (0.007)	3.6x10^{-8}	0.038 (0.006)	5.6x10^{-9}	EUR	1.00	No		
ADRB1	rs7076938	10	115,789,375	T	C	0.73	0.036 (0.004)	4.7x10^{-18}	0.035 (0.004)	4.7x10^{-18}	TA		Yes		
	rs740746	10	115,792,787	A	G	0.73	0.036 (0.004)	3.8x10^{-18}	0.035 (0.004)	6.4x10^{-18}	EUR	0.99	Yes		
	rs1801253	10	115,805,056	C	G	0.71	0.032 (0.004)	3.0x10^{-14}	0.031 (0.004)	2.6x10^{-14}	Previous	0.99	Yes		
PLEKHA1	rs2421016	10	124,167,512	T	C	0.49	0.021 (0.004)	1.8x10^{-8}	0.021 (0.004)	6.1x10^{-9}	TA/EUR		Yes		
INS-IGF2	rs72851023	11	2,130,620	T	C	0.07	0.048 (0.008)	2.9x10^{-10}	0.046 (0.007)	6.8x10^{-10}	TA/EUR		No	rs868332	0.49
MTNR1B	rs10830963	11	92,708,710	G	C	0.28	0.023 (0.004)	2.9x10^{-8}	0.022 (0.004)	1.0x10^{-7}	EUR		Yes		

Locus	**SNP**	**Chr**	**Position (b37, bp)**	**Alleles**		**EAF**	**European ancestry**		**Trans-ancestry**		**Status**[a]	**EUR r^2 with lead TA**	**Present in HapMap?**	**Best proxy in HapMap**	
				Effect	**Other**		**β (SE)**	***P*-value**	**β (SE)**	***P*-value**				**SNP**	**EUR r^2**
APOLD1	rs11055034	12	12,890,626	C	A	0.73	0.022 (0.004)	1.8×10^{-7}	0.023 (0.004)	2.3×10^{-8}	TA		Yes		
ABCC9	rs139975827	12	22,068,161	G	A	0.62	0.025 (0.004)	1.1×10^{-8}	0.022 (0.004)	1.0×10^{-7}	EUR		No	rs4148656	0.67
ITPR2	rs12823128	12	26,872,730	T	C	0.54	0.021 (0.004)	1.9×10^{-8}	0.020 (0.004)	3.2×10^{-8}	TA		Yes		
	rs2306547	12	26,877,885	C	T	0.54	0.021 (0.004)	1.8×10^{-8}	0.020 (0.004)	3.2×10^{-8}	EUR	0.96	Yes		
HMGA2	rs1351394	12	66,351,826	T	C	0.49	0.044 (0.004)	1.9×10^{-32}	0.043 (0.004)	2.0×10^{-33}	TA/EUR		Yes		
	rs1042725	12	66,358,347	C	T	0.51	0.043 (0.004)	3.1×10^{-32}	0.042 (0.004)	7.1×10^{-32}	Previous	0.93	Yes		
IGF1	rs7964361	12	102,994,878	A	G	0.09	0.039 (0.007)	4.7×10^{-9}	0.038 (0.007)	9.7×10^{-9}	TA/EUR		Yes		
LINC00332	rs2324499	13	40,662,001	G	C	0.68	0.022 (0.004)	7.3×10^{-8}	0.023 (0.004)	8.3×10^{-9}	TA		Yes		
	rs7998537	13	40,662,742	G	A	0.68	0.022 (0.004)	3.9×10^{-8}	0.022 (0.004)	1.8×10^{-8}	EUR	1.00	Yes		
RB1	rs2854355	13	48,882,363	G	A	0.27	0.023 (0.004)	9.8×10^{-8}	0.024 (0.004)	2.2×10^{-8}	TA		No	rs9568028	0.88
	rs34217484	13	48,854,550	A	T	0.26	0.024 (0.004)	4.8×10^{-8}	0.023 (0.004)	5.8×10^{-8}	EUR	0.85	No		
RNF219-AS1	rs1819436	13	78,580,283	C	T	0.87	0.033 (0.006)	6.3×10^{-9}	0.033 (0.005)	1.8×10^{-9}	TA/EUR		No	rs944379	0.88
FES	rs12906125	15	91,427,612	G	A	0.68	0.023 (0.004)	1.7×10^{-8}	0.023 (0.004)	1.0×10^{-8}	TA/EUR		No	rs6227	0.87
IGF1R	rs7402982	15	99,193,269	A	G	0.43	0.023 (0.004)	2.3×10^{-9}	0.023 (0.004)	1.1×10^{-9}	TA/EUR		No	rs8028620	0.55
GPR139	rs1011939	16	19,992,996	G	A	0.30	0.022 (0.004)	1.3×10^{-7}	0.024 (0.004)	2.7×10^{-9}	TA		No	rs1858988	0.70
CLDN7	rs113086489	17	7,171,356	T	C	0.56	0.031 (0.004)	9.1×10^{-16}	0.030 (0.004)	1.3×10^{-15}	TA/EUR		No	rs5417	0.80
SUZ12P1-CRLF3	rs144843919	17	29,037,339	G	A	0.97	0.066 (0.012)	1.4×10^{-8}	0.068 (0.011)	1.5×10^{-9}	TA/EUR		No	rs8073965	0.22
SP6-SP2	rs12942207	17	45,968,294	C	T	0.30	0.022 (0.004)	5.1×10^{-8}	0.024 (0.004)	3.0×10^{-9}	TA		No	rs11079800	0.91
	rs72833480	17	45,964,861	A	G	0.29	0.023 (0.004)	4.6×10^{-8}	0.023 (0.004)	2.1×10^{-8}	EUR	0.94	No		
ACTL9	rs61154119	19	8,787,750	T	G	0.84	0.028 (0.005)	1.1×10^{-7}	0.028 (0.005)	2.3×10^{-8}	TA		No	rs2967684	1
PEPD	rs10402712	19	33,926,013	A	G	0.26	0.022 (0.004)	4.4×10^{-7}	0.023 (0.004)	2.3×10^{-8}	TA		No	rs17833935	0.54

Locus	**SNP**	**Chr**	**Position**	**Alleles**		**EAF**	**European ancestry**		**Trans-ancestry**		**Status**[a]	**EUR r^2 with lead TA**	**Present in HapMap?**	**Best proxy in HapMap**	
			(b37, bp)	**Effect**	**Other**		**β (SE)**	***P*-value**	**β (SE)**	***P*-value**				**SNP**	**EUR r^2**
JAG1	rs6040076	20	10,658,882	C	G	0.49	0.023 (0.004)	$2.0\text{x}10^{-9}$	0.022 (0.004)	$7.2\text{x}10^{-9}$	TA/EUR		No	rs2206815	0.85
C20orf203	rs28530618	20	31,275,581	A	G	0.49	0.026 (0.004)	$7.7\text{x}10^{-12}$	0.024 (0.004)	$8.4\text{x}10^{-11}$	TA/EUR		No	rs6057610	0.82
MAFB	rs6016377	20	39,172,728	T	C	0.43	0.024 (0.004)	$9.5\text{x}10^{-10}$	0.024 (0.004)	$3.7\text{x}10^{-10}$	TA/EUR		Yes		
NRIP1	rs2229742	21	16,339,172	G	C	0.87	0.036 (0.006)	$2.2\text{x}10^{-9}$	0.034 (0.006)	$1.5\text{x}10^{-8}$	TA/EUR		Yes		
KREMEN1	rs134594	22	29,468,456	C	T	0.35	0.023 (0.004)	$1.0\text{x}10^{-8}$	0.022 (0.004)	$2.2\text{x}10^{-8}$	TA/EUR		Yes		
SREBF2	rs62240962	22	42,259,524	C	T	0.91	0.047 (0.007)	$9.7\text{x}10^{-12}$	0.047 (0.007)	$3.7\text{x}10^{-12}$	TA/EUR		No	rs10483213	0.70
PLAC1	rs11096402	X	133,827,868	G	A	0.28	0.028 (0.005)	$1.3\text{x}10^{-9}$	N/A	N/A	EUR		Yes		

Chr, chromosome; bp, base pair; EAF, effect allele frequency; SE, standard error.

[a] Status indicates whether the SNP was lead in European ancestry (EUR) or trans-ancestry (TA) meta-analysis. Previous denotes previously reported lead SNP[5] at established loci.

Supplementary Table 5. Loci with multiple distinct association signals attaining genome-wide significance (*P*<5x10^{-8}) in approximate conditional meta-analysis of 143,677 individuals of European ancestry, using 5,000 white British participants from UK BioBank as a reference for linkage disequilibrium.

Locus	Index variant	Chr	Position (b37, bp)	Alleles	EAF	Unconditional meta-analysis		Conditional meta-analysis			UKBB reference r^2	Present in HapMap?	Best proxy in HapMap	
				Effect/ Other		β (SE)	*P*-value	Conditioned on	β (SE)	*P*-value			SNP	EUR r^2
ZBTB7B	rs3753639	1	154,986,091	C/T	0.24	0.031 (0.004)	7.3x10^{-12}	rs4330912	0.034 (0.005)	2.2x10^{-14}	0.019	No	rs905938	0.77
	rs4330912	1	155,969,428	G/C	0.64	0.021 (0.004)	1.8x10^{-7}	rs3753639	0.025 (0.004)	5.4x10^{-10}		No	rs12043212	0.93
HMGA1	rs9368777	6	33,788,637	C/G	0.58	0.022 (0.004)	2.2x10^{-8}	rs1187118	0.021 (0.004)	3.3x10^{-8}	0.000	No	rs4304152	0.57
	rs1187118	6	34,169,020	A/T	0.17	0.030 (0.005)	3.6x10^{-9}	rs9368777	0.030 (0.005)	5.4x10^{-9}		No	rs1776877	0.95
PTCH1	rs12551019	9	96,949,079	C/T	0.68	0.022 (0.004)	3.1x10^{-8}	rs3780573	0.024 (0.004)	5.1x10^{-9}	0.001	Yes		
	rs3780573	9	98,239,503	A/G	0.10	0.055 (0.006)	7.0x10^{-18}	rs12551019	0.057 (0.006)	1.2x10^{-18}		No	rs3824488	1.00

Chr, chromosome; bp, base pair; EAF, effect allele frequency; SE, standard error.

Supplementary Table 6. Candidate gene(s) at birth weight loci.

Locus	Lead SNP	Chr	Position (b37)	Candidate gene(s) in the locus[a]	Reports on eQTL[b]	Literature search for nearby genes (300kb)	Coding variants (EUR r^2 with the lead SNP)
WNT4-ZBTB40	rs2473248	1	22,536,643	*WNT4[P,N], CDC42[B]*	*WNT4:* Cerebellum and temporal cortex eQTL; *CDC42:* Whole blood eQTL (proxy SNP)		-
ZBTB7B	rs3753639	1	154,986,091	*SHC1[B], S100A7[P]*		*SHC1*: The Shc adaptor proteins are key transducers of growth promotion and gene expression, and are phosphorylated by all known receptor tyrosine.	-
FCGR2B	rs72480273	1	161,644,871	*ATF6[B], APOA2[P], FCGR2B[N]*	*ATF6:* Cerebellum and temporal cortex eQTL; *FCGR2B:* Whole blood, cerebellum and temporal cortex eQTL	*HSPA6*: higher expression of HSPA6 in placental vascular disease (PVD) vs controls; HSPA6 encodes HSP70 which was found to be upregulated in PVD vs control placenta and microvascular endothelial cells. HSP70 mRNA and protein expression also correlated negatively with infant birth weight (PMID:18372927).	-
DTL	rs61830764	1	212,289,976	*DTL[N]*			-
ATAD2B	rs7575873	2	23,962,647	*ATAD2B[N], FKBP1B[P]*	*PFN4:* Lymphoblastoid eQTL		-
EPAS1	rs1374204	2	46,484,205	*RHOQ[B], SOCS5[P]*	*EPAS1, PRKCE*: Cerebellum and temporal cortex eQTL	*EPAS1*: involved in the hypoxic response and is suggested to be responsible for the genetic adaptation of high-altitude hypoxia in Tibetans. PMID 25501874 found associations of 2 variants with BW in small sample-sized Tibetans.	-
PTH1R	rs2242116	3	46,941,116	*PTH1R[B,N], CCR1[P]*	*CCDC12:* Whole blood, cerebellum and temporal cortex eQTL		-
ADCY5	rs11719201	3	123,068,744	*ADCY5[B,N], HCLS1[P]*	*ADCY5:* Cerebellum and temporal cortex eQTL (proxy SNP)		-
CPA3	rs10935733	3	148,622,968	*AGTR1[B,P]*	*CPA3,CPB1: eQTL* (proxy SNP)	*AGTR1* = angiotensin II receptor gene: good candidate as the protein mediates processes important for placentation. Levels of protein higher in umbilical cord and maternal peripheral blood in preeclampsia than in controls; levels of mRNA higher in placenta of preeclampsia than control pregnancies; birth weight negatively correlated with levels in cord (PMID 23302726).	-
CCNL1-LEKR1	rs13322435	3	156,795,468	*LEKR1[N], IL12A[P]*	*LEKR1:* Temporal cortex eQTL; CCNL1: Whole blood, cerebellum and temporal cortex eQTL		-
LCORL	rs925098	4	17,919,811	*LCORL[N], SLIT2[P]*	*LCORL:* Cerebellum and temporal cortex eQTL	Adipose tissue and muscle expression in cattle of *NCAPG* and *LCORL* associated with feed intake and weight gain in cattle (these are in a QTL for body weight in cattle).	-
HHIP	rs6537307	4	145,601,863	*HHIP[N], ANAPC10[P]*	*HHIP:* Cerebellum and temporal cortex eQTL		-
5q11.2	rs854037	5	57,091,783	*ACTBL2[N], IL6ST[P]*			-
EBF1	rs7729301	5	157,886,953	*EBF1[N,B], FABP6[P]*			-
CDKAL1	rs35261542	6	20,675,792	*CDKAL1[B], SOX4[P]*	*CDKAL1:* Cerebellum and temporal cortex eQTL		-

Locus	Lead SNP	Chr	Position (b37)	Candidate gene(s) in the locus[a]	Reports on eQTL[b]	Literature search for nearby genes (300kb)	Coding variants (EUR r^2 with the lead SNP)
HIST1H2BE	rs9379832	6	26,186,200	*HIST1H2BE[N,B], BTN2A2[P]*			-
HMGA1	rs7742369	6	34,165,721	*HMGA1[N,B], GRM4[B], MAPK14[P]*	*HMGA1:* Cerebellum and temporal cortex eQTL		-
L3MBTL3	rs1415701	6	130,345,835	*L3MBTL3[E,N], SAMD3[E], ENPP1[P]*	*L3MBTL3, SAMD3:* Whole blood, cerebellum and temporal cortex eQTLs		-
ESR1	rs1101081	6	152,032,917	*ESR1[N,B], LATS1[P]*	*ESR1: M*onocyte, cerebellum and temporal cortex eQTL (for proxy SNP)		-
GNA12	rs798489	7	2,801,803	*GNA12[N,E], PDGFA[N]*	*GNA12:* Nerve tibial, lymphoblastid, whole blood, cerebellum and temporal cortex eQTL		-
IGF2BP3	rs11765649	7	23,479,013	*IGF2BP3[N,B], NPY[P]*	*CCDC126: lymphoblastoid eQTL*		-
TBX20	rs6959887	7	35,295,365	*TBX20[N], SEPT7[P]*	*TBX20:* Cerebellum and temporal cortex eQTL		-
YKT6-GCK	rs138715366	7	44,246,271	*YKT6[N], GCK[B]*		*GCK* mutations reduce birth weight and increase fasting glucose (Hattersley et al 1999, Nat Genet).	-
MLXIPL	rs62466330	7	73,056,805	*MLXIPL[N], FZD9[P]*	*MLXIPL:* Cerebellum and temporal cortex eQTL (for proxy SNP)		-
ANK1-NKX6-3	rs13266210	8	41,533,514	*ANK1[N,B], SFRP1[P]*	*ANK1:* Cerebellum, temporal cortex and lung eQTL		-
TRIB1	rs6989280	8	126,508,746	*TRIB1[N], MYC[P]*	*TRIB1:* Cerebellum and temporal cortex eQTL		-
SLC45A4	rs12543725	8	142,247,979	*SLC45A4[N,E], PTK2[B,P]*	*SLC45A4:* Whole blood, cerebellum and temporal cortex eQTL		-
PTCH1	rs28510415	9	98,245,026	*PTCH1[N,B], FOXE1[P]*	*PTCH1:* Whole blood, cerebellum and temporal cortex eQTL (for proxy SNP)	*FANCC*: mutations result in Fanconi anaemia (associated with low birth weight and shorter stature).	-
LPAR1	rs2150052	9	113,945,067	*LPAR1[N,E,B,P]*	*LPAR1:* whole blood eQTL		-
PHF19	rs7847628	9	123,631,225	*C5[B], DAB2IP[P]*	*C5:* naïve monocyte, whole blood, cerebellum and temporal cortex eQTL		-
STRBP	rs700059	9	125,824,055	*STRBP[E], C5[P]*	*STRBP:* Whole blood, cerebellum and temporal cortex eQTL		-
HHEX-IDE	rs61862780	10	94,468,643	*IDE[B], PLCE1[P]*	*HHEX:* monocyte, whole blood, cerebellum and temporal cortex eQTL		-
NT5C2	rs74233809	10	104,913,940	*NT5C2[N], CHUK[P]*		*CYP17A1*: mutation in maternal *CYP17A1* is associated with small for gestational age (SGA) (PMID 14665706)	-
ADRB1	rs7076938	10	115,789,375	*ADRB1[N,C,B], AFAP1L2[P]*	*ADRB1: cerebellum and temporal cortex eQTL*		rs1801253 (G389R, r^2=0.99, damaging)
PLEKHA1	rs2421016	10	124,167,512	*PLEKHA1[N,E], FGFR2[P]*	*PLEKHA1:* Whole blood, cerebellum and temporal cortex eQTL		-
INS-IGF2	rs72851023	11	2,130,620	*INS-IGF2[N,B,imp]*			-

Locus	Lead SNP	Chr	Position (b37)	Candidate gene(s) in the locus[a]	Reports on eQTL[b]	Literature search for nearby genes (300kb)	Coding variants (EUR r^2 with the lead SNP)
MTNR1B	rs10830963	11	92,708,710	*MTNR1B[N,B,P]*	*MTNR1B:* Cerebellum and temporal cortex eQTL		-
APOLD1	rs11055034	12	12,890,626	*CDKN1B[B,E,P], HEBP1[B]*	*CDKN1B:* Cerebellum and temporal cortex eQTL		-
ABCC9	rs139975827	12	22,068,161	*ABCC9[N], KRAS[P]*			-
ITPR2	rs12823128	12	26,872,730	*ITPR2[N,B]*	*ITPR2:* Cerebellum and temporal cortex eQTL		-
HMGA2	rs1351394	12	66,351,826	*HMGA2[N,B], IRAK3[P]*	*HMGA2:* Cerebellum and temporal cortex eQTL	*HMGA2:* 12q14 microdeletion syndrome implicates *HMGA2* as causal to height (PMID: 17220210 and 19298872).	-
IGF1	rs7964361	12	102,994,878	*IGF1[N,B,P]*			-
LINC00332	rs2324499	13	40,662,001	*LINC00332[N], TNFSF11[P]*			-
RB1	rs2854355	13	48,882,363	*RB1[N,B,P,imp], LPAR6[imp,B]*	*RB1:* Whole blood, cerebellum and temporal cortex eQTL		-
RNF219-AS1	rs1819436	13	78,580,283	*EDNRB[B,P]*	*EDNRB:* Monocyte, cerebellum and temporal cortex eQTL (for proxy SNP)		-
FES	rs12906125	15	91,427,612	*FES[N,E], MESP1[P]*	*FES:* Thyroid, whole blood, cerebellum, temporal cortex and tibial nerve eQTL	*FURIN*: a ubiquitous proprotein convertase, the major processing enzyme of the secretory pathway. It is involved in processing proinsulin to insulin, and in processing proIGF2 (PMID 9660813).	-
IGF1R	rs7402982	15	99,193,269	*IGF1R[B]*			-
GPR139	rs1011939	16	19,992,996	*GPR139[N], RPS15A[P]*			-
CLDN7	rs113086489	17	7,171,356	*SLC2A4[B], POLR2A[S], DVL2[P]*	*SLC2A4:* Cerebellum and temporal cortex eQTL; *DVL2:* monocyte, whole blood, cerebellum and temporal cortex eQTL (for proxy SNP)	*SLC2A4 (GLUT4):* an insulin responsive glucose transporter. PMID 24062248 showed lower mRNA in preadipocytes from LBW vs NBW. Protein level of SLCA24 was lower in adipose tissue of LBW men compared to NMW (PMID 17063325).	-
SUZ12P1-CRLF3	rs144843919	17	29,037,339	*SUZ12P1[N]*			-
SP6-SP2	rs12942207	17	45,968,294	*SP2[N], NGFR[P]*	*SP2:* Whole blood, cerebellum and temporal cortex eQTL (for proxy SNP)		-
ACTL9	rs61154119	19	8,787,750	*ACTL9[N], INSR[P]*			-
PEPD	rs10402712	19	33,926,013	*CEBPA[B]*		*CEBPA:* an adipogenic transcription factor involved in adipocyte differentiation. Expression levels lower in smaller pig fetuses (PMID 21354690).	-
JAG1	rs6040076	20	10,658,882	*JAG1[N], MKKS[P]*	*JAG1:* Cerebellum and temporal cortex eQTL (proxy SNP)	*JAG1* is a ligand that interacts with receptors in the notch signalling pathway. Notch pathway plays an important role during placental development; notch pathway downregulation is associated with preeclampsia, and specifically JAG1 mRNA levels downregulated in preeclampsia placental samples vs controls (PMID 25962154).	-
C20orf203	rs28530618	20	31,275,581	*BAK1P1[E], FOXS1[P]*	*BAK1P1:* thyroid eQTL (for proxy SNP)		-

Locus	Lead SNP	Chr	Position (b37)	Candidate gene(s) in the locus[a]	Reports on eQTL[b]	Literature search for nearby genes (300kb)	Coding variants (EUR r^2 with the lead SNP)
MAFB	rs6016377	20	39,172,728	*MAFB[N], PLCG1[P]*	*MAFB:* Cerebellum and temporal cortex eQTL (for proxy SNP)	Lots of literature on importance of MAFB in transcriptional regulation in embryonic islets, e.g. analysis of Mafa(-/-) and pancreas-specific Mafa(Δpanc) deletion mutant mice demonstrated a primary role for MafA in adult β-cell activity, different from the embryonic importance of MafB (PMID 24520122).	-
NRIP1	rs2229742	21	16,339,172	*NRIP1[N,C], SAMSN1[P]*	*NRIP1:* Cerebellum and temporal cortex eQTL		rs2229742 (R448G, lead SNP, damaging)
KREMEN1	rs134594	22	29,468,456	*KREMEN1[N,E], YWHAH[P]*	*KREMEN1:* Monocyte, heart, whole blood, cerebellum and temporal cortex eQTL		-
SREBF2	rs62240962	22	42,259,524	*SREBF2[N,B], PDGFB[P]*			-
PLAC1	rs11096402	X	133,827,868	*PLAC1[N]*		*PLAC1* shows placenta-specific expression in human (PMID: 10995572). A mutant mouse model showed *PLAC1* as a paternally imprinted, X-linked gene essential for normal placental and embryonic development (PMID: 22729990).	-

[a] B = biological candidate, C = coding variant, E = eQTL (from GTEx), N=nearest, P = best ranked gene in PPI network, imp = imprinted gene.

[b] eQTL reported from GTEx v4, GEUVADIS, and 11 other studies for the lead variant. When there was no eQTL report for the lead variant, eQTL reports for the proxy SNPs (r^2>0.8 with the lead variant) are shown.

Supplementary Table 7. Summary of 99% credible sets at 62 distinct autosomal association signals.

Locus	Index variant	Chr	Position (b37, bp)	MANTRA $\log_{10}$BF	99% credible set		
					Variants	Distance (bp)	Interval (bp)
WNT4-ZBTB40	rs2473248	1	22,536,643	7.68	7	17,534	22,536,643-22,554,176
ZBTB7B	rs3753639	1	154,986,091	12.19	6	22,088	154,984,363-155,006,450
	rs4330912	1	155,969,428	7.93	45	403,839	155,612,197-156,016,035
FCGR2B	rs72480273	1	161,644,871	7.48	37	173,221	161,500,712-161,673,932
DTL	rs61830764	1	212,289,976	6.02	56	702,234	211,830,044-212,532,277
ATAD2B	rs7575873	2	23,962,647	8.87	234	477,824	23,887,437-24,365,260
EPAS1	rs1374204	2	46,484,205	27.22	4	695	46,484,188-46,484,882
PTH1R	rs2242116	3	46,941,116	6.65	54	243,837	46,925,539-47,169,375
ADCY5	rs11719201	3	123,068,744	24.38	6	16,621	123,065,778-123,082,398
CPA3	rs10935733	3	148,622,968	7.91	80	33,654	148,591,725-148,625,378
CCNL1-LEKR1	rs13322435	3	156,795,468	40.24	11	3,265	156,795,468-156,798,732
LCORL	rs925098	4	17,919,811	13.56	15	123,806	17,901,679-18,025,484
HHIP	rs6537307	4	145,601,863	10.43	43	137,679	145,520,608-145,658,286
5q11.2	rs854037	5	57,091,783	5.77	63	276,269	56,906,160-57,182,428
EBF1	rs7729301	5	157,886,953	7.62	50	77380	157,884,706-157,962,085
CDKAL1	rs35261542	6	20,675,792	26.41	7	14,242	20,673,880-20,688,121
HIST1H2BE	rs9379832	6	26,186,200	6.64	5	26,542	26,180,634-26,207,175
HMGA1	rs9368777	6	33,788,637	6.20	91	570,460	33,292,543-33,863,002
	rs1187118	6	34,169,020	6.94	27	148,294	34,095,696-34,243,989
L3MBTL3	rs1415701	6	130,345,835	9.03	2	4,601	130,341,235-130,345,835
ESR1	rs1101081	6	152,032,917	17.69	14	20,968	152,029,556-152,050,523
GNA12	rs798489	7	2,801,803	7.01	114	160,777	2,752,152-2,912,928
IGF2BP3	rs11765649	7	23,479,013	7.58	23	111,149	23,474,687-23,585,835
TBX20	rs6959887	7	35,295,365	6.75	113	109,117	35,196,208-35,305,324
YKT6-GCK	rs138715366	7	44,246,271	24.10	1	1	44,246,271-44,246,271
MLXIPL	rs62466330	7	73,056,805	9.60	102	221,896	72,836,230-73,058,025
ANK1-NKX6-3	rs13266210	8	41,533,514	9.22	17	28,742	41,508,577-41,537,318
TRIB1	rs6989280	8	126,508,746	5.69	39	411,117	126,114,947-126,526,063
SLC45A4	rs12543725	8	142,247,979	7.18	10	13,200	142,239,381-142,252,580
PTCH1	rs12551019	9	96,949,079	6.96	40	652,934	96,900,505-97,553,438
	rs3780573	9	98,239,503	16.44	23	53,294	98,212,608-98,265,901

Locus	Index variant	Chr	Position (b37, bp)	MANTRA $\log_{10}$BF	99% credible set		
					Variants	Distance (bp)	Interval (bp)
LPAR1	rs2150052	9	113,945,067	6.29	60	214,738	113,828,811-114,043,548
PHF19	rs7847628	9	123,631,225	6.95	5	90,924	123,631,225-123,722,148
STRBP	rs700059	9	125,824,055	10.35	135	432,744	125,605,840-126,038,583
HHEX-IDE	rs61862780	10	94,468,643	12.40	31	134,694	94,358,023-94,492,716
NT5C2	rs74233809	10	104,913,940	7.25	98	404,547	104,655,350-105,059,896
ADRB1	rs7076938	10	115,789,375	15.69	4	9,521	115,789,375-115,798,895
PLEKHA1	rs2421016	10	124,167,512	6.90	26	70,596	124,127,990-124,198,585
INS-IGF2	rs72851023	11	2,130,620	7.89	48	145,434	2,078,742-2,224,175
MTNR1B	rs10830963	11	92,708,710	5.78	52	499,464	92,225,858-92,725,321
APOLD1	rs11055034	12	12,890,626	6.33	13	42,180	12,849,241-12,891,420
ABCC9	rs139975827	12	22,068,161	5.64	72	133,773	22,027,182-22,160,954
ITPR2	rs12823128	12	26,872,730	6.12	114	291,548	26,759,026-27,050,573
HMGA2	rs1351394	12	66,351,826	30.74	7	32,282	66,343,810-66,376,091
IGF1	rs7964361	12	102,994,878	6.71	42	213,557	102,867,636-103,081,192
LINC00332	rs2324499	13	40,662,001	6.83	41	95,318	40,583,503-40,678,820
RB1	rs2854355	13	48,882,363	6.23	143	403,044	48,797,661-49,200,704
RNF219-AS1	rs1819436	13	78,580,283	7.44	105	220,228	78,443,297-78,663,524
FES	rs12906125	15	91,427,612	6.68	24	36,382	91,404,705-91,441,086
IGF1R	rs7402982	15	99,193,269	7.59	5	15,682	99,177,595-99,193,276
GPR139	rs1011939	16	19,992,996	7.20	55	53,120	19,992,996-20,461,115
CLDN7	rs113086489	17	7,171,356	13.41	29	84,570	7,101,292-7,185,861
SUZ12P1-CRLF3	rs144843919	17	29,037,339	7.60	21	520,396	28,780,178-29,300,573
SP6-SP2	rs12942207	17	45,968,294	7.04	21	90,685	45,940,310-46,030,994
ACTL9	rs61154119	19	8,787,750	6.24	21	4,455	8,785,744-8,790,198
PEPD	rs10402712	19	33,926,013	6.40	35	218,599	33,784,657-34,003,255
JAG1	rs6040076	20	10,658,882	6.72	43	164,577	10,539,775-10,704,351
C20orf203	rs28530618	20	31,275,581	8.69	63	114,192	31,214,234-31,328,425
MAFB	rs6016377	20	39,172,728	8.15	33	72,001	39,144,286-39,216,286
NRIP1	rs2229742	21	16,339,172	6.69	4	85,250	16,339,172-16,424,421
KREMEN1	rs134594	22	29,468,456	6.41	56	52,177	29,461,150-29,513,326
SREBF2	rs62240962	22	42,259,524	10.01	4	189,151	42,070,374-42,259,524

Chr, chromosome; bp, base pair; BF, Bayes factor.

Supplementary Table 8. BW credible set enrichment for DNaseI hypersensitive sites.

(a) 128 cell-type DHS annotation and 4 genic annotation tested for enrichment individually

Cell type	Lower 95%CI[a]	Effect[a]	Upper 95%CI[a]	Tissue	Category
iPS_6_9	-20.00	0.35	1.74	Stem cell	Stem cell
iPS_4_7	-20.00	0.82	2.04	Stem cell	Stem cell
iPS_19_7	-1.22	0.96	2.09	Stem cell	Stem cell
iPS_19_11	-1.40	0.80	1.93	Stem cell	Stem cell
hESCT0	-0.10	1.26	2.16	Stem cell	Stem cell
HESC	-20.00	0.21	1.79	Stem cell	Stem cell
NPC	0.94	2.14	2.99	Brain	Progenitor cell
HMVEC_dNeo	0.24	1.62	2.54	Neonatal blood vessel	Neonatal
HMVEC_dLyNeo	0.48	1.71	2.58	Neonatal blood vessel	Neonatal
HMVEC_dBlNeo	-0.82	1.00	2.01	Neonatal blood vessel	Neonatal
NHDF_Neo	1.22	2.29	3.12	Skin	Neonatal
fThymus	0.88	1.94	2.75	Foetal thymus	Foetal
fTestes	0.88	1.97	2.79	Foetal testes	Foetal
fStomach	0.40	1.63	2.50	Foetal stomach	Foetal
fSpleen	0.75	1.86	2.68	Foetal spleen	Foetal
fSpinal_cord	0.52	1.58	2.38	Foetal skin	Foetal
fSkin_fibro_upper_back	-0.86	1.43	2.44	Foetal skin	Foetal
fSkin_fibro_scalp	-4.83	1.03	2.17	Foetal skin	Foetal
fSkin_fibro_leg_R_quad	-20.00	0.84	2.11	Foetal skin	Foetal
fSkin_fibro_leg_L_quad	-0.89	1.23	2.25	Foetal skin	Foetal
fSkin_fibro_bicep_R	-20.00	0.73	2.05	Foetal skin	Foetal
fSkin_fibro_bicep_L	-20.00	1.09	2.24	Foetal skin	Foetal
fSkin_fibro_back	-20.00	0.04	1.75	Foetal skin	Foetal
fSkin_fibro_abdomen	-3.50	1.30	2.41	Foetal skin	Foetal
fSkin	-20.00	1.13	2.31	Foetal skin	Foetal
fPlacenta	0.80	1.72	2.49	Foetal placenta	Foetal
fMuscle_upper_trunk	0.70	1.74	2.55	Foetal muscle	Foetal
fMuscle_upper_limb_sk	-0.08	1.43	2.35	Foetal muscle	Foetal
fMuscle_upper_back	0.48	1.70	2.54	Foetal muscle	Foetal
fMuscle_trunk	0.63	1.72	2.54	Foetal muscle	Foetal
fMuscle_lower_limb	0.53	1.53	2.33	Foetal muscle	Foetal
fMuscle_leg	0.22	1.60	2.49	Foetal muscle	Foetal
fMuscle_back	0.34	1.37	2.17	Foetal muscle	Foetal
fMuscle_arm	0.46	1.73	2.60	Foetal muscle	Foetal
fLung_R	0.76	1.84	2.65	Foetal lung	Foetal
fLung_L	0.09	1.50	2.41	Foetal lung	Foetal
fLung	-1.03	1.34	2.42	Foetal lung	Foetal
fKidney_renal_pelvis_R	1.23	2.12	2.87	Foetal kidney	Foetal
fKidney_renal_pelvis_L	0.51	1.62	2.45	Foetal kidney	Foetal
fKidney_renal_pelvis	0.60	1.69	2.52	Foetal kidney	Foetal
fKidney_renal_cortex_R	0.03	1.44	2.35	Foetal kidney	Foetal
fKidney_renal_cortex_L	0.91	1.88	2.67	Foetal kidney	Foetal
fKidney_R	0.52	1.63	2.45	Foetal kidney	Foetal
fKidney_L	0.70	1.81	2.65	Foetal kidney	Foetal
fKidney	0.42	1.65	2.51	Foetal kidney	Foetal
fIntestine_Sm	-0.17	1.29	2.22	Foetal intestine	Foetal
fIntestine_Lg	0.25	1.63	2.55	Foetal intestine	Foetal
fHeart	0.21	1.56	2.45	Foetal heart	Foetal
fBrain	0.65	1.90	2.78	Foetal brain	Foetal

Cell type	Lower 95%_CI[a]	Effect[a]	Upper 95%_CI[a]	Tissue	Category
fAdrenal	0.54	1.69	2.52	Foetal adrenal	Foetal
WI_38_TAM	-3.99	0.83	1.95	Embryonic	Embryonic
WI_38	-20.00	0.43	1.87	Embryonic	Embryonic
Trophoblast	-20.00	1.21	2.36	Embryonic	Embryonic
Mesendoderm	-0.52	1.15	2.15	Embryonic	Embryonic
Skin_Melanocytes	-0.05	1.40	2.33	Skin	Adult
Skin_Keratinocytes	-20.00	0.84	2.00	Skin	Adult
Skin_Fibroblasts	0.81	1.81	2.64	Skin	Adult
NHEK	-20.00	0.57	1.98	Skin	Adult
NHDF_Ad	-0.75	1.09	2.09	Skin	Adult
BJ	-0.05	1.65	2.64	Skin	Adult
AG10803	-0.12	1.50	2.46	Skin	Adult
AG09309	-20.00	1.03	2.20	Skin	Adult
AG04449	-0.32	1.50	2.47	Skin	Adult
PrEC	-20.00	0.83	2.13	Prostate	Adult
LNCap	-20.00	1.28	2.42	Prostate	Adult
SkMC	-0.82	1.33	2.38	Muscle	Adult
HSMM_D	-20.00	0.66	1.83	Muscle	Adult
HSMM	-20.00	-1.29	1.31	Muscle	Adult
NHLF	-2.24	0.96	2.08	Lung	Adult
IMR90	-20.00	0.61	1.93	Lung	Adult
HPF	-1.69	1.00	2.10	Lung	Adult
AG04450	0.03	1.60	2.56	Lung	Adult
HRGEC	-0.64	1.57	2.60	Kidney	Adult
HCM	-20.00	0.79	1.99	Heart	Adult
HCFaa	-0.48	1.25	2.25	Heart	Adult
HCF	-2.09	1.13	2.20	Heart	Adult
HGF	0.49	1.88	2.79	Gingival	Adult
AG09319	-0.49	1.54	2.56	Gingival	Adult
HFF_MyC	-1.06	1.16	2.21	Foreskin	Adult
HFF	0.51	1.74	2.62	Foreskin	Adult
HConF	-20.00	0.94	2.12	Eye	Adult
SAEC	-20.00	0.92	2.11	Epithelium	Adult
RPTEC	-20.00	-0.11	1.55	Epithelium	Adult
HRPEpiC	-20.00	0.20	1.67	Epithelium	Adult
HRE	-1.34	1.17	2.20	Epithelium	Adult
HRCE	-20.00	0.82	2.02	Epithelium	Adult
HPdLF	-20.00	0.55	1.91	Epithelium	Adult
HNPCEpiC	-0.11	1.42	2.36	Epithelium	Adult
HIPEpiC	-0.16	1.38	2.32	Epithelium	Adult
HEEpiC	-0.05	1.51	2.45	Epithelium	Adult
HCPEpiC	0.06	1.53	2.45	Epithelium	Adult
HAEpiC	-0.87	1.21	2.23	Epithelium	Adult
HVMF	-0.07	1.53	2.49	Connective	Adult
vHMEC	-0.13	1.36	2.29	Breast	Adult
HMF	-0.37	1.35	2.31	Breast	Adult
HMEC	0.27	1.69	2.60	Breast	Adult
NHA	-1.48	1.16	2.22	Brain	Adult
HAsp	-20.00	0.63	1.91	Brain	Adult
HAh	-20.00	0.59	1.80	Brain	Adult
HAc	-20.00	0.63	1.97	Brain	Adult
HUVEC	-0.57	1.36	2.38	Blood vessel	Adult

Cell type	Lower 95%_CI[a]	Effect[a]	Upper 95%_CI[a]	Tissue	Category
HPAF	-20.00	0.95	2.08	Blood vessel	Adult
HPAEC	-1.23	1.34	2.44	Blood vessel	Adult
HMVEC_LLy	-0.39	1.32	2.34	Blood vessel	Adult
HMVEC_LBl	-4.39	0.70	1.90	Blood vessel	Adult
HMVEC_dLyAd	-20.00	1.02	2.24	Blood vessel	Adult
HMVEC_dBlAd	0.03	1.46	2.38	Blood vessel	Adult
HMVEC_dAd	-0.79	1.37	2.44	Blood vessel	Adult
HBMEC	-1.98	0.88	1.96	Blood vessel	Adult
AoAF	-20.00	0.73	1.92	Blood vessel	Adult
hTH2	0.28	1.54	2.43	Blood	Adult
hTH17	-20.00	1.00	2.39	Blood	Adult
hTH1	0.19	1.61	2.53	Blood	Adult
H9_P42	-0.80	1.24	2.27	Blood	Adult
H1_P18	-0.07	1.40	2.35	Blood	Adult
GM12878	-0.72	1.24	2.30	Blood	Adult
GM12865	-20.00	0.73	2.07	Blood	Adult
GM12864	-20.00	0.85	2.10	Blood	Adult
GM06990	-20.00	0.98	2.19	Blood	Adult
CD8	0.34	1.73	2.66	Blood	Adult
CD56	-1.01	1.06	2.13	Blood	Adult
CD4	-0.49	1.28	2.29	Blood	Adult
CD34	-0.15	1.50	2.49	Blood	Adult
CD3_CordBlood	-1.52	1.56	2.69	Blood	Adult
CD3	-2.48	1.09	2.30	Blood	Adult
CD20	-2.52	0.90	2.01	Blood	Adult
CD19	0.29	1.71	2.66	Blood	Adult
CD14	-0.70	1.07	2.10	Blood	Adult
TSS	-0.87	1.37	2.42	Genic	Genic
3UTR	-20.00	1.04	2.47	Genic	Genic
5UTR	-47.50	-2.00	2.14	Genic	Genic
CDS	-2.08	1.03	2.48	Genic	Genic

(b) Six categorical fields from ENCODE tested for enrichment in a joint model

Annotation	Lower 95% CI[a]	Effect[a]	Upper 95% CI[a]
Neonatal DHS	0.60	1.59	2.40
Foetal DHS	0.57	1.43	2.37
Genic	-0.85	0.63	1.61
Stem_cell DHS	-1.35	0.09	1.04
Adult DHS	-1.12	-0.26	0.62
Embryonic DHS	-3.95	-1.49	-0.39

[a] Estimated effects of enrichment and 95% CI are natural log transformed. We considered an annotation enriched if the 95% CI of the estimated effects of enrichment did not overlap zero.

Supplementary Table 9. Genetic variance explained.

Study	***N***	**By 62 known and novel SNPs**		**By 55 novel SNPs**	
		Variance explained	SE	Variance explained	SE
HAPO	1338	0.020	0.011	0.013	0.010
NFBC1966	5402	0.029	0.007	0.020	0.006
Generation R	2537	0.049	0.013	0.026	0.009

SE, standard error. HAPO study is independent of the birth weight meta-analysis whilst NFBC1966 and Generation R (European component) are part of the meta-analysis.

Supplementary Table 10. Look-up of maternal genotype effect on offspring BW (unadjusted for foetal genotype) in up to 68,254 mothers for the 60 BW loci detected in foetal birth weight GWAS.

Locus	**Lead SNP**	**Allele**		**Foetal (European ancestry) GWAS**		**Maternal GWAS**					**Foetal Beta - Maternal Beta**[a]
		Effect	**Other**	**β**	**SE**	**EAF**	**β**	**SE**	***P*-value**	***N***	
WNT4-ZBTB40	rs2473248	C	T	0.033	0.006	0.88	0.013	0.010	0.20	48,632	0.020
ZBTB7B	rs3753639	C	T	0.031	0.004	0.25	0.017	0.008	0.03	48,632	0.014
FCGR2B	rs72480273	C	A	0.031	0.005	0.19	0.013	0.008	0.11	48,632	0.018
DTL	rs61830764	A	G	0.022	0.004	0.37	-0.002	0.007	0.76	48,632	0.020
ATAD2B	rs7575873	A	G	0.038	0.004	0.87	-0.011	0.010	0.27	48,632	0.028
EPAS1	rs1374204	T	C	0.047	0.004	0.69	0.024	0.006	5.6×10^{-5}	68,252	0.023
PTH1R	rs2242116	A	G	0.022	0.004	0.37	0.019	0.006	9.3×10^{-4}	67,542	0.004
ADCY5	rs11719201	T	C	0.046	0.004	0.25	-0.001	0.008	0.85	48,632	0.045
CPA3	rs10935733	T	C	0.022	0.004	0.40	0.015	0.007	0.02	48,632	0.007
CCNL1-LEKR1	rs13322435	A	G	0.053	0.004	0.59	0.026	0.006	9.5×10^{-6}	68,250	0.027
LCORL	rs925098	G	A	0.034	0.004	0.28	0.025	0.006	2.9×10^{-5}	68,254	0.009
HHIP	rs6537307	G	A	0.025	0.004	0.49	0.019	0.005	4.4×10^{-4}	68,247	0.006
5q11.2	rs854037	A	G	0.027	0.005	0.80	0.009	0.007	0.18	68,219	0.018
EBF1	rs7729301	A	G	0.024	0.004	0.74	0.039	0.007	8.9×10^{-8}	48,632	-0.015
CDKAL1	rs35261542	C	A	0.044	0.004	0.74	0.004	0.007	0.60	48,632	0.040
HIST1H2BE	rs9379832	A	G	0.023	0.004	0.73	0.008	0.007	0.30	48,632	0.015
HMGA1	rs7742369	G	A	0.028	0.005	0.19	0.017	0.007	0.01	68,253	0.011
L3MBTL3	rs1415701	G	A	0.025	0.004	0.73	0.037	0.006	3.7×10^{-9}	66,897	-0.012
ESR1	rs1101081	C	T	0.038	0.004	0.72	0.021	0.007	3.8×10^{-3}	48,632	0.017
GNA12	rs798489	C	T	0.023	0.004	0.72	0.023	0.006	1.6×10^{-4}	68,253	0.001
IGF2BP3	rs11765649	T	C	0.027	0.004	0.74	0.015	0.007	0.04	48,632	0.012
TBX20	rs6959887	A	G	0.023	0.004	0.61	0.009	0.006	0.10	68,232	0.014
YKT6-GCK	rs138715366	C	T	0.241	0.023	0.99	0.137	0.038	2.8×10^{-4}	48,632	0.104
MLXIPL	rs62466330	C	T	0.051	0.011	0.07	0.022	0.013	0.08	48,632	0.029
ANK1-NKX6-3	rs13266210	A	G	0.031	0.005	0.78	0.005	0.007	0.43	68,252	0.026
TRIB1	rs6989280	G	A	0.022	0.004	0.72	0.020	0.006	1.3×10^{-3}	67,520	0.003
SLC45A4	rs12543725	G	A	0.023	0.004	0.58	0.021	0.005	1.4×10^{-4}	68,222	0.002
PTCH1	rs28510415	G	A	0.056	0.007	0.09	0.034	0.011	2.2×10^{-3}	48,632	0.022
LPAR1	rs2150052	T	A	0.021	0.004	0.50	0.017	0.005	1.4×10^{-3}	68,245	0.004
PHF19	rs7847628	G	A	0.023	0.004	0.68	0.009	0.007	0.20	48,632	0.014
STRBP	rs700059	G	A	0.033	0.005	0.16	0.018	0.008	0.02	68,251	0.016

Locus	Lead SNP	Allele		Foetal (European ancestry) GWAS		Maternal GWAS					Foetal Beta - Maternal Beta[a]
		Effect	Other	β	SE	EAF	β	SE	*P*-value	*N*	
HHEX-IDE	rs61862780	T	C	0.028	0.004	0.49	-0.004	0.006	0.55	48,632	0.024
NT5C2	rs74233809	C	T	0.037	0.007	0.08	0.005	0.012	0.70	48,632	0.032
ADRB1	rs7076938	T	C	0.036	0.004	0.73	0.010	0.006	0.09	68,254	0.026
PLEKHA1	rs2421016	T	C	0.021	0.004	0.48	0.016	0.005	$3.3x10^{-3}$	68,253	0.005
INS-IGF2	rs72851023	T	C	0.048	0.008	0.08	0.015	0.012	0.24	48,632	0.033
MTNR1B	rs10830963	G	C	0.023	0.004	0.29	0.048	0.006	$5.1x10^{-15}$	67,603	-0.025
APOLD1	rs11055034	C	A	0.022	0.004	0.71	0.002	0.006	0.74	67,597	0.020
ABCC9	rs139975827	G	A	0.027	0.007	0.63	-0.010	0.007	0.13	48,632	0.017
ITPR2	rs12823128	T	C	0.021	0.004	0.53	0.009	0.005	0.08	68,187	0.012
HMGA2	rs1351394	T	C	0.044	0.004	0.49	0.034	0.005	$1.4x10^{-10}$	68,247	0.010
IGF1	rs7964361	A	G	0.039	0.007	0.10	0.018	0.010	0.06	68,251	0.021
LINC00332	rs2324499	G	C	0.022	0.004	0.68	0.012	0.006	0.05	68,213	0.011
RB1	rs2854355	G	A	0.023	0.004	0.26	0.017	0.007	0.03	48,632	0.007
RNF219-AS1	rs1819436	C	T	0.033	0.006	0.88	0.007	0.010	0.50	48,632	0.026
FES	rs12906125	G	A	0.023	0.004	0.68	0.029	0.007	$1.8x10^{-5}$	48,632	-0.006
IGF1R	rs7402982	A	G	0.023	0.004	0.41	0.021	0.007	$1.7x10^{-3}$	48,632	0.002
GPR139	rs1011939	G	A	0.022	0.004	0.28	0.007	0.007	0.34	48,632	0.015
CLDN7	rs113086489	T	C	0.031	0.004	0.54	0.022	0.007	$7.7x10^{-4}$	48,632	0.009
SUZ12P1-CRLF3	rs144843919	G	A	0.066	0.012	0.96	0.041	0.018	0.02	48,632	0.025
SP6-SP2	rs12942207	C	T	0.022	0.004	0.30	0.010	0.007	0.14	48,632	0.012
ACTL9	rs61154119	T	G	0.028	0.005	0.85	0.047	0.009	$1.5x10^{-7}$	48,632	-0.019
PEPD	rs10402712	A	G	0.022	0.004	0.26	-0.002	0.007	0.76	48,632	0.020
JAG1	rs6040076	C	G	0.023	0.004	0.51	0.015	0.007	0.02	48,632	0.008
C20orf203	rs28530618	A	G	0.026	0.004	0.47	0.003	0.006	0.62	48,632	0.023
MAFB	rs6016377	T	C	0.024	0.004	0.45	0.005	0.006	0.35	67,909	0.019
NRIP1	rs2229742	G	C	0.036	0.006	0.88	0.018	0.009	0.04	68,155	0.018
KREMEN1	rs134594	C	T	0.023	0.004	0.36	0.004	0.006	0.53	66,634	0.020
SREBF2	rs62240962	C	T	0.047	0.007	0.92	0.027	0.012	0.02	48,632	0.020
PLAC1	rs11096402	G	A	0.028	0.005	0.24	0.001	0.003	0.82	45,353	0.027

SE, standard error, EAF, effect allele frequency. The lead SNPs at *MTNR1B, HMGA2* and *L3MBTL3* attained genome-wide significance in the maternal, as well as the foetal GWAS. [a]Foetal GWAS effect size subtracted from maternal GWAS effect size: 55/60 beta values were more positive in the foetal GWAS (aligned to BW-raising allele) than in the maternal GWAS (2-tailed binomial sign test $P=1x10^{-11}$).

Supplementary Table 11. Maternal and foetal conditional analyses in 12,909 mother-child pairs.

Locus	Index variant	EA/ NEA	Maternal effect on offspring birth weight						Foetal effect on birth weight					
			Unadjusted			Adjusted for foetal genotype			Unadjusted			Adjusted for maternal genotype		
			β	SE	*P*-value	β	SE	*P*-value	β	SE	*P*-value	β	SE	*P*-value
WNT4-ZBTB40	rs2473248	C/T	0.004	0.018	0.82	-0.006	0.020	0.76	0.033	0.018	0.06	0.039	0.020	0.05
ZBTB7B	rs3753639	C/T	0.022	0.015	0.16	-0.005	0.017	0.79	0.060	0.016	9.8x10^{-5}	0.060	0.018	5.7x10^{-4}
FCGR2B	rs72480273	C/A	0.034	0.017	0.05	0.018	0.019	0.34	0.042	0.017	0.01	0.031	0.019	0.11
DTL	rs61830764	A/G	0.026	0.014	0.06	0.016	0.016	0.31	0.029	0.014	0.04	0.027	0.016	0.09
ATAD2B	rs7575873	A/G	0.018	0.019	0.35	0.007	0.022	0.74	0.042	0.019	0.03	0.047	0.022	0.03
EPAS1	rs1374204	T/C	0.032	0.013	0.02	0.008	0.015	0.60	0.056	0.013	2.6x10^{-5}	0.047	0.015	1.9x10^{-3}
PTH1R	rs2242116	A/G	0.025	0.013	0.05	0.031	0.015	0.03	0.002	0.013	0.86	-0.013	0.014	0.38
ADCY5	rs11719201	T/C	0.000	0.015	1.00	-0.025	0.017	0.15	0.057	0.015	2.2x10^{-4}	0.075	0.017	1.5x10^{-5}
CPA3	rs10935733	T/C	-0.004	0.013	0.73	-0.006	0.014	0.66	0.007	0.013	0.57	0.013	0.014	0.36
CCNL1-LEKR1	rs13322435	A/G	0.028	0.013	0.03	-0.015	0.014	0.31	0.091	0.013	7.9x10^{-13}	0.097	0.014	9.7x10^{-12}
LCORL	rs925098	G/A	0.012	0.014	0.39	-0.017	0.016	0.29	0.057	0.014	3.1x10^{-5}	0.060	0.015	1.0x10^{-4}
HHIP	rs6537307	G/A	0.028	0.013	0.03	0.003	0.014	0.85	0.057	0.013	1.1x10^{-5}	0.057	0.015	7.8x10^{-5}
5q11.2	rs854037	A/G	0.019	0.015	0.20	0.016	0.017	0.35	0.022	0.015	0.15	0.011	0.017	0.52
EBF1	rs7729301	A/G	0.036	0.014	8.8x10^{-3}	0.040	0.015	9.6x10^{-3}	0.024	0.014	0.08	0.010	0.016	0.52
CDKAL1	rs35261542	C/A	0.003	0.014	0.81	-0.028	0.016	0.07	0.057	0.014	4.3x10^{-5}	0.071	0.016	6.1x10^{-6}
HIST1H2BE	rs9379832	A/G	-0.005	0.014	0.74	-0.012	0.016	0.45	0.022	0.014	0.12	0.026	0.016	0.10
HMGA1	rs7742369	G/A	0.027	0.015	0.08	0.006	0.017	0.72	0.043	0.015	4.9x10^{-3}	0.035	0.017	0.04
L3MBTL3	rs1415701	G/A	0.035	0.014	0.01	0.019	0.016	0.22	0.052	0.014	2.7x10^{-4}	0.041	0.016	0.01
ESR1	rs1101081	C/T	0.009	0.014	0.51	-0.004	0.016	0.82	0.029	0.014	0.04	0.033	0.016	0.04
GNA12	rs798489	C/T	0.018	0.015	0.22	0.011	0.017	0.50	0.034	0.015	0.02	0.029	0.017	0.08
IGF2BP3	rs11765649	T/C	0.007	0.015	0.64	0.006	0.017	0.74	0.017	0.015	0.25	0.013	0.017	0.45
TBX20	rs6959887	A/G	0.018	0.013	0.15	-0.002	0.014	0.89	0.040	0.013	1.7x10^{-3}	0.036	0.014	0.01
YKT6-GCK	rs138715366	C/T	-0.030	0.087	0.73	-0.147	0.097	0.13	0.186	0.087	0.03	0.230	0.098	0.02
MLXIPL	rs62466330	C/T	0.019	0.028	0.50	-0.015	0.031	0.62	0.104	0.028	2.2x10^{-4}	0.129	0.031	3.3x10^{-5}
ANK1-NKX6-3	rs13266210	A/G	0.013	0.015	0.41	0.009	0.017	0.61	0.018	0.015	0.24	0.023	0.017	0.18
TRIB1	rs6989280	G/A	0.014	0.014	0.32	0.019	0.016	0.24	-0.003	0.014	0.84	-0.012	0.016	0.46
SLC45A4	rs12543725	G/A	0.012	0.013	0.36	0.004	0.015	0.79	0.013	0.013	0.31	0.014	0.015	0.34
PTCH1	rs28510415	G/A	0.037	0.023	0.11	-0.005	0.026	0.84	0.105	0.023	8.0x10^{-6}	0.105	0.027	7.2x10^{-5}
LPAR1	rs2150052	T/A	0.019	0.013	0.13	0.008	0.014	0.56	0.017	0.013	0.17	0.010	0.014	0.47
PHF19	rs7847628	G/A	0.020	0.013	0.13	0.018	0.015	0.24	0.022	0.013	0.11	0.017	0.015	0.25
STRBP	rs700059	G/A	0.017	0.016	0.27	-0.006	0.018	0.76	0.053	0.016	8.0x10^{-4}	0.062	0.018	4.5x10^{-4}
HHEX-IDE	rs61862780	T/C	0.012	0.013	0.36	-0.015	0.014	0.29	0.053	0.013	3.0x10^{-5}	0.059	0.014	3.1x10^{-5}

Locus	**Index variant**	**EA/ NEA**	**Maternal effect on offspring birth weight**						**Foetal effect on birth weight**					
			Unadjusted			**Adjusted for foetal genotype**			**Unadjusted**			**Adjusted for maternal genotype**		
			β	**SE**	***P*-value**	**β**	**SE**	***P*-value**	**β**	**SE**	***P*-value**	**β**	**SE**	***P*-value**
NT5C2	rs74233809	C/T	-0.002	0.021	0.94	-0.010	0.024	0.67	0.016	0.021	0.44	0.011	0.024	0.64
ADRB1	rs7076938	T/C	0.045	0.014	8.8x10^{-4}	0.032	0.015	0.03	0.050	0.014	2.6x10^{-4}	0.037	0.015	0.02
PLEKHA1	rs2421016	T/C	0.017	0.012	0.17	0.018	0.014	0.19	0.006	0.012	0.63	0.001	0.014	0.95
INS-IGF2	rs72851023	T/C	0.031	0.027	0.26	0.008	0.031	0.79	0.060	0.028	0.03	0.061	0.031	0.05
MTNR1B	rs10830963	G/C	0.047	0.015	1.7x10^{-3}	0.035	0.017	0.04	0.049	0.015	9.8x10^{-4}	0.032	0.017	0.06
APOLD1	rs11055034	C/A	-0.003	0.014	0.83	-0.013	0.016	0.42	0.005	0.014	0.72	0.011	0.016	0.51
ABCC9	rs139975827	G/A	0.005	0.014	0.72	-0.011	0.015	0.47	0.033	0.014	0.02	0.041	0.015	0.01
ITPR2	rs12823128	T/C	-0.003	0.013	0.83	-0.016	0.015	0.28	0.022	0.013	0.10	0.024	0.015	0.10
HMGA2	rs1351394	T/C	0.023	0.013	0.07	0.007	0.015	0.65	0.038	0.013	3.0x10^{-3}	0.038	0.014	0.01
IGF1	rs7964361	A/G	-0.005	0.023	0.85	-0.016	0.026	0.55	0.025	0.023	0.28	0.030	0.026	0.25
LINC00332	rs2324499	G/C	0.006	0.013	0.68	0.001	0.015	0.96	0.019	0.013	0.15	0.019	0.015	0.22
RB1	rs2854355	G/A	-0.013	0.015	0.37	-0.027	0.016	0.10	0.020	0.015	0.18	0.029	0.016	0.07
RNF219-AS1	rs1819436	C/T	0.040	0.018	0.03	0.013	0.020	0.52	0.057	0.018	1.8x10^{-3}	0.046	0.020	0.02
FES	rs12906125	G/A	0.006	0.014	0.66	-0.004	0.016	0.82	0.016	0.014	0.27	0.012	0.016	0.47
IGF1R	rs7402982	A/G	0.015	0.013	0.24	0.003	0.015	0.83	0.025	0.013	0.06	0.027	0.015	0.07
GPR139	rs1011939	G/A	0.015	0.014	0.27	0.013	0.015	0.39	0.008	0.014	0.57	0.000	0.015	1.00
CLDN7	rs113086489	T/C	0.018	0.013	0.16	0.002	0.014	0.89	0.043	0.013	5.7x10^{-4}	0.044	0.014	1.9x10^{-3}
SUZ12P1-CRLF3	rs144843919	G/A	0.003	0.037	0.93	-0.030	0.041	0.47	0.045	0.038	0.24	0.047	0.043	0.27
SP6-SP2	rs12942207	C/T	-0.001	0.014	0.92	-0.003	0.016	0.82	0.007	0.014	0.63	0.008	0.015	0.59
ACTL9	rs61154119	T/G	-0.005	0.016	0.75	-0.022	0.018	0.23	0.032	0.016	0.05	0.041	0.018	0.02
PEPD	rs10402712	A/G	-0.013	0.014	0.36	-0.028	0.016	0.07	0.016	0.014	0.26	0.025	0.016	0.11
JAG1	rs6040076	C/G	0.000	0.013	0.98	-0.007	0.015	0.64	0.010	0.013	0.43	0.017	0.015	0.24
C20orf203	rs28530618	A/G	0.015	0.013	0.23	0.013	0.014	0.34	0.006	0.013	0.63	0.003	0.014	0.85
MAFB	rs6016377	T/C	0.000	0.013	0.99	-0.021	0.015	0.16	0.042	0.013	1.4x10^{-3}	0.058	0.015	9.9x10^{-5}
NRIP1	rs2229742	G/C	0.026	0.023	0.26	0.018	0.026	0.49	0.031	0.023	0.17	0.018	0.026	0.49
KREMEN1	rs134594	C/T	0.016	0.013	0.22	0.007	0.015	0.64	0.017	0.013	0.20	0.015	0.015	0.30
SREBF2	rs62240962	C/T	0.019	0.026	0.47	0.005	0.029	0.87	0.049	0.026	0.06	0.049	0.029	0.09
PLAC1[a]	rs11096402	G/A	0.009	0.022	0.68	-0.004	0.024	0.88	0.013	0.024	0.60	0.014	0.027	0.61

[a] For analysis of the *PLAC1* locus on the X chromosome, we used female offsprings only: N = 4,940 mother-child pairs

EA: Effect Allele. NEA: Non Effect Allele. SE: standard error. Effects (beta values) are aligned to the BW-raising allele as reported in Extended Data Table 1a.

Supplementary Table 12. Summary results of LD Score regression analyses between birth weight and various diseases, metabolic and anthropometric traits.

(a) Birth weight and other traits

Phenotype1	Phenotype2	Genetic Correlation (r_g)	SE	z	*P*-value	Sample size of phenotype 2	Number of SNPs	Reference (PMID)
Birth weight	Infant head circumference	0.389	0.073	5.30	1.2x10^{-7}	10,770	1,019,674	22504419
Birth weight	Birth length	0.805	0.058	13.98	2.0x10^{-44}	28,460	983,823	25281659
Birth weight	Height (2014)	0.406	0.027	15.18	4.8x10^{-52}	253,300	1,049,262	25282103
Birth weight	Height (2010)	0.401	0.028	14.09	4.6x10^{-45}	133,900	1,026,905	20881960
Birth weight	Height (women)	0.400	0.032	12.59	2.4x10^{-36}	73,140	1,028,514	23754948
Birth weight	Height (men)	0.384	0.035	11.00	3.7x10^{-28}	60,590	1,024,139	23754948
Birth weight	Extreme height	0.399	0.043	9.20	3.5x10^{-20}	16,200	739,427	23563607
Birth weight	Body mass index (2015)	0.114	0.025	4.49	7.3x10^{-6}	322,200	1,050,986	25673413
Birth weight	Body mass index (2010)	0.120	0.033	3.66	3.0x10^{-4}	123,900	1,028,235	20935630
Birth weight	Extreme Body mass index	0.116	0.048	2.40	0.017	16,070	738,850	23563607
Birth weight	Body mass index (men)	0.148	0.040	3.67	2.4x10^{-4}	58,670	1,025,063	23754948
Birth weight	Body mass index (women)	0.096	0.035	2.76	0.006	67,960	1,029,327	23754948
Birth weight	Weight (men)	0.377	0.039	9.57	1.1x10^{-21}	58,350	1,025,155	23754948
Birth weight	Weight (women)	0.280	0.036	7.70	1.4x10^{-14}	67,590	1,029,320	23754948
Birth weight	Waist-hip ratio (2015)	-0.052	0.031	-1.66	0.097	212,200	1,048,211	25673412
Birth weight	Waist-hip ratio (adjusted for BMI - 2015)	-0.159	0.032	-4.93	8.3x10^{-7}	210,100	1,051,567	25673412
Birth weight	Waist-hip ratio (adjusted for BMI - 2010)	-0.189	0.041	-4.59	4.4x10^{-6}	77,220	1,027,370	20935629
Birth weight	Waist-hip ratio (men)	-0.080	0.053	-1.51	0.132	34,640	1,025,922	23754948
Birth weight	Waist-hip ratio (women)	-0.060	0.054	-1.11	0.268	42,730	1,029,620	23754948
Birth weight	Extreme waist-hip ratio	-0.254	0.071	-3.57	3.6x10^{-4}	10,260	674,047	23563607
Birth weight	Hip circumference	0.281	0.030	9.30	1.4x10^{-20}	213,000	1,048,111	25673412
Birth weight	Hip circumference (adjusted for BMI)	0.314	0.033	9.49	2.3x10^{-21}	211,100	1,049,874	25673412
Birth weight	Hip circumference (men)	0.339	0.063	5.34	9.3x10^{-8}	32,850	1,030,276	23754948
Birth weight	Hip circumference (women)	0.260	0.057	4.54	5.6x10^{-6}	40,360	1,031,503	23754948
Birth weight	Waist circumference	0.177	0.028	6.29	3.9x10^{-10}	232,100	1,048,634	25673412
Birth weight	Waist circumference (adjusted for BMI)	0.128	0.032	4.03	5.7x10^{-5}	231,400	1,049,871	25673412
Birth weight	Waist circumference (men)	0.218	0.053	4.11	3.9x10^{-5}	38,310	1,025,680	23754948
Birth weight	Waist circumference (women)	0.135	0.047	2.86	0.004	47,320	1,027,090	23754948
Birth weight	Obesity (class 1)	0.102	0.035	2.97	0.003	98,700	965,717	23563607
Birth weight	Obesity (class 2)	0.099	0.040	2.46	0.014	72,550	890,085	23563607

Phenotype1	Phenotype2	Genetic Correlation (r_g)	SE	z	*P*-value	Sample size of phenotype 2	Number of SNPs	Reference (PMID)
Birth weight	Obesity (class 3)	0.136	0.055	2.48	0.013	50,360	621,425	23563607
Birth weight	Childhood obesity	0.192	0.049	3.95	$7.8x10^{-5}$	13,850	1,057,303	22484627
Birth weight	Overweight	0.061	0.033	1.83	0.067	158,900	1,012,975	23563607
Birth weight	Anorexia nervosa	0.029	0.033	0.91	0.365	17,770	1,042,946	24514567
Birth weight	Crohn's disease	0.047	0.044	1.07	0.284	20,883	1,066,772	26192919
Birth weight	Irritable bowel syndrome	0.009	0.052	0.18	0.858	27,432	1,091,971	26192919
Birth weight	Rheumatoid arthritis	-0.004	0.046	-0.08	0.935	25,710	986,060	20453842
Birth weight	Lumbar spine bone mineral density	-0.027	0.043	-0.63	0.531	31,800	1,061,087	22504420
Birth weight	Lumbar spine bone mineral density (men)	-0.098	0.064	-1.53	0.127	9,980	1,060,919	22504420
Birth weight	Lumbar spine bone mineral density (women)	-0.003	0.044	-0.07	0.943	22,180	1,064,756	22504420
Birth weight	Femoral neck bone mineral density	0.013	0.039	0.34	0.736	32,960	1,065,335	22504420
Birth weight	Femoral neck bone mineral density (men)	-0.019	0.057	-0.33	0.745	9,971	1,056,535	22504420
Birth weight	Femoral neck bone mineral density (women)	0.020	0.050	0.40	0.686	22,990	1,069,031	22504420
Birth weight	Coronary artery disease	-0.295	0.051	-5.80	$6.5x10^{-9}$	84,270	932,642	21378990
Birth weight	Systolic blood pressure (adjusted for BMI)	-0.263	0.039	-6.72	$1.8x10^{-11}$	69,395	990,423	21909115
Birth weight	Systolic blood pressure (unadjusted for BMI)	-0.215	0.030	-7.21	$5.5x10^{-13}$	127,969	1,186,583	UK Biobank data
Birth weight	Diastolic blood pressure (adjusted for BMI)	-0.224	0.042	-5.35	$8.7x10^{-8}$	69,395	990,446	21909115
Birth weight	Triglycerides (2010)	-0.167	0.038	-4.41	$1.0x10^{-5}$	96,600	1,024,575	20686565
Birth weight	Triglycerides (2013)	-0.112	0.031	-3.61	$3.0x10^{-4}$	177,900	1,026,718	24097068
Birth weight	Total cholesterol (2010)	-0.127	0.040	-3.21	0.001	100,200	1,026,024	20686565
Birth weight	Total cholesterol (2013)	-0.105	0.033	-3.17	0.002	187,400	1,027,605	24097068
Birth weight	Low density lipoprotein (2010)	-0.136	0.047	-2.90	0.004	95,450	1,024,730	20686565
Birth weight	Low density lipoprotein (2013)	-0.102	0.036	-2.87	0.004	173,100	1,026,705	24097068
Birth weight	High density lipoprotein (2010)	0.087	0.039	2.23	0.026	99,900	1,026,029	20686565
Birth weight	High density lipoprotein (2013)	0.056	0.029	1.97	0.048	187,200	1,027,731	24097068
Birth weight	Type 2 diabetes	-0.271	0.056	-4.88	$1.1x10^{-6}$	69,030	976,437	22885922
Birth weight	Fasting insulin	-0.150	0.071	-2.10	0.036	46,190	1,054,692	20081858
Birth weight	Fasting insulin (adjusting for BMI)	-0.178	0.055	-3.26	0.001	51,750	1,121,151	22581228
Birth weight	HbA1c	-0.166	0.060	-2.75	0.006	46,368	1,109,233	20858683
Birth weight	2hr glucose	-0.245	0.094	-2.62	0.009	15,230	1,028,518	20081857
Birth weight	Fasting glucose	-0.073	0.054	-1.35	0.178	46,190	1,056,257	20081858
Birth weight	Fasting glucose (adjusting for BMI)	-0.126	0.048	-2.61	0.009	58,074	1,121,150	22581228
Birth weight	HOMA-IR	-0.133	0.072	-1.84	0.066	46,190	1,053,709	20081858
Birth weight	HOMA-B	-0.065	0.065	-1.00	0.317	46,190	1,053,581	20081858

Phenotype1	**Phenotype2**	**Genetic Correlation (r_g)**	**SE**	**z**	***P*-value**	**Sample size of phenotype 2**	**Number of SNPs**	**Reference (PMID)**
Birth weight	Educational attainment (college)	0.111	0.042	2.63	0.009	126,600	1,017,448	25201988
Birth weight	Educational attainment (years)	0.105	0.043	2.43	0.015	126,600	1,014,207	25201988
Birth weight	Childhood intelligence	0.123	0.075	1.64	0.100	17,990	800,741	25201988
Birth weight	Autism	-0.089	0.053	-1.69	0.091	10,263	944,654	23453885
Birth weight	ADHD	-0.107	0.103	-1.04	0.300	3,351	1,065,753	20732625
Birth weight	Major depressive disorder	-0.076	0.074	-1.02	0.306	18,760	887,434	22472876
Birth weight	Bipolar disorder	0.026	0.047	0.56	0.578	16,730	800,584	21926972
Birth weight	Alzheimer's disease	-0.039	0.080	-0.49	0.622	74,050	1,142,332	24162737
Birth weight	Schizophrenia	-0.022	0.044	-0.49	0.624	21,860	846,564	21926974
Birth weight	Pubertal growth - height at age 10 in females and 12 in males - targets take-off phase of growth spurt	0.271	0.051	5.28	$1.3x10^{-7}$	13,960	1,009,067	23449627
Birth weight	Pubertal growth - height at age 12 in males	0.305	0.072	4.23	$2.3x10^{-5}$	6,986	1,017,307	23449627
Birth weight	Pubertal growth - height at age 10 in females	0.221	0.061	3.63	$3.0x10^{-4}$	6,974	1,036,441	23449627
Birth weight	Pubertal growth - total amount of growth across the pubertal growth period	0.162	0.062	2.61	0.009	10,800	1,037,500	23449627
Birth weight	Pubertal growth - total amount of growth across the pubertal growth period (males)	0.173	0.080	2.15	0.032	5,043	1,039,045	23449627
Birth weight	Pubertal growth - total amount of growth across the pubertal growth period (females)	0.142	0.083	1.70	0.089	5,756	1,038,734	23449627
Birth weight	Pubertal growth - total amount of growth in late adolescence, targeting the timing of peak height growth velocity	0.109	0.075	1.46	0.145	4,282	1,039,103	23449627
Birth weight	Pubertal growth - total amount of growth in late adolescence (males)	0.041	0.081	0.51	0.613	4,282	1,039,103	23449627
Birth weight	Pubertal growth - total amount of growth in late adolescence (females)	0.230	0.112	2.06	0.039	4,946	1,038,829	23449627
Birth weight	Age at menarche (2014)	0.029	0.031	0.93	0.354	133,000	1,057,631	25231870
Birth weight	Pubertal growth - Tanner scale	-0.137	0.125	-1.10	0.273	9,918	969,224	23449627
Birth weight	Pubertal growth - Tanner scale (males)	-0.453	0.650	-0.97	0.486	3,769	969,224	23449627
Birth weight	Pubertal growth - Tanner scale (females)	-0.037	0.138	-0.27	0.786	6,149	969,224	23449627
Birth weight	Asthma	0.050	0.069	0.72	0.471	10,770	1,019,674	20860503
Birth weight	Ever smoked	0.007	0.045	0.15	0.878	28,460	983,823	20418890
Birth weight	Former smoker	0.097	0.061	1.58	0.114	253,300	1,049,262	20418890
Birth weight	Cigarettes per day	-0.042	0.064	-0.67	0.505	133,900	1,026,905	20418890
Birth weight	Smoking start age	0.041	0.087	0.47	0.636	73,140	1,028,514	20418890

(b) Glucose-Related Phenotypes

Phenotype1	**Phenotype2**	**Genetic Correlation (rg)**	**SE**	**z**	***P*-value**	**Sample size of phenotype 2**	**Number of SNPs**	**Reference (PMID)**
Type 2 diabetes	Fasting glucose	0.587	0.097	6.07	1.3×10^{-9}	46,190	1,056,257	20081858
Type 2 diabetes	2hr glucose	0.301	0.12	2.47	0.014	15,230	1,028,518	20081857
Type 2 diabetes	Fasting insulin	0.435	0.12	3.56	4.0×10^{-4}	46,190	1,054,692	20081858
Type 2 diabetes	HOMA-B	-0.002	0.11	-0.01	0.989	46,190	1,053,581	20081858

SE, standard error; BMI, body mass index; ADHD, attention deficit hyperactive disorder; HOMA-IR, homeostasis model assessment of insulin resistance; HOMA-B, homeostasis model assessment of beta cell function.

Supplementary Table 13. Estimating the proportion of the BW-adult phenotype covariance attributable to genotyped SNPs in UK Biobank and the Northern Finland Birth Cohort (NFBC) 1966 data.

Adult phenotype	***N*[a]**	**Phenotypic correlation with BW**	**Genetic correlation with BW (SE)**	**Residual correlation with BW (SE)**	**Genetic covariance with BW, gcov (SE)**	**Residual covariance with BW, rcov (SE)**	**Proportion of covariance explained by genetic variants directly genotyped: gcov/(gcov+rcov)[b] (95% CI)**
UK Biobank							
Type 2 diabetes	56,654	-0.034	-0.124 (0.081)	-0.001 (0.010)	-0.012 (0.008)	-0.001 (0.008)	0.96 (0.36, 1.56)
Systolic blood pressure (unadjusted for BMI)	57,581	-0.072	-0.201 (0.037)	-0.011 (0.011)	-0.045 (0.008)	-0.008 (0.008)	0.85 (0.70, 0.99)
Systolic blood pressure (adjusted for BMI)	57,319	-0.084	-0.216 (0.030)	-0.042 (0.010)	-0.052 (0.007)	-0.031 (0.007)	0.62 (0.54, 0.71)
Diastolic blood pressure (adjusted for BMI)	57,230	-0.072	-0.156 (0.030)	-0.045 (0.010)	-0.038 (0.007)	-0.033 (0.007)	0.54 (0.44, 0.64)
Coronary artery disease	57,715	-0.002	-0.174 (0.182)	0.004 (0.009)	-0.008 (0.007)	0.003 (0.008)	N/A
Height	57,638	0.228	0.332 (0.026)	0.194 (0.015)	0.106 (0.008)	0.091 (0.007)	0.54 (0.50, 0.58)
Height (men)	23,385	0.202	0.343 (0.060)	0.214 (0.041)	0.108 (0.019)	0.090 (0.018)	0.55 (0.45, 0.64)
Height (women)	34,253	0.2	0.367 (0.037)	0.174 (0.029)	0.131 (0.013)	0.072 (0.012)	0.65 (0.58, 0.71)
Weight (men)	23,371	0.15	0.199 (0.074)	0.118 (0.027)	0.050 (0.018)	0.080 (0.018)	0.38 (0.24, 0.53)
Weight (women)	34,233	0.094	0.206 (0.049)	0.058 (0.019)	0.056 (0.013)	0.040 (0.013)	0.58 (0.45, 0.72)
Body mass index	57,402	0.043	0.063 (0.036)	0.031 (0.011)	0.014 (0.008)	0.023 (0.008)	0.39 (0.17, 0.61)
Body mass index (men)	34,077	0.045	0.049 (0.051)	0.019 (0.019)	0.013 (0.013)	0.013 (0.013)	0.49 (-0.01, 0.98)
Body mass index (women)	23,325	0.024	0.072 (0.087)	0.037 (0.025)	0.015 (0.018)	0.028 (0.018)	0.35 (-0.06, 0.77)
Obesity (class 1)	33,622	0.048	0.080 (0.051)	0.040 (0.020)	0.021 (0.013)	0.027 (0.013)	0.44 (0.17, 0.71)

Adult phenotype	***N*[a]**	**Phenotypic correlation with BW**	**Genetic correlation with BW (SE)**	**Residual correlation with BW (SE)**	**Genetic covariance with BW, gcov (SE)**	**Residual covariance with BW, rcov (SE)**	**Proportion of covariance explained by genetic variants directly genotyped: gcov/(gcov+rcov)[b] (95% CI)**
Obesity (class 2)	23,846	0.028	0.016 (0.061)	0.050 (0.029)	0.005 (0.018)	0.032 (0.017)	0.13 (-0.37, 0.63)
Obesity (class 3)	20,966	0.01	-0.088 (0.105)	0.046 (0.026)	-0.017 (0.020)	0.036 (0.020)	N/A
Overweight	57,451	0.042	0.052 (0.045)	0.035 (0.010)	0.009 (0.008)	0.028 (0.008)	0.25 (0.04, 0.46)
Waist-hip ratio	57,590	0.077	-0.049 (0.041)	0.015 (0.010)	-0.010 (0.008)	0.012 (0.008)	N/A
Waist-hip ratio (adjusted for BMI)	57,388	0.065	-0.115 (0.042)	0.007 (0.010)	-0.022 (0.008)	0.005 (0.008)	N/A
Waist-hip ratio (men)	23,387	0.004	-0.081 (0.110)	0.026 (0.022)	-0.013 (0.018)	0.022 (0.018)	N/A
Waist-hip ratio (women)	34,203	-0.011	-0.023 (0.055)	-0.002 (0.018)	-0.006 (0.013)	-0.001 (0.013)	0.80 (-1.07, 2.68)
Waist circumference	57,641	0.103	0.084 (0.041)	0.091 (0.010)	0.017 (0.008)	0.072 (0.008)	0.19 (0.10, 0.28)
Waist circumference (adjusted for BMI)	57,435	0.129	0.147 (0.041)	0.008 (0.011)	0.029 (0.008)	0.006 (0.008)	0.83 (0.60, 1.05)
Waist circumference (men)	23,318	0.072	0.090 (0.089)	0.047 (0.025)	0.019 (0.018)	0.035 (0.018)	0.35 (0.01, 0.68)
Waist circumference (women)	34,252	0.014	0.083 (0.052)	0.017 (0.018)	0.021 (0.013)	0.012 (0.013)	0.63 (0.25, 1.01)
Hip circumference	57,559	0.066	0.173 (0.036)	0.033 (0.011)	0.039 (0.008)	0.025 (0.008)	0.61 (0.48, 0.73)
Hip circumference (adjusted for BMI)	57,359	0.070	0.292 (0.037)	0.015 (0.011)	0.065 (0.008)	0.011 (0.008)	0.85 (0.75, 0.96)
Hip circumference (men)	23,376	0.102	0.193 (0.082)	0.058 (0.026)	0.044 (0.018)	0.041 (0.018)	0.51 (0.30, 0.73)
Hip circumference (women)	34,183	0.046	0.146 (0.053)	0.026 (0.018)	0.037 (0.013)	0.019 (0.013)	0.66 (0.43, 0.89)
Age at menarche	33,518	0.022	0.021 (0.054)	0.008 (0.019)	0.005 (0.013)	0.006 (0.013)	0.49 (-0.72, 1.71)
Asthma	57,715	-0.019	-0.014 (0.054)	-0.007 (0.010)	-0.002 (0.008)	-0.006 (0.008)	0.25 (-0.67, 1.16)

Adult phenotype	***N*[a]**	**Phenotypic correlation with BW**	**Genetic correlation with BW (SE)**	**Residual correlation with BW (SE)**	**Genetic covariance with BW, gcov (SE)**	**Residual covariance with BW, rcov (SE)**	**Proportion of covariance explained by genetic variants directly genotyped: gcov/(gcov+rcov)[b] (95% CI)**
Ever smoked	56,960	0.042	-0.011 (0.049)	0.043 (0.010)	-0.002 (0.008)	0.035 (0.008)	N/A
Former smoker	50,907	0.046	-0.038 (0.059)	0.048 (0.011)	-0.006 (0.009)	0.040 (0.009)	N/A
Cigarettes per day	50,641	0.044	-0.053 (0.052)	0.049 (0.011)	-0.009 (0.009)	0.040 (0.009)	N/A
Smoking start age	19,639	-0.024	0.465 (0.239)	-0.054 (0.024)	0.043 (0.020)	-0.048 (0.020)	N/A
NFBC1966							
Triglycerides	4,954	-0.065	-0.448 (0.224)	0.022 (0.049)	-0.083 (0.038)	0.018 (0.039)	N/A
Total cholesterol	4,970	-0.021	-0.271 (0.137)	0.080 (0.054)	-0.078 (0.039)	0.057 (0.038)	N/A
High density lipoprotein	4,972	0.020	0.101 (0.125)	-0.017 (0.055)	0.031 (0.039)	-0.011 (0.038)	N/A
Low density lipoprotein	4,970	-0.013	-0.223 (0.119)	0.093 (0.058)	-0.074 (0.039)	0.062 (0.038)	N/A
Fasting glucose	4,465	-0.042	-0.184 (0.173)	0.006 (0.058)	-0.045 (0.042)	0.005 (0.042)	N/A
Fasting insulin	4,441	-0.100	-0.180 (0.214)	-0.087 (0.056)	-0.036 (0.043)	-0.067 (0.043)	0.35 (-0.07, 1.28)

[a] The number of case/control was T2D: 1,488/55,166, CAD: 1,959/55,756, obesity1: 19,820/13,802, obesity2: 4,026/13,802, obesity3: 1,146/13,802, overweight: 37,631/19,820, asthma: 7,131/50,584, ever smoker: 24,774/32,186, and former smoker: 18,721/32,186 The covariance for these traits were on the observed scale.

[b] We have put N/A (not applicable) when the genetic and residual covariances are in the opposite direction and it is not relevant to calculate gcov/(gcov + rcov). Although genetic covariance is subject to high uncertainty, there is a general pattern across both UK Biobank and the NFBC1966 that the phenotypic covariation between low BW and future cardiometabolic risk is at least in part genetically mediated.

Supplementary Table 14. List of 77 reported imprinted regions used in the current analysis.

Gene	**Type**	**Entrez ID**	**Chr**	**Gene Start site (bp, b37)**	**Gene End site (bp, b37)**
CPA4	GTEX Primary	51200	7	129,932,973	129,964,020
CST1	GTEX Primary	1469	20	23,728,189	23,731,574
DIRAS3	GTEX Primary	9077	1	68,511,644	68,516,460
DLK1	GTEX Primary	8788	14	101,193,201	101,201,467
FAM50B	GTEX Primary	26240	6	3,849,631	3,851,551
GRB10	GTEX Primary	2887	7	50,657,759	50,861,159
H19	GTEX Primary	283120	11	2,016,405	2,019,065
IGF2	GTEX Primary	3481	11	2,150,346	2,170,833
IGF2AS	GTEX Primary	51214	11	2,161,757	2,169,896
INPP5F	GTEX Primary	22876	10	121,485,608	121,588,659
KCNQ1	GTEX Primary	3784	11	2,466,220	2,870,340
KIF25	GTEX Primary	3834	6	168,418,552	168,445,769
L3MBTL1	GTEX Primary	26013	20	42,136,319	42,170,534
LPAR6	GTEX Primary	10161	13	48,985,181	49,018,840
MAGEL2	GTEX Primary	54551	15	23,888,695	23,892,993
MAGI2	GTEX Primary	9863	7	77,646,373	79,082,890
MEG3	GTEX Primary	55384	14	101,292,444	101,327,360
MEG8	GTEX Primary	79104	14	101,361,106	101,373,305
MEST	GTEX Primary	4232	7	130,126,045	130,146,131
NAP1L5	GTEX Primary	266812	4	89,617,065	89,619,023
NDN	GTEX Primary	4692	15	23,930,553	23,932,450
NTM	GTEX Primary	50863	11	131,240,370	132,206,716
PEG10	GTEX Primary	23089	7	94,285,636	94,299,006
PEG3	GTEX Primary	5178	19	57,321,444	57,352,094
PLAGL1	GTEX Primary	5325	6	144,261,436	144,385,735
PPIEL	GTEX Primary	728448	1	39,987,951	40,025,370
PPP2R5D	GTEX Primary	5528	6	42,952,329	42,980,080
PWRN1	GTEX Primary	791114	15	24,803,303	24,832,926
SGK2	GTEX Primary	10110	20	42,187,634	42,214,273
SNRPN	GTEX Primary	6638	15	25,068,793	25,223,729
SNURF	GTEX Primary	8926	15	25,200,069	25,223,729
SYCE1	GTEX Primary	93426	10	135,367,403	135,382,876
UBE3A	GTEX Primary	7337	15	25,582,395	25,684,128
UGT2B4	GTEX Primary	7363	4	70,345,882	70,361,626
UTS2	GTEX Primary	10911	1	7,907,671	7,913,551
ZDBF2	GTEX Primary	57683	2	207,139,522	207,179,148
ZNF331	GTEX Primary	55422	19	54,024,176	54,083,523
ZNF597	GTEX Primary	146434	16	3,486,109	3,493,490
ABCA6	GTEX suggestive (S4 unique)	23460	17	67,074,846	67,138,015
BMP8A	GTEX suggestive (S4 unique)	353500	1	39,957,317	39,995,541
CHIT1	GTEX suggestive (S4 unique)	1118	1	203,185,206	203,198,860
DLGAP2	GTEX suggestive (S4 unique)	9228	8	1,449,568	1,656,642
DZIP1	GTEX suggestive (S4 unique)	22873	13	96,230,455	96,296,957
EMR1	GTEX suggestive (S4 unique)	2015	19	6,887,581	6,940,464
FKBP10	GTEX suggestive (S4 unique)	60681	17	39,968,961	39,979,469
GPR1	GTEX suggestive (S4 unique)	2825	2	207,040,041	207,082,771
GTSF1	GTEX suggestive (S4 unique)	121355	12	54,849,735	54,867,386
GUCY1B2	GTEX suggestive (S4 unique)	2974	13	51,568,646	51,640,293
KIR3DX1	GTEX suggestive (S4 unique)	90011	19	55,043,908	55,055,195
LRRTM1	GTEX suggestive (S4 unique)	347730	2	80,529,002	80,531,487

Gene	**Type**	**Entrez ID**	**Chr**	**Gene Start site (bp, b37)**	**Gene End site (bp, b37)**
MYOM2	GTEX suggestive (S4 unique)	9172	8	1,993,157	2,093,380
RTL1	GTEX suggestive (S4 unique)	388015	14	101,346,991	101,351,184
SERPINA6	GTEX suggestive (S4 unique)	866	14	94,770,584	94,789,688
SLC10A2	GTEX suggestive (S4 unique)	6555	13	103,696,347	103,719,196
THNSL2	GTEX suggestive (S4 unique)	55258	2	88,469,834	88,486,146
ANO1	GTEX consistent (S6)	55107	11	69,924,407	70,035,652
CALCR	GTEX consistent (S6)	799	7	93,053,798	93,204,042
CDKN1C	GTEX consistent (S6)	1028	11	2,904,447	2,906,995
COPG2	GTEX consistent (S6)	26958	7	130,146,079	130,353,598
DCN	GTEX consistent (S6)	1634	12	91,539,034	91,576,806
DIO3	GTEX consistent (S6)	1735	14	102,027,687	102,029,789
DLX5	GTEX consistent (S6)	1749	7	96,649,701	96,654,143
GABRA5	GTEX consistent (S6)	2558	15	27,111,865	27,194,357
GABRG3	GTEX consistent (S6)	2567	15	27,216,428	27,778,373
GLIS3	GTEX consistent (S6)	169792	9	3,824,127	4,300,035
GNAS-AS1	GTEX consistent (S6)	149775	20	57,393,972	57,425,958
KLF14	GTEX consistent (S6)	136259	7	130,417,395	130,418,888
MKRN3	GTEX consistent (S6)	7681	15	23,810,453	23,813,166
NNAT	GTEX consistent (S6)	4826	20	36,149,606	36,152,090
C15orf2	GTEX consistent (S6)	23742	15	24,920,540	24,928,593
PON3	GTEX consistent (S6)	5446	7	94,989,183	95,025,687
RB1	GTEX consistent (S6)	5925	13	48,877,882	49,056,026
RBP5	GTEX consistent (S6)	83758	12	7,276,279	7,281,466
SGCE	GTEX consistent (S6)	8910	7	94,214,535	94,285,521
TH	GTEX consistent (S6)	7054	11	2,185,158	2,193,035
TSPAN32	GTEX consistent (S6)	10077	11	2,323,242	2,339,430
TSSC4	GTEX consistent (S6)	10078	11	2,423,522	2,425,106

These 77 regions were highlighted in reference 10: Baran Y *et al*. *Genome Res* **25**, 927-936 (2015).

Supplementary Table 15. Comparison of variance in BW between individuals heterozygous and homozygous for each of the 59 autosomal BW index SNPs (plus *DLK1*) in 57,715 UK Biobank samples.

Locus	**Index variant**	**Alleles A/B**	**Variance**			**Effect**		
			AA	**AB**	**BB**	**β**	**SE**	***P*-value**
WNT4-ZBTB40	rs2473248	T/C	1.008	0.971	1.007	-0.015	0.006	0.99
ZBTB7B	rs3753639	T/C	0.994	1.004	1.026	0.002	0.005	0.34
FCGR2B	rs72480273	A/C	0.995	1.008	1.012	0.008	0.005	6.4x10^{-2}
DTL	rs61830764	G/A	0.997	0.993	1.031	-0.004	0.005	0.81
ATAD2B	rs7575873	A/G	1.007	0.978	0.964	-0.014	0.006	0.99
EPAS1	rs1374204	C/T	0.968	0.999	1.005	-0.002	0.005	0.68
PTH1R	rs2242116	A/G	1.003	0.987	1.013	-0.010	0.005	0.98
ADCY5	rs11719201	C/T	0.984	1.019	1.023	0.016	0.005	1.1x10^{-3}
CPA3	rs10935733	T/C	0.999	1.007	0.990	0.009	0.005	3.7x10^{-2}
CCNL1-LEKR1	rs13322435	A/G	1.016	0.993	0.981	-0.007	0.005	0.91
LCORL	rs925098	G/A	1.011	0.996	1.001	-0.002	0.005	0.64
HHIP	rs6537307	A/G	0.972	1.004	1.019	0.005	0.005	0.18
5q11.2	rs854037	A/G	1.004	0.990	1.008	-0.009	0.005	0.95
EBF1	rs7729301	G/A	1.028	0.990	1.003	-0.007	0.005	0.93
CDKAL1	rs35261542	C/A	1.004	0.998	0.969	2x10^{-4}	0.005	0.48
HIST1H2BE	rs9379832	A/G	1.004	0.995	0.995	-0.004	0.005	0.80
HMGA1	rs7742369	A/G	0.995	1.005	1.044	0.002	0.005	0.36
L3MBTL3	rs1415701	G/A	1.006	0.990	1.006	-0.009	0.005	0.96
ESR1	rs1101081	C/T	1.003	0.999	0.979	0.001	0.005	0.39
GNA12	rs798489	C/T	1.005	0.993	0.997	-0.005	0.005	0.81
IGF2BP3	rs11765649	T/C	1.004	0.991	1.007	-0.005	0.005	0.83
TBX20	rs6959887	A/G	0.998	1.001	0.999	0.004	0.005	0.21
YKT6-GCK	rs138715366	C/T	1.001	0.888	0.657	-0.070	0.019	1.00
MLXIPL	rs62466330	T/C	0.995	1.028	1.036	0.016	0.007	1.3x10^{-2}
ANK1-NKX6-3	rs13266210	A/G	1.007	0.984	1.009	-0.013	0.005	0.99
TRIB1	rs6989280	G/A	0.997	1.005	0.992	0.005	0.005	0.18
SLC45A4	rs12543725	G/A	1.009	0.994	0.999	-0.009	0.005	0.97
PTCH1	rs28510415	A/G	0.999	0.999	1.017	1x10^{-4}	0.007	0.49
LPAR1	rs2150052	A/T	0.980	1.002	1.015	0.002	0.005	0.37
PHF19	rs7847628	A/G	0.984	1.002	1.001	0.003	0.005	0.30
STRBP	rs700059	G/A	0.989	1.018	0.994	0.015	0.006	4.4x10^{-3}
HHEX-IDE	rs61862780	T/C	1.005	0.996	1.003	-0.005	0.005	0.82
NT5C2	rs74233809	T/C	0.999	0.998	1.136	3x10^{-4}	0.007	0.48
ADRB1	rs7076938	C/T	0.992	1.003	0.998	6x10^{-4}	0.005	0.45
PLEKHA1	rs2421016	C/T	0.988	1.007	0.998	0.008	0.005	6.1x10^{-2}
INS-IGF2	rs72851023	C/T	0.996	1.022	1.013	0.013	0.007	3.4x10^{-2}
MTNR1B	rs10830963	C/G	0.994	1.008	0.997	0.005	0.005	0.18
APOLD1	rs11055034	C/A	1.002	1.000	0.985	2x10^{-4}	0.005	0.49
ABCC9	rs139975827	G/A	1.006	1.000	0.982	2x10^{-4}	0.005	0.48
ITPR2	rs12823128	T/C	1.014	0.993	0.998	-0.006	0.005	0.87
HMGA2	rs1351394	T/C	1.003	1.001	0.993	9x10^{-4}	0.005	0.43
IGF1	rs7964361	G/A	0.999	1.006	0.991	0.003	0.007	0.35
LINC00332	rs2324499	G/C	1.000	0.998	1.004	-0.003	0.005	0.70
RB1	rs2854355	A/G	0.991	1.008	1.024	0.008	0.005	5.4x10^{-2}
RNF219-AS1	rs1819436	T/C	1.034	1.003	0.998	5x10^{-4}	0.006	0.47
DLK1	rs6575803	C/T	1.002	0.991	0.987	-0.007	0.006	0.87
FES	rs12906125	G/A	1.004	0.993	1.010	-0.005	0.005	0.86
IGF1R	rs7402982	A/G	0.994	0.998	1.006	-0.003	0.005	0.73

Locus	**Index variant**	**Alleles A/B**	**Variance**			**Effect**		
			AA	**AB**	**BB**	**β**	**SE**	***P*-value**
GPR139	rs1011939	G/A	1.022	1.006	0.991	0.005	0.005	0.14
CLDN7	rs113086489	C/T	0.991	1.002	1.002	0.001	0.005	0.41
SUZ12P1-CRLF3	rs144843919	G/A	1.000	0.990	0.955	-0.006	0.010	0.72
SP6-SP2	rs12942207	C/T	1.018	1.005	0.992	0.006	0.005	0.12
ACTL9	rs61154119	T/G	0.998	1.007	0.974	0.003	0.006	0.30
PEPD	rs10402712	G/A	1.005	0.993	0.998	-0.004	0.005	0.78
JAG1	rs6040076	G/C	0.989	1.003	1.003	0.004	0.005	0.22
C20orf203	rs28530618	A/G	1.002	1.000	0.997	$4\text{x}10^{-4}$	0.005	0.47
MAFB	rs6016377	C/T	0.988	0.999	1.021	$2\text{x}10^{-4}$	0.005	0.48
NRIP1	rs2229742	G/C	1.002	0.991	0.939	-0.006	0.006	0.83
KREMEN1	rs134594	C/T	1.020	1.009	0.983	0.005	0.005	0.14
SREBF2	rs62240962	C/T	1.003	0.985	0.983	-0.008	0.007	0.89

The beta value is a parameter of the Brown-Forsythe test that measures how different the mean absolute deviations (MADs) are from the respective group medians in the heterozygous vs the homozygous group. SE, standard error.

Supplementary Table 16. Parent-of-origin specific analysis at 59 autosomal BW loci (plus *DLK1*) in 4,908 ALSPAC mother-child pairs.

Locus	SNP	EA/ NEA	Paternal transmission			Maternal transmission			*P*_het
			β	SE	*P*-value	β	SE	*P*-value	
WNT4-ZBTB40	rs2473248	C/T	0.019	0.042	0.65	0.189	0.076	1.3x10^{-2}	6.1x10^{-2}
ZBTB7B	rs3753639	C/T	0.012	0.034	0.72	0.078	0.045	8.5x10^{-2}	0.34
FCGR2B	rs72480273	C/A	0.097	0.037	8.0x10^{-3}	0.060	0.047	0.20	0.17
DTL	rs61830764	A/G	0.067	0.031	2.8x10^{-2}	0.096	0.030	1.7x10^{-3}	0.44
ATAD2B	rs7575873	A/G	0.080	0.041	5.3x10^{-2}	0.086	0.072	0.23	0.36
EPAS1	rs1374204	T/C	0.094	0.032	3.7x10^{-3}	0.121	0.037	1.1x10^{-3}	0.98
PTH1R	rs2242116	A/G	0.007	0.031	0.83	0.064	0.033	5.2x10^{-2}	9.8x10^{-2}
ADCY5	rs11719201	T/C	0.137	0.034	4.5x10^{-3}	0.062	0.035	7.5x10^{-2}	0.11
CPA3	rs10935733	T/C	0.052	0.029	7.7x10^{-2}	0.013	0.031	0.67	0.19
CCNL1-LEKR1	rs13322435	A/G	0.117	0.031	1.4x10^{-4}	0.088	0.032	5.9x10^{-3}	0.48
LCORL	rs925098	G/A	0.128	0.033	1.1x10^{-4}	0.063	0.042	0.13	0.18
HHIP	rs6537307	G/A	0.080	0.030	8.1x10^{-3}	0.071	0.030	1.9x10^{-2}	0.79
5q11.2	rs854037	A/G	0.078	0.037	3.5x10^{-2}	0.081	0.043	5.8x10^{-2}	0.90
EBF1	rs7729301	A/G	-0.006	0.034	0.86	-0.028	0.041	0.50	0.67
CDKAL1	rs35261542	C/A	0.101	0.033	2.1x10^{-3}	0.040	0.041	0.32	8.3x10^{-2}
HIST1H2BE	rs9379832	A/G	0.034	0.033	0.30	0.037	0.038	0.33	0.83
HMGA1	rs7742369	G/A	0.046	0.038	0.23	0.161	0.051	1.6x10^{-3}	0.10
L3MBTL3	rs1415701	G/A	0.029	0.033	0.38	0.092	0.042	2.8x10^{-2}	9.2x10^{-2}
ESR1	rs1101081	C/T	0.074	0.033	2.5x10^{-2}	0.025	0.039	0.53	0.16
GNA12	rs798489	C/T	0.011	0.033	0.74	0.043	0.040	0.29	0.35
IGF2BP3	rs11765649	T/C	-0.013	0.033	0.69	0.054	0.036	0.14	0.14
TBX20	rs6959887	A/G	0.035	0.032	0.27	0.035	0.033	0.29	0.94
YKT6-GCK	rs138715366	C/T	0.235	0.166	0.16	0.032	0.468	0.95	0.66
MLXIPL	rs62466330	C/T	0.107	0.053	4.5x10^{-2}	0.166	0.094	7.8x10^{-2}	0.87
ANK1-NKX6-3	rs13266210	A/G	0.039	0.036	0.28	-0.031	0.041	0.45	0.21
TRIB1	rs6989280	G/A	-0.012	0.034	0.73	0.018	0.040	0.66	0.60
SLC45A4	rs12543725	G/A	0.052	0.030	8.6x10^{-2}	0.047	0.030	0.12	0.90
PTCH1	rs28510415	G/A	0.091	0.047	5.4x10^{-2}	0.212	0.092	2.1x10^{-2}	0.39
LPAR1	rs2150052	T/A	-0.001	0.030	0.97	0.092	0.030	2.0x10^{-3}	2.4x10^{-3}
PHF19	rs7847628	G/A	0.038	0.032	0.23	0.004	0.037	0.92	0.28
STRBP	rs700059	G/A	0.043	0.041	0.29	-0.029	0.070	0.68	0.22
HHEX-IDE	rs61862780	T/C	0.085	0.030	4.7x10^{-3}	0.050	0.030	9.6x10^{-2}	0.32
NT5C2	rs74233809	C/T	-0.018	0.051	0.73	0.040	0.068	0.56	0.51
ADRB1	rs7076938	T/C	0.023	0.033	0.49	0.078	0.041	5.5x10^{-2}	0.27
PLEKHA1	rs2421016	T/C	0.024	0.031	0.43	0.036	0.031	0.24	0.77
INS-IGF2	rs72851023	T/C	0.116	0.051	2.2x10^{-2}	0.108	0.107	0.31	0.56
MTNR1B	rs10830963	G/C	0.024	0.033	0.46	0.058	0.040	0.15	0.53
APOLD1	rs11055034	C/A	0.122	0.032	1.7x10^{-4}	0.053	0.039	0.17	3.2x10^{-2}
ABCC9	rs139975827	G/A	0.045	0.031	0.15	0.017	0.032	0.59	0.46
ITPR2	rs12823128	T/C	0.064	0.030	3.0x10^{-2}	-0.003	0.029	0.91	7.7x10^{-2}
HMGA2	rs1351394	T/C	0.015	0.031	0.63	0.082	0.031	8.3x10^{-3}	8.0x10^{-2}
IGF1	rs7964361	A/G	-0.045	0.049	0.36	0.091	0.099	0.36	0.33
LINC00332	rs2324499	G/C	0.012	0.032	0.70	0.041	0.034	0.22	0.70
RB1	rs2854355	G/A	0.031	0.033	0.35	-0.012	0.042	0.77	0.25
RNF219-AS1	rs1819436	C/T	0.038	0.042	0.36	0.136	0.079	8.4x10^{-2}	0.39
DLK1	rs6575803	C/T	0.104	0.045	2.2x10^{-2}	0.205	0.091	2.5x10^{-2}	0.40
FES	rs12906125	G/A	0.019	0.032	0.55	0.095	0.035	6.7x10^{-3}	9.3x10^{-2}
IGF1R	rs7402982	A/G	0.047	0.031	0.13	0.036	0.032	0.25	0.78

Locus	**SNP**	**EA/ NEA**	**Paternal transmission**			**Maternal transmission**			***P*_het**
			β	**SE**	***P*-value**	**β**	**SE**	***P*-value**	
GPR139	rs1011939	G/A	-0.028	0.032	0.38	0.021	0.038	0.59	0.29
CLDN7	rs113086489	T/C	0.061	0.031	$4.9\text{x}10^{-2}$	0.050	0.031	0.11	0.83
SUZ12P1-CRLF3	rs144843919	G/A	0.003	0.071	0.96	0.182	0.113	0.11	0.20
SP6-SP2	rs12942207	C/T	0.050	0.032	0.12	0.027	0.038	0.48	0.32
ACTL9	rs61154119	T/G	0.056	0.038	0.14	0.164	0.062	$8.7\text{x}10^{-3}$	$5.6\text{x}10^{-2}$
PEPD	rs10402712	A/G	0.077	0.033	$2.1\text{x}10^{-2}$	0.001	0.034	0.98	0.10
JAG1	rs6040076	C/G	0.028	0.031	0.36	0.001	0.031	0.97	0.53
C20orf203	rs28530618	A/G	0.053	0.031	$8.3\text{x}10^{-2}$	0.013	0.031	0.68	0.26
MAFB	rs6016377	T/C	0.054	0.031	$8.0\text{x}10^{-2}$	0.008	0.031	0.80	0.20
NRIP1	rs2229742	G/C	0.020	0.046	0.66	0.030	0.095	0.75	0.89
KREMEN1	rs134594	C/T	0.024	0.031	0.43	0.052	0.035	0.13	0.75
SREBF2	rs62240962	C/T	-0.004	0.052	0.94	0.088	0.065	0.18	0.40

EA, effect allele; NEA, non effect allele; SE, standard error; *P*_het, *P*-value for difference in BW between AB heterozygote offspring inheriting allele A from mother and B from father, and those inheriting A from father and B from mother.

Supplementary Table 17. Association of BW signals with various adult metabolic and anthropometric traits. (GWAS look-ups)

Provided in a separate Excel file.

Supplementary Table 18. Effect of transmitted and untransmitted maternal haplotype scores on BW in 5,201 ALSPAC mother-child pairs.

Haplotype score	**Height**			**Systolic blood pressure**			**Type 2 diabetes**		
	β	**SE**	***P*-value**	**β**	**SE**	***P*-value**	**β**	**SE**	***P*-value**
M1 (C1)	0.128	0.013	1.6×10^{-21}	-6.82	3.36	0.04	-0.44	1.73	0.80
M2	0.010	0.012	0.39	-6.40	2.63	0.02	1.66	1.42	0.24
C2	0.066	0.012	1.2×10^{-7}	0.14	2.62	0.96	-2.94	1.47	0.045

Beta values are in grams per weighted trait-raising allele. SE, standard error.
M1(C1), maternal transmitted haplotype score; M2, Maternal untransmitted haplotype score; C2, paternal transmitted haplotype score.

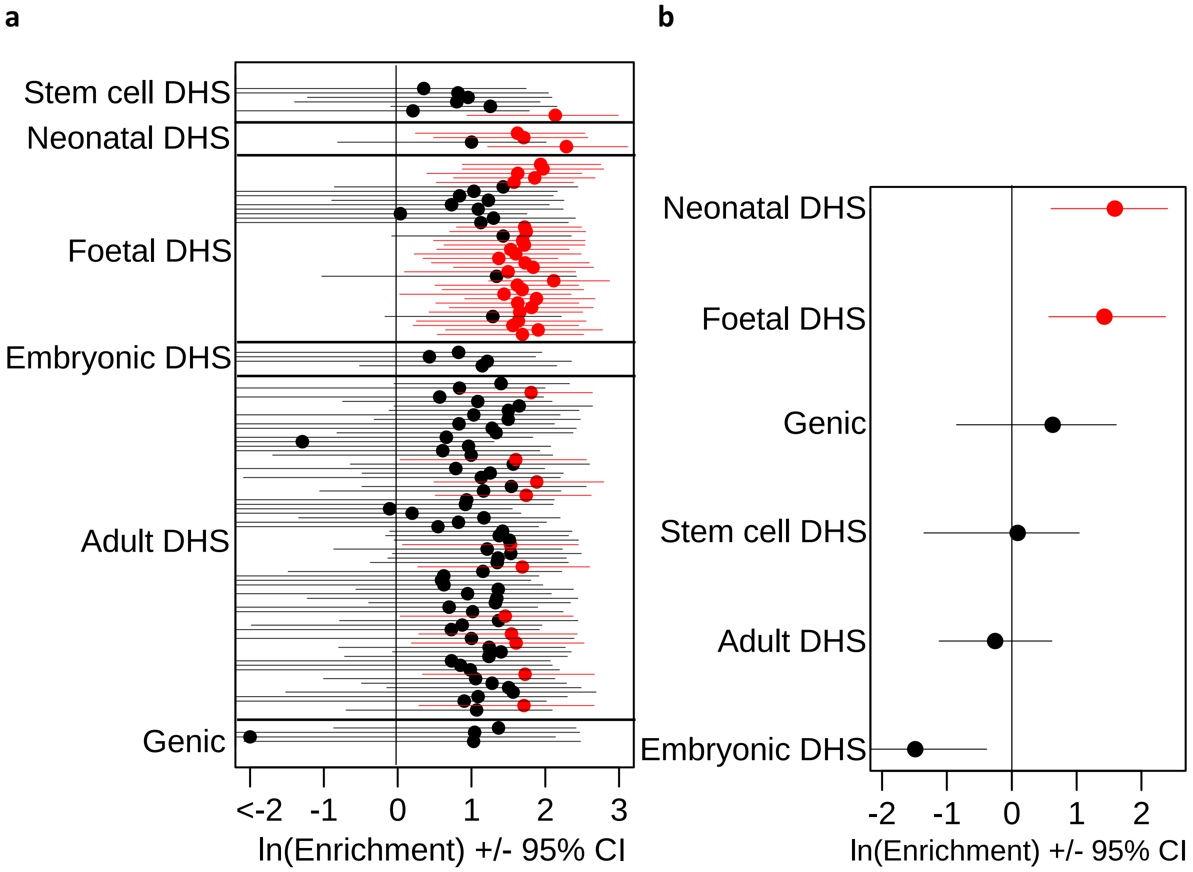
Supplementary Table 19. Reciprocal approximate conditional analyses at *YKT6-GCK* variants associated with birth weight (BW) or fasting glucose (FG), in European ancestry meta-analysis of up to 143,677 individuals.

Variant (chr:position)	Type	EA/ NEA	EAF (Eur)	BW SNP conditioned on FG SNP				FG SNP conditioned on BW SNP			
				Unconditioned *P*	**Conditioned on**	**Variant type**	**Conditioned *P***	**Variant**	**Conditioned on**	**Unconditioned *P***	**Conditioned *P***
rs138715366 (7:44246271)	BW lead SNP (at *YKT6* intron 1)	T/C	0.0089	7.2×10^{-26}	unconditioned	-	-	-	-	-	-
					rs878521	*GCK* FG primary (ENGAGE[1])	1.3×10^{-25}	rs878521	rs138715366	0.12	0.28
					rs10259649	*GCK* FG secondary (ENGAGE[1])	7.7×10^{-26}	rs10259649	rs138715366	0.52	0.63
					rs4607517	*GCK* FG (MAGIC[2])	2.6×10^{-25}	rs4607517	rs138715366	3.2×10^{-4}	1.2×10^{-3}
					rs10278336	*GCK* T2D (DIAGRAM[3])	1.8×10^{-25}	rs10278336	rs138715366	0.057	0.19
rs78412508 (7:44223858)	BW second strongest SNP (at *GCK* intron 3)	A/G	0.0095	8.9×10^{-24}	unconditioned	-	-	-	-	-	-
					rs878521	*GCK* FG primary (ENGAGE[1])	1.6×10^{-23}	rs878521	rs78412508	0.12	0.27
					rs10259649	*GCK* FG secondary (ENGAGE[1])	9.7×10^{-24}	rs10259649	rs78412508	0.52	0.66
					rs4607517	*GCK* FG (MAGIC[2])	3.1×10^{-23}	rs4607517	rs78412508	3.2×10^{-4}	1.2×10^{-3}
					rs10278336	*GCK* T2D (DIAGRAM[3])	2.2×10^{-23}	rs10278336	rs78412508	0.057	0.18

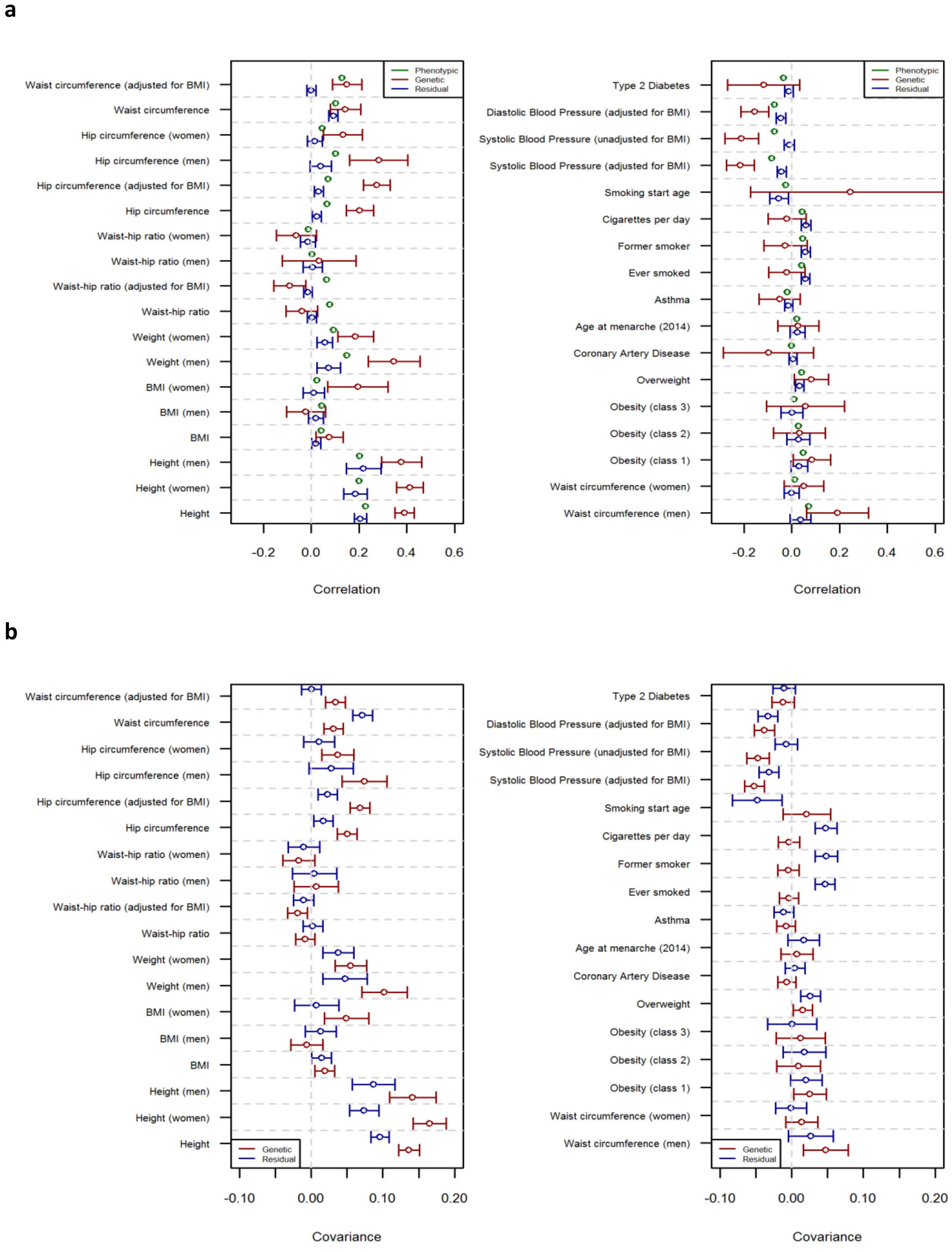
EA, effect allele; NEA, non effect allele, EAF, effect allele frequency; Eur, European; BW, birth weight; FG, fasting glucose; T2D, type 2 diabetes.

1. Horikoshi M *et al*. PLoS Genet 11, e1005230 (2015).
2. Dupuis J *et al*. Nat Genet 42, 105-116 (2010).
3. Morris AP *et al*. Nat Genet 44, 981-990 (2012).

Supplementary Figure 1. BW association enrichment for DNaseI hypersensitive (DHS) sites in 128 cell types and four genic annotations. a, Each cell type DHS annotation and four gene-based annotations were individually tested for enrichment using the Bayes Factors for all variants in the 62 credible sets. The effect estimate (filled circle) and 95% CI (horizontal line) are plotted on the *x* axis. The 128 cell types (listed on the *y* axis; see Supplementary Table 8 for details) are categorised according to the description fields from ENCODE (stem cell, neonatal, foetal, embryonic and adult groups). We considered an annotation enriched if the 95% CI did not overlap zero (highlighted in red). **b,** Estimated effect of enrichment (filled circle) and 95% CI (horizontal line) for each categorical field, tested in a joint model, are plotted (see Methods).



Supplementary Figure 2. Estimates of phenotypic, genetic and residual correlations (a) and estimates of genetic and residual covariance (b) between birth weight and adult metabolic or anthropometric traits in UK Biobank 'white British' samples (up to N=57,715). See details in Supplementary Table 13.



Full grants and funding supports for contributing studies.

1958 British Birth Cohort acknowledges use of phenotype and genotype data from the British 1958 Birth Cohort DNA collection, funded by the Medical Research Council grant G0000934 and the Wellcome Trust grant 068545/Z/02. Genotyping for the B58C-WTCCC subset was funded by the Wellcome Trust grant 076113/B/04/Z. The B58C-T1DGC genotyping utilised resources provided by the Type 1 Diabetes Genetics Consortium, a collaborative clinical study sponsored by the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), National Institute of Allergy and Infectious Diseases (NIAID), National Human Genome Research Institute (NHGRI), National Institute of Child Health and Human Development (NICHD), and Juvenile Diabetes Research Foundation International (JDRF) and supported by U01 DK062418. B58C-T1DGC GWAS data were deposited by the Diabetes and Inflammation Laboratory, Cambridge Institute for Medical Research (CIMR), University of Cambridge, which is funded by Juvenile Diabetes Research Foundation International, the Wellcome Trust and the National Institute for Health Research Cambridge Biomedical Research Centre; the CIMR is in receipt of a Wellcome Trust Strategic Award (079895). The B58C-GABRIEL genotyping was supported by a contract from the European Commission Framework Programme 6 (018996) and grants from the French Ministry of Research.

ALSPAC is supported by the UK Medical Research Council and the Wellcome Trust (Grant ref: 102215/2/13/2), and the University of Bristol provide core support for ALSPAC.

Barcelona Supercomputing Center This work has been sponsored by the grant SEV-2011-00067 of Severo Ochoa Program, awarded by the Spanish Government. This work was supported by an EFSD/Lilly research fellowship.

CHOP was financially supported by an Institute Development Award from the Children’s Hospital of Philadelphia, a Research Development Award from the Cotswold Foundation, NIH grant R01 HD056465 and the Daniel B. Burke Endowed Chair for Diabetes Research (SFAG).

CLHNS was supported by National Institutes of Health grants DK078150, TW05596 and HL085144 and pilot funds from RR20649, ES10126, and DK056350.

The **CoLaus** study was and is supported by research grants from GlaxoSmithKline, the Faculty of Biology and Medicine of Lausanne, and the Swiss National Science Foundation (grants 33CSCO-122661, 33CS30-139468 and 33CS30-148401).

COPSACs greatly acknowledge the private and public research funding allocated to COPSAC and listed on www.copsac.com, with special thanks to The Lundbeck Foundation; Ministry of Health; Danish Council for Strategic Research; The Danish Council for Independent Research and The Capital Region Research Foundation as core supporters. The funding agencies did not have any influence on study design, data collection and analysis, decision to publish or preparation of the manuscript. No pharmaceutical company was involved in the study.

DNBC was established with the support of a major grant from the Danish National Research Foundation. Additional support for the DNBC has been obtained from the Danish Pharmacists’ Fund, the Egmont Foundation, the March of Dimes Birth Defects Foundation, the Augustinus Foundation and the Health Fund of the Danish Health Insurance Societies. The generation of GWAS genotype data for the DNBC samples was carried out within the GENEVA consortium with funding provided through the NIH Genes, Environment and Health Initiative (GEI) (U01HG004423, U01HG004438, U01HG004446).

EPIC-Norfolk is supported by Cancer Research UK (SP2024-0201 and SP2024-0204) and the Medical Research Council (G9502233).

The **ERF** study as a part of EUROSPAN (European Special Populations Research Network) was supported by European Commission FP6 STRP grant number 018947 (LSHG-CT-2006-01947) and also received funding from the European Community's Seventh Framework Programme (FP7/2007-2013)/grant agreement HEALTH-F4-2007-201413 by the European Commission under the programme "Quality of Life and Management of the Living Resources" of 5th Framework Programme (no. QLG2-CT-2002-01254). The ERF study was further supported by ENGAGE consortium and Center for Medical Systems Biology (CMSB). High-throughput analysis of the ERF data was supported by joint grant from Netherlands Organisation for Scientific Research and the Russian Foundation for Basic Research (NWO-RFBR 047.017.043).

The **Fenland** Study is funded by the Medical Research Council (MC_U106179471) and Wellcome Trust.

The general design of **Generation R** Study is made possible by financial support from the Erasmus Medical Center, Rotterdam, the Erasmus University Rotterdam, the Netherlands Organization for Health Research and Development (ZonMw), the Netherlands Organisation for Scientific Research (NWO), the Ministry of Health, Welfare and Sport and the Ministry of Youth and Families.

GOYA study was conducted as part of the activities of the Gene-diet Interactions in Obesity project (GENDINOB, www.gendinob.dk) and the MRC Integrative Epidemiology Unit at the University of Bristol (MC_UU_12013/1-9).

HAPO was supported by US National Institutes of Health (NIH) grants (HD34242, HD34243, HG004415, and DK099820) and by the American Diabetes Association.

HBCS received financial support from the Academy of Finland (project grants 120315, 129287, 218029 and 267561).

Hong Kong HAPO follow-up study was supported by Research Grant Council General Research Fund (CU473408, CU471713) and CUHK Faculty of Medicine Outstanding Fellowship.

INMA study was funded by grants from Instituto de Salud Carlos III (Red INMA G03/176 and CB06/02/0041), FIS-FEDER 03/1615, 04/1509, 04/1112, 04/1931, 05/1079, 05/1052, 06/1213, 07/0314, 09/02647, 11/01007, 11/02591, 13/02032, 13/1944, PI041436, PI081151, 11/00178, 97/0588, 00/0021-2, PI061756, PS0901958, 14/00891, and 14/01687, Spanish Ministry of Science and Innovation (SAF2008-00357), European Commission (ENGAGE project and grant agreement HEALTH-F4-2007-201413), Fundació La Marató de TV3, Generalitat de Catalunya-CIRIT 1999SGR 00241 and Conselleria de Sanitat Generalitat Valenciana. Part of the DNA extractions and genotyping was performed at the Spanish National Genotyping Centre (CEGEN-Barcelona).

Inter99 The Novo Nordisk Foundation Center for Basic Metabolic Research is an independent Research Center at the University of Copenhagen partially funded by an unrestricted donation from the Novo Nordisk Foundation (www.metabol.ku.dk). The study was financially supported by research grants from the Danish Research Council, the Danish Centre for Health Technology Assessment, Novo Nordisk Inc., Research Foundation of Copenhagen County, Ministry of Internal Affairs and Health, the Danish Heart Foundation, the Danish Pharmaceutical Association, the Augustinus Foundation, the Ib Henriksen Foundation, the Becket Foundation, and the Danish Diabetes Association.

Leipzig-Childhood-Obesity was supported by grants from Integrated Research and Treatment Center (IFB) Adiposity Diseases 01EO1001, from the German Research Foundation for the Collaborative Research Center CRC1085 “Atherobesity” project C05, and by the European Commission (Beta-JUDO n° 279153).

The **NEO** study is supported by the participating Departments, the Division and the Board of Directors of the Leiden University Medical Center, and by the Leiden University, Research Profile Area Vascular and Regenerative Medicine.

The Northern Finland Birth Cohort (NFBC) Research program, including the study of the NFBC 1966 and 1986 studies, received financial support from Academy of Finland (1114194, 24300796), NHLBI grant 5R01HL087679 through the STAMPEED program (1RL1MH083268-01), ENGAGE project and grant agreement HEALTH-F4-2007-201413, the Medical Research Council (grant G0500539, centre grant G0600705, PrevMetSyn), and the Wellcome Trust (project grant GR069224), UK. The program is currently being funded by the H2020-633595 DynaHEALTH action and Academy of Finland EGEA-project.

NTR obtained funding from the Netherlands Organization for Scientific Research (NWO: MagW/ZonMW grants 916-76-125, 904-61-090, 985-10-002,904-61-193,480-04-004, 400-05-717, 481-08-011, 451- 04-034, 463-06-001, 912-10-020, Addiction- 31160008 Middelgroot-911-09-032, Spinozapremie 56-464-14192), Center for Medical Systems Biology (CMSB, NWO Genomics), NBIC/BioAssist/RK(2008.024), Biobanking and Biomolecular Resources Research Infrastructure (BBMRI-NL), the VU University's Institute for Health and Care Research (EMGO+) and Neuroscience Campus Amsterdam (NCA), the European Science Foundation (ESF, EU/QLRT-2001-01254), the European Community's Seventh Framework Program (FP7/2007- 2013), ENGAGE (HEALTH-F4-2007-201413); the European Research Council (ERC Advanced, 230374), Rutgers University Cell and DNA Repository (National Institute of Mental Health (NIMH) U24 MH068457-06), and the National Institutes of Health (NIH, R01D0042157-01A; 1RC2MH089995-01; R01DK092127-01). Part of the genotyping and analyses were funded by the Genetic Association Information Network (GAIN) of the Foundation for the US National Institutes of Health, and by grants from GAIN and the NIMH (MH081802).

ORCADES was supported by the Chief Scientist Office of the Scottish Government (CZB/4/276 and CZB/4/710), the Royal Society, the MRC Human Genetics Unit, Arthritis Research UK and the European Union framework program 6 EUROSPAN project (contract no. LSHG-CT-2006-018947).

The **PANIC** study has been financially supported by grants from Ministry of Social Affairs and Health of Finland, Ministry of Education and Culture of Finland, Finnish Innovation Fund Sitra, Social Insurance Institution of Finland, Finnish Cultural Foundation, Juho Vainio Foundation, Foundation for Paediatric Research, Paavo Nurmi Foundation, Paulo Foundation, Diabetes Research Foundation, Research Committee of the Kuopio University Hospital Catchment Area (State Research Funding), Kuopio University Hospital (EVO funding number 5031343) and the city of Kuopio.

RAINE study was supported by the National Health and Medical Research Council of Australia (grant numbers 572613, 403981 and 003209) and the Canadian Institutes of Health Research (grant number MOP-82893).

SCORM was funded by National Medical Research Foundation, Singapore (NMRC/0975/2005) and Biomedical Research Council, Singapore (BMRC 06/1/21/19/466).

SORBS was supported by grants from the German Research Council (DFG - SFB 1052 “Obesity mechanisms”; A01, B01, B03, C01 and SPP 1629 TO 718/2-1), from the German Diabetes Association and from the DHFD (Diabetes Hilfs- und Forschungsfonds Deutschland).

STRIP was supported by Academy of Finland (grants 206374, 251360 and 276861); Juho Vainio Foundation; Finnish Cardiac Research Foundation; Finnish Cultural Foundation; Finnish Ministry of Education and Culture; Sigrid Juselius Foundation; Yrjö Jahnsson Foundation; C.G. Sundell Foundation;

Special Governmental Grants for Health Sciences Research, Turku University Hospital; Foundation for Pediatric Research; and Turku University Foundation.

TEENAGE study has been co-financed by the European Union (European Social Fund (ESF)) and Greek national funds through the Operational Program “Education and Lifelong Learning” of the National Strategic Reference Framework (NSRF)—Research Funding Program: Heracleitus II. Investing in knowledge society through the European Social Fund. This work was funded by the Wellcome Trust (098051).

TDCOB received supports from the Danish Innovation Foundation and The Region Zealand Health and Medical Research Foundation. This study was partly supported by grants from the Program Committee for Individuals, Disease and Society of the Danish Innovation Foundation (grant numbers: 0603-00484B and 0603-00457B) and was part of the research activities in The Impact of our Genomes on Individual Treatment Response in Obese Children (TARGET, www.target.ku.dk) and the Indo-Danish bi-lateral project, Genetics and Systems Biology of Childhood Obesity in India and Denmark (BioChild, www.biochild.ku.dk).

The Novo Nordisk Foundation Center for Basic Metabolic Research, an independent Research Center at the University of Copenhagen, partially funded by an unrestricted donation from the Novo Nordisk Foundation.

University of Oxford, UK, was funded by the British Heart Foundation (grant code SP/13/2/30111), the European Commission (ENGAGE: HEALTH-F4-2007-201413), Medical Research Council (G0601261), and the Wellcome Trust (090532, 098381).

The **Young Finns Study** has been financially supported by the Academy of Finland: grants 286284 (T.L.), 134309 (Eye), 126925, 121584, 124282, 129378 (Salve), 117787 (Gendi), and 41071 (Skidi); the Social Insurance Institution of Finland; Kuopio, Tampere and Turku University Hospital Medical Funds (grant X51001 for T.L.); Juho Vainio Foundation; Paavo Nurmi Foundation; Finnish Foundation of Cardiovascular Research (T.L.); Finnish Cultural Foundation; Tampere Tuberculosis Foundation (T.L.); Emil Aaltonen Foundation (T.L.); and Yrjö Jahnsson Foundation (T.L.).

Grants and funding supports for CHARGE Consortium Hematology Working Group

AGES Funding for Age, Gene/Environment Susceptibility Reykjavik Study (AGES) was made possible by NIA/NIH contract AG000932-2 (2009) Characterization of Normal Genomic Variability. AGES is funded by NIH contract N01-AG-12100, the NIA Intramural Research Program, Hjartavernd (the Icelandic Heart Association) and the Althingi (the Icelandic Parliament).

ARIC The Atherosclerosis Risk in the Communities Study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute contracts (HHSN268201100005C, HHSN268201100006C, HHSN2682 01100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C and HHSN268 201100012C), R01HL087641, R01HL59367 and R01HL086694; National Human Genome Research Institute contract (U01HG 004402) and National Institutes of Health contract (HHSN 268200625226C). Infrastructure was partly supported by grant number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research. ARIC is also supported by University of North Carolina at Chapel Hill (funded by N01-HC-55015), Baylor Medical College (N01- HC-55016), University of Mississippi Medical Center (N01-HC- 55021), University of Minnesota (N01-HC-55019), Johns Hopkins University (N01-HC-55020), University of Texas Houston (N01-HC- 55017) and University of North Carolina (N01-HC-55018).

CHS Cardiovascular Health Study research was supported by NHLBI contracts HHSN268201200036C, HHSN268200800007C, N01HC55222, N01HC85079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, N01HC85086; and NHLBI grants U01HL080295, R01HL087652, R01HL105756, R01HL103612, and R01HL120393 with additional contribution from the National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided through R01AG023629 from the National Institute on Aging (NIA). A full list of principal CHS investigators and institutions can be found at CHS-NHLBI.org. The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR000124, and the National Institute of Diabetes and Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center.

FHS The National Heart, Lung, and Blood Institute’s Framingham Heart Study is a joint project of the National Institutes of Health and Boston University School of Medicine and was supported by the National Heart, Lung, and Blood Institute’s Framingham Heart Study (contract No. N01-HC-25195) and its contract with Affymetrix for genotyping services (contract No. N02-HL-6-4278). Analyses reflect the efforts and resource development from the Framingham Heart Study investigators participating in the SNP Health Association Resource (SHARe) project. A portion of this research was conducted using the Linux Cluster for Genetic Analysis (LinGA-II) funded by the Robert Dawson Evans Endowment of the Department of Medicine at the Boston University School of Medicine and Boston Medical Center.

Rotterdam Study The generation and management of GWAS genotype data for the Rotterdam Study (RS I, RS II, RS III) was executed by the Human Genotyping Facility of the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, Rotterdam, The Netherlands. The GWAS datasets are supported by the Netherlands Organisation of Scientific Research NWO Investments (nr. 175.010.2005.011, 911-03-012), the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, the Research Institute for Diseases in the Elderly (014-93-015; RIDE2), the Netherlands Genomics Initiative (NGI)/Netherlands Organisation for Scientific Research (NWO) Netherlands Consortium for Healthy Aging (NCHA), project nr. 050-060-810. The Rotterdam Study is funded by Erasmus Medical Center and Erasmus University, Rotterdam, Netherlands Organization for the Health Research and Development (ZonMw), the Research Institute for Diseases in the Elderly (RIDE), the Ministry of Education, Culture and Science, the Ministry for Health, Welfare and Sports, the European Commission (DG XII), and the Municipality of Rotterdam.

The InChianti Study was supported as a ‘targeted project’ (ICS 110.1RS97.71) by the Italian Ministry of Health, by the US National Institute on Aging (contracts N01-AG-916413, N01- AG-821336, 263 MD 9164 13 and 263 MD 821336) and in part by the Intramural Research Program, National Institute on Aging and National Institutes of Health, USA.

Grants and funding supports for individuals

R.N.B. is funded by the Wellcome Trust and Royal Society (grant: 104150/Z/14/Z). N.M.W. is supported by a National Health and Medical Research Council Early Career Fellowship (APP1104818), a University of Queensland Early Career Researcher Grant (2014002959) and a University of Western Australia - University of Queensland Bilateral Research Collaboration Award (2014001711). B.F. is supported by an Oak Foundation fellowship and by a grant from the Novo Nordisk Foundation (12955). N.R.v.Z. has received salary support from the Innovative Medicines Initiative and the Juvenile Diabetes Research Foundation. T.S.A. was funded by the Gene-Diet Interactions in Obesity (GENDINOB) project and acknowledges the same. N.V-T. is funded by a pre-doctoral grant from the Agència de Gestió d’Ajuts

Universitaris i de Recerca (2015 FI_B 00636), Generalitat de Catalunya. V.L. and I.P. were funded in part through the European Union's Seventh Framework Programme (FP7/2007–2013), ENGAGE project, grant agreement HEALTH-F4-2007-201413. L.A.D received a College of Medical, Veterinary and Life Sciences Medical Research Council Doctoral Training Grant Scholarship (G0900185-1/1). J.M.M. was supported by Sara Borrell Fellowship from the Instituto Carlos III and Beatriu de Pinós fellowship from the Agency for Management of University and Research Grants (AGAUR). N.R. is funded by the Medical Research Council, UK (MR/K011480/1). S.K.G. is supported by HL122684. S.E.J. is funded by the Medical Research Council (grant: MR/M005070/1). M.A.T. is supported by a Wellcome Trust Institutional Strategic Support Award (WT097835MF). J.T. is funded by a Diabetes Research and Wellness Foundation Fellowship. A.R.W. and T.M.F. are supported by the European Research Council grant: 323195 SZ-245 50371-GLUCOSEGENES-FP7-IDEAS-ERC. I.P. is supported by Elsie Widdowson fellowship from the Imperial College London, UK. S.B-G. was FI-DGR Fellowship from FIDGR 2013 from Agència de Gestió d’Ajuts Universitaris i de Recerca (AGAUR, Generalitat de Catalunya). G.H. works within the MRC Integrative Epidemiology Unit at the University of Bristol (MC_UU_12013/1-9). G.M. is supported by core ALSPAC funding Grant ref: 102215/2/13/2). S.M.M. was partly funded by a Research Councils UK Fellowship. E.Z. is supported by the Wellcome Trust (098051). H.N.K. is awarded EU-FP7 Marie Curie Actions - Career Integration Grant (CIG-293511). S.S. and M-R.J. have received funding from the European Union’s Horizon 2020 research and innovation programme [under grant agreement No 633595] for the DynaHEALTH action. A.T.H. is a Wellcome Trust Senior Investigator (098395/Z/12/Z) and an NIHR Senior Investigator (NF-SI-0611-10219). P.V. received funding from the Swiss National Science Foundation (grant no: 33CSCO-122661 and FN 33CSC0-139468), GlaxoSmithKline and the Faculty of Biology and Medicine of Lausanne, Switzerland, to conduct the CoLaus study. D.M-K. was supported by Dutch Science Organization (ZonMW-VENI Grant 916.14.023). C.Pisinger is funded by the Health Foundation (Helsefonden). C.Power at UCL Institute of Child Health, with support from the National Institute for Health Research Biomedical Research Centre at Great Ormond Street Hospital for Children NHS Foundation Trust and University College London. B.R.W. is funded by British Heart Foundation and the Wellcome Trust. V.W.V.J. received an additional grant from the Netherlands Organization for Health Research and Development (NWO, ZonMw-VIDI 016.136.361) and a European Research Council Consolidator Grant (ERC-2014-CoG-648916). S.F.A.G. is funded by the Daniel B. Burke Endowed Chair for Diabetes Research. D.A.L. works within the MRC Integrative Epidemiology Unit at the University of Bristol (MC_UU_12013/5). G.D.S. works within the MRC Integrative Epidemiology Unit at the University of Bristol (MC_UU_12013/1). A.P.M. is a Wellcome Trust Senior Research Fellow (grant number WT098017) and acknowledges funding under WT090532 and WT064890. J.F.F. has received funding from the European Union’s Horizon 2020 research and innovation programme under grant agreement No 633595 for the DynaHEALTH action. N.J.T. works within the MRC Integrative Epidemiology Unit at the University of Bristol (MC_UU_12013/3). D.M.E. is funded by an Australian Research Council Future Fellowship (FT130101709) and works within the MRC Integrative Epidemiology Unit at the University of Bristol (MC_UU_12013/4). M.I.M. is a Wellcome Trust Senior Investigator (grant number 098381) and a NIHR Senior Investigator. R.M.F. is a Sir Henry Dale Fellow (Wellcome Trust and Royal Society grant: 104150/Z/14/Z).

Study acknowledgements

ALSPAC We are extremely grateful to all the families who took part in this study, the midwives for their help in recruiting them, and the whole ALSPAC team, which includes interviewers, computer and laboratory technicians, clerical workers, research scientists, volunteers, managers, receptionists and nurses. GWAS data were generated by Sample Logistics and Genotyping Facilities at the Wellcome Trust Sanger Institute and LabCorp (Laboratory Corporation of America) using support from 23andMe.

Barcelona Supercomputing Center acknowledges PRACE for awarding us access to MareNostrum supercomputer, based in Spain at Barcelona.

CHOP authors thank the network of primary care clinicians and the patients and families for their contribution to this project and to clinical research facilitated by the Pediatric Research Consortium (PeRC) at The Children’s Hospital of Philadelphia. R. Chiavacci, E. Dabaghyan, A. (Hope) Thomas, K. Harden, A. Hill, C. Johnson-Honesty, C. Drummond, S. Harrison, F. Salley, C. Gibbons, K. Lilliston, C. Kim, E. Frackelton, G. Otieno, K. Thomas, C. Hou, K. Thomas and M.L. Garris provided expert assistance with genotyping and/or data collection and management. The authors would also like to thank S. Kristinsson, L.A. Hermannsson and A. Krisbjörnsson of Raförninn ehf for extensive software design and contributions.

CLHNS We thank the USC-Office of Population Studies Foundation, Inc. research and data collection teams and the study participants who generously provided their time for this study.

COPSAC2000, COPSAC2010 and COPSAC-REGISTRY gratefully express our gratitude to the participants of the COPSAC2000, COPSAC2010 and COPSAC-REGISTRY cohort study for all their support and commitment. We also acknowledge and appreciate the unique efforts of the COPSAC research team.

DNBC We are very grateful to all the women and children taking part in the DNBC.

EPIC-Norfolk We thank all EPIC-Norfolk study participants and staff for their contribution to the study.

ERF We are grateful to all study participants and their relatives, general practitioners and neurologists for their contributions and to P. Veraart for her help in genealogy, J. Vergeer for the supervision of the laboratory work and P. Snijders for his help in data collection.

Fenland We are grateful to all the volunteers for their time and help, and to the General Practitioners and practice staff for assistance with recruitment. We thank the Fenland Study Investigators, Fenland Study Co-ordination team and the Epidemiology Field, Data and Laboratory teams.

The Generation R Study is conducted by the Erasmus Medical Center in close collaboration with the School of Law and Faculty of Social Sciences of the Erasmus University Rotterdam, the Municipal Health Service Rotterdam area, Rotterdam, the Rotterdam Homecare Foundation, Rotterdam and the Stichting Trombosedienst & Artsenlaboratorium Rijnmond (STAR-MDC), Rotterdam. We gratefully acknowledge the contribution of children and parents, general practitioners, hospitals, midwives and pharmacies in Rotterdam. The study protocol was approved by the Medical Ethical Committee of the Erasmus Medical Center, Rotterdam. Written informed consent was obtained for all participants. The generation and management of GWAS genotype data was executed by the Human Genotyping Facility of the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, Rotterdam, the Netherlands. We thank Pascal Arp, Mila Jhamai, Marijn Verkerk, Lizbeth Herrera and Marjolein Peters for their help in creating, managing and QC of the GWAS database. Also Karol Estrada and Carolina Medina-Gomez for their support in creation and analysis of imputed data. We would like to thank Anis Abuseiris, Karol Estrada, Dr. Tobias A. Knoch, and Rob de Graaf as well as their institutions Biophysical Genomics, Erasmus MC Rotterdam, The Netherlands, and especially the national German MediGRID and Services@MediGRID part of the German D-Grid, both funded by the German Bundesministerium fuer Forschung und Technology under grants #01 AK 803 A-H and # 01 IG 07015 G for access to their grid resources.

GINIplus&LISAplus We thank all families for participation in the studies and the LISAplus and GINIplus study teams for their excellent work. The GINIplus study team wishes to acknowledge the following: Helmholtz Zentrum Muenchen - German Research Center for Environmental Health, Institute of Epidemiology I, Munich (Heinrich J, Brüske I, Schulz H, Standl M, Thiering E, Tiesler CMT, Chen C-M, Schnappinger M); Department of Pediatrics, Marien-Hospital, Wesel (Berdel D, von Berg A); Department of Pediatrics, Ludwig Maximilians University, Munich (Koletzko S); Department of Pediatrics, Technical University, Munich (Bauer CP, Hoffmann U); IUF – Leibniz Research Institute for Environmental Medicine, Düsseldorf (Krämer U, Link E, Cramer C). The LISAplus study team wishes to acknowledge the following: Helmholtz Zentrum Muenchen - German Research Center for Environment and Health, Institute of Epidemiology I, Neuherberg (Heinrich J, Brüske I, Schulz H, Standl M, Thiering E, Tiesler CMT, Chen C-M, Schnappinger M); Department of Pediatrics, Marien-Hospital, Wesel (von Berg A); Bad Honnef (Schaaf B); UFZ-Centre for Environmental Research Leipzig-Halle, Department of Environmental Immunology (Lehmann I); IUF – Leibniz Research Institute for Environmental Medicine, Düsseldorf (Krämer U); Department of Pediatrics, Technical University, Munich (Bauer CP, Hoffman U).

GOYA We thank all the participants of the study.

The Helsinki Birth Cohort Study (HBCS/HBCS 1934-44) thanks Professor David Barker and Tom Forsen. The DNA extraction, sample quality control, biobank up-keep and aliquotting were performed at the National Institute for Health and Welfare, Helsinki, Finland.

INMA authors are grateful to Silvia Fochs, Anna Sànchez, Maribel López, Nuria Pey, Muriel Ferrer, Amparo Quiles, Sandra Pérez, Gemma León, Elena Romero, Maria Andreu, Nati Galiana, Maria Dolores Climent and Amparo Cases for their assistance in contacting the families and administering the questionnaires. The authors would particularly like to thank all the participants for their generous collaboration. A full roster of the INMA Project Investigators can be found at http://www.proyectoinma.org/presentacion-inma/listado-investigadores/en_listado-investigadores.html.

Inter99 study We thank all participants and our committed staff.

Leipzig-Childhood-Obesity are grateful to all the patients and families for contributing to the study. We highly appreciate the support of the Obesity Team and Auxo Team of the Leipzig University Children’s Hospital for management of the patients and to the Pediatric Research Center Lab Team for support with DNA banking.

The authors of the **NEO study** thank all individuals who participated in the Netherlands Epidemiology in Obesity study, all participating general practitioners for inviting eligible participants and all research nurses for collection of the data. We thank the NEO study group and Ingeborg de Jonge for the coordination and data management of the NEO study. The genotyping in the NEO study was supported by the Centre National de Génotypage (Paris, France), headed by Jean-Francois Deleuze.

NFBC 1966 and 1986 We thank the late professor Paula Rantakallio (launch of NFBC1966), the participants in the 31- and 46-years-old study and the NFBC project center. We thank professor Anna-Liisa Hartikainen (launch of NFBC1986), the participants in the study and the NFBC project center.

NTR We would like to thank all twins and their families whom are cooperating in our research. We would like to thank the Avera Human Genetics research lab for their close collaboration, DNA typing and sample logistics.

ORCADES DNA extractions were performed at the Wellcome Trust Clinical Research Facility in Edinburgh. We would like to acknowledge the invaluable contributions of Lorraine Anderson and the research nurses in Orkney, the administrative team in Edinburgh and the people of Orkney.

PANIC We are grateful to the children and their parents for participating in the PANIC study and to the whole research team for their contribution in carrying out the study.

RAINE authors are grateful to the Raine Study participants and their families, and to the Raine Study research staff for cohort coordination and data collection. The authors gratefully acknowledge the

NH&MRC for their long term contribution to funding the study over the last 25 years and also the following Institutions for providing funding for Core Management of the Raine Study: The University of Western Australia (UWA), Raine Medical Research Foundation, UWA Faculty of Medicine, Dentistry and Health Sciences, Telethon Kids Institute and Women and Infants Research Foundation (King Edward Memorial Hospital), Curtin University and Edith Cowan University. The authors gratefully acknowledge the assistance of the Western Australian DNA Bank (National Health and Medical Research Council of Australia National Enabling Facility). This work was supported by resources provided by the Pawsey Supercomputing Centre with funding from the Australian Government and the Government of Western Australia.

TDCOB The Danish Childhood Obesity Biobank would like to thank all children, youths, and their families for participation in the studies and thus providing opportunities to detect novel insights in regards to childhood obesity.

TEENAGE We would like to thank all study participants and their families as well as all volunteers for their contribution in this study. We thank the following staff from the Sample Management and Genotyping Facilities at the Wellcome Trust Sanger Institute for sample preparation, quality control and genotyping: Dave Jones, Doug Simpkin, Emma Gray, Hannah Blackburn and Sarah Edkins.

YFS gratefully acknowledge the expert technical assistance in the statistical analyses by Ville Aalto and Irina Lisinen.

CHARGE Consortium Hematology Working Group Details of the acknowledgements are described in Ganesh et al, *Nat Genet* (2009)[80].

UK Biobank This study has been conducted using the UK Biobank Resource.