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**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 <sup>a,b</sup>	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 & LISApplus (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.

<sup>a</sup>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).

<sup>b</sup>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) <sup>a</sup>	Sample quality control		SNP scaffold quality control			Prephasing software	Imputation		Association analysis		Lambda (M/F)
		Call rate	Additional filters	Call rate	HWE <i>P</i> -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%	$1 \times 10^{-4}$	MAF<1%	MaCH	Minimac	1000G Mar 2012	ProbABEL	GA	1.01/1.00
ALSPAC	I550	97%	Heterozygosity, relatedness, ancestry outliers	95%	$5 \times 10^{-7}$	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%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-3	0.96/0.96
CoLaus	A5	90%	Relatedness, ancestry outliers	90%	$1 \times 10^{-7}$	MAF<1%	MaCH	Minimac	1000G Mar 2012	In-house	None	0.99/1.00
COPSAC-2000	I550	97.5%	Heterozygosity, relatedness, ancestry outliers	98%	$1 \times 10^{-6}$	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%	$1 \times 10^{-6}$	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%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	QuickTest	GA, PC1-5	1.00/1.00
DNBC	I660	96%	Heterozygosity, ancestry outliers, sex discrepancy	98%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	1.00/1.00
ERF	Various	98%	Relatedness, ancestry outliers, sex discrepancy	98%	$5 \times 10^{-8}$	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%	$1 \times 10^{-6}$	MAC<1	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-10	1.00/1.01
Fenland (GA+)	AUKBB	95%	Sex discrepancy, identity	95%	$1 \times 10^{-6}$	MAC<2	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1-10	1.00/1.01
Fenland (GA-)	AUKBB	95%	Sex discrepancy, identity	95%	$1 \times 10^{-6}$	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%	$1 \times 10^{-6}$	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%	$1 \times 10^{-5}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	0.99/1.00
GOYA	I610	95%	Heterozygosity, ancestry outliers, sex discrepancy	95%	$1 \times 10^{-7}$	MAF<1%	MaCH	MaCH	1000G Mar 2012	QuickTest	None	1.00/0.99
HBCS	I670	95%	Heterozygosity, relatedness, ancestry outliers	95%	$1 \times 10^{-6}$	MAF<1%	MaCH	MaCH	1000G Mar 2012	mach2qtl	GA	1.02/1.02

Study	Genotyping array(s) <sup>a</sup>	Sample quality control		SNP scaffold quality control			Prephasing software	Imputation		Association analysis		Lambda (M/F)
		Call rate	Additional filters	Call rate	HWE <i>p</i> -value	Frequency		Software	Reference panel	Software	Covariates or adjustment	
INMA	IOQ	98%	Heterozygosity, relatedness, ancestry outliers, duplicates	95%	$1.1 \times 10^{-6}$	MAF<1%	IMPUTE2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	1.00/0.99
INTER99	ICM	95%	Relatedness, ancestry outliers, sex discrepancy	95%	$1 \times 10^{-4}$	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%)	$1 \times 10^{-4}$	MAF<1%	IMPUTE2	IMPUTE2	1000G Mar 2012	SNPTEST	GA	0.95/0.96
NEO	ICE	98%	Heterozygosity, relatedness, ancestry outliers, sex discrepancy	98%	$1 \times 10^{-6}$	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%)	$5.7 \times 10^{-7}$	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%)	$5.7 \times 10^{-7}$ ( $1 \times 10^{-4}$ 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%	$1 \times 10^{-5}$	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%)	$1 \times 10^{-6}$	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%	$1 \times 10^{-6}$	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%	$5.7 \times 10^{-7}$	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%	$1 \times 10^{-4}$	MAF<1%	MaCH	Minimac	1000G Mar 2012	ProbABEL	Kinship matrix	1.01/1.01
STRIP	A5, A6	95%	Heterozygosity, ancestry outliers, twins	95%	$1 \times 10^{-6}$	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%)	$1 \times 10^{-4}$	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%)	$1 \times 10^{-4}$	MAF<1%	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	None	1.02/0.98

TDCOB-cases	IOE	95%	Heterozygosity, relatedness, ancestry outliers	95%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1	1.02/1.01
TDCOB-controls	ICE	95%	Heterozygosity, relatedness, ancestry outliers	95%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	GA, PC1	1.02/1.05
YFS	I670	95%	Heterozygosity, relatedness, sex discrepancy, duplicates	95%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-4	0.99/1.01

(b) Component 2: UK BioBank

Study	Genotyping array(s) <sup>a</sup>	Sample quality control		SNP scaffold quality control			Prephasing software	Imputation		Association analysis		Lambda
		Call rate	Additional filters	Call rate	HWE <i>P</i> -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) <sup>a</sup>	Sample quality control		SNP scaffold quality control			Prephasing software	Imputation		Association analysis		Lambda (M/F)
		Call rate	Additional filters	Call rate	HWE <i>P</i> -value	Frequency		Software	Reference panel	Software	Covariates or adjustment	
CHOP-AA	I550, I610	95%	Relatedness, ancestry outliers, sex discrepancy	95%	$1 \times 10^{-6}$	MAF<1%	SHAPEIT2	IMPUTE2	1000G Mar 2012	SNPTEST	PC1-3	0.98/0.98
CLHNS	ICM	98.6%	Relatedness, sex discrepancy	97%	$1 \times 10^{-6}$	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%	$1 \times 10^{-7}$	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%	$1 \times 10^{-7}$	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%	$1 \times 10^{-7}$	MAF<1%	MaCH	Minimac	1000G Mar 2012	mach2qtl	GA, PC1	0.99/0.95
SCORM	I550	95%	Heterozygosity, relatedness, sex discrepancy	95%	$1 \times 10^{-6}$	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.

<sup>a</sup>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 (IQ); 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 ( $P < 5 \times 10^{-8}$ ).**

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.86	0.039	0.008	$5.0 \times 10^{-7}$	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	$1.1 \times 10^{-8}$	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	$1.1 \times 10^{-9}$	148,081	0.72

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.23	0.038	0.006	$3.9 \times 10^{-9}$	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	$7.3 \times 10^{-12}$	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	$1.3 \times 10^{-12}$	146,817	0.72

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.16	0.029	0.007	$8.7 \times 10^{-5}$	70,594	0.14
Component 2: UKBB	0.19	0.033	0.007	$2.3 \times 10^{-6}$	67,786	N/A
European ancestry meta-analysis	0.17	0.031	0.005	$8.0 \times 10^{-10}$	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	$1.5 \times 10^{-9}$	147,035	0.86

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.38	0.031	0.006	$1.0 \times 10^{-7}$	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	$5.6 \times 10^{-8}$	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	$4.5 \times 10^{-8}$	146,813	0.18

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.88	0.040	0.008	$4.9 \times 10^{-7}$	71,639	0.98
Component 2: UKBB	0.87	0.036	0.008	$6.3 \times 10^{-6}$	67,786	N/A
European ancestry meta-analysis	0.88	0.038	0.006	$1.3 \times 10^{-11}$	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	$6.2 \times 10^{-11}$	149,529	0.35

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.70	0.050	0.006	$1.0 \times 10^{-16}$	66,667	0.94
Component 2: UKBB	0.70	0.044	0.006	$9.7 \times 10^{-14}$	67,786	N/A
European ancestry meta-analysis	0.70	0.047	0.004	$6.2 \times 10^{-29}$	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	$1.5 \times 10^{-29}$	143,107	0.82

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

Analysis	EAf	$\beta$	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	$5.5 \times 10^{-6}$	67,786	N/A
European ancestry meta-analysis	0.38	0.022	0.004	$1.4 \times 10^{-8}$	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	$1.2 \times 10^{-8}$	153,773	0.94

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.22	0.052	0.006	$5.2 \times 10^{-18}$	75,884	0.34
Component 2: UKBB	0.24	0.039	0.006	$4.0 \times 10^{-10}$	67,786	N/A
European ancestry meta-analysis	0.23	0.046	0.004	$2.4 \times 10^{-26}$	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	$6.4 \times 10^{-27}$	152,934	0.35

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.42	0.023	0.005	$2.2 \times 10^{-5}$	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	$9.2 \times 10^{-9}$	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	$6.2 \times 10^{-10}$	149,529	0.33

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.60	0.063	0.005	$1.0 \times 10^{-30}$	71,640	0.0091
Component 2: UKBB	0.60	0.042	0.006	$3.4 \times 10^{-13}$	67,786	N/A
European ancestry meta-analysis	0.60	0.053	0.004	$3.7 \times 10^{-41}$	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	$1.3 \times 10^{-42}$	149,529	0.14

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.28	0.040	0.006	$4.8 \times 10^{-12}$	71,640	0.46
Component 2: UKBB	0.26	0.027	0.006	$9.0 \times 10^{-6}$	67,786	N/A
European ancestry meta-analysis	0.27	0.034	0.004	$5.4 \times 10^{-16}$	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	$1.3 \times 10^{-15}$	149,528	0.060

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.50	0.023	0.005	$1.5 \times 10^{-5}$	71,645	0.35
Component 2: UKBB	0.49	0.029	0.005	$1.1 \times 10^{-7}$	67,786	N/A
European ancestry meta-analysis	0.50	0.025	0.004	$9.5 \times 10^{-12}$	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	$1.3 \times 10^{-12}$	148,988	0.80

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.81	0.038	0.007	$7.8 \times 10^{-9}$	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	$2.2 \times 10^{-8}$	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	$3.5 \times 10^{-8}$	149,532	0.010

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

Analysis	EAf	$\beta$	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	$1.0 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.73	0.024	0.004	$1.6 \times 10^{-8}$	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	$1.3 \times 10^{-9}$	153,773	0.78

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.72	0.047	0.006	$6.1 \times 10^{-17}$	75,881	0.94
Component 2: UKBB	0.74	0.041	0.006	$1.4 \times 10^{-11}$	67,786	N/A
European ancestry meta-analysis	0.73	0.044	0.004	$4.4 \times 10^{-27}$	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	$9.7 \times 10^{-29}$	153,769	0.42

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.67	0.029	0.006	$7.2 \times 10^{-7}$	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	$6.6 \times 10^{-8}$	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	$1.2 \times 10^{-8}$	148,264	0.42

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

Analysis	EAf	$\beta$	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	$2.4 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.18	0.028	0.005	$1.0 \times 10^{-8}$	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	$1.1 \times 10^{-8}$	146,606	0.16

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.75	0.025	0.006	$2.3 \times 10^{-5}$	75,880	0.69
Component 2: UKBB	0.73	0.025	0.006	$3.2 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.74	0.025	0.004	$2.6 \times 10^{-9}$	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	$4.0 \times 10^{-11}$	153,768	0.40

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.72	0.044	0.006	$5.4 \times 10^{-14}$	71,641	0.95
Component 2: UKBB	0.73	0.031	0.006	$2.7 \times 10^{-7}$	67,786	N/A
European ancestry meta-analysis	0.72	0.038	0.004	$1.6 \times 10^{-19}$	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	$6.1 \times 10^{-20}$	149,530	0.28

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

Analysis	EAf	$\beta$	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	$1.0 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.73	0.023	0.004	$2.0 \times 10^{-8}$	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	$5.0 \times 10^{-9}$	153,378	0.84

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

Analysis	EAf	$\beta$	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	$1.3 \times 10^{-7}$	67,786	N/A
European ancestry meta-analysis	0.75	0.027	0.004	$5.8 \times 10^{-10}$	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	$1.0 \times 10^{-9}$	149,531	0.60

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.61	0.031	0.005	$1.4 \times 10^{-9}$	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	$1.5 \times 10^{-9}$	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	$1.0 \times 10^{-8}$	153,757	0.054

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.9908	0.227	0.034	$1.7 \times 10^{-11}$	64,557	0.86
Component 2: UKBB	0.9915	0.253	0.031	$7.1 \times 10^{-16}$	67,786	N/A
European ancestry meta-analysis	0.9911	0.241	0.023	$7.2 \times 10^{-26}$	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	$1.4 \times 10^{-26}$	135,635	0.16

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.06	0.052	0.011	$1.9 \times 10^{-6}$	74,414	0.24
Component 2: UKBB	0.07	0.046	0.011	$1.5 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.07	0.049	0.008	$1.2 \times 10^{-10}$	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	$5.9 \times 10^{-12}$	150,015	0.23

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

Analysis	EAf	$\beta$	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	$1.5 \times 10^{-9}$	67,786	N/A
European ancestry meta-analysis	0.79	0.031	0.005	$1.3 \times 10^{-11}$	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	$1.6 \times 10^{-11}$	148,991	0.32

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.73	0.026	0.006	$5.6 \times 10^{-6}$	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	$2.2 \times 10^{-7}$	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	$5.0 \times 10^{-8}$	153,775	0.92

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.59	0.023	0.005	$1.1 \times 10^{-5}$	71,645	0.39
Component 2: UKBB	0.59	0.023	0.005	$3.0 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.59	0.023	0.004	$1.2 \times 10^{-9}$	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	$1.9 \times 10^{-9}$	148,084	0.65

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.09	0.041	0.009	$1.4 \times 10^{-5}$	66,960	0.40
Component 2: UKBB	0.10	0.070	0.009	$1.7 \times 10^{-14}$	67,786	N/A
European ancestry meta-analysis	0.09	0.056	0.007	$1.5 \times 10^{-17}$	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	$4.0 \times 10^{-16}$	143,400	0.0055

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.50	0.021	0.005	$8.6 \times 10^{-5}$	71,638	0.23
Component 2: UKBB	0.51	0.021	0.005	$7.5 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.50	0.021	0.004	$2.2 \times 10^{-8}$	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	$2.8 \times 10^{-8}$	148,079	0.99

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.68	0.028	0.006	$1.1 \times 10^{-6}$	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	$1.0 \times 10^{-8}$	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	$5.4 \times 10^{-9}$	149,528	0.17

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

Analysis	EAf	$\beta$	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	$2.1 \times 10^{-7}$	67,786	N/A
European ancestry meta-analysis	0.14	0.033	0.005	$4.7 \times 10^{-10}$	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	$1.2 \times 10^{-12}$	148,080	0.21

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.51	0.027	0.005	$9.2 \times 10^{-8}$	75,884	0.37
Component 2: UKBB	0.51	0.029	0.005	$7.6 \times 10^{-8}$	67,786	N/A
European ancestry meta-analysis	0.51	0.028	0.004	$3.0 \times 10^{-14}$	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	$9.5 \times 10^{-15}$	153,773	0.80

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

Analysis	EAf	$\beta$	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	$3.0 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.08	0.037	0.007	$5.2 \times 10^{-8}$	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	$1.8 \times 10^{-9}$	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	$1.3 \times 10^{-15}$	75,885	0.79
Component 2: UKBB	0.73	0.025	0.006	$4.5 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.73	0.036	0.004	$4.7 \times 10^{-18}$	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	$4.7 \times 10^{-18}$	153,774	0.19

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.50	0.022	0.005	$1.0 \times 10^{-5}$	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	$1.8 \times 10^{-8}$	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	$6.1 \times 10^{-9}$	153,759	0.83

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.07	0.055	0.011	$6.7 \times 10^{-7}$	67,990	0.014
Component 2: UKBB	0.08	0.041	0.010	$8.0 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.07	0.048	0.008	$2.9 \times 10^{-10}$	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	$6.8 \times 10^{-10}$	143,591	0.64

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.28	0.029	0.006	$5.1 \times 10^{-7}$	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	$2.9 \times 10^{-8}$	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	$1.0 \times 10^{-7}$	153,765	0.23

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.74	0.028	0.006	$2.1 \times 10^{-6}$	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	$1.8 \times 10^{-7}$	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	$2.3 \times 10^{-8}$	153,595	0.32

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.61	0.027	0.007	$4.9 \times 10^{-5}$	55,417	0.72
Component 2: UKBB	0.63	0.023	0.006	$5.8 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.62	0.025	0.004	$1.1 \times 10^{-8}$	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	$1.0 \times 10^{-7}$	131,858	0.22

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

Analysis	EAf	$\beta$	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	$3.8 \times 10^{-6}$	67,786	N/A
European ancestry meta-analysis	0.54	0.021	0.004	$1.9 \times 10^{-8}$	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	$3.2 \times 10^{-8}$	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	$7.6 \times 10^{-21}$	75,885	0.40
Component 2: UKBB	0.49	0.039	0.005	$3.1 \times 10^{-13}$	67,786	N/A
European ancestry meta-analysis	0.49	0.044	0.004	$1.9 \times 10^{-32}$	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	$2.0 \times 10^{-33}$	153,773	0.72

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.08	0.038	0.009	$5.6 \times 10^{-5}$	71,642	0.63
Component 2: UKBB	0.09	0.040	0.010	$2.3 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.09	0.039	0.007	$4.7 \times 10^{-9}$	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	$9.7 \times 10^{-9}$	148,692	0.20

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.68	0.026	0.006	$7.9 \times 10^{-6}$	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	$7.3 \times 10^{-8}$	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	$8.3 \times 10^{-9}$	148,080	0.64

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

Analysis	EAf	$\beta$	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	$9.8 \times 10^{-8}$	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	$2.2 \times 10^{-8}$	146,215	0.63

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.86	0.041	0.008	$2.4 \times 10^{-7}$	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	$6.3 \times 10^{-9}$	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	$1.8 \times 10^{-9}$	147,633	0.80

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

Analysis	EAf	$\beta$	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	$1.1 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.68	0.023	0.004	$1.7 \times 10^{-8}$	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	$1.0 \times 10^{-8}$	151,384	0.75

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.43	0.022	0.005	$4.9 \times 10^{-5}$	71,637	0.24
Component 2: UKBB	0.41	0.024	0.006	$1.3 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.43	0.023	0.004	$2.3 \times 10^{-9}$	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	$1.1 \times 10^{-9}$	149,526	0.61

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

Analysis	EAf	$\beta$	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	$1.3 \times 10^{-7}$	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	$2.7 \times 10^{-9}$	153,702	0.66

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.57	0.033	0.005	$7.1 \times 10^{-10}$	71,640	0.10
Component 2: UKBB	0.55	0.028	0.005	$2.6 \times 10^{-7}$	67,786	N/A
European ancestry meta-analysis	0.56	0.031	0.004	$9.1 \times 10^{-16}$	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	$1.3 \times 10^{-15}$	149,530	0.77

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

Analysis	EAf	$\beta$	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	$1.0 \times 10^{-8}$	67,786	N/A
European ancestry meta-analysis	0.96	0.066	0.012	$1.4 \times 10^{-8}$	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	$1.5 \times 10^{-9}$	127,992	0.068

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.31	0.025	0.006	$2.2 \times 10^{-5}$	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	$5.1 \times 10^{-8}$	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	$3.0 \times 10^{-9}$	148,075	0.75

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.84	0.030	0.007	$6.4 \times 10^{-5}$	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	$1.1 \times 10^{-7}$	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	$2.3 \times 10^{-8}$	139,853	0.98

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

Analysis	EAf	$\beta$	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	$4.4 \times 10^{-7}$	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	$2.3 \times 10^{-8}$	149,530	0.72

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.48	0.023	0.005	$3.1 \times 10^{-5}$	71,638	0.82
Component 2: UKBB	0.51	0.023	0.005	$1.8 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.49	0.023	0.004	$2.0 \times 10^{-9}$	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	$7.2 \times 10^{-9}$	148,079	0.24

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.50	0.032	0.005	$5.0 \times 10^{-9}$	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	$7.7 \times 10^{-12}$	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	$8.4 \times 10^{-11}$	148,264	0.18

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.41	0.028	0.005	$3.8 \times 10^{-7}$	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	$9.5 \times 10^{-10}$	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	$3.7 \times 10^{-10}$	149,528	0.27

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.85	0.037	0.008	$6.6 \times 10^{-6}$	75,886	0.66
Component 2: UKBB	0.90	0.034	0.009	$9.1 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.87	0.036	0.006	$2.2 \times 10^{-9}$	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	$1.5 \times 10^{-8}$	152,936	0.092

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.35	0.022	0.006	$8.9 \times 10^{-5}$	69,554	0.36
Component 2: UKBB	0.35	0.023	0.006	$3.2 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.35	0.023	0.004	$1.0 \times 10^{-8}$	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	$2.2 \times 10^{-8}$	145,995	0.25

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.91	0.054	0.010	$2.6 \times 10^{-8}$	68,286	0.69
Component 2: UKBB	0.92	0.040	0.010	$6.0 \times 10^{-5}$	67,786	N/A
European ancestry meta-analysis	0.91	0.047	0.007	$9.7 \times 10^{-12}$	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	$3.7 \times 10^{-12}$	143,887	0.69

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

Analysis	EAf	$\beta$	SE	P-value	N	Q P-value
Component 1: European ancestry	0.28	0.027	0.007	$2.0 \times 10^{-4}$	37,417	0.73
Component 2: UKBB	0.24	0.028	0.006	$1.8 \times 10^{-6}$	57,620	N/A
European ancestry meta-analysis	0.25	0.028	0.005	$1.3 \times 10^{-9}$	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 ( $P < 5 \times 10^{-8}$ ) 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 <sup>a</sup>	EUR $r^2$ with lead TA	Present in HapMap?	Best proxy in HapMap	
				Effect	Other		$\beta$ (SE)	P-value	$\beta$ (SE)	P-value				SNP	EUR $r^2$
<i>WNT4-ZBTB40</i>	rs2473248	1	22,536,643	C	T	0.87	0.033 (0.006)	$1.1 \times 10^{-8}$	0.033 (0.005)	$1.1 \times 10^{-9}$	TA/EUR		No	rs2744726	0.99
<i>ZBTB7B</i>	rs3753639	1	154,986,091	C	T	0.24	0.031 (0.004)	$7.3 \times 10^{-12}$	0.031 (0.004)	$1.3 \times 10^{-12}$	TA/EUR		No	rs905938	0.77
<i>FCGR2B</i>	rs72480273	1	161,644,871	C	A	0.17	0.031 (0.005)	$8.0 \times 10^{-10}$	0.030 (0.005)	$1.5 \times 10^{-9}$	TA/EUR		No	rs17413015	0.97
<i>DTL</i>	rs61830764	1	212,289,976	A	G	0.38	0.022 (0.004)	$5.6 \times 10^{-8}$	0.022 (0.004)	$4.5 \times 10^{-8}$	TA		No	rs1387815	0.51
<i>ATAD2B</i>	rs7575873	2	23,962,647	A	G	0.88	0.038 (0.006)	$1.3 \times 10^{-11}$	0.036 (0.006)	$6.2 \times 10^{-11}$	TA		No	rs718139	0.98
	rs181211713	2	23,965,445	G	A	0.87	0.038 (0.006)	$1.2 \times 10^{-11}$	0.036 (0.005)	$7.3 \times 10^{-11}$	EUR	0.94	No		
<i>EPAS1</i>	rs1374204	2	46,484,205	T	C	0.70	0.047 (0.004)	$6.2 \times 10^{-29}$	0.046 (0.004)	$1.5 \times 10^{-29}$	TA		Yes		
	rs17034876	2	46,484,310	T	C	0.70	0.047 (0.004)	$2.6 \times 10^{-29}$	0.046 (0.004)	$1.9 \times 10^{-29}$	EUR	0.99	Yes		
<i>PTH1R</i>	rs2242116	3	46,941,116	A	G	0.38	0.022 (0.004)	$1.4 \times 10^{-8}$	0.021 (0.004)	$1.2 \times 10^{-8}$	TA		Yes		
	rs2168443	3	46,947,087	T	A	0.38	0.023 (0.004)	$3.5 \times 10^{-9}$	0.021 (0.004)	$1.3 \times 10^{-8}$	EUR	0.99	Yes		
<i>ADCY5</i>	rs11719201	3	123,068,744	T	C	0.23	0.046 (0.004)	$2.4 \times 10^{-26}$	0.046 (0.004)	$6.4 \times 10^{-27}$	TA/EUR		No	rs7613951	0.97
	rs9883204	3	123,096,820	T	C	0.25	0.041 (0.004)	$8.4 \times 10^{-22}$	0.040 (0.004)	$6.1 \times 10^{-22}$	Previous	0.85	Yes		
<i>CPA3</i>	rs10935733	3	148,622,968	T	C	0.41	0.022 (0.004)	$9.2 \times 10^{-9}$	0.023 (0.004)	$6.2 \times 10^{-10}$	TA/EUR		No	rs12496367	0.81
<i>CCNL1-LEKR1</i>	rs13322435	3	156,795,468	A	G	0.60	0.053 (0.004)	$3.7 \times 10^{-41}$	0.052 (0.004)	$1.3 \times 10^{-42}$	TA		Yes		
	rs900399	3	156,798,732	A	G	0.61	0.052 (0.004)	$2.2 \times 10^{-41}$	0.051 (0.004)	$2.9 \times 10^{-41}$	EUR	0.92	Yes		
	rs900400	3	156,798,775	T	C	0.61	0.053 (0.004)	$1.1 \times 10^{-40}$	0.051 (0.004)	$8.4 \times 10^{-41}$	Previous	0.92	Yes		
<i>LCORL</i>	rs925098	4	17,919,811	G	A	0.27	0.034 (0.004)	$5.4 \times 10^{-16}$	0.032 (0.004)	$1.3 \times 10^{-15}$	TA		Yes		
	rs2724475	4	17,946,432	T	C	0.27	0.034 (0.004)	$5.3 \times 10^{-16}$	0.032 (0.004)	$1.3 \times 10^{-15}$	EUR	0.97	Yes		
	rs724577	4	17,993,410	A	C	0.27	0.033 (0.004)	$1.7 \times 10^{-15}$	0.031 (0.004)	$1.5 \times 10^{-14}$	Previous	0.98	Yes		

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

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

Locus	SNP	Chr	Position	Alleles		EAF	European ancestry		Trans-ancestry		Status <sup>a</sup>	EUR $r^2$ with lead TA	Present in HapMap?	Best proxy in HapMap	
			(b37, bp)	Effect	Other		$\beta$ (SE)	P-value	$\beta$ (SE)	P-value				SNP	EUR $r^2$
APOLD1	rs11055034	12	12,890,626	C	A	0.73	0.022 (0.004)	$1.8 \times 10^{-7}$	0.023 (0.004)	$2.3 \times 10^{-8}$	TA		Yes		
ABCC9	rs139975827	12	22,068,161	G	A	0.62	0.025 (0.004)	$1.1 \times 10^{-8}$	0.022 (0.004)	$1.0 \times 10^{-7}$	EUR		No	rs4148656	0.67
ITPR2	rs12823128	12	26,872,730	T	C	0.54	0.021 (0.004)	$1.9 \times 10^{-8}$	0.020 (0.004)	$3.2 \times 10^{-8}$	TA		Yes		
	rs2306547	12	26,877,885	C	T	0.54	0.021 (0.004)	$1.8 \times 10^{-8}$	0.020 (0.004)	$3.2 \times 10^{-8}$	EUR	0.96	Yes		
HMGA2	rs1351394	12	66,351,826	T	C	0.49	0.044 (0.004)	$1.9 \times 10^{-32}$	0.043 (0.004)	$2.0 \times 10^{-33}$	TA/EUR		Yes		
	rs1042725	12	66,358,347	C	T	0.51	0.043 (0.004)	$3.1 \times 10^{-32}$	0.042 (0.004)	$7.1 \times 10^{-32}$	Previous	0.93	Yes		
IGF1	rs7964361	12	102,994,878	A	G	0.09	0.039 (0.007)	$4.7 \times 10^{-9}$	0.038 (0.007)	$9.7 \times 10^{-9}$	TA/EUR		Yes		
LINCO0332	rs2324499	13	40,662,001	G	C	0.68	0.022 (0.004)	$7.3 \times 10^{-8}$	0.023 (0.004)	$8.3 \times 10^{-9}$	TA		Yes		
	rs7998537	13	40,662,742	G	A	0.68	0.022 (0.004)	$3.9 \times 10^{-8}$	0.022 (0.004)	$1.8 \times 10^{-8}$	EUR	1.00	Yes		
RB1	rs2854355	13	48,882,363	G	A	0.27	0.023 (0.004)	$9.8 \times 10^{-8}$	0.024 (0.004)	$2.2 \times 10^{-8}$	TA		No	rs9568028	0.88
	rs34217484	13	48,854,550	A	T	0.26	0.024 (0.004)	$4.8 \times 10^{-8}$	0.023 (0.004)	$5.8 \times 10^{-8}$	EUR	0.85	No		
RNF219-AS1	rs1819436	13	78,580,283	C	T	0.87	0.033 (0.006)	$6.3 \times 10^{-9}$	0.033 (0.005)	$1.8 \times 10^{-9}$	TA/EUR		No	rs944379	0.88
FES	rs12906125	15	91,427,612	G	A	0.68	0.023 (0.004)	$1.7 \times 10^{-8}$	0.023 (0.004)	$1.0 \times 10^{-8}$	TA/EUR		No	rs6227	0.87
IGF1R	rs7402982	15	99,193,269	A	G	0.43	0.023 (0.004)	$2.3 \times 10^{-9}$	0.023 (0.004)	$1.1 \times 10^{-9}$	TA/EUR		No	rs8028620	0.55
GPR139	rs1011939	16	19,992,996	G	A	0.30	0.022 (0.004)	$1.3 \times 10^{-7}$	0.024 (0.004)	$2.7 \times 10^{-9}$	TA		No	rs1858988	0.70
CLDN7	rs113086489	17	7,171,356	T	C	0.56	0.031 (0.004)	$9.1 \times 10^{-16}$	0.030 (0.004)	$1.3 \times 10^{-15}$	TA/EUR		No	rs5417	0.80
SUZ12P1-CRLF3	rs144843919	17	29,037,339	G	A	0.97	0.066 (0.012)	$1.4 \times 10^{-8}$	0.068 (0.011)	$1.5 \times 10^{-9}$	TA/EUR		No	rs8073965	0.22
SP6-SP2	rs12942207	17	45,968,294	C	T	0.30	0.022 (0.004)	$5.1 \times 10^{-8}$	0.024 (0.004)	$3.0 \times 10^{-9}$	TA		No	rs11079800	0.91
	rs72833480	17	45,964,861	A	G	0.29	0.023 (0.004)	$4.6 \times 10^{-8}$	0.023 (0.004)	$2.1 \times 10^{-8}$	EUR	0.94	No		
ACTL9	rs61154119	19	8,787,750	T	G	0.84	0.028 (0.005)	$1.1 \times 10^{-7}$	0.028 (0.005)	$2.3 \times 10^{-8}$	TA		No	rs2967684	1
PEPD	rs10402712	19	33,926,013	A	G	0.26	0.022 (0.004)	$4.4 \times 10^{-7}$	0.023 (0.004)	$2.3 \times 10^{-8}$	TA		No	rs17833935	0.54

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

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

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

**Supplementary Table 5. Loci with multiple distinct association signals attaining genome-wide significance ( $P < 5 \times 10^{-8}$ ) 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		$\beta$ (SE)	$P$ -value	Conditioned on	$\beta$ (SE)	$P$ -value			SNP	EUR $r^2$
ZBTB7B	rs3753639	1	154,986,091	C/T	0.24	0.031 (0.004)	$7.3 \times 10^{-12}$	rs4330912	0.034 (0.005)	$2.2 \times 10^{-14}$	0.019	No	rs905938	0.77
	rs4330912	1	155,969,428	G/C	0.64	0.021 (0.004)	$1.8 \times 10^{-7}$	rs3753639	0.025 (0.004)	$5.4 \times 10^{-10}$		No	rs12043212	0.93
HMGA1	rs9368777	6	33,788,637	C/G	0.58	0.022 (0.004)	$2.2 \times 10^{-8}$	rs1187118	0.021 (0.004)	$3.3 \times 10^{-8}$	0.000	No	rs4304152	0.57
	rs1187118	6	34,169,020	A/T	0.17	0.030 (0.005)	$3.6 \times 10^{-9}$	rs9368777	0.030 (0.005)	$5.4 \times 10^{-9}$		No	rs1776877	0.95
PTCH1	rs12551019	9	96,949,079	C/T	0.68	0.022 (0.004)	$3.1 \times 10^{-8}$	rs3780573	0.024 (0.004)	$5.1 \times 10^{-9}$	0.001	Yes		
	rs3780573	9	98,239,503	A/G	0.10	0.055 (0.006)	$7.0 \times 10^{-18}$	rs12551019	0.057 (0.006)	$1.2 \times 10^{-18}$		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 <sup>a</sup>	Reports on eQTL <sup>b</sup>	Literature search for nearby genes (300kb)	Coding variants (EUR $r^2$ with the lead SNP)
<i>WNT4-ZBTB40</i>	rs2473248	1	22,536,643	<i>WNT4</i> [P,N], <i>CDC42</i> [B]	<i>WNT4</i> : Cerebellum and temporal cortex eQTL; <i>CDC42</i> : Whole blood eQTL (proxy SNP)		-
<i>ZBTB7B</i>	rs3753639	1	154,986,091	<i>SHC1</i> [B], <i>S100A7</i> [P]		<i>SHC1</i> : The Shc adaptor proteins are key transducers of growth promotion and gene expression, and are phosphorylated by all known receptor tyrosine.	-
<i>FCGR2B</i>	rs72480273	1	161,644,871	<i>ATF6</i> [B], <i>APOA2</i> [P], <i>FCGR2B</i> [N]	<i>ATF6</i> : Cerebellum and temporal cortex eQTL; <i>FCGR2B</i> : Whole blood, cerebellum and temporal cortex eQTL	<i>HSPA6</i> : 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).	-
<i>DTL</i>	rs61830764	1	212,289,976	<i>DTL</i> [N]			-
<i>ATAD2B</i>	rs7575873	2	23,962,647	<i>ATAD2B</i> [N], <i>FKBP1B</i> [P]	<i>PFN4</i> : Lymphoblastoid eQTL		-
<i>EPAS1</i>	rs1374204	2	46,484,205	<i>RHOQ</i> [B], <i>SOC5</i> [P]	<i>EPAS1</i> , <i>PRKCE</i> : Cerebellum and temporal cortex eQTL	<i>EPAS1</i> : 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.	-
<i>PTH1R</i>	rs2242116	3	46,941,116	<i>PTH1R</i> [B,N], <i>CCR1</i> [P]	<i>CCDC12</i> : Whole blood, cerebellum and temporal cortex eQTL		-
<i>ADCY5</i>	rs11719201	3	123,068,744	<i>ADCY5</i> [B,N], <i>HCLS1</i> [P]	<i>ADCY5</i> : Cerebellum and temporal cortex eQTL (proxy SNP)		-
<i>CPA3</i>	rs10935733	3	148,622,968	<i>AGTR1</i> [B,P]	<i>CPA3</i> , <i>CPB1</i> : eQTL (proxy SNP)	<i>AGTR1</i> = 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).	-
<i>CCNL1-LEKR1</i>	rs13322435	3	156,795,468	<i>LEKR1</i> [N], <i>IL12A</i> [P]	<i>LEKR1</i> : Temporal cortex eQTL; <i>CCNL1</i> : Whole blood, cerebellum and temporal cortex eQTL		-
<i>LCORL</i>	rs925098	4	17,919,811	<i>LCORL</i> [N], <i>SLIT2</i> [P]	<i>LCORL</i> : Cerebellum and temporal cortex eQTL	Adipose tissue and muscle expression in cattle of <i>NCAPG</i> and <i>LCORL</i> associated with feed intake and weight gain in cattle (these are in a QTL for body weight in cattle).	-
<i>HHIP</i>	rs6537307	4	145,601,863	<i>HHIP</i> [N], <i>ANAPC10</i> [P]	<i>HHIP</i> : Cerebellum and temporal cortex eQTL		-
<i>5q11.2</i>	rs854037	5	57,091,783	<i>ACTBL2</i> [N], <i>IL6ST</i> [P]			-
<i>EBF1</i>	rs7729301	5	157,886,953	<i>EBF1</i> [N,B], <i>FABP6</i> [P]			-
<i>CDKAL1</i>	rs35261542	6	20,675,792	<i>CDKAL1</i> [B], <i>SOX4</i> [P]	<i>CDKAL1</i> : Cerebellum and temporal cortex eQTL		-

Locus	Lead SNP	Chr	Position (b37)	Candidate gene(s) in the locus <sup>a</sup>	Reports on eQTL <sup>b</sup>	Literature search for nearby genes (300kb)	Coding variants (EUR $r^2$ with the lead SNP)
<i>HIST1H2BE</i>	rs9379832	6	26,186,200	<i>HIST1H2BE</i> [N,B], <i>BTN2A2</i> [P]			-
<i>HMGA1</i>	rs7742369	6	34,165,721	<i>HMGA1</i> [N,B], <i>GRM4</i> [B], <i>MAPK14</i> [P]	<i>HMGA1</i> : Cerebellum and temporal cortex eQTL		-
<i>L3MBTL3</i>	rs1415701	6	130,345,835	<i>L3MBTL3</i> [E,N], <i>SAMD3</i> [E], <i>ENPP1</i> [P]	<i>L3MBTL3</i> , <i>SAMD3</i> : Whole blood, cerebellum and temporal cortex eQTLs		-
<i>ESR1</i>	rs1101081	6	152,032,917	<i>ESR1</i> [N,B], <i>LATS1</i> [P]	<i>ESR1</i> : Monocyte, cerebellum and temporal cortex eQTL (for proxy SNP)		-
<i>GNA12</i>	rs798489	7	2,801,803	<i>GNA12</i> [N,E], <i>PDGFA</i> [N]	<i>GNA12</i> : Nerve tibial, lymphoblastid, whole blood, cerebellum and temporal cortex eQTL		-
<i>IGF2BP3</i>	rs11765649	7	23,479,013	<i>IGF2BP3</i> [N,B], <i>NPY</i> [P]	<i>CCDC126</i> : lymphoblastoid eQTL		-
<i>TBX20</i>	rs6959887	7	35,295,365	<i>TBX20</i> [N], <i>SEPT7</i> [P]	<i>TBX20</i> : Cerebellum and temporal cortex eQTL		-
<i>YKT6-GCK</i>	rs138715366	7	44,246,271	<i>YKT6</i> [N], <i>GCK</i> [B]		<i>GCK</i> mutations reduce birth weight and increase fasting glucose (Hattersley et al 1999, Nat Genet).	-
<i>MLXIPL</i>	rs62466330	7	73,056,805	<i>MLXIPL</i> [N], <i>FZD9</i> [P]	<i>MLXIPL</i> : Cerebellum and temporal cortex eQTL (for proxy SNP)		-
<i>ANK1-NKX6-3</i>	rs13266210	8	41,533,514	<i>ANK1</i> [N,B], <i>SFRP1</i> [P]	<i>ANK1</i> : Cerebellum, temporal cortex and lung eQTL		-
<i>TRIB1</i>	rs6989280	8	126,508,746	<i>TRIB1</i> [N], <i>MYC</i> [P]	<i>TRIB1</i> : Cerebellum and temporal cortex eQTL		-
<i>SLC45A4</i>	rs12543725	8	142,247,979	<i>SLC45A4</i> [N,E], <i>PTK2</i> [B,P]	<i>SLC45A4</i> : Whole blood, cerebellum and temporal cortex eQTL		-
<i>PTCH1</i>	rs28510415	9	98,245,026	<i>PTCH1</i> [N,B], <i>FOXE1</i> [P]	<i>PTCH1</i> : Whole blood, cerebellum and temporal cortex eQTL (for proxy SNP)	<i>FANCC</i> : mutations result in Fanconi anaemia (associated with low birth weight and shorter stature).	-
<i>LPAR1</i>	rs2150052	9	113,945,067	<i>LPAR1</i> [N,E,B,P]	<i>LPAR1</i> : whole blood eQTL		-
<i>PHF19</i>	rs7847628	9	123,631,225	<i>C5</i> [B], <i>DAB2IP</i> [P]	<i>C5</i> : naïve monocyte, whole blood, cerebellum and temporal cortex eQTL		-
<i>STRBP</i>	rs700059	9	125,824,055	<i>STRBP</i> [E], <i>C5</i> [P]	<i>STRBP</i> : Whole blood, cerebellum and temporal cortex eQTL		-
<i>HHEX-IDE</i>	rs61862780	10	94,468,643	<i>IDE</i> [B], <i>PLCE1</i> [P]	<i>HHEX</i> : monocyte, whole blood, cerebellum and temporal cortex eQTL		-
<i>NTSC2</i>	rs74233809	10	104,913,940	<i>NTSC2</i> [N], <i>CHUK</i> [P]		<i>CYP17A1</i> : mutation in maternal <i>CYP17A1</i> is associated with small for gestational age (SGA) (PMID 14665706)	-
<i>ADRB1</i>	rs7076938	10	115,789,375	<i>ADRB1</i> [N,C,B], <i>AFAP1L2</i> [P]	<i>ADRB1</i> : cerebellum and temporal cortex eQTL		rs1801253 (G389R, $r^2=0.99$ , damaging)
<i>PLEKHA1</i>	rs2421016	10	124,167,512	<i>PLEKHA1</i> [N,E], <i>FGFR2</i> [P]	<i>PLEKHA1</i> : Whole blood, cerebellum and temporal cortex eQTL		-
<i>INS-IGF2</i>	rs72851023	11	2,130,620	<i>INS-IGF2</i> [N,B,imp]			-

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

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

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

<sup>b</sup>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 <sub>10</sub> BF	99% credible set		
					Variants	Distance (bp)	Interval (bp)
<i>WNT4-ZBTB40</i>	rs2473248	1	22,536,643	7.68	7	17,534	22,536,643-22,554,176
<i>ZBTB7B</i>	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
<i>FCGR2B</i>	rs72480273	1	161,644,871	7.48	37	173,221	161,500,712-161,673,932
<i>DTL</i>	rs61830764	1	212,289,976	6.02	56	702,234	211,830,044-212,532,277
<i>ATAD2B</i>	rs7575873	2	23,962,647	8.87	234	477,824	23,887,437-24,365,260
<i>EPAS1</i>	rs1374204	2	46,484,205	27.22	4	695	46,484,188-46,484,882
<i>PTH1R</i>	rs2242116	3	46,941,116	6.65	54	243,837	46,925,539-47,169,375
<i>ADCY5</i>	rs11719201	3	123,068,744	24.38	6	16,621	123,065,778-123,082,398
<i>CPA3</i>	rs10935733	3	148,622,968	7.91	80	33,654	148,591,725-148,625,378
<i>CCNL1-LEKR1</i>	rs13322435	3	156,795,468	40.24	11	3,265	156,795,468-156,798,732
<i>LCORL</i>	rs925098	4	17,919,811	13.56	15	123,806	17,901,679-18,025,484
<i>HHIP</i>	rs6537307	4	145,601,863	10.43	43	137,679	145,520,608-145,658,286
<i>5q11.2</i>	rs854037	5	57,091,783	5.77	63	276,269	56,906,160-57,182,428
<i>EBF1</i>	rs7729301	5	157,886,953	7.62	50	77380	157,884,706-157,962,085
<i>CDKAL1</i>	rs35261542	6	20,675,792	26.41	7	14,242	20,673,880-20,688,121
<i>HIST1H2BE</i>	rs9379832	6	26,186,200	6.64	5	26,542	26,180,634-26,207,175
<i>HMGA1</i>	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
<i>L3MBTL3</i>	rs1415701	6	130,345,835	9.03	2	4,601	130,341,235-130,345,835
<i>ESR1</i>	rs1101081	6	152,032,917	17.69	14	20,968	152,029,556-152,050,523
<i>GNA12</i>	rs798489	7	2,801,803	7.01	114	160,777	2,752,152-2,912,928
<i>IGF2BP3</i>	rs11765649	7	23,479,013	7.58	23	111,149	23,474,687-23,585,835
<i>TBX20</i>	rs6959887	7	35,295,365	6.75	113	109,117	35,196,208-35,305,324
<i>YKT6-GCK</i>	rs138715366	7	44,246,271	24.10	1	1	44,246,271-44,246,271
<i>MLXIPL</i>	rs62466330	7	73,056,805	9.60	102	221,896	72,836,230-73,058,025
<i>ANK1-NKX6-3</i>	rs13266210	8	41,533,514	9.22	17	28,742	41,508,577-41,537,318
<i>TRIB1</i>	rs6989280	8	126,508,746	5.69	39	411,117	126,114,947-126,526,063
<i>SLC45A4</i>	rs12543725	8	142,247,979	7.18	10	13,200	142,239,381-142,252,580
<i>PTCH1</i>	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	MANTRA log <sub>10</sub> BF	99% credible set		
			(b37, bp)		Variants	Distance (bp)	Interval (bp)
<i>LPAR1</i>	rs2150052	9	113,945,067	6.29	60	214,738	113,828,811-114,043,548
<i>PHF19</i>	rs7847628	9	123,631,225	6.95	5	90,924	123,631,225-123,722,148
<i>STRBP</i>	rs700059	9	125,824,055	10.35	135	432,744	125,605,840-126,038,583
<i>HHEX-IDE</i>	rs61862780	10	94,468,643	12.40	31	134,694	94,358,023-94,492,716
<i>NT5C2</i>	rs74233809	10	104,913,940	7.25	98	404,547	104,655,350-105,059,896
<i>ADRB1</i>	rs7076938	10	115,789,375	15.69	4	9,521	115,789,375-115,798,895
<i>PLEKHA1</i>	rs2421016	10	124,167,512	6.90	26	70,596	124,127,990-124,198,585
<i>INS-IGF2</i>	rs72851023	11	2,130,620	7.89	48	145,434	2,078,742-2,224,175
<i>MTNR1B</i>	rs10830963	11	92,708,710	5.78	52	499,464	92,225,858-92,725,321
<i>APOLD1</i>	rs11055034	12	12,890,626	6.33	13	42,180	12,849,241-12,891,420
<i>ABCC9</i>	rs139975827	12	22,068,161	5.64	72	133,773	22,027,182-22,160,954
<i>ITPR2</i>	rs12823128	12	26,872,730	6.12	114	291,548	26,759,026-27,050,573
<i>HMGA2</i>	rs1351394	12	66,351,826	30.74	7	32,282	66,343,810-66,376,091
<i>IGF1</i>	rs7964361	12	102,994,878	6.71	42	213,557	102,867,636-103,081,192
<i>LINC00332</i>	rs2324499	13	40,662,001	6.83	41	95,318	40,583,503-40,678,820
<i>RB1</i>	rs2854355	13	48,882,363	6.23	143	403,044	48,797,661-49,200,704
<i>RNF219-AS1</i>	rs1819436	13	78,580,283	7.44	105	220,228	78,443,297-78,663,524
<i>FES</i>	rs12906125	15	91,427,612	6.68	24	36,382	91,404,705-91,441,086
<i>IGF1R</i>	rs7402982	15	99,193,269	7.59	5	15,682	99,177,595-99,193,276
<i>GPR139</i>	rs1011939	16	19,992,996	7.20	55	53,120	19,992,996-20,461,115
<i>CLDN7</i>	rs113086489	17	7,171,356	13.41	29	84,570	7,101,292-7,185,861
<i>SUZ12P1-CRLF3</i>	rs144843919	17	29,037,339	7.60	21	520,396	28,780,178-29,300,573
<i>SP6-SP2</i>	rs12942207	17	45,968,294	7.04	21	90,685	45,940,310-46,030,994
<i>ACTL9</i>	rs61154119	19	8,787,750	6.24	21	4,455	8,785,744-8,790,198
<i>PEPD</i>	rs10402712	19	33,926,013	6.40	35	218,599	33,784,657-34,003,255
<i>JAG1</i>	rs6040076	20	10,658,882	6.72	43	164,577	10,539,775-10,704,351
<i>C20orf203</i>	rs28530618	20	31,275,581	8.69	63	114,192	31,214,234-31,328,425
<i>MAFB</i>	rs6016377	20	39,172,728	8.15	33	72,001	39,144,286-39,216,286
<i>NRIP1</i>	rs2229742	21	16,339,172	6.69	4	85,250	16,339,172-16,424,421
<i>KREMEN1</i>	rs134594	22	29,468,456	6.41	56	52,177	29,461,150-29,513,326
<i>SREBF2</i>	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 <sup>a</sup>	Effect <sup>a</sup>	Upper 95%CI <sup>a</sup>	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 <sup>a</sup>	Effect <sup>a</sup>	Upper 95%_CI <sup>a</sup>	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 <sup>a</sup>	Effect <sup>a</sup>	Upper 95% CI <sup>a</sup>	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_LBI	-4.39	0.70	1.90	Blood vessel	Adult
HMVEC_dLyAd	-20.00	1.02	2.24	Blood vessel	Adult
HMVEC_dBIAd	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 <sup>a</sup>	Effect <sup>a</sup>	Upper 95% CI <sup>a</sup>
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

<sup>a</sup>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	<i>N</i>	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 <sup>a</sup>
		Effect	Other	$\beta$	SE	EAF	$\beta$	SE	P-value	N	
<i>WNT4-ZBTB40</i>	rs2473248	C	T	0.033	0.006	0.88	0.013	0.010	0.20	48,632	0.020
<i>ZBTB7B</i>	rs3753639	C	T	0.031	0.004	0.25	0.017	0.008	0.03	48,632	0.014
<i>FCGR2B</i>	rs72480273	C	A	0.031	0.005	0.19	0.013	0.008	0.11	48,632	0.018
<i>DTL</i>	rs61830764	A	G	0.022	0.004	0.37	-0.002	0.007	0.76	48,632	0.020
<i>ATAD2B</i>	rs7575873	A	G	0.038	0.004	0.87	-0.011	0.010	0.27	48,632	0.028
<i>EPAS1</i>	rs1374204	T	C	0.047	0.004	0.69	0.024	0.006	5.6x10 <sup>-5</sup>	68,252	0.023
<i>PTH1R</i>	rs2242116	A	G	0.022	0.004	0.37	0.019	0.006	9.3x10 <sup>-4</sup>	67,542	0.004
<i>ADCY5</i>	rs11719201	T	C	0.046	0.004	0.25	-0.001	0.008	0.85	48,632	0.045
<i>CPA3</i>	rs10935733	T	C	0.022	0.004	0.40	0.015	0.007	0.02	48,632	0.007
<i>CCNL1-LEKR1</i>	rs13322435	A	G	0.053	0.004	0.59	0.026	0.006	9.5x10 <sup>-6</sup>	68,250	0.027
<i>LCORL</i>	rs925098	G	A	0.034	0.004	0.28	0.025	0.006	2.9x10 <sup>-5</sup>	68,254	0.009
<i>HHIP</i>	rs6537307	G	A	0.025	0.004	0.49	0.019	0.005	4.4x10 <sup>-4</sup>	68,247	0.006
<i>5q11.2</i>	rs854037	A	G	0.027	0.005	0.80	0.009	0.007	0.18	68,219	0.018
<i>EBF1</i>	rs7729301	A	G	0.024	0.004	0.74	0.039	0.007	8.9x10 <sup>-8</sup>	48,632	-0.015
<i>CDKAL1</i>	rs35261542	C	A	0.044	0.004	0.74	0.004	0.007	0.60	48,632	0.040
<i>HIST1H2BE</i>	rs9379832	A	G	0.023	0.004	0.73	0.008	0.007	0.30	48,632	0.015
<i>HMGA1</i>	rs7742369	G	A	0.028	0.005	0.19	0.017	0.007	0.01	68,253	0.011
<i>L3MBTL3</i>	rs1415701	G	A	0.025	0.004	0.73	0.037	0.006	3.7x10 <sup>-9</sup>	66,897	-0.012
<i>ESR1</i>	rs1101081	C	T	0.038	0.004	0.72	0.021	0.007	3.8x10 <sup>-3</sup>	48,632	0.017
<i>GNA12</i>	rs798489	C	T	0.023	0.004	0.72	0.023	0.006	1.6x10 <sup>-4</sup>	68,253	0.001
<i>IGF2BP3</i>	rs11765649	T	C	0.027	0.004	0.74	0.015	0.007	0.04	48,632	0.012
<i>TBX20</i>	rs6959887	A	G	0.023	0.004	0.61	0.009	0.006	0.10	68,232	0.014
<i>YKT6-GCK</i>	rs138715366	C	T	0.241	0.023	0.99	0.137	0.038	2.8x10 <sup>-4</sup>	48,632	0.104
<i>MLXIPL</i>	rs62466330	C	T	0.051	0.011	0.07	0.022	0.013	0.08	48,632	0.029
<i>ANK1-NKX6-3</i>	rs13266210	A	G	0.031	0.005	0.78	0.005	0.007	0.43	68,252	0.026
<i>TRIB1</i>	rs6989280	G	A	0.022	0.004	0.72	0.020	0.006	1.3x10 <sup>-3</sup>	67,520	0.003
<i>SLC45A4</i>	rs12543725	G	A	0.023	0.004	0.58	0.021	0.005	1.4x10 <sup>-4</sup>	68,222	0.002
<i>PTCH1</i>	rs28510415	G	A	0.056	0.007	0.09	0.034	0.011	2.2x10 <sup>-3</sup>	48,632	0.022
<i>LPAR1</i>	rs2150052	T	A	0.021	0.004	0.50	0.017	0.005	1.4x10 <sup>-3</sup>	68,245	0.004
<i>PHF19</i>	rs7847628	G	A	0.023	0.004	0.68	0.009	0.007	0.20	48,632	0.014
<i>STRBP</i>	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 <sup>a</sup>
		Effect	Other	β	SE	EAF	β	SE	P-value	N	
<i>HHEX-IDE</i>	rs61862780	T	C	0.028	0.004	0.49	-0.004	0.006	0.55	48,632	0.024
<i>NT5C2</i>	rs74233809	C	T	0.037	0.007	0.08	0.005	0.012	0.70	48,632	0.032
<i>ADRB1</i>	rs7076938	T	C	0.036	0.004	0.73	0.010	0.006	0.09	68,254	0.026
<i>PLEKHA1</i>	rs2421016	T	C	0.021	0.004	0.48	0.016	0.005	3.3x10 <sup>-3</sup>	68,253	0.005
<i>INS-IGF2</i>	rs72851023	T	C	0.048	0.008	0.08	0.015	0.012	0.24	48,632	0.033
<i>MTNR1B</i>	rs10830963	G	C	0.023	0.004	0.29	0.048	0.006	5.1x10 <sup>-15</sup>	67,603	-0.025
<i>APOLD1</i>	rs11055034	C	A	0.022	0.004	0.71	0.002	0.006	0.74	67,597	0.020
<i>ABCC9</i>	rs139975827	G	A	0.027	0.007	0.63	-0.010	0.007	0.13	48,632	0.017
<i>ITPR2</i>	rs12823128	T	C	0.021	0.004	0.53	0.009	0.005	0.08	68,187	0.012
<i>HMGA2</i>	rs1351394	T	C	0.044	0.004	0.49	0.034	0.005	1.4x10 <sup>-10</sup>	68,247	0.010
<i>IGF1</i>	rs7964361	A	G	0.039	0.007	0.10	0.018	0.010	0.06	68,251	0.021
<i>LINC00332</i>	rs2324499	G	C	0.022	0.004	0.68	0.012	0.006	0.05	68,213	0.011
<i>RB1</i>	rs2854355	G	A	0.023	0.004	0.26	0.017	0.007	0.03	48,632	0.007
<i>RNF219-AS1</i>	rs1819436	C	T	0.033	0.006	0.88	0.007	0.010	0.50	48,632	0.026
<i>FES</i>	rs12906125	G	A	0.023	0.004	0.68	0.029	0.007	1.8x10 <sup>-5</sup>	48,632	-0.006
<i>IGF1R</i>	rs7402982	A	G	0.023	0.004	0.41	0.021	0.007	1.7x10 <sup>-3</sup>	48,632	0.002
<i>GPR139</i>	rs1011939	G	A	0.022	0.004	0.28	0.007	0.007	0.34	48,632	0.015
<i>CLDN7</i>	rs113086489	T	C	0.031	0.004	0.54	0.022	0.007	7.7x10 <sup>-4</sup>	48,632	0.009
<i>SUZ12P1-CRLF3</i>	rs144843919	G	A	0.066	0.012	0.96	0.041	0.018	0.02	48,632	0.025
<i>SP6-SP2</i>	rs12942207	C	T	0.022	0.004	0.30	0.010	0.007	0.14	48,632	0.012
<i>ACTL9</i>	rs61154119	T	G	0.028	0.005	0.85	0.047	0.009	1.5x10 <sup>-7</sup>	48,632	-0.019
<i>PEPD</i>	rs10402712	A	G	0.022	0.004	0.26	-0.002	0.007	0.76	48,632	0.020
<i>JAG1</i>	rs6040076	C	G	0.023	0.004	0.51	0.015	0.007	0.02	48,632	0.008
<i>C20orf203</i>	rs28530618	A	G	0.026	0.004	0.47	0.003	0.006	0.62	48,632	0.023
<i>MAFB</i>	rs6016377	T	C	0.024	0.004	0.45	0.005	0.006	0.35	67,909	0.019
<i>NRIP1</i>	rs2229742	G	C	0.036	0.006	0.88	0.018	0.009	0.04	68,155	0.018
<i>KREMEN1</i>	rs134594	C	T	0.023	0.004	0.36	0.004	0.006	0.53	66,634	0.020
<i>SREBF2</i>	rs62240962	C	T	0.047	0.007	0.92	0.027	0.012	0.02	48,632	0.020
<i>PLAC1</i>	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. <sup>a</sup>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  $P=1 \times 10^{-11}$ ).

**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		
			$\beta$	SE	P-value	$\beta$	SE	P-value	$\beta$	SE	P-value	$\beta$	SE	P-value
<i>WNT4-ZBTB40</i>	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
<i>ZBTB7B</i>	rs3753639	C/T	0.022	0.015	0.16	-0.005	0.017	0.79	0.060	0.016	$9.8 \times 10^{-5}$	0.060	0.018	$5.7 \times 10^{-4}$
<i>FCGR2B</i>	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
<i>DTL</i>	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
<i>ATAD2B</i>	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
<i>EPAS1</i>	rs1374204	T/C	0.032	0.013	0.02	0.008	0.015	0.60	0.056	0.013	$2.6 \times 10^{-5}$	0.047	0.015	$1.9 \times 10^{-3}$
<i>PTH1R</i>	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
<i>ADCY5</i>	rs11719201	T/C	0.000	0.015	1.00	-0.025	0.017	0.15	0.057	0.015	$2.2 \times 10^{-4}$	0.075	0.017	$1.5 \times 10^{-5}$
<i>CPA3</i>	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
<i>CCNL1-LEKR1</i>	rs13322435	A/G	0.028	0.013	0.03	-0.015	0.014	0.31	0.091	0.013	$7.9 \times 10^{-13}$	0.097	0.014	$9.7 \times 10^{-12}$
<i>LCORL</i>	rs925098	G/A	0.012	0.014	0.39	-0.017	0.016	0.29	0.057	0.014	$3.1 \times 10^{-5}$	0.060	0.015	$1.0 \times 10^{-4}$
<i>HHIP</i>	rs6537307	G/A	0.028	0.013	0.03	0.003	0.014	0.85	0.057	0.013	$1.1 \times 10^{-5}$	0.057	0.015	$7.8 \times 10^{-5}$
<i>5q11.2</i>	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
<i>EBF1</i>	rs7729301	A/G	0.036	0.014	$8.8 \times 10^{-3}$	0.040	0.015	$9.6 \times 10^{-3}$	0.024	0.014	0.08	0.010	0.016	0.52
<i>CDKAL1</i>	rs35261542	C/A	0.003	0.014	0.81	-0.028	0.016	0.07	0.057	0.014	$4.3 \times 10^{-5}$	0.071	0.016	$6.1 \times 10^{-6}$
<i>HIST1H2BE</i>	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
<i>HMGA1</i>	rs7742369	G/A	0.027	0.015	0.08	0.006	0.017	0.72	0.043	0.015	$4.9 \times 10^{-3}$	0.035	0.017	0.04
<i>L3MBTL3</i>	rs1415701	G/A	0.035	0.014	0.01	0.019	0.016	0.22	0.052	0.014	$2.7 \times 10^{-4}$	0.041	0.016	0.01
<i>ESR1</i>	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
<i>GNA12</i>	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
<i>IGF2BP3</i>	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
<i>TBX20</i>	rs6959887	A/G	0.018	0.013	0.15	-0.002	0.014	0.89	0.040	0.013	$1.7 \times 10^{-3}$	0.036	0.014	0.01
<i>YKT6-GCK</i>	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
<i>MLXIPL</i>	rs62466330	C/T	0.019	0.028	0.50	-0.015	0.031	0.62	0.104	0.028	$2.2 \times 10^{-4}$	0.129	0.031	$3.3 \times 10^{-5}$
<i>ANK1-NKX6-3</i>	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
<i>TRIB1</i>	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
<i>SLC45A4</i>	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
<i>PTCH1</i>	rs28510415	G/A	0.037	0.023	0.11	-0.005	0.026	0.84	0.105	0.023	$8.0 \times 10^{-6}$	0.105	0.027	$7.2 \times 10^{-5}$
<i>LPAR1</i>	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
<i>PHF19</i>	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
<i>STRBP</i>	rs700059	G/A	0.017	0.016	0.27	-0.006	0.018	0.76	0.053	0.016	$8.0 \times 10^{-4}$	0.062	0.018	$4.5 \times 10^{-4}$
<i>HHEX-IDE</i>	rs61862780	T/C	0.012	0.013	0.36	-0.015	0.014	0.29	0.053	0.013	$3.0 \times 10^{-5}$	0.059	0.014	$3.1 \times 10^{-5}$

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		
			$\beta$	SE	P-value	$\beta$	SE	P-value	$\beta$	SE	P-value	$\beta$	SE	P-value
<i>NT5C2</i>	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
<i>ADRB1</i>	rs7076938	T/C	0.045	0.014	$8.8 \times 10^{-4}$	0.032	0.015	0.03	0.050	0.014	$2.6 \times 10^{-4}$	0.037	0.015	0.02
<i>PLEKHA1</i>	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
<i>INS-IGF2</i>	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
<i>MTNR1B</i>	rs10830963	G/C	0.047	0.015	$1.7 \times 10^{-3}$	0.035	0.017	0.04	0.049	0.015	$9.8 \times 10^{-4}$	0.032	0.017	0.06
<i>APOLD1</i>	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
<i>ABCC9</i>	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
<i>ITPR2</i>	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
<i>HMGA2</i>	rs1351394	T/C	0.023	0.013	0.07	0.007	0.015	0.65	0.038	0.013	$3.0 \times 10^{-3}$	0.038	0.014	0.01
<i>IGF1</i>	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
<i>LINC00332</i>	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
<i>RB1</i>	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
<i>RNF219-AS1</i>	rs1819436	C/T	0.040	0.018	0.03	0.013	0.020	0.52	0.057	0.018	$1.8 \times 10^{-3}$	0.046	0.020	0.02
<i>FES</i>	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
<i>IGF1R</i>	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
<i>GPR139</i>	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
<i>CLDN7</i>	rs113086489	T/C	0.018	0.013	0.16	0.002	0.014	0.89	0.043	0.013	$5.7 \times 10^{-4}$	0.044	0.014	$1.9 \times 10^{-3}$
<i>SUZ12P1-CRLF3</i>	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
<i>SP6-SP2</i>	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
<i>ACTL9</i>	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
<i>PEPD</i>	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
<i>JAG1</i>	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
<i>C20orf203</i>	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
<i>MAFB</i>	rs6016377	T/C	0.000	0.013	0.99	-0.021	0.015	0.16	0.042	0.013	$1.4 \times 10^{-3}$	0.058	0.015	$9.9 \times 10^{-5}$
<i>NRIP1</i>	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
<i>KREMEN1</i>	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
<i>SREBF2</i>	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
<i>PLAC1<sup>a</sup></i>	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

<sup>a</sup>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	$1.2 \times 10^{-7}$	10,770	1,019,674	22504419
Birth weight	Birth length	0.805	0.058	13.98	$2.0 \times 10^{-44}$	28,460	983,823	25281659
Birth weight	Height (2014)	0.406	0.027	15.18	$4.8 \times 10^{-52}$	253,300	1,049,262	25282103
Birth weight	Height (2010)	0.401	0.028	14.09	$4.6 \times 10^{-45}$	133,900	1,026,905	20881960
Birth weight	Height (women)	0.400	0.032	12.59	$2.4 \times 10^{-36}$	73,140	1,028,514	23754948
Birth weight	Height (men)	0.384	0.035	11.00	$3.7 \times 10^{-28}$	60,590	1,024,139	23754948
Birth weight	Extreme height	0.399	0.043	9.20	$3.5 \times 10^{-20}$	16,200	739,427	23563607
Birth weight	Body mass index (2015)	0.114	0.025	4.49	$7.3 \times 10^{-6}$	322,200	1,050,986	25673413
Birth weight	Body mass index (2010)	0.120	0.033	3.66	$3.0 \times 10^{-4}$	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	$2.4 \times 10^{-4}$	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	$1.1 \times 10^{-21}$	58,350	1,025,155	23754948
Birth weight	Weight (women)	0.280	0.036	7.70	$1.4 \times 10^{-14}$	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	$8.3 \times 10^{-7}$	210,100	1,051,567	25673412
Birth weight	Waist-hip ratio (adjusted for BMI - 2010)	-0.189	0.041	-4.59	$4.4 \times 10^{-6}$	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	$3.6 \times 10^{-4}$	10,260	674,047	23563607
Birth weight	Hip circumference	0.281	0.030	9.30	$1.4 \times 10^{-20}$	213,000	1,048,111	25673412
Birth weight	Hip circumference (adjusted for BMI)	0.314	0.033	9.49	$2.3 \times 10^{-21}$	211,100	1,049,874	25673412
Birth weight	Hip circumference (men)	0.339	0.063	5.34	$9.3 \times 10^{-8}$	32,850	1,030,276	23754948
Birth weight	Hip circumference (women)	0.260	0.057	4.54	$5.6 \times 10^{-6}$	40,360	1,031,503	23754948
Birth weight	Waist circumference	0.177	0.028	6.29	$3.9 \times 10^{-10}$	232,100	1,048,634	25673412
Birth weight	Waist circumference (adjusted for BMI)	0.128	0.032	4.03	$5.7 \times 10^{-5}$	231,400	1,049,871	25673412
Birth weight	Waist circumference (men)	0.218	0.053	4.11	$3.9 \times 10^{-5}$	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	$7.8 \times 10^{-5}$	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	$6.5 \times 10^{-9}$	84,270	932,642	21378990
Birth weight	Systolic blood pressure (adjusted for BMI)	-0.263	0.039	-6.72	$1.8 \times 10^{-11}$	69,395	990,423	21909115
Birth weight	Systolic blood pressure (unadjusted for BMI)	-0.215	0.030	-7.21	$5.5 \times 10^{-13}$	127,969	1,186,583	UK Biobank data
Birth weight	Diastolic blood pressure (adjusted for BMI)	-0.224	0.042	-5.35	$8.7 \times 10^{-8}$	69,395	990,446	21909115
Birth weight	Triglycerides (2010)	-0.167	0.038	-4.41	$1.0 \times 10^{-5}$	96,600	1,024,575	20686565
Birth weight	Triglycerides (2013)	-0.112	0.031	-3.61	$3.0 \times 10^{-4}$	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	$1.1 \times 10^{-6}$	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	$1.3 \times 10^{-7}$	13,960	1,009,067	23449627
Birth weight	Pubertal growth - height at age 12 in males	0.305	0.072	4.23	$2.3 \times 10^{-5}$	6,986	1,017,307	23449627
Birth weight	Pubertal growth - height at age 10 in females	0.221	0.061	3.63	$3.0 \times 10^{-4}$	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	$1.3 \times 10^{-9}$	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	$4.0 \times 10^{-4}$	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 <sup>a</sup>	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) <sup>b</sup> (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 <sup>a</sup>	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) <sup>b</sup> (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 <sup>a</sup>	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) <sup>b</sup> (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
<b>NFBC1966</b>							
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)

<sup>a</sup>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.

<sup>b</sup>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)
<i>CPA4</i>	GTEX Primary	51200	7	129,932,973	129,964,020
<i>CST1</i>	GTEX Primary	1469	20	23,728,189	23,731,574
<i>DIRAS3</i>	GTEX Primary	9077	1	68,511,644	68,516,460
<i>DLK1</i>	GTEX Primary	8788	14	101,193,201	101,201,467
<i>FAM50B</i>	GTEX Primary	26240	6	3,849,631	3,851,551
<i>GRB10</i>	GTEX Primary	2887	7	50,657,759	50,861,159
<i>H19</i>	GTEX Primary	283120	11	2,016,405	2,019,065
<i>IGF2</i>	GTEX Primary	3481	11	2,150,346	2,170,833
<i>IGF2AS</i>	GTEX Primary	51214	11	2,161,757	2,169,896
<i>INPP5F</i>	GTEX Primary	22876	10	121,485,608	121,588,659
<i>KCNQ1</i>	GTEX Primary	3784	11	2,466,220	2,870,340
<i>KIF25</i>	GTEX Primary	3834	6	168,418,552	168,445,769
<i>L3MBTL1</i>	GTEX Primary	26013	20	42,136,319	42,170,534
<i>LPAR6</i>	GTEX Primary	10161	13	48,985,181	49,018,840
<i>MAGEL2</i>	GTEX Primary	54551	15	23,888,695	23,892,993
<i>MAGI2</i>	GTEX Primary	9863	7	77,646,373	79,082,890
<i>MEG3</i>	GTEX Primary	55384	14	101,292,444	101,327,360
<i>MEG8</i>	GTEX Primary	79104	14	101,361,106	101,373,305
<i>MEST</i>	GTEX Primary	4232	7	130,126,045	130,146,131
<i>NAP1L5</i>	GTEX Primary	266812	4	89,617,065	89,619,023
<i>NDN</i>	GTEX Primary	4692	15	23,930,553	23,932,450
<i>NTM</i>	GTEX Primary	50863	11	131,240,370	132,206,716
<i>PEG10</i>	GTEX Primary	23089	7	94,285,636	94,299,006
<i>PEG3</i>	GTEX Primary	5178	19	57,321,444	57,352,094
<i>PLAGL1</i>	GTEX Primary	5325	6	144,261,436	144,385,735
<i>PPIEL</i>	GTEX Primary	728448	1	39,987,951	40,025,370
<i>PPP2R5D</i>	GTEX Primary	5528	6	42,952,329	42,980,080
<i>PWRN1</i>	GTEX Primary	791114	15	24,803,303	24,832,926
<i>SGK2</i>	GTEX Primary	10110	20	42,187,634	42,214,273
<i>SNRPN</i>	GTEX Primary	6638	15	25,068,793	25,223,729
<i>SNURF</i>	GTEX Primary	8926	15	25,200,069	25,223,729
<i>SYCE1</i>	GTEX Primary	93426	10	135,367,403	135,382,876
<i>UBE3A</i>	GTEX Primary	7337	15	25,582,395	25,684,128
<i>UGT2B4</i>	GTEX Primary	7363	4	70,345,882	70,361,626
<i>UTS2</i>	GTEX Primary	10911	1	7,907,671	7,913,551
<i>ZDBF2</i>	GTEX Primary	57683	2	207,139,522	207,179,148
<i>ZNF331</i>	GTEX Primary	55422	19	54,024,176	54,083,523
<i>ZNF597</i>	GTEX Primary	146434	16	3,486,109	3,493,490
<i>ABCA6</i>	GTEX suggestive (S4 unique)	23460	17	67,074,846	67,138,015
<i>BMP8A</i>	GTEX suggestive (S4 unique)	353500	1	39,957,317	39,995,541
<i>CHIT1</i>	GTEX suggestive (S4 unique)	1118	1	203,185,206	203,198,860
<i>DLGAP2</i>	GTEX suggestive (S4 unique)	9228	8	1,449,568	1,656,642
<i>DZIP1</i>	GTEX suggestive (S4 unique)	22873	13	96,230,455	96,296,957
<i>EMR1</i>	GTEX suggestive (S4 unique)	2015	19	6,887,581	6,940,464
<i>FKBP10</i>	GTEX suggestive (S4 unique)	60681	17	39,968,961	39,979,469
<i>GPR1</i>	GTEX suggestive (S4 unique)	2825	2	207,040,041	207,082,771
<i>GTSF1</i>	GTEX suggestive (S4 unique)	121355	12	54,849,735	54,867,386
<i>GUCY1B2</i>	GTEX suggestive (S4 unique)	2974	13	51,568,646	51,640,293
<i>KIR3DX1</i>	GTEX suggestive (S4 unique)	90011	19	55,043,908	55,055,195
<i>LRRTM1</i>	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)
<i>MYOM2</i>	GTEX suggestive (S4 unique)	9172	8	1,993,157	2,093,380
<i>RTL1</i>	GTEX suggestive (S4 unique)	388015	14	101,346,991	101,351,184
<i>SERPINA6</i>	GTEX suggestive (S4 unique)	866	14	94,770,584	94,789,688
<i>SLC10A2</i>	GTEX suggestive (S4 unique)	6555	13	103,696,347	103,719,196
<i>THNSL2</i>	GTEX suggestive (S4 unique)	55258	2	88,469,834	88,486,146
<i>ANO1</i>	GTEX consistent (S6)	55107	11	69,924,407	70,035,652
<i>CALCR</i>	GTEX consistent (S6)	799	7	93,053,798	93,204,042
<i>CDKN1C</i>	GTEX consistent (S6)	1028	11	2,904,447	2,906,995
<i>COPG2</i>	GTEX consistent (S6)	26958	7	130,146,079	130,353,598
<i>DCN</i>	GTEX consistent (S6)	1634	12	91,539,034	91,576,806
<i>DIO3</i>	GTEX consistent (S6)	1735	14	102,027,687	102,029,789
<i>DLX5</i>	GTEX consistent (S6)	1749	7	96,649,701	96,654,143
<i>GABRA5</i>	GTEX consistent (S6)	2558	15	27,111,865	27,194,357
<i>GABRG3</i>	GTEX consistent (S6)	2567	15	27,216,428	27,778,373
<i>GLIS3</i>	GTEX consistent (S6)	169792	9	3,824,127	4,300,035
<i>GNAS-AS1</i>	GTEX consistent (S6)	149775	20	57,393,972	57,425,958
<i>KLF14</i>	GTEX consistent (S6)	136259	7	130,417,395	130,418,888
<i>MKRN3</i>	GTEX consistent (S6)	7681	15	23,810,453	23,813,166
<i>NNAT</i>	GTEX consistent (S6)	4826	20	36,149,606	36,152,090
<i>C15orf2</i>	GTEX consistent (S6)	23742	15	24,920,540	24,928,593
<i>PON3</i>	GTEX consistent (S6)	5446	7	94,989,183	95,025,687
<i>RB1</i>	GTEX consistent (S6)	5925	13	48,877,882	49,056,026
<i>RBP5</i>	GTEX consistent (S6)	83758	12	7,276,279	7,281,466
<i>SGCE</i>	GTEX consistent (S6)	8910	7	94,214,535	94,285,521
<i>TH</i>	GTEX consistent (S6)	7054	11	2,185,158	2,193,035
<i>TSPAN32</i>	GTEX consistent (S6)	10077	11	2,323,242	2,339,430
<i>TSSC4</i>	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	$\beta$	SE	P-value
<i>WNT4-ZBTB40</i>	rs2473248	T/C	1.008	0.971	1.007	-0.015	0.006	0.99
<i>ZBTB7B</i>	rs3753639	T/C	0.994	1.004	1.026	0.002	0.005	0.34
<i>FCGR2B</i>	rs72480273	A/C	0.995	1.008	1.012	0.008	0.005	$6.4 \times 10^{-2}$
<i>DTL</i>	rs61830764	G/A	0.997	0.993	1.031	-0.004	0.005	0.81
<i>ATAD2B</i>	rs7575873	A/G	1.007	0.978	0.964	-0.014	0.006	0.99
<i>EPAS1</i>	rs1374204	C/T	0.968	0.999	1.005	-0.002	0.005	0.68
<i>PTH1R</i>	rs2242116	A/G	1.003	0.987	1.013	-0.010	0.005	0.98
<i>ADCY5</i>	rs11719201	C/T	0.984	1.019	1.023	0.016	0.005	$1.1 \times 10^{-3}$
<i>CPA3</i>	rs10935733	T/C	0.999	1.007	0.990	0.009	0.005	$3.7 \times 10^{-2}$
<i>CCNL1-LEKR1</i>	rs13322435	A/G	1.016	0.993	0.981	-0.007	0.005	0.91
<i>LCORL</i>	rs925098	G/A	1.011	0.996	1.001	-0.002	0.005	0.64
<i>HHIP</i>	rs6537307	A/G	0.972	1.004	1.019	0.005	0.005	0.18
<i>5q11.2</i>	rs854037	A/G	1.004	0.990	1.008	-0.009	0.005	0.95
<i>EBF1</i>	rs7729301	G/A	1.028	0.990	1.003	-0.007	0.005	0.93
<i>CDKAL1</i>	rs35261542	C/A	1.004	0.998	0.969	$2 \times 10^{-4}$	0.005	0.48
<i>HIST1H2BE</i>	rs9379832	A/G	1.004	0.995	0.995	-0.004	0.005	0.80
<i>HMGA1</i>	rs7742369	A/G	0.995	1.005	1.044	0.002	0.005	0.36
<i>L3MBTL3</i>	rs1415701	G/A	1.006	0.990	1.006	-0.009	0.005	0.96
<i>ESR1</i>	rs1101081	C/T	1.003	0.999	0.979	0.001	0.005	0.39
<i>GNA12</i>	rs798489	C/T	1.005	0.993	0.997	-0.005	0.005	0.81
<i>IGF2BP3</i>	rs11765649	T/C	1.004	0.991	1.007	-0.005	0.005	0.83
<i>TBX20</i>	rs6959887	A/G	0.998	1.001	0.999	0.004	0.005	0.21
<i>YKT6-GCK</i>	rs138715366	C/T	1.001	0.888	0.657	-0.070	0.019	1.00
<i>MLXIPL</i>	rs62466330	T/C	0.995	1.028	1.036	0.016	0.007	$1.3 \times 10^{-2}$
<i>ANK1-NKX6-3</i>	rs13266210	A/G	1.007	0.984	1.009	-0.013	0.005	0.99
<i>TRIB1</i>	rs6989280	G/A	0.997	1.005	0.992	0.005	0.005	0.18
<i>SLC45A4</i>	rs12543725	G/A	1.009	0.994	0.999	-0.009	0.005	0.97
<i>PTCH1</i>	rs28510415	A/G	0.999	0.999	1.017	$1 \times 10^{-4}$	0.007	0.49
<i>LPAR1</i>	rs2150052	A/T	0.980	1.002	1.015	0.002	0.005	0.37
<i>PHF19</i>	rs7847628	A/G	0.984	1.002	1.001	0.003	0.005	0.30
<i>STRBP</i>	rs700059	G/A	0.989	1.018	0.994	0.015	0.006	$4.4 \times 10^{-3}$
<i>HHEX-IDE</i>	rs61862780	T/C	1.005	0.996	1.003	-0.005	0.005	0.82
<i>NT5C2</i>	rs74233809	T/C	0.999	0.998	1.136	$3 \times 10^{-4}$	0.007	0.48
<i>ADRB1</i>	rs7076938	C/T	0.992	1.003	0.998	$6 \times 10^{-4}$	0.005	0.45
<i>PLEKHA1</i>	rs2421016	C/T	0.988	1.007	0.998	0.008	0.005	$6.1 \times 10^{-2}$
<i>INS-IGF2</i>	rs72851023	C/T	0.996	1.022	1.013	0.013	0.007	$3.4 \times 10^{-2}$
<i>MTNR1B</i>	rs10830963	C/G	0.994	1.008	0.997	0.005	0.005	0.18
<i>APOLD1</i>	rs11055034	C/A	1.002	1.000	0.985	$2 \times 10^{-4}$	0.005	0.49
<i>ABCC9</i>	rs139975827	G/A	1.006	1.000	0.982	$2 \times 10^{-4}$	0.005	0.48
<i>ITPR2</i>	rs12823128	T/C	1.014	0.993	0.998	-0.006	0.005	0.87
<i>HMGA2</i>	rs1351394	T/C	1.003	1.001	0.993	$9 \times 10^{-4}$	0.005	0.43
<i>IGF1</i>	rs7964361	G/A	0.999	1.006	0.991	0.003	0.007	0.35
<i>LINC00332</i>	rs2324499	G/C	1.000	0.998	1.004	-0.003	0.005	0.70
<i>RB1</i>	rs2854355	A/G	0.991	1.008	1.024	0.008	0.005	$5.4 \times 10^{-2}$
<i>RNF219-AS1</i>	rs1819436	T/C	1.034	1.003	0.998	$5 \times 10^{-4}$	0.006	0.47
<i>DLK1</i>	rs6575803	C/T	1.002	0.991	0.987	-0.007	0.006	0.87
<i>FES</i>	rs12906125	G/A	1.004	0.993	1.010	-0.005	0.005	0.86
<i>IGF1R</i>	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	$\beta$	SE	P-value
<i>GPR139</i>	rs1011939	G/A	1.022	1.006	0.991	0.005	0.005	0.14
<i>CLDN7</i>	rs113086489	C/T	0.991	1.002	1.002	0.001	0.005	0.41
<i>SUZ12P1-CRLF3</i>	rs144843919	G/A	1.000	0.990	0.955	-0.006	0.010	0.72
<i>SP6-SP2</i>	rs12942207	C/T	1.018	1.005	0.992	0.006	0.005	0.12
<i>ACTL9</i>	rs61154119	T/G	0.998	1.007	0.974	0.003	0.006	0.30
<i>PEPD</i>	rs10402712	G/A	1.005	0.993	0.998	-0.004	0.005	0.78
<i>JAG1</i>	rs6040076	G/C	0.989	1.003	1.003	0.004	0.005	0.22
<i>C20orf203</i>	rs28530618	A/G	1.002	1.000	0.997	$4 \times 10^{-4}$	0.005	0.47
<i>MAFB</i>	rs6016377	C/T	0.988	0.999	1.021	$2 \times 10^{-4}$	0.005	0.48
<i>NRIP1</i>	rs2229742	G/C	1.002	0.991	0.939	-0.006	0.006	0.83
<i>KREMEN1</i>	rs134594	C/T	1.020	1.009	0.983	0.005	0.005	0.14
<i>SREBF2</i>	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			<i>P</i> <sub>het</sub>
			$\beta$	SE	<i>P</i> -value	$\beta$	SE	<i>P</i> -value	
<i>WNT4-ZBTB40</i>	rs2473248	C/T	0.019	0.042	0.65	0.189	0.076	$1.3 \times 10^{-2}$	$6.1 \times 10^{-2}$
<i>ZBTB7B</i>	rs3753639	C/T	0.012	0.034	0.72	0.078	0.045	$8.5 \times 10^{-2}$	0.34
<i>FCGR2B</i>	rs72480273	C/A	0.097	0.037	$8.0 \times 10^{-3}$	0.060	0.047	0.20	0.17
<i>DTL</i>	rs61830764	A/G	0.067	0.031	$2.8 \times 10^{-2}$	0.096	0.030	$1.7 \times 10^{-3}$	0.44
<i>ATAD2B</i>	rs7575873	A/G	0.080	0.041	$5.3 \times 10^{-2}$	0.086	0.072	0.23	0.36
<i>EPAS1</i>	rs1374204	T/C	0.094	0.032	$3.7 \times 10^{-3}$	0.121	0.037	$1.1 \times 10^{-3}$	0.98
<i>PTH1R</i>	rs2242116	A/G	0.007	0.031	0.83	0.064	0.033	$5.2 \times 10^{-2}$	$9.8 \times 10^{-2}$
<i>ADCY5</i>	rs11719201	T/C	0.137	0.034	$4.5 \times 10^{-3}$	0.062	0.035	$7.5 \times 10^{-2}$	0.11
<i>CPA3</i>	rs10935733	T/C	0.052	0.029	$7.7 \times 10^{-2}$	0.013	0.031	0.67	0.19
<i>CCNL1-LEKR1</i>	rs13322435	A/G	0.117	0.031	$1.4 \times 10^{-4}$	0.088	0.032	$5.9 \times 10^{-3}$	0.48
<i>LCORL</i>	rs925098	G/A	0.128	0.033	$1.1 \times 10^{-4}$	0.063	0.042	0.13	0.18
<i>HHIP</i>	rs6537307	G/A	0.080	0.030	$8.1 \times 10^{-3}$	0.071	0.030	$1.9 \times 10^{-2}$	0.79
<i>5q11.2</i>	rs854037	A/G	0.078	0.037	$3.5 \times 10^{-2}$	0.081	0.043	$5.8 \times 10^{-2}$	0.90
<i>EBF1</i>	rs7729301	A/G	-0.006	0.034	0.86	-0.028	0.041	0.50	0.67
<i>CDKAL1</i>	rs35261542	C/A	0.101	0.033	$2.1 \times 10^{-3}$	0.040	0.041	0.32	$8.3 \times 10^{-2}$
<i>HIST1H2BE</i>	rs9379832	A/G	0.034	0.033	0.30	0.037	0.038	0.33	0.83
<i>HMGA1</i>	rs7742369	G/A	0.046	0.038	0.23	0.161	0.051	$1.6 \times 10^{-3}$	0.10
<i>L3MBTL3</i>	rs1415701	G/A	0.029	0.033	0.38	0.092	0.042	$2.8 \times 10^{-2}$	$9.2 \times 10^{-2}$
<i>ESR1</i>	rs1101081	C/T	0.074	0.033	$2.5 \times 10^{-2}$	0.025	0.039	0.53	0.16
<i>GNA12</i>	rs798489	C/T	0.011	0.033	0.74	0.043	0.040	0.29	0.35
<i>IGF2BP3</i>	rs11765649	T/C	-0.013	0.033	0.69	0.054	0.036	0.14	0.14
<i>TBX20</i>	rs6959887	A/G	0.035	0.032	0.27	0.035	0.033	0.29	0.94
<i>YKT6-GCK</i>	rs138715366	C/T	0.235	0.166	0.16	0.032	0.468	0.95	0.66
<i>MLXIPL</i>	rs62466330	C/T	0.107	0.053	$4.5 \times 10^{-2}$	0.166	0.094	$7.8 \times 10^{-2}$	0.87
<i>ANK1-NKX6-3</i>	rs13266210	A/G	0.039	0.036	0.28	-0.031	0.041	0.45	0.21
<i>TRIB1</i>	rs6989280	G/A	-0.012	0.034	0.73	0.018	0.040	0.66	0.60
<i>SLC45A4</i>	rs12543725	G/A	0.052	0.030	$8.6 \times 10^{-2}$	0.047	0.030	0.12	0.90
<i>PTCH1</i>	rs28510415	G/A	0.091	0.047	$5.4 \times 10^{-2}$	0.212	0.092	$2.1 \times 10^{-2}$	0.39
<i>LPAR1</i>	rs2150052	T/A	-0.001	0.030	0.97	0.092	0.030	$2.0 \times 10^{-3}$	$2.4 \times 10^{-3}$
<i>PHF19</i>	rs7847628	G/A	0.038	0.032	0.23	0.004	0.037	0.92	0.28
<i>STRBP</i>	rs700059	G/A	0.043	0.041	0.29	-0.029	0.070	0.68	0.22
<i>HHEX-IDE</i>	rs61862780	T/C	0.085	0.030	$4.7 \times 10^{-3}$	0.050	0.030	$9.6 \times 10^{-2}$	0.32
<i>NTSC2</i>	rs74233809	C/T	-0.018	0.051	0.73	0.040	0.068	0.56	0.51
<i>ADRB1</i>	rs7076938	T/C	0.023	0.033	0.49	0.078	0.041	$5.5 \times 10^{-2}$	0.27
<i>PLEKHA1</i>	rs2421016	T/C	0.024	0.031	0.43	0.036	0.031	0.24	0.77
<i>INS-IGF2</i>	rs72851023	T/C	0.116	0.051	$2.2 \times 10^{-2}$	0.108	0.107	0.31	0.56
<i>MTNR1B</i>	rs10830963	G/C	0.024	0.033	0.46	0.058	0.040	0.15	0.53
<i>APOLD1</i>	rs11055034	C/A	0.122	0.032	$1.7 \times 10^{-4}$	0.053	0.039	0.17	$3.2 \times 10^{-2}$
<i>ABCC9</i>	rs139975827	G/A	0.045	0.031	0.15	0.017	0.032	0.59	0.46
<i>ITPR2</i>	rs12823128	T/C	0.064	0.030	$3.0 \times 10^{-2}$	-0.003	0.029	0.91	$7.7 \times 10^{-2}$
<i>HMGA2</i>	rs1351394	T/C	0.015	0.031	0.63	0.082	0.031	$8.3 \times 10^{-3}$	$8.0 \times 10^{-2}$
<i>IGF1</i>	rs7964361	A/G	-0.045	0.049	0.36	0.091	0.099	0.36	0.33
<i>LINC00332</i>	rs2324499	G/C	0.012	0.032	0.70	0.041	0.034	0.22	0.70
<i>RB1</i>	rs2854355	G/A	0.031	0.033	0.35	-0.012	0.042	0.77	0.25
<i>RNF219-AS1</i>	rs1819436	C/T	0.038	0.042	0.36	0.136	0.079	$8.4 \times 10^{-2}$	0.39
<i>DLK1</i>	rs6575803	C/T	0.104	0.045	$2.2 \times 10^{-2}$	0.205	0.091	$2.5 \times 10^{-2}$	0.40
<i>FES</i>	rs12906125	G/A	0.019	0.032	0.55	0.095	0.035	$6.7 \times 10^{-3}$	$9.3 \times 10^{-2}$
<i>IGF1R</i>	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			<i>P</i> _het
			$\beta$	SE	<i>P</i> -value	$\beta$	SE	<i>P</i> -value	
<i>GPR139</i>	rs1011939	G/A	-0.028	0.032	0.38	0.021	0.038	0.59	0.29
<i>CLDN7</i>	rs113086489	T/C	0.061	0.031	$4.9 \times 10^{-2}$	0.050	0.031	0.11	0.83
<i>SUZ12P1-CRLF3</i>	rs144843919	G/A	0.003	0.071	0.96	0.182	0.113	0.11	0.20
<i>SP6-SP2</i>	rs12942207	C/T	0.050	0.032	0.12	0.027	0.038	0.48	0.32
<i>ACTL9</i>	rs61154119	T/G	0.056	0.038	0.14	0.164	0.062	$8.7 \times 10^{-3}$	$5.6 \times 10^{-2}$
<i>PEPD</i>	rs10402712	A/G	0.077	0.033	$2.1 \times 10^{-2}$	0.001	0.034	0.98	0.10
<i>JAG1</i>	rs6040076	C/G	0.028	0.031	0.36	0.001	0.031	0.97	0.53
<i>C20orf203</i>	rs28530618	A/G	0.053	0.031	$8.3 \times 10^{-2}$	0.013	0.031	0.68	0.26
<i>MAFB</i>	rs6016377	T/C	0.054	0.031	$8.0 \times 10^{-2}$	0.008	0.031	0.80	0.20
<i>NRIP1</i>	rs2229742	G/C	0.020	0.046	0.66	0.030	0.095	0.75	0.89
<i>KREMEN1</i>	rs134594	C/T	0.024	0.031	0.43	0.052	0.035	0.13	0.75
<i>SREBF2</i>	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		
	$\beta$	SE	<i>P</i> -value	$\beta$	SE	<i>P</i> -value	$\beta$	SE	<i>P</i> -value
M1 (C1)	0.128	0.013	$1.6 \times 10^{-21}$	-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	$1.2 \times 10^{-7}$	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.

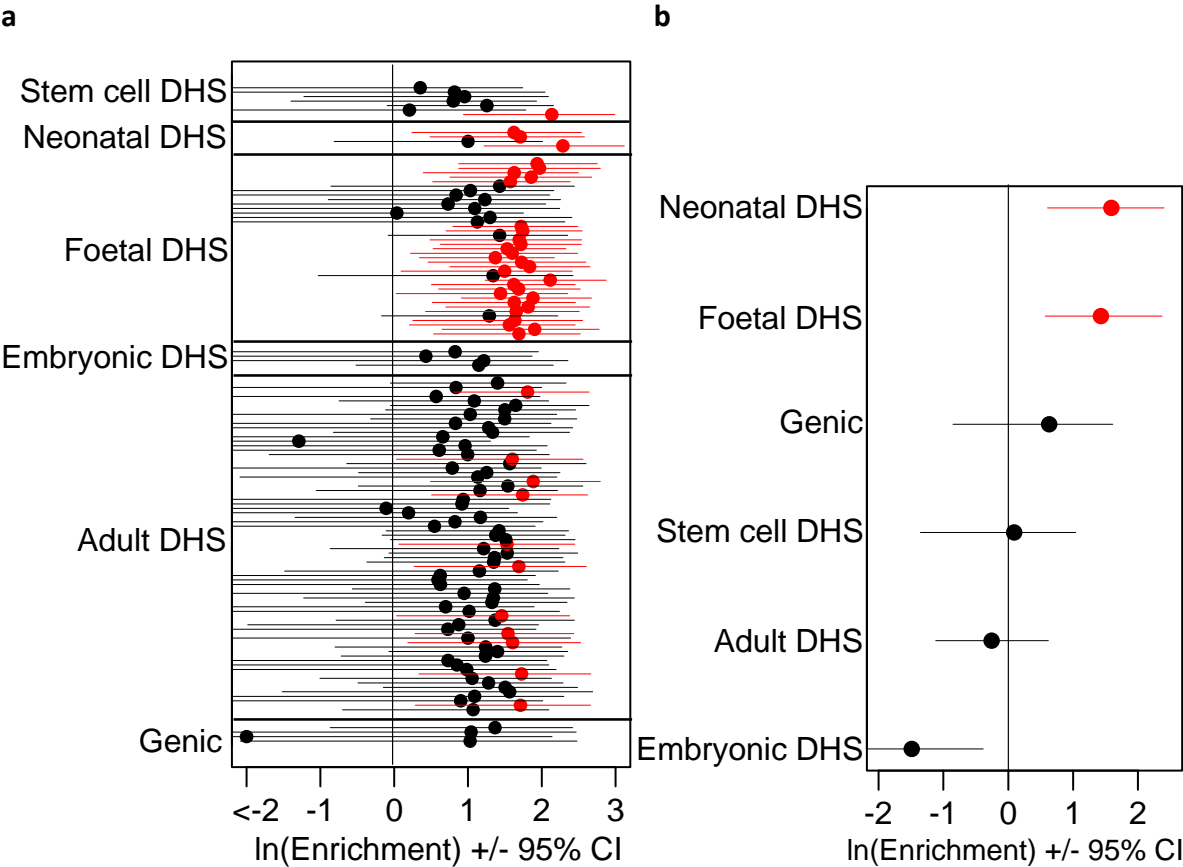
**Supplementary Table 19. Reciprocal approximate conditional analyses at *YKT6-GCK* variants associated with birth weight (BW) or fasting glucose (FG), in European ancestry meta-analysis of up to 143,677 individuals.**

Variant (chr:position)	Type	EA/ NEA	EAF (Eur)	BW SNP conditioned on FG SNP				FG SNP conditioned on BW SNP			
				Uncondit ioned <i>P</i>	Conditioned on	Variant type	Conditio ned <i>P</i>	Variant	Conditioned on	Uncondit ioned <i>P</i>	Conditio ned <i>P</i>
rs138715366 (7:44246271)	BW lead SNP (at <i>YKT6</i> intron 1)	T/C	0.0089	7.2x10 <sup>-26</sup>	unconditioned	-	-	-	-	-	-
					rs878521	<i>GCK</i> FG primary (ENGAGE <sup>1</sup> )	1.3x10 <sup>-25</sup>	rs878521	rs138715366	0.12	0.28
					rs10259649	<i>GCK</i> FG secondary (ENGAGE <sup>1</sup> )	7.7x10 <sup>-26</sup>	rs10259649	rs138715366	0.52	0.63
					rs4607517	<i>GCK</i> FG (MAGIC <sup>2</sup> )	2.6x10 <sup>-25</sup>	rs4607517	rs138715366	3.2x10 <sup>-4</sup>	1.2x10 <sup>-3</sup>
					rs10278336	<i>GCK</i> T2D (DIAGRAM <sup>3</sup> )	1.8x10 <sup>-25</sup>	rs10278336	rs138715366	0.057	0.19
rs78412508 (7:44223858)	BW second strongest SNP (at <i>GCK</i> intron 3)	A/G	0.0095	8.9x10 <sup>-24</sup>	unconditioned	-	-	-	-	-	-
					rs878521	<i>GCK</i> FG primary (ENGAGE <sup>1</sup> )	1.6x10 <sup>-23</sup>	rs878521	rs78412508	0.12	0.27
					rs10259649	<i>GCK</i> FG secondary (ENGAGE <sup>1</sup> )	9.7x10 <sup>-24</sup>	rs10259649	rs78412508	0.52	0.66
					rs4607517	<i>GCK</i> FG (MAGIC <sup>2</sup> )	3.1x10 <sup>-23</sup>	rs4607517	rs78412508	3.2x10 <sup>-4</sup>	1.2x10 <sup>-3</sup>
					rs10278336	<i>GCK</i> T2D (DIAGRAM <sup>3</sup> )	2.2x10 <sup>-23</sup>	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.

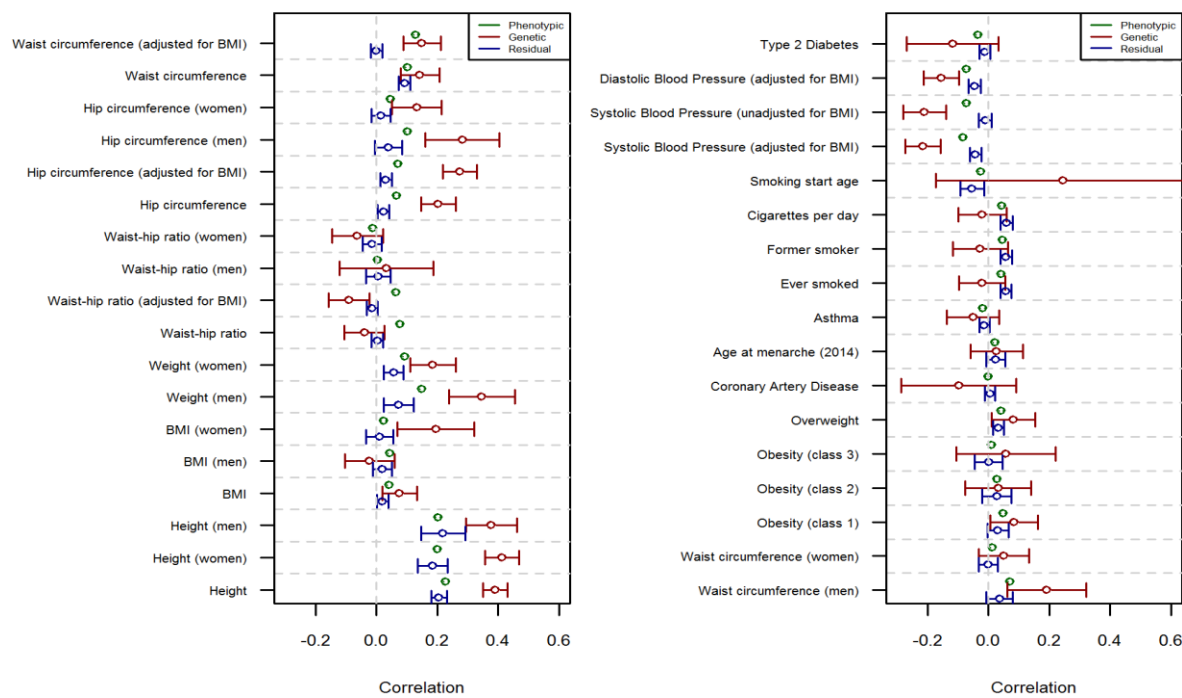
- 1. Horikoshi M *et al.* PLoS Genet 11, e1005230 (2015).
- 2. Dupuis J *et al.* Nat Genet 42, 105-116 (2010).
- 3. Morris AP *et al.* Nat Genet 44, 981-990 (2012).

**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).

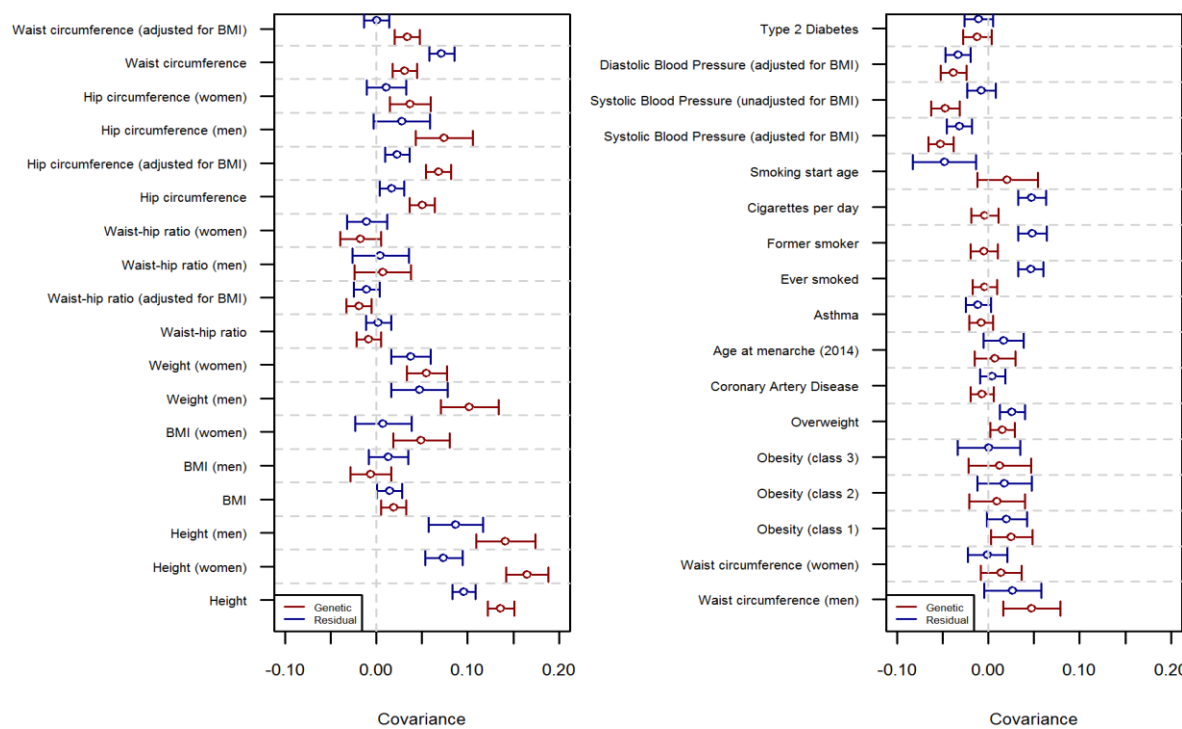


**Supplementary Figure 2. Estimates of phenotypic, genetic and residual correlations (a) and estimates of genetic and residual covariance (b) between birth weight and adult metabolic or anthropometric traits in UK Biobank ‘white British’ samples (up to N=57,715). See details in Supplementary Table 13.**

**a**



**b**



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