

## Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution

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### Declaration:

I.B. and spouse own stock in Incyte Ltd and GlaxoSmithKline. J.H. is a member of the Scientific Advisory Board, Correlagen, Inc. A.P. is employed by Amgen. K.S., V.S., G.T., U.T. and G.B.W. are employed by deCODE Genetics.

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### Supplementary Table 1: Study-specific information on study design, sample quality control, and sample size

Short	Name		Study design	Call rate*	Other Exclusions	Sample size		References
	Full					Total	In WHR analyses	
<b>Discovery Stage</b>								
ADVANCE (Cases) *	Atherosclerotic Disease, Vascular Function, and Genetic Epidemiology	Population-based case-control (multi ethnic)	>98.5%	1) duplicates; 2) missing weight or height	275	NA	Assimes TL et al. Hum Mol Genet. 2008 Aug 1;17(15):2320-8	
ADVANCE (Controls) *	As above	As above	>98.5%	As above	311	NA	As above	
AGES Reykjavik~	Age, Gene/Environment Susceptibility-Reykjavik Study	Population-based	≥ 97%	1) mismatch with previous genotypes; 2) remove A/T & G/C SNPs; 3) remove SNPs not in HapMap	3219	NA	Harris et al. American Journal of Epidemiology (2007) vol. 165 (9) pp. 1076-87	
Amish	Amish Heredity and Phenotype Intervention Heart Study	Founder population	≥ 93%	1) Misidentified pedigree relationships; 2) Misidentified sex	910	900	Mitchell BD et al. Am Heart J 823:828, 2008; Heard-Costa NL et al. PLoS Genet. 2009 Jun;5(6):e1000539	
ARIC	The Atherosclerosis Risk in Communities Study	Population-based	≥ 90%	1) True sex/gender mismatch; 2) Discordant genotype with earlier TaqMan genotyping. If >10/47 genotypes discordant -> exclude; 3) First-degree relative; 4) PC>8SD in Eigenstrat run (10 iterations with 10 PCs); 5) Outlier based on average IBS; 6) missing	8,861	8,104	Atherosclerosis Risk in Communities (ARIC) Study: design and objectives. 1989. ARIC Investigators. Am. J. Epidemiol. 129: 687-702; Heard-Costa, NL et al. 2009. Plos Genet. 5(6): e1000539	
B58C (T1DGC)	British 1958 birth cohort (Type 1 Diabetes Genetic Consortium controls)	Population-based	≥ 98%	1) contamination; 2) non-European identity; 3) Missing body height.	2,592	2,490	Strachan DP et al. Int J Epidemiol 2007; 36:522-531; Barrett JC et al. Nat Genet 2009 May 10	
B58C (WTCCC)	British 1958 birth cohort (Wellcome Trust Case Control Consortium controls)	Population-based	≥ 97%	1) contamination; 2) non-European identity and relatedness; 3) Missing body height.	1,502	1,422	The Wellcome Trust Case Control Consortium, Nature 447, 661-678 (2007). Power, C. & Elliott, J. Cohort profile: 1958 British birth cohort (National Child Development)	
BRIGHT	The British Genetics of Hypertension (BRIGHT) Study	Hypertension cases	≥ 97%	1) heterozygosity <23% or >30%; 2) external discordance; 3) non-European ancestry; 4) duplicate/first/second degree relatives.	2,000	1,895	Caulfield M et al. , Lancet. 2003 Jun 21; 361(9375):2118-23	
CHS	The Cardiovascular Health Study	Population-based	>95%	1) Prevalent clinical CVD; 2) African-americans; 3) Sex discordant; 4) Missing body weight and height	3,238	3,217	Fried LP et al. Ann Epidemiol. 1991; 1: 263-276	
CoLaus	Cohorte Lausannoise	Population-based	>90%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing height	6,188	5,405	Firmann et al. BMC Cardiovascular Disorders 2008, 8:6	
deCODE	deCODE genetics sample set	Population-based	≥ 96%	Missing body weight and height.	38,446	5,883	Thorleifsson G et al. Nat Genet. 41, 18-24 (2009)	
DGI (Cases)	Diabetes Genetics Initiative of Broad Institute of Harvard and MIT, Lund University, and Novartis Institutes of BioMedical Research	Case control for diabetes	≥ 95%	1) Related individuals; 2. Sample contamination; 3) Missing body weight and height.	1,658	958	Saxena et al. Science 316, 1331-6 (2007)	
DGI (Controls)	As above	As above	≥ 95%	As above	1,595	469	As above	
EGCUT	Estonian Genome Center, University of Tartu	Population-based	≥ 95%	1) Related individuals and duplicates; 2) Sex mismatch; 3) Phenotype missing	1,412	423	Nelis M et al. PLoS ONE 4(5): e5472; Metspalu A. 62, 97-101 (2004)	
EPIC-Obesity Study	European Prospective Investigation into Cancer and Nutrition - Obesity Study	Population-based	≥ 94%	1) heterozygosity <23% or >30%; 2) >5.0% discordance in SNP pairs with r2=1 in HapMap; 3) ethnic outliers; 4) related individuals and duplicates; 5) Missing body weight and height.	2,566	2,415	Day NE et al. British Journal of Cancer 80, 95-103 (1999); Loos RJ et al. Nat Genet 40, 768-775 (2008)	
ERF (EUROSPAN)	The Erasmus Rucphen Family (EUROSPAN)	Family-based	> 95%	1) excess heterozygosity based on FDR; 2) ethnic outliers; 3) sex mismatch; 4) missing phenotype	2,300	2,090	Aulchenko YS et al. Eur J Hum Genet 12, 527-534; Pecioska S et al. PLoS One 5, e8541 (2010)	
Fenland	The Fenland Study	Population-based	≥ 95%	1) heterozygosity <27.3% or >28.8%; 2) duplicate check; 3) relatedness check	1,500	1,402	Willer et al. Nat Genet. 2009 Jan;41(1):25-34	
FHS (Cases)	The Family Heart Study	Case-Controls	≥ 98%	1) technical errors; 2) discrepancies between reported sex and sex-diagnostic markers	463	441	M. Higgins et al. Am J Epidemiol 143, 1219-1228 (1996)	
FHS (Controls)	As above	As above	≥ 98%	As above	434	416	As above	
FRAM	The Framingham Heart Study	Population-based, multi-generational	≥ 97%	1) pHWE <1e-6 call rate <97%; 2) mishap p <1e-9; 3) MAF <0.01; 4) Mendelian errors >100; 5) SNPs not in Hapmap; strand issues merging with Hapmap	9,274	325	DAWBER TR et al. Ann N Y Acad Sci. 1963; 107:539-556; Feinleib M et al. Prev Med. 1975; 4:518-525; Splansky GL et al. Am J Epidemiol. 2007; 165:1328-1335	
FTC	Finnish Twin Cohort	Monozygotic Twins	≥ 95%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body weight and body mass index.	152 pairs	138 pairs	Aulchenko YS et al. Nat Genet. 2009 Jan, 41(1):47-55. Epub 2008 Dec 7	
FUSION (Controls)	Finland-United States Investigation of NIDDM Genetics	case-control study	> 97.5%	related individuals; missing BMI or height	1,174	1,169	Scott LJ et al. Science 316(5829):1341-5 (2007)	

FUSION (Cases)	As above	As above	> 97.5%	As above	1,161	1,084	As above
GENMETS (Cases)	Health 2000 / GENMETS substudy	Metabolic syndrome case-control	≥ 95%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body weight and body mass index.	932	857	<a href="http://www.terveys2000.fi/indexe.html">http://www.terveys2000.fi/indexe.html</a>
GENMETS (Controls)	As above	As above	≥ 95%	As above	948	869	As above
KORA S3	Kooperative Gesundheitsforschung in der Region Augsburg, third survey	Population-based	≥ 93%	1) german passport; 2) missing height.	1,644	1,644	Heid IM et al. 2010 Atherosclerosis. 2010 Feb;208(2):412-20. Epub 2009 Dec 2
KORA S4	Kooperative Gesundheitsforschung in der Region Augsburg, forth survey	Population-based	≥ 93%	1) german passport; 2) missing height.	1,814	1,814	Heid et al. Obesity (Silver Spring). 2008 Feb;16(2):369-76
MICROS	MICROS (EUROSPAN)	Population-based	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	1,098	293	Johansson A et al. Hum Mol Genet. 18(2), 373-80 (2009); Hicks, AA et al. PLoS Genet. 5(10):e1000672 (2009)
NFBC1966	Northern Finland Birth Cohort (NFBC) 1966	Population-based	≥ 95%	1) gender discrepancy with genetic data from X-linked markers; 2) withdrawn consent; 3) duplicates and first and second degree relatives; 4) contaminated samples	5,654	4,773	Sabatti C. et al. Nat Genet (2008)
NHS	The Nurses' Health Studies	Nested case-control	>90%	1) Low genotyping completion (<90%); 2) Unclear identity and admixed origin; 3) Missing height.	2,368	1,632	Hunter DJ et al. Nat Genet. (2007). Jul;39(7):870-4
NSPHS †	Northern Sweden Population Health Study (EUROSPAN)	Population-based	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	647		Johansson A. et al. Hum Mol Genet. 18(2), 373-80 (2009) Hicks, AA et al. PLoS Genet. 5(10):e1000672 (2009)
NTRNESDA (Cases)	Netherlands Twin Register & the Netherlands Study of Depression and Anxiety	Case-control	≥ 95%	1) evidence of sample contamination (heterozygosity); 2) ethnic outliers; 3) related individuals and duplicates; 5) missing body height.	1,860	1,723	Boomsma DI et al. Int J Methods Psychiatr Res 2008; 17: 121–140; Boomsma DI et al. Eur J Hum Genet 2008; 16: 335–342
NTRNESDA (Controls)	As above	As above	≥ 95%	As above	1,860	1,786	As above
ORCADES	Orkney Complex Disease Study (part of EUROSPAN)	Population-based	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	719	697	Johansson A et al. CHum Mol Genet. 18(2), 373-80 (2009).; Hicks, AA. et al. PLoS Genet. 5(10):e1000672 (2009)
PROCARDIS	Precocious coronary artery disease	coronary artery disease case-control	> 95%	none	2,573	2,539	Broadbent, H.M. et al. Hum Mol Genet 17, 806-14 (2008)
RS1	Rotterdam Study I	Population-based	≥ 97.5%	1) gender mismatch with typed X-linked markers; 2) excess autosomal heterozygosity > 0.336~FDR>0.1%; 3) duplicates and/or 1st or 2nd degree relatives using IBS probabilities >97% from PLINK; 4) ethnic outliers using IBS distances > 3SD from PLINK; 5) Missing phenotype	7,983	5,468	Visscher 2001 A comparison of body mass index, waist-hip ratio and waist circumference ...: the Rotterdam study; Estrada, 2009 GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data; Hofman 2009 The Rotterdam Study: 2010 objectives and design update; Hofman 1991 Determinants of disease and disability in the elderly: the Rotterdam Elderly Study
SARDINIA	The Sardinia Study	Population-based	≥ 90%	1) Morquio syndrome; 2) Missing height	6,148	4,301	Pilia G et al. Plos Genetics 2, e132 (2006); Willer CJ et al. Nat Genet 40, 161-16
SHIP	Study of Health in Pomerania	Population-based	≥ 92%	1) missing genotype or phenotype data	4,310	4,092	John U et al. Soz-Präventivmed 46: 186- 194 (2001)
T2D_WTCCC	WTCCC Type 2 Diabetes cases	case series	≥ 97%	1) heterozygosity <23% or >30%; 2) discrepancy with external identifying information; 3) ethnic outliers; 4) related individuals and duplicates;	1,999	1,903	The Wellcome Trust Case Control Consortium, Nature 447, 661-678 (2007)
TwinsUK	TwinsUK	Twins pair	≥ 95%	1) heterozygosity <33% or >37%; 2) ethnic outliers; 3) related individuals and duplicates; 4) Missing body weight and height.	2,226	1,094	Spector TD et al. Twin Res Hum Genet 9, 899-906 (2006); Spector TD et al. Twin Res 5, 440-443 (2002)
VIS	VIS and KORCULA (EUROSPAN)	Population-based	≥ 97%	1) ethnic outliers; 2) duplicates; 3) Missing height.	795	783	Johansson A et al. Hum Mol Genet. 18(2), 373-80 (2009); Hicks, AA. et al. PLoS Genet. 5(10):e1000672 (2009)

Follow-up Stage							
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In silico follow-up studies							
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BHS	Busselton Health Study	Population-based	≥ 75%	1) ethnic outliers; 2) related individuals and duplicates; 3) Missing body waist and hip.	1,366	1,284	James AL et al. Am J Respir Crit Care Med 2005;171:109-14
Corogene	Genetic Predisposition of Coronary Heart Disease in Patients Verified with Coronary Angiogram	Population-based	≥ 95%	1) missing gender; 2) related individuals and duplicates 3) (For this specific analysis) Missing body height	4,130	2,063	Soranzo N et al., Nat. Genet. 41, 1182-1190 (2009)
EGCUT	Estonian Genome Center, University of Tartu	Population-based	≥ 95%	1) Related individuals and duplicates; 2) Sex mismatch 3) Phenotype missing	345	345	Nelis M et al. Drug Development Research 62, 97-101 (2004)
FHS	Family Heart Study	Case-Control	≥ 98%	1) technical errors; 2) discrepancies between sex and sex-markers	1808	1463	M. Higgins et al., Am J Epidemiol 143, 1219–1228 (1996).
GOOD	Gothenburg Osteoporosis and Obesity Determinants Study	Population-based	≥ 97.5%	1) heterozygosity > 33%; 2) ethnic outliers; 3) related individuals and duplicates.	1056	937	Lorentzon M. et al. J Bone Miner Res 20, 1334-1341 (2005)

HBCS	Helsinki Birth Cohort Study	Population-based birth cohort	≥ 95%	1) related individuals and duplicates; 2) Missing height	1,872	1,723	Ylihärsilä H et al. Am J Clin Nutr. 2008 Jun, 87(6):1769-75; Kajantie E et al. Int J Epidemiol 2005; 34:655-663
NHS	The Nurses' Health Study	Nested case-control	>98%	1) Low genotyping completion (<98%); 2) Unclear identity and admixed origin; 3) related individuals and duplicates; 4) DNA contamination; 5) Missing height;	3,221	2,196	Qi L et al. Hum Mol Genet. 2010 Feb 10
RS-II	Rotterdam Study II	Population-based	≥ 97.5%	1) gender mismatch with typed X-linked markers; 2) excess autosomal heterozygosity (F<0.055); 3) duplicates and/or 1st degree relatives using IBD PIHAT >40% from PLINK; 4) ethnic outliers IBS distances > 4SD mean HaMAP CEU cluster from PLINK; 5) Missing body weight and height.	3,011	1,915	Visscher 2001 A comparison of body mass index, waist-hip ratio and waist circumference ...: the Rotterdam study; Estrada 2009 GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data; Hofman 2009 The Rotterdam Study: 2010 objectives and design update, Hofman, 1991 Determinants of disease and disability in the elderly: the Rotterdam Elderly Study
SORBS	Sorbs are self-contained population from Eastern Germany, European Descent	Population-based	≥ 94%	1) gender mismatch; 2) ethnic outliers; 3) duplicates; 4) Missing body weight and height.	1,097	907	Tönjes A et al. Eur J Hum Genet. 2010 Jan;18(1):104-10
WGHS	Women's Genome Health Study	Population-based	>98%	1) includes only WGHS participants with confirmed, self-reported European ancestry; 2) all SNPs have HWE p>10E-6; 3) all SNPs have genotype for >90% samples; 4) only samples with biometric measures included	23,294	20,529	Ridker PM et al. Women's Genome Health Study Working Group. Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy american women
YFS	The Cardiovascular Risk in Young Finns Study	Population-based	≥ 95%	1) missing gender; 2) related individuals and duplicates; 3) Missing body height	2,443	1,999	Raitakari OT et al. Int J Epidemiol. 2008; 37:1220-6
<b>De-novo follow-up studies</b>							
BCG	Barry Caerphilly Growth Study	Population-based	> 90%	1. Missing phenotype; 2. Missing DNA	659	634	Martin RM et al. American Journal of Clinical Nutrition, 77: 1489-97, 2003
BPPP	Botnia Prevalence, Prediction and Prevention of Diabetes study	Population-based	≥ 95%	1. Missing phenotypes; 2. Missing DNA	3505	3463	Isomaa B et al., Diabetologia 2010, in press
BWHHS	British Women's Heart and Health Study	Population based	> 90%	1. Missing phenotypes; 2. Missing DNA	3757	3687	Lawlor DA et al. Journal of Epidemiology & Community Health., 57: 134-40, 2003
DESIR	Data from the Epidemiological Study on the Insulin Resistance Syndrome	Population-based	≥ 95%	1. Missing DNA; 2. Missing phenotypes; 3. Non Europeans or born outside continental France	5212	4535	Balkau B. Rev Epidemiol Sante Publique. 1996 Aug;44(4):373-5. French
DIAGEN	Diabetes Genetics	Population-based	≥ 88%	Missing phenotypes	1,855	1,777	Fischer S. et al. Diabetes Care 29, 1645-50 (2006)
EGCUT	Estonian Genome Center, University of Tartu	Population-based	≥ 95%	1) Related individuals and duplicates; 2) Sex mismatch; 3) Phenotype missing	3779	3779	Nelis M et al. Drug Development Research 62, 97-101 (2004)
EPIC-Norfolk	European Prospective Investigation into Cancer and Nutrition - Norfolk	Population-based	≥ 95%	1. Missing phenotypes; 2. Missing DNA	19086	18484	Day NE et al. British Journal of Cancer 80, 95-103 (1999)
FINRISK	FINRISK 97	Population-based	≥ 95%	1. Missing phenotypes; 2. Missing DNA	8447	7903	Vartiainen E et al. Int. J. Epidemiol. 29, 49-56 (2000)
FUSION T2D (Cases)	FUSION stage 2 Cases	Case-Control	≥ 94%	Missing phenotypes	1,233	1,224	Scott LJ et al. Science 316, 1341-5 (2007)
FUSION T2D (Controls)	FUSION stage2 Controls	As above	≥ 94%	As above	3,704	3,688	As above
HUNT2	Nord-Trøndelag Health (HUNT) 2 Study	Population-based	≥ 92%	Missing phenotypes	6,399	4,836	Midtjell K. et al. Diabetes Care 22, 1813-1820 (1999); Holmen, J. et al. Norwegian Journal of Epidemiology 13, 19-32 (2003)
Inter99	A population-based primary prevention study on cardiovascular disease and type 2 diabetes	Population-based	≥ 95%	1. Missing phenotypes; 2. Missing DNA	6,514	6,497	Jørgensen et al. Eur J Cardiovasc Prev Rehabil. 2003 Oct;10(5):377-86
KORA2	Kooperative Gesundheitsforschung in der Region Augsburg, 2nd survey	Population-based	≥ 90%	1. Missing phenotypes; Missing DNA	3,692	3,691	Holzappel C et al., Int J Obesity 2010 Apr 13; epub ahead of print.
KORA3	Kooperative Gesundheitsforschung in der Region Augsburg, 3rd survey	Population-based	≥ 90%	1. Missing phenotypes; 2. Missing DNA	1,498	1,324	Heid et. al. Obesity (Silver Spring). 2008 Feb;16(2):369-76
KORA4	Kooperative Gesundheitsforschung in der Region Augsburg,, 4th survey	Population-based	≥ 90%	1. Missing phenotypes; 2. Missing DNA	1,502	1,502	Heid et. al. Obesity (Silver Spring). 2008 Feb;16(2):369-76
METSIM	Metabolic Syndrome in Men	Population-based	≥ 94%	Missing phenotypes	8,182	8,166	Stancakova A. et al. Diabetes 58, 1212-21 (2009)
NFBC1986	Northern Finland Birth Cohort 1986	Population-based	≥ 95%	1. Missing DNA; 2. Missing phenotypes; 3. Related	9,479	5,370	Järvelin MR et al. 1997 Jul;11(3):298-312
OBB	Oxford Biobank	Population-based	≥ 90%	1. Missing phenotypes; 2. Missing DNA	1,469	1,469	Tan GD et al. Diabetologia. 2006;49:158-68
R58	British 1958 birth cohort replication set	Population-based		Missing phenotypes	1,345	1,281	Strachan DP et al. Int J Epidemiol 2007;36:522-531. Power C, Elliott J. Int J Epidemiol 2006;35:34-41

\* Study contributed only for Waist circumference

~Study contributed only for Waist circumference

† Study contributed only for Hip circumference

**Supplementary Table 2: Random effect model results and between-study heterogeneity of the 14 identified WHR loci.**

Lead SNP	Nearby genes	Random effects Overall		Overall	Women	Men		$P^a$	
		Beta	P	$I^2$ (%)	$P^a$	$I^2$ (%)	$P^a$		
rs9491696	<i>RSPO3</i>	0.041	9.38E-38	4.8	0.338	16.3	0.139	0.0	0.499
rs6905288	<i>VEGFA</i>	0.036	4.30E-25	1.4	0.440	0.0	0.737	0.0	0.895
rs984222	<i>TBX15-WARS2</i>	0.034	4.15E-26	0.0	0.796	0.0	0.863	0.0	0.662
rs1055144	<i>NFE2L3</i>	0.035	1.59E-15	15.7	0.086	15.7	0.149	8.0	0.300
rs10195252	<i>GRB14</i>	0.032	6.82E-10	50.9	1.99E-09	42.7	3.48E-04	22.5	0.071
rs4846567	<i>LYPLAL1</i>	0.034	9.43E-11	42.5	2.69E-06	36.8	2.55E-03	4.2	0.384
rs1011731	<i>DNM3-PIGC</i>	0.025	2.02E-10	22.1	0.024	4.8	0.368	31.6	0.012
rs718314	<i>ITPR2-SSPN</i>	0.029	1.07E-12	16.8	0.075	0.0	0.489	22.8	0.065
rs1294421	<i>LY86</i>	0.028	1.91E-18	0.0	0.852	0.0	0.494	0.0	0.822
rs1443512	<i>HOXC13</i>	0.030	8.83E-12	20.4	0.034	8.0	0.297	22.2	0.069
rs6795735	<i>ADAMTS9</i>	0.025	6.15E-12	9.0	0.229	1.6	0.442	0.0	0.785
rs4823006	<i>ZNRF3-KREMEN1</i>	0.023	5.15E-11	4.7	0.346	7.2	0.318	0.087	0.473
rs6784615	<i>NISCH-STAB1</i>	0.047	1.90E-08	19.9	0.040	0.0	0.885	44.2	2.04E-04
rs6861681	<i>CPEB4</i>	0.022	1.83E-09	2.9	0.400	0.0	0.634	20.7	0.096

Random effects model results according to DerSimonian and Laird<sup>1</sup> (P-value and beta coefficient) and  $I^2$  measures (including P-value based on Q statistics) of between-study heterogeneity of the WHR SNP-associations for the joint discovery and follow-up meta-analysis are given. In the overall (sex-combined) analysis, 2 SNPs showed  $I^2 > 30\%$ , which was also pronounced in the women, but not in the men. All 14 associations remained genome-wide significant ( $P < 5.00E-08$ ).

**Supplementary Table 3: Details on the association of 14 WHR SNPs with other anthropometric measures.**

Lead SNP*	Nearby genes	BMI		Waist circumference		Hip circumference	
		<i>P</i>	Beta	<i>P</i> <sup>a</sup>	Beta	<i>P</i>	Beta
rs9491696	<i>RSPO3</i>	0.510	0.002	1.18E-06	0.016	9.62E-04	-0.011
rs6905288	<i>VEGFA</i>	0.104	-0.006	0.011	0.010	1.70E-03	-0.012
rs984222	<i>TBX15-WARS2</i>	3.20E-06	-0.015	0.154	0.005	3.27E-04	-0.013
rs1055144	<i>NFE2L3</i>	0.745	-0.001	1.40E-05	0.018	0.129	-0.006
rs10195252	<i>GRB14</i>	2.00E-03	-0.010	0.368	0.003	2.99E-09	-0.021
rs4846567	<i>LYPLAL1</i>	4.09E-03	-0.010	0.138	-0.006	3.28E-18	-0.035
rs1011731	<i>DNM3-PIGC</i>	0.129	-0.005	0.092	0.006	2.10E-03	-0.011
rs718314	<i>ITPR2-SSPN</i>	0.039	-0.007	0.347	0.004	1.30E-04	-0.015
rs1294421	<i>LY86</i>	0.760	-0.001	0.082	0.006	2.63E-04	-0.013
rs1443512	<i>HOXC13</i>	0.803	-0.001	4.85E-03	0.011	8.21E-03	-0.011
rs6795735	<i>ADAMTS9</i>	0.216	-0.004	0.232	0.004	0.043	-0.008
rs4823006	<i>ZNRF3-KREMEN1</i>	0.400	-0.003	0.159	0.005	0.023	-0.008
rs6784615	<i>NISCH-STAB1</i>	0.844	-0.001	0.205	0.009	0.047	-0.015
rs6861681	<i>CPEB4</i>	2.43E-03	-0.011	0.322	0.004	0.102	-0.007

*P*-values and beta coefficients (in the direction of the WHR increasing allele) for the joint discovery and follow-up meta-analysis of the association of the 14 WHR SNPs with body-mass-index (BMI, up to 242,530 subjects), WC (up to 199,498 subjects) and HIP (up to 193,276 subjects).



**Supplementary Table 4: Spearman correlation coefficients of WHR with anthropometric and metabolic traits.**

Trait	Study <sup>a</sup>	Women		Men	
		unadj. for BMI	adj. for BMI	unadj. for BMI	adj. for BMI
<b>BMI</b>	FRAM	0.48	0.05 ( $P=0.03$ )	0.57	0.06 ( $P=0.03$ )
	ERF	0.44	0.01 ( $P=0.45$ )	0.58	0.07 ( $P=0.02$ )
	KORA	0.46	0.06	0.56	0.05 ( $P=0.004$ )
<b>Waist Circumference</b>	FRAM	0.74	0.40	0.73	0.32
	ERF	0.69	0.36	0.77	0.39
	KORA	0.72	0.40	0.78	0.38
<b>Hip Circumference</b>	FRAM	0.31	-0.09	0.30	-0.15
	ERF	0.16	-0.26	0.34	-0.12
	KORA	0.26	-0.10	0.29	-0.14
<b>VAT<sup>b</sup></b>	FRAM	0.56	0.32	0.56	0.29
	ERF	NA	NA	NA	NA
	KORA	NA	NA	NA	NA
<b>SAT<sup>b</sup></b>	FRAM	0.44	0.14	0.52	0.16
	ERF	NA	NA	NA	NA
	KORA	NA	NA	NA	NA
<b>Android-gynoid fat ratio<sup>c</sup></b>	FRAM	NA	NA	NA	NA
	ERF	0.64	0.42	0.58	0.44
	KORA	NA	NA	NA	NA
<b>HDL-cholesterol</b>	FRAM	-0.40	-0.27	-0.23	-0.09
	ERF	-0.33	-0.24	-0.26	-0.12
	KORA	-0.29	-0.17	-0.22	-0.09
<b>Fasting Triglycerides</b>	FRAM	0.40	0.26	0.30	0.16
	ERF	0.33	0.24	0.37	0.25
	KORA <sup>d</sup>	0.29	0.21	0.26	0.14
<b>Fasting Glucose</b>	FRAM	0.29	0.16	0.14	0.08 ( $p=0.003$ )
	ERF	0.18	0.066 ( $P=0.019$ )	0.22	0.10
	KORA	NA	NA	NA	NA
<b>Fasting Insulin</b>	FRAM	NA	NA	NA	NA
	ERF	0.37	0.17	0.37	0.13
	KORA	NA	NA	NA	NA
<b>HOMA IR</b>	FRAM	NA	NA	NA	NA
	ERF	0.37	0.17	0.39	0.15
	KORA	NA	NA	NA	NA

All phenotypes were age-adjusted.  $P$ -values are stated unless  $P < 0.001$ . NA = not available; VAT = visceral abdominal fat; SAT = subcutaneous abdominal fat; HOMA-IR = insulin resistance index; unadj. = unadjusted; adj. = adjusted.

<sup>a</sup> three population-based studies: FRAM (1719 women, 1567 men)\* 4<sup>th</sup> examination, ERF (1534 women, 1237 men), and KORA S3 & S4 (3976 women, 3912 men).

<sup>b</sup> VAT/SAT sample size for FRAM exam 7 consists of 658 women and 608 men

<sup>c</sup> from DXA;

<sup>d</sup> Fasting triglyceride sample size consists of 841 men and 773 women in KORA S3 & S4

## Supplementary Table 5: Details on the association of the 14 WHR SNPs with metabolic traits

(a) Combined from other consortia and our *de novo* genotyped follow-up studies

SNP	Nearby genes	HDL		LDL		TG		GLUC	
		P	Zscore	P	Zscore	P	Zscore	P	Zscore
rs9491696	<i>RSPO3</i>	2.16E-03	-3.067	0.333	0.968	6.12E-04	3.426	0.931	0.087
rs6905288	<i>VEGFA</i> <i>TBX15-</i>	0.028	-2.194	0.067	1.830	1.55E-05	4.322	0.283	-1.074
rs984222	<i>WARS2</i>	0.393	-0.855	0.469	0.724	0.070	1.812	0.910	0.113
rs1055144	<i>NFE2L3</i>	0.168	1.379	0.712	-0.369	0.126	1.529	0.891	0.137
rs10195252	<i>GRB14</i>	0.008	-2.653	4.53E-04	3.507	7.38E-09	5.782	0.089	1.699
rs4846567	<i>LYPLAL1</i>	0.246	-1.160	0.327	0.980	0.018	2.366	0.347	0.941
rs1011731	<i>DNM3-PIGC</i>	0.208	-1.260	0.163	1.395	0.202	1.277	0.080	1.750
rs718314	<i>ITPR2-SSPN</i>	0.110	-1.599	0.560	-0.583	0.046	1.996	0.379	0.881
rs1294421	<i>LY86</i>	0.660	-0.440	0.548	0.600	0.796	0.258	0.240	1.176
rs1443512	<i>HOXC13</i>	0.333	-0.969	0.044	-2.012	0.220	1.225	0.816	-0.233
rs6795735	<i>ADAMTS9</i> <i>ZNRF3-</i>	0.013	-2.486	0.388	0.863	0.063	1.863	0.042	2.031
rs4823006	<i>KREMEN1</i> <i>NISCH-</i>	0.110	-1.597	0.180	1.340	0.030	2.168	0.489	-0.691
rs6784615	<i>STAB1</i>	0.143	-1.464	0.339	0.957	0.050	1.958	0.942	0.073
rs6861681	<i>CPEB4</i>	0.817	-0.232	0.910	-0.114	0.016	2.407	0.062	-1.868

SNP	Nearby genes	INS		HOMA-IR		2h GLUC		T2D	
		P	Zscore	P	Zscore	P	Zscore	P	OR
rs9491696	<i>RSPO3</i>	1.65E-03	3.146	2.42E-03	3.033	0.834	0.210	0.055	0.944
rs6905288	<i>VEGFA</i> <i>TBX15-</i>	0.215	1.239	0.246	1.160	0.239	1.178	0.160	1.047
rs984222	<i>WARS2</i>	0.390	-0.860	0.488	-0.693	0.792	-0.264	0.802	0.992
rs1055144	<i>NFE2L3</i>	0.126	1.529	0.081	1.747	0.729	-0.347	0.123	1.057
rs10195252	<i>GRB14</i>	5.01E-06	4.564	1.86E-06	4.768	0.053	1.932	0.284	1.060
rs4846567	<i>LYPLAL1</i>	1.09E-05	4.398	9.82E-06	4.421	0.905	0.119	0.112	1.057
rs1011731	<i>DNM3-PIGC</i>	0.080	1.752	0.048	1.980	0.209	1.258	0.305	1.052
rs718314	<i>ITPR2-SSPN</i>	0.011	2.552	1.53E-03	3.169	0.385	-0.868	0.041	1.075
rs1294421	<i>LY86</i>	0.831	0.214	0.811	0.240	0.202	-1.276	0.682	1.013
rs1443512	<i>HOXC13</i>	0.813	0.236	0.854	0.184	0.646	-0.460	0.337	0.967
rs6795735	<i>ADAMTS9</i> <i>ZNRF3-</i>	0.414	0.817	0.307	1.022	0.057	1.907	0.002	1.124
rs4823006	<i>KREMEN1</i> <i>NISCH-</i>	0.316	1.002	0.475	0.714	0.961	-0.049	0.778	1.009
rs6784615	<i>STAB1</i>	3.96E-03	2.881	0.017	2.377	0.268	1.108	0.015	1.190
rs6861681	<i>CPEB4</i>	0.195	1.297	0.488	0.693	0.854	-0.184	0.323	1.033

The 14 WHR SNPs were tested for association with other traits by meta-analysis of GWA data from previous reports<sup>2-5</sup> together with our non-overlapping *de novo* follow-up studies. HDL-C, high density lipoprotein cholesterol; LDL-C, low density lipoprotein cholesterol; GLUC, fasting glucose; INS, fasting insulin; HOMA-IR, index of insulin resistance; 2-hr glucose, glucose levels 2 hours after an oral glucose challenge; T2d, type 2 diabetes. Meta-analysis of linear regression results was performed using the weighted Z-score method – except for T2D, for which logistic regression results were meta-analyzed using the fixed effect model. Z-scores and odds ratios (OR) are given per change of WHR-increasing allele.

b) From GWA and follow-up data of other consortia

SNP	Nearby genes	HDL-C		LDL-C		TG		GLUC	
		P	Zscore	P	Zscore	P	Zscore	P	Beta
rs9491696	<i>RSPO3</i>	1.04E-03	-3.281	0.253	1.143	0.098	1.657	0.957	0.000
rs6905288	<i>VEGFA</i>	0.038	-2.074	0.657	0.444	0.028	2.203	0.129	-0.006
rs984222	<i>TBX15- WARS2</i>	0.472	-0.719	0.739	0.334	0.060	1.884	0.845	0.000
rs1055144	<i>NFE2L3</i>	0.860	0.177	0.280	-1.080	0.936	0.080	0.924	0.000
rs10195252	<i>GRB14</i>	5.01E-03	-2.804	3.36E-03	2.933	0.011	2.543	0.974	0.000
rs4846567	<i>LYPLAL1</i>	0.011	-2.540	0.488	0.693	0.040	2.049	0.352	0.004
rs1011731	<i>DNM3-PIGC</i>	0.259	-1.130	0.778	0.282	0.297	1.042	0.118	0.006
rs718314	<i>ITPR2-SSPN</i>	0.017	-2.395	0.413	0.819	0.024	2.256	0.534	0.003
rs1294421	<i>LY86</i>	0.330	0.973	0.663	-0.435	0.519	-0.646	0.501	0.003
rs1443512	<i>HOXC13</i>	0.318	-0.999	0.436	-0.779	0.571	0.567	0.741	0.001
rs6795735	<i>ADAMTS9</i>	5.93E-03	-2.752	0.852	0.186	0.142	1.467	0.024	0.008
rs4823006	<i>ZNRF3- KREMEN1</i>	0.022	-2.285	7.57E-08	2.671	0.030	2.170	0.389	-0.003
rs6784615	<i>NISCH- STAB1</i>	0.523	-0.639	0.542	0.610	0.351	0.932	0.956	0.000
rs6861681	<i>CPEB4</i>	0.157	-1.416	0.900	0.126	0.069	1.816	0.267	-0.005

SNP	Nearby genes	INS		HOMA-IR		2h GLUC		T2D	
		P	Beta	P	Beta	P	Beta	P	OR
rs9491696	<i>RSPO3</i>	2.11E-03	0.012	5.60E-03	0.011	0.772	-0.006	0.055	0.944
rs6905288	<i>VEGFA</i>	0.827	-0.000	0.697	-0.002	0.270	0.023	0.160	1.047
rs984222	<i>TBX15- WARS2</i>	0.906	-0.000	0.998	0	0.307	-0.020	0.802	0.992
rs1055144	<i>NFE2L3</i>	0.163	0.007	0.124	0.008	0.928	0.002	0.123	1.057
rs10195252	<i>GRB14</i>	2.49E-03	0.012	1.85E-03	0.013	0.013	0.048	0.284	1.060
rs4846567	<i>LYPLAL1</i>	8.57E-04	0.014	7.69E-04	0.015	0.922	-0.002	0.112	1.057
rs1011731	<i>DNM3-PIGC</i>	0.017	0.009	6.87E-03	0.011	0.374	0.017	0.305	1.052
rs718314	<i>ITPR2-SSPN</i>	6.91E-03	0.012	1.24E-03	0.015	0.184	-0.029	0.041	1.075
rs1294421	<i>LY86</i>	0.641	-0.002	0.572	-0.002	0.084	-0.034	0.682	1.013
rs1443512	<i>HOXC13</i>	0.710	0.002	0.744	0.002	0.889	-0.003	0.337	0.967
rs6795735	<i>ADAMTS9</i>	0.092	0.007	0.086	0.007	0.101	0.031	0.002	1.124
rs4823006	<i>ZNRF3- KREMEN1</i>	0.292	0.004	0.380	0.004	0.837	-0.004	0.778	1.009
rs6784615	<i>NISCH- STAB1</i>	0.049	0.016	0.154	0.012	0.822	-0.010	0.015	1.190
rs6861681	<i>CPEB4</i>	0.012	0.011	0.048	0.009	0.752	-0.006	0.323	1.033

As in Supplementary Table 5a, but restricted to the GWA data of the previous reports<sup>2-5</sup>. These data cannot be considered independent from our discovery because some studies overlap. Meta-analysis of linear regression results was performed using the weighted Z-score method for lipid traits (HDL-C, LDL-C, TG) and using a fixed effect model for glucose and insulin traits (GLUC, INS, HOMA-IR, 2h GLUC). For T2D, logistic regression results were meta-analyzed using the fixed effect model. Z-scores, beta-coefficients, and odds ratios (OR) are given per change of WHR-increasing allele.

(c) From *de novo* genotyped follow-up studies

SNP	Nearby genes	HDL		LDL		TG		GLUC	
		P	Beta	P	Beta	P	Beta	P	Beta
rs9491696	<i>RSPO3</i>	0.232	-0.008	0.790	0.002	1.77E-03	0.014	0.933	0.000
rs6905288	<i>VEGFA</i>	0.271	-0.008	0.039	0.016	1.23E-04	0.018	0.687	0.001
rs984222	<i>TBX15- WARS2</i>	0.615	-0.004	0.499	0.006	0.462	0.004	0.926	0.000
rs1055144	<i>NFE2L3</i>	0.094	0.015	0.639	0.005	0.047	0.011	0.922	0.000
rs10195252	<i>GRB14</i>	0.286	-0.008	0.037	0.016	3.71E-08	0.025	1.77E-03	0.009
rs4846567	<i>LYPLAL1</i>	0.481	0.006	0.486	0.006	0.185	0.007	0.785	0.000
rs1011731	<i>DNM3-PIGC</i>	0.491	-0.005	0.104	0.013	0.433	0.003	0.415	0.002
rs718314	<i>ITPR2-SSPN</i>	0.943	0.000	0.103	-0.014	0.572	0.003	0.492	0.002
rs1294421	<i>LY86</i>	0.145	-0.011	0.223	0.010	0.343	0.004	0.244	0.003
rs1443512	<i>HOXC13</i>	0.679	-0.004	0.044	-0.019	0.254	0.006	0.324	0.003
rs6795735	<i>ADAMTS9</i>	0.373	-0.006	0.322	0.008	0.240	0.005	0.824	0.000
rs4823006	<i>ZNRF3- KREMEN1</i>	0.939	-0.000	0.508	-0.009	0.351	0.004	0.918	0.000
rs6784615	<i>NISCH- STAB1</i>	0.166	-0.019	0.462	0.011	0.072	0.019	0.954	0.000
rs6861681	<i>CPEB4</i>	0.351	0.008	0.789	-0.002	0.110	0.008	0.075	0.006
SNP	Nearby gene	INS		HOMA-IR		2h GLUC		T2D	
		P	Beta	P	Beta	P	Beta	P	OR
rs9491696	<i>RSPO3</i>	0.294	0.007	0.189	0.009	0.514	0.010	NA	NA
rs6905288	<i>VEGFA</i>	0.010	0.017	7.71E-03	0.018	0.597	0.008	NA	NA
rs984222	<i>TBX15- WARS2</i>	0.165	-0.010	0.213	-0.009	0.450	0.012	NA	NA
rs1055144	<i>NFE2L3</i>	0.516	0.005	0.412	0.007	0.532	-0.012	NA	NA
rs10195252	<i>GRB14</i>	2.28E-04	0.024	1.03E-04	0.028	0.924	0.002	NA	NA
rs4846567	<i>LYPLAL1</i>	3.30E-03	0.021	3.43E-03	0.022	0.767	0.005	NA	NA
rs1011731	<i>DNM3-PIGC</i>	0.673	-0.003	0.648	-0.003	0.376	0.013	NA	NA
rs718314	<i>ITPR2-SSPN</i>	0.674	0.003	0.460	0.006	0.815	0.004	NA	NA
rs1294421	<i>LY86</i>	0.264	0.008	0.192	0.010	0.931	0.001	NA	NA
rs1443512	<i>HOXC13</i>	0.895	-0.000	0.871	-0.001	0.589	-0.009	NA	NA
rs6795735	<i>ADAMTS9</i>	0.291	-0.007	0.476	-0.005	0.310	0.016	NA	NA
rs4823006	<i>ZNRF3- KREMEN1</i>	0.840	0.001	0.962	-0.000	0.877	0.003	NA	NA
rs6784615	<i>NISCH- STAB1</i>	0.025	0.033	0.035	0.034	0.056	0.051	NA	NA
rs6861681	<i>CPEB4</i>	0.148	-0.010	0.089	-0.012	0.932	0.002	NA	NA

As in Supplementary Table 5a, but restricted to our *de novo* genotyped follow-up studies, which are independent from our discovery studies. Meta-analysis of linear regression results was performed using the weighted Z-score method. Z-scores are given per change of WHR-increasing allele. NA = not available.

**Supplementary Table 6: Summary of PANTHER pathway analyses**

Biological process	Number of genes in			<i>Punadj</i>	<i>Padj-I</i>	<i>Padj-II</i>
	biological process	associated regions				
		observed	expected			
Developmental processes	2168	25	7.56	5.8E-08	2.3E-03	0.12
mRNA transcription regulation	1472	18	5.13	2.7E-06	2.7E-03	0.18
mRNA transcription	1926	19	6.72	3.0E-05	5.0E-03	0.27
Neurogenesis	594	10	2.07	4.2E-05	0.018	0.30
Ectoderm development	699	10	2.44	1.6E-04	0.042	0.39
Nucleoside, nucleotide and nucleic acid metabolism	3356	23	11.70	1.3E-03	0.019	0.64
Porphyrim metabolism	17	2	0.06	1.6E-03	4.5E-04	0.67
Stress response	202	4	0.70	5.5E-03	4.5E-03	0.86
Segment specification	103	3	0.36	5.6E-03	0.014	0.87
Mesoderm development	556	6	1.94	0.013	0.050	0.96
Angiogenesis	55	2	0.19	0.016	8.6E-03	0.97
Hematopoiesis	77	2	0.27	0.030	0.013	0.99
NO mediated signal transduction	11	1	0.04	0.038	4.5E-03	1

For the 48 independent SNPs with WHR discovery association  $P < 1.00E-05$  that map to 32 distinct loci, the neighboring 95 genes were selected (details see **Supplementary Note**). Of these, 89 genes were available in the PANTHER database (including 25,431 genes). For each biological process, this gene set was tested for enrichment for that process using Fisher's exact test (*Punadj*).

To adjust for bias, e.g. due to non-random SNP coverage in relation to genes, (i) random SNP sets were created from the 2,8 million SNPs in the GWS by permutation matching the original 48 SNPs on frequency, distance to and the size of nearest gene, (ii) for each random SNP set, the set of neighboring genes was identified and tested for enrichment for a certain biological process, (iii) an adjusted  $P$  was computed as the fraction of random SNP sets that produced  $P$ -values lower than or equal to the original *Punadj* for this biological process (*Padj-I*).

To additionally adjust for the number of processes tested, a further adjusted  $P$  was computed as the fraction of random sets that – for any process - produced a  $P$ -value equal or lower than the original *Punadj* (*Padj-II*).

**Supplementary Table 7: Differential expression between abdominal and gluteal fat for five of the genes in the 14 WHR associated loci.**

Gene	Log2 Fold change <sup>a</sup>	abdominal fat expression <sup>b</sup>		gluteal fat expression <sup>b</sup>		<i>P</i>	
		Mean	SD	Mean	SD	Unadjusted	adjusted
<b>RSPO3</b>	<b>-1.608</b>	<b>8.555</b>	<b>0.849</b>	<b>6.976</b>	<b>0.582</b>	<b>2.80E-14</b>	<b>4.20E-13</b>
VEGFA	-0.084	4.424	0.368	4.325	0.501	3.45E-01	5.58E-01
<b>TBX15</b>	<b>0.589</b>	<b>7.033</b>	<b>0.277</b>	<b>7.719</b>	<b>0.377</b>	<b>3.00E-09</b>	<b>2.25E-08</b>
<b>WARS2</b>	<b>-0.194</b>	<b>4.593</b>	<b>0.267</b>	<b>4.420</b>	<b>0.277</b>	<b>4.63E-03</b>	<b>1.74E-02</b>
NFE2L3	NA	NA	NA	NA	NA	NA	NA
AA553656 <sup>c</sup>	-	-	-	-	-	-	-
GRB14	0.305	4.603	0.798	5.437	0.915	7.95E-02	1.99E-01
LYPLAL1	-0.015	9.462	0.228	9.600	0.224	7.69E-01	8.24E-01
DNM3	n.a.	NA	NA	NA	NA	NA	NA
PIGC	0.022	7.524	0.152	7.518	0.161	5.75E-01	7.18E-01
<b>ITPR2</b>	<b>0.302</b>	<b>3.391</b>	<b>0.447</b>	<b>3.698</b>	<b>0.350</b>	<b>2.18E-04</b>	<b>1.09E-03</b>
SSPN	-0.087	8.283	0.322	8.176	0.348	2.85E-01	5.34E-01
LY86	-0.234	5.054	0.743	4.917	0.928	2.28E-01	4.88E-01
HOXC13	NA	NA	NA	NA	NA	NA	NA
ADAMTS9	-0.032	4.104	0.374	4.160	0.359	6.87E-01	7.93E-01
KREMEN1	n.a.	NA	NA	NA	NA	NA	NA
ZNRF3	0.081	6.391	0.416	6.700	0.386	3.72E-01	5.58E-01
NISCH	0.049	9.061	0.249	9.046	0.287	5.09E-01	6.94E-01
<b>STAB1</b>	<b>0.289</b>	<b>4.885</b>	<b>0.505</b>	<b>5.088</b>	<b>0.497</b>	<b>1.11E-02</b>	<b>3.34E-02</b>
CPEB4	-0.003	6.253	0.239	6.151	0.391	9.75E-01	9.75E-01

*P*-value and Fold Change are given for the overall expression comparison between subcutaneous gluteal fat and abdominal fat tissue from 49 individuals. The *P*-value refers to the F-test for difference in expression levels between the gluteal and abdominal fat. The adjusted *P* is adjusted for testing 15 expressed genes by false discovery rate (see **Online Material** and **Supplementary Note**). Findings are highlighted in bold font where the *P* < 0.05.

NA = Not available (expression probes not expressed above background, not available for analysis); SD = standard deviation.

<sup>a</sup> difference in mean log<sub>2</sub>(gene expression) between gluteal fat and abdominal fat tissue (an increase of 1 on this scale indicates a doubling of RNA levels in gluteal fat relative to levels in abdominal fat, i.e. a two-fold increase). <sup>b</sup> on log<sub>2</sub> scale. <sup>c</sup> not present on the arrays for analysis.

## Supplementary Table 8: Study-specific descriptives

Study	available phenotypes	trait	men							correlation with BMI	correlation with height	women							
			n	mean	sd	median	min	max	n			mean	sd	median	min	max	correlation with BMI	correlation with height	
<b>Discovery Stage</b>																			
ADVANCE Cases	Height, BMI, Weight, WC	Age (yrs)	114	40.42	3.98	41.20	20.40	45.10	-0.10	-0.12	161	49.46	4.68	50.50	34.00	55.00	0.01	-0.15	
		BMI (kg/m <sup>2</sup> )	114	31.39	5.77	30.89	19.48	54.32	1.00	0.15	161	31.40	8.17	30.65	17.30	61.08	1.00	-0.14	
		Weight (kg)	114	99.03	21.16	97.59	64.05	181.44	0.92	0.49	161	83.98	21.78	81.74	48.58	153.00	0.95	0.16	
		Height (m)	114	1.77	0.07	1.77	1.61	1.95	0.15	1.00	161	1.64	0.07	1.64	1.48	1.84	-0.14	1.00	
		WC (cm)	114	101.75	13.61	101.35	76.10	135.10	0.93	0.31	160	93.98	18.59	92.30	60.50	145.20	0.95	-0.01	
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
		ADVANCE Controls	Height, BMI, Weight, WC	Age (yrs)	128	40.46	3.23	41.20	33.40	46.80	-0.03	0.15	183	48.69	4.45	49.80	34.80	55.40	0.09
BMI (kg/m <sup>2</sup> )	128	27.00		4.48	26.21	17.86	49.38	1.00	0.02	181	26.08	6.36	24.65	15.76	54.12	1.00	-0.14		
Weight (kg)	128	86.45		16.38	84.37	51.48	158.76	0.88	0.43	182	71.35	17.13	68.27	40.23	140.71	0.92	0.21		
Height (m)	128	1.79		0.07	1.78	1.58	1.96	0.02	1.00	181	1.66	0.06	1.66	1.45	1.80	-0.14	1.00		
WC (cm)	128	92.95		12.17	91.00	70.00	150.00	0.89	0.16	179	79.42	12.72	75.90	60.10	121.00	0.90	-0.03		
Hip (cm)	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
WHR (cm/cm)	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
AGES Reykjavik~	Height, BMI, Weight, WC	Age (yrs)		1352	76.52	5.32	76.00	67.00	94.00	-0.13	-0.28	1867	76.34	5.55	76.00	66.00	95.00	-0.13	-0.36
BMI (kg/m <sup>2</sup> )		1351	26.99	3.78	26.72	15.88	40.60	1.00	0.04	1865	27.19	4.85	26.79	14.83	48.47	1.00	-0.05		
Weight (kg)		1351	83.16	13.33	81.60	42.00	144.70	0.89	0.48	1865	70.46	13.29	69.30	37.20	128.30	0.92	0.33		
Height (m)		1351	1.75	0.06	1.75	1.53	1.96	0.04	1.00	1865	1.61	0.06	1.61	1.39	1.83	-0.05	1.00		
WC (cm)		1351	102.54	10.48	102.00	51.00	144.00	0.89	0.23	1865	99.54	13.14	99.00	59.00	159.50	0.86	0.07		
Hip (cm)																			
WHR (cm/cm)																			
Amish		Height, BMI, Weight, WC, WHR	Age (yrs)	465	45.80	16.50	43.00	20.00	98.00	0.24	-0.38	435	47.50	15.10	48.00	20.00	95.00	0.24	-0.40
BMI (kg/m <sup>2</sup> )	464		26.30	3.50	26.00	18.60	39.00	1.00	-0.05	435	28.50	5.60	28.20	16.90	47.10	1.00	-0.22		
Weight (kg)	464		75.60	11.70	77.00	49.40	112.80	0.87	0.45	435	73.40	14.30	71.60	37.80	114.30	0.93	0.16		
Height (m)	465		1.73	0.06	1.73	1.48	1.94	-0.05	1.00	435	1.61	0.06	1.61	1.39	1.75	-0.22	1.00		
WC (cm)	465		92.00	10.60	90.60	71.90	132.00	0.89	0.06	435	86.20	11.90	85.00	63.70	120.00	0.89	-0.11		
Hip (cm)	465		101.70	6.60	101.00	87.20	131.00	0.86	0.25	435	106.10	11.50	105.00	76.00	146.00	0.91	0.00		
WHR (cm/cm)	465		0.90	0.10	0.90	0.80	1.10	0.65	-0.13	435	0.80	0.10	0.80	0.70	1.10	0.32	-0.20		
ARIC	Height, BMI, Weight, WC, WHR		Age (yrs)	3821	54.69	5.69	55.00	44.00	66.00	-0.04	-0.16	4283	53.97	5.67	54.00	44.00	66.00	0.04	-0.15
BMI (kg/m <sup>2</sup> )		3820	27.48	4.01	26.98	17.21	56.26	1.00	-0.03	4283	26.62	5.50	25.45	14.38	55.20	1.00	-0.08		
Weight (kg)		3820	85.55	13.76	84.09	44.55	182.27	0.89	0.43	4283	69.97	14.95	66.82	36.36	141.82	0.94	0.26		
Height (m)		3821	1.76	0.06	1.76	1.49	1.99	-0.03	1.00	4283	1.62	0.06	1.62	1.37	1.87	-0.08	1.00		
WC (cm)		3821	99.73	10.45	99.00	68.00	171.00	0.91	0.19	4283	93.06	14.87	91.00	52.00	158.00	0.89	0.03		
Hip (cm)		3821	102.83	7.61	102.00	61.00	165.00	0.86	0.30	4283	104.22	10.89	102.00	56.00	173.00	0.91	0.14		
WHR (cm/cm)		3821	0.97	0.05	0.97	0.62	1.39	0.58	-0.04	4283	0.89	0.08	0.89	0.49	1.19	0.49	-0.11		
B58C-T1DGC		Height, BMI, Weight, WC, WHR	Age (yrs)	1259	45.31	0.34	45.33	44.50	46.00	-0.02	-0.05	1328	45.27	0.34	45.25	44.50	46.00	0.00	-0.04
BMI (kg/m <sup>2</sup> )	1259		28.02	4.19	27.56	16.84	51.63	1.00	-0.03	1328	26.97	5.58	25.73	17.18	52.20	1.00	-0.07		
Weight (kg)	1259		87.05	14.41	86.00	50.80	177.10	0.89	0.43	1328	71.63	15.45	68.40	43.00	155.30	0.93	0.29		
Height (m)	1261		1.76	0.07	1.76	1.55	1.99	-0.03	1.00	1330	1.63	0.06	1.63	1.40	1.85	-0.07	1.00		
WC (cm)	1198		98.69	10.95	98.00	65.20	154.90	0.87	0.19	1292	85.58	12.82	83.50	61.70	138.30	0.90	0.10		
Hip (cm)	1198		105.94	7.31	105.30	87.40	149.40	0.81	0.33	1292	105.27	11.48	103.30	80.40	170.50	0.91	0.16		
WHR (cm/cm)	1198		0.93	0.06	0.93	0.68	1.31	0.59	-0.03	1292	0.81	0.06	0.81	0.55	1.09	0.44	-0.02		
B58C-WTCCC	Height, BMI, Weight, WC, WHR		Age (yrs)	741	44.89	0.34	44.75	44.50	45.60	-0.01	-0.04	738	44.89	0.35	44.75	44.50	45.60	0.02	0.02
BMI (kg/m <sup>2</sup> )		741	27.84	4.29	27.23	15.93	48.41	1.00	-0.05	738	26.92	5.44	25.56	17.34	56.55	1.00	-0.10		
Weight (kg)		741	86.56	14.63	85.20	51.00	137.50	0.87	0.39	738	70.96	14.68	68.20	41.80	139.40	0.91	0.29		
Height (m)		741	1.76	0.07	1.76	1.52	2.02	-0.05	1.00	738	1.62	0.06	1.63	1.42	1.80	-0.10	1.00		
WC (cm)		700	98.85	10.91	97.95	66.10	138.20	0.86	0.17	722	85.53	12.29	83.20	61.20	131.40	0.89	0.07		

		Hip (cm)	700	106.04	7.48	105.30	80.20	140.10	0.79	0.32									
		WHR (cm/cm)	700	0.93	0.06	0.93	0.71	1.12	0.64	-0.05		722	105.16	10.82	103.00	81.20	152.40	0.88	0.15
											722	0.81	0.06	0.81	0.61	1.03	0.51	-0.05	
BRIGHT	Height, BMI, Weight, WC, WHR	Age (yrs)	719	56.29	11.15	57.00	21.00	84.00	-0.12	-0.24	1087	57.43	11.23	58.00	21.00	85.00	0.07	-0.24	
		BMI (kg/m <sup>2</sup> )	719	27.74	3.28	27.68	17.20	38.26	1.00	-0.06	1087	27.36	4.04	27.03	16.85	41.66	1.00	-0.08	
		Weight (kg)	719	84.22	11.90	83.45	51.00	121.00	0.80	0.54	1087	71.19	11.55	69.90	41.70	122.80	0.87	0.41	
		Height (m)	719	1.74	0.07	1.74	1.51	1.95	-0.06	1.00	1087	1.61	0.06	1.61	1.39	1.81	-0.08	1.00	
		WC (cm)	668	97.71	8.88	98.00	65.35	127.00	0.77	0.19	984	85.74	10.49	85.00	51.00	128.00	0.82	0.12	
		Hip (cm)	667	103.82	6.54	104.00	84.00	124.00	0.66	0.35	982	104.04	9.34	104.00	72.00	146.00	0.81	0.18	
		WHR (cm/cm)	667	0.94	0.06	0.94	0.63	1.39	0.43	-0.08	982	0.82	0.07	0.82	0.56	1.21	0.34	-0.03	
CHS	Height, BMI, Weight, WC, WHR	Age (yrs)	1281	73.00	5.70	72.00	65.00	95.00	-0.15	-0.22	1957	71.90	5.20	71.00	65.00	98.00	-0.14	-0.23	
		BMI (kg/m <sup>2</sup> )	1276	26.40	3.50	26.10	18.60	44.20	-	-0.04	1952	26.40	4.80	25.80	18.50	48.30	-	-0.05	
		Weight (kg)	1276	79.70	11.90	79.00	50.00	145.00	0.86	0.46	1952	67.10	12.90	65.50	37.30	133.20	0.91	0.04	
		Height (m)	1277	1.73	0.07	1.73	1.51	1.93	-0.04	-	1955	1.59	0.06	1.59	1.24	1.78	-0.04	-	
		WC (cm)	1274	97.70	9.70	97.00	70.00	145.50	0.86	0.17	1944	90.80	13.40	90.00	55.00	143.00	0.79	0.07	
		Hip (cm)	1274	101.10	7.60	101.00	45.50	155.00	0.79	0.24	1943	102.10	10.40	100.50	52.00	153.00	0.88	0.17	
		WHR (cm/cm)	1274	0.97	0.07	0.97	0.72	2.30	0.37	-0.03	1943	0.89	0.09	0.89	0.54	2.10	0.26	-0.06	
CoLaus	Height, BMI, Weight, WC, WHR	Age (yrs)	2547	52.92	10.77	52.20	34.90	75.10	0.18	-0.19	2862	53.90	10.70	53.70	35.00	75.40	0.16	-0.20	
		BMI (kg/m <sup>2</sup> )	2547	26.64	4.19	26.20	11.70	81.10	1.00	-0.15	2861	25.20	4.90	24.20	8.10	59.20	1.00	-0.21	
		Weight (kg)	2547	81.54	13.41	79.90	36.50	175.40	0.85	0.38	2861	66.40	13.00	64.00	21.40	171.00	0.91	0.22	
		Height (m)	2547	1.75	0.07	1.75	1.33	1.98	-0.15	1.00	2862	1.63	0.07	1.63	1.31	1.85	-0.21	1.00	
		WC (cm)	2546	95.91	11.22	95.00	64.00	163.00	0.85	0.08	2862	83.50	12.50	82.00	49.00	162.00	0.87	-0.05	
		Hip (cm)	2544	102.98	7.93	102.00	74.00	170.00	0.77	0.22	2861	100.70	10.30	99.00	66.00	168.00	0.88	0.05	
		WHR (cm/cm)	2544	0.93	0.06	0.93	0.58	1.24	0.59	-0.11	2861	0.83	0.07	0.82	0.52	1.25	0.45	-0.15	
DECODE	Height, BMI, Weight, WC, WHR	Age (yrs)	2610	63.50	16.40	78.00	18.00	103.00	-0.13	-0.34	3273	58.40	18.60	38.00	11.50	98.00	-0.15	-0.33	
		BMI (kg/m <sup>2</sup> )	2610	28.60	4.90	27.80	14.70	59.20	1.00	0.08	3273	29.00	6.40	33.90	13.70	73.50	1.00	0.00	
		Weight (kg)	2610	90.80	17.70	73.00	40.40	216.00	0.92	0.46	3273	79.50	18.70	92.30	33.00	220.00	0.94	0.33	
		Height (m)	2610	1.78	0.07	1.62	1.51	2.01	0.08	1.00	3273	1.65	0.06	1.65	1.42	1.92	0.00	1.00	
		WC (cm)	2610	102.40	14.10	91.00	32.00	181.00	0.75	0.18	3273	96.60	15.90	111.00	46.00	165.00	0.70	0.08	
		Hip (cm)	2610	106.40	9.60	95.00	40.00	175.00	0.70	0.27	3273	107.90	12.30	120.00	54.00	165.00	0.78	0.16	
		WHR (cm/cm)	2610	0.96	0.09	0.96	0.36	2.25	0.48	0.04	3273	0.89	0.09	0.93	0.57	1.34	0.28	-0.04	
DGI (Cases)	Height, BMI, Weight, WC, WHR	Age (yrs)	509	61.85	9.85	62.89	37.10	84.96	-0.12	-0.28	449	64.23	9.84	64.98	36.79	84.47	-0.25	-0.27	
		BMI (kg/m <sup>2</sup> )	509	28.24	3.87	28.02	18.29	46.71	1.00	0.01	449	28.80	4.85	28.30	18.51	53.73	1.00	-0.05	
		Weight (kg)	509	85.85	13.63	85.00	56.00	148.00	0.86	0.47	449	74.23	13.44	73.00	43.80	141.00	0.90	0.35	
		Height (m)	509	1.74	0.07	1.74	1.43	1.95	0.01	1.00	449	1.60	0.06	1.60	1.41	1.80	-0.05	1.00	
		WC (cm)	509	101.40	10.85	101.00	58.00	146.00	0.81	0.20	449	93.43	11.41	93.00	67.00	135.00	0.81	0.10	
		Hip (cm)	509	102.68	7.89	102.00	55.00	134.00	0.68	0.26	449	105.02	10.21	104.00	79.00	147.00	0.76	0.15	
		WHR (cm/cm)	509	0.99	0.06	0.99	0.64	1.28	0.51	-0.01	449	0.89	0.07	0.88	0.68	1.19	0.34	-0.04	
DGI (Controls)	Height, BMI, Weight, WC, WHR	Age (yrs)	241	59.21	9.48	60.05	35.54	78.63	-0.08	-0.39	228	58.32	9.31	58.66	36.83	80.41	0.00	-0.22	
		BMI (kg/m <sup>2</sup> )	241	27.03	3.23	26.61	20.57	37.12	1.00	0.08	228	26.82	4.16	26.44	19.83	42.77	1.00	-0.19	
		Weight (kg)	241	82.98	11.71	81.50	57.40	116.60	0.87	0.53	228	70.67	11.45	70.00	48.00	120.70	0.86	0.29	
		Height (m)	241	1.75	0.06	1.75	1.59	1.92	0.08	1.00	228	1.62	0.06	1.63	1.43	1.78	-0.19	1.00	
		WC (cm)	241	96.98	9.18	96.00	73.00	132.00	0.83	0.28	228	85.16	9.89	84.00	66.00	124.00	0.78	0.03	
		Hip (cm)	241	100.75	7.04	101.00	54.00	119.00	0.72	0.24	228	101.98	8.38	101.75	83.00	132.50	0.79	0.12	
		WHR (cm/cm)	241	0.96	0.08	0.96	0.82	1.61	0.46	0.16	228	0.83	0.06	0.83	0.69	1.11	0.33	-0.08	
EGCUT	Height, BMI, Weight, WC, WHR	Age (yrs)	195	32.00	13.20	26.00	18.00	69.00	0.41	-0.18	228	37.90	14.80	36.00	18.00	69.00	0.42	-0.20	
		BMI (kg/m <sup>2</sup> )	195	25.00	4.20	24.50	16.70	50.70	1.00	-0.03	228	26.10	6.20	24.50	16.60	54.20	1.00	-0.16	
		Weight (kg)	195	82.00	14.70	80.00	54.00	150.00	0.89	0.43	228	71.60	16.60	68.00	42.00	137.00	0.94	0.17	
		Height (m)	195	1.81	0.07	1.81	1.64	2.03	-0.03	1.00	228	1.66	0.06	1.65	1.47	1.83	-0.16	1.00	
		WC (cm)	195	89.70	13.10	88.00	60.00	164.00	0.85	0.11	228	84.90	15.70	81.00	53.00	140.00	0.90	-0.04	
		Hip (cm)	195	100.90	9.70	100.00	61.00	145.00	0.74	0.26	228	104.20	13.40	102.00	66.00	152.00	0.87	0.08	
		WHR (cm/cm)	195	0.89	0.09	0.88	0.73	1.31	0.47	-0.08	228	0.81	0.08	0.80	0.55	1.14	0.50	-0.17	
EPIC-Obesity Study	Height, BMI, Weight, WC, WHR	Age (yrs)	1130	59.82	9.02	60.00	40.00	77.00	0.08	-0.25	1284	58.74	9.00	59.00	39.00	77.00	0.17	-0.28	
		BMI (kg/m <sup>2</sup> )	1130	26.61	3.20	26.22	16.85	42.06	1.00	-0.07	1284	26.19	4.39	25.50	16.09	47.57	1.00	-0.16	
		Weight (kg)	1130	80.42	11.09	79.40	42.80	134.00	0.83	0.49	1284	67.98	11.62	66.20	44.60	119.00	0.90	0.27	



		Height (m)	1130	1.74	0.07	1.74	1.52	1.97	-0.07	1.00	1284	1.61	0.06	1.61	1.38	1.83	-0.16	1.00
		WC (cm)	1130	95.83	9.46	95.00	67.00	133.20	0.85	0.17	1284	81.92	10.76	80.10	56.00	128.00	0.86	-0.01
		Hip (cm)	1130	102.87	6.22	102.35	84.00	135.10	0.78	0.32	1284	103.54	9.10	102.00	83.10	149.90	0.89	0.09
		WHR (cm/cm)	1130	0.93	0.06	0.93	0.76	1.22	0.58	-0.04	1284	0.79	0.06	0.78	0.65	1.09	0.43	-0.13
ERF (EUROSPAN)	Height, BMI, Weight, WC, WHR	Age (yrs)	890	50.14	14.98	50.67	18.00	88.60	0.14	-0.49	1170	49.30	15.34	49.52	18.03	92.10	0.27	-0.42
		BMI (kg/m <sup>2</sup> )	890	27.14	3.98	26.78	15.85	42.44	1.00	-0.08	1170	26.36	4.77	25.64	15.54	45.37	1.00	-0.11
		Weight (kg)	890	82.70	13.52	81.40	48.00	133.30	0.86	0.43	1170	68.96	13.14	67.00	42.10	133.90	0.90	0.32
		Height (m)	890	1.75	0.07	1.75	1.52	1.96	-0.08	1.00	1170	1.61	0.07	1.62	1.41	1.83	-0.11	1.00
		WC (cm)	890	93.75	11.33	93.20	62.50	134.60	0.87	-0.04	1170	81.52	11.74	80.30	56.70	130.00	0.89	-0.05
		Hip (cm)	890	99.49	7.49	98.80	81.50	147.50	0.84	0.28	1170	101.37	9.33	100.40	79.00	151.00	0.85	0.20
		WHR (cm/cm)	890	0.94	0.08	0.95	0.72	1.19	0.56	-0.29	1170	0.80	0.08	0.80	0.61	1.17	0.51	-0.25
Fenland	Height, BMI, Weight, WC, WHR	Age (yrs)	615	44.48	7.32	45.00	30.00	57.00	0.08	-0.09	787	45.34	7.18	46.00	30.00	57.00	0.09	-0.11
		BMI (kg/m <sup>2</sup> )	615	27.62	4.07	27.27	18.62	56.66	1.00	-0.01	787	26.68	5.46	25.44	17.27	55.39	1.00	-0.07
		Weight (kg)	615	86.76	13.87	85.50	49.40	155.70	0.83	0.46	787	71.48	15.25	68.30	42.40	142.50	0.93	0.28
		Height (m)	615	1.77	0.07	1.77	1.59	2.01	-0.01	1.00	787	1.64	0.06	1.64	1.43	1.90	-0.07	1.00
		WC (cm)	615	98.69	11.61	97.55	74.00	184.20	0.76	0.20	787	86.99	12.77	85.00	61.05	141.20	0.89	0.10
		Hip (cm)	615	104.82	7.39	104.50	86.00	148.05	0.78	0.35	787	103.75	11.61	102.10	75.50	165.50	0.92	0.13
		WHR (cm/cm)	615	0.94	0.07	0.94	0.76	1.91	0.42	0.00	787	0.84	0.06	0.84	0.69	1.03	0.36	0.00
FHS (Cases)	Height, BMI, Weight, WC, WHR	Age (yrs)	220	54.20	11.87	55.75	26.38	74.14	0.02	-0.27	243	57.43	10.08	58.42	26.48	84.00	-0.04	-0.32
		BMI (kg/m <sup>2</sup> )	208	28.51	4.68	28.15	15.96	45.72	1.00	-0.18	233	28.27	6.51	26.75	18.43	50.18	1.00	-0.02
		Weight (kg)	208	89.04	15.03	87.77	51.71	146.51	0.89	0.27	233	73.87	17.94	69.40	45.36	1.00	0.95	0.29
		Height (m)	208	1.77	0.07	1.77	1.58	1.96	-0.18	1.00	233	1.62	0.06	1.62	1.42	1.79	-0.02	1.00
		WC (cm)	208	102.62	11.96	103.00	70.00	146.00	0.91	0.01	233	98.69	16.34	97.00	69.00	162.00	0.90	0.10
		Hip (cm)	208	105.42	9.32	104.00	81.00	150.00	0.87	0.15	233	107.69	13.23	104.00	86.00	162.00	0.09	0.16
		WHR (cm/cm)	208	0.97	0.06	0.97	0.75	1.09	0.51	-0.22	233	0.91	0.08	0.92	0.72	1.08	0.40	-0.04
FHS (Controls)	BMI, Weight, WC, WHR	Age (yrs)	218	52.09	12.20	54.19	26.99	76.86	0.10	-0.18	216	58.25	8.57	59.10	27.33	81.09	-0.06	-0.11
		BMI (kg/m <sup>2</sup> )	208	27.74	3.59	27.10	19.56	42.51	1.00	-0.07	207	26.64	4.66	25.61	17.48	43.39	1.00	0.04
		Weight (kg)	208	87.22	13.09	84.80	57.61	131.09	0.83	0.50	207	70.34	13.59	67.59	43.09	122.05	0.93	0.41
		Height (m)	208	1.77	0.07	1.78	1.55	1.98	-0.07	1.00	207	1.62	0.06	1.63	1.46	1.81	0.04	1.00
		WC (cm)	207	99.74	9.92	99.00	72.00	132.00	0.87	0.18	207	93.29	13.35	92.00	61.00	139.00	0.83	0.17
		Hip (cm)	207	104.28	7.22	103.00	87.00	132.00	0.82	0.36	207	106.03	9.17	105.00	88.00	145.00	0.89	0.28
		WHR (cm/cm)	207	0.96	0.05	0.96	0.80	1.09	0.53	-0.13	207	0.88	0.08	0.88	0.68	1.06	0.44	0.01
FRAM	Height, BMI, Weight, WC, hip, WHR	Age (yrs)	1562	51.40	10.09	51.00	26.00	80.00	0.07	-0.22	1715	51.00	9.80	50.00	22.00	77.00	0.19	-0.27
		BMI (kg/m <sup>2</sup> )	1556	27.64	3.87	27.22	17.71	46.91	1.00	-0.07	1711	26.08	5.53	24.63	13.79	66.62	1.00	-0.12
		Weight (kg)	1562	84.92	13.21	83.46	29.94	149.23	0.84	0.44	1715	68.35	14.85	64.86	39.92	181.44	0.90	0.28
		Height (m)	1557	1.75	0.07	1.75	1.24	1.97	-0.07	1.00	1711	1.62	0.06	1.62	1.41	1.82	-0.12	1.00
		WC (cm)	1562	97.61	10.52	96.52	63.50	144.78	0.86	0.16	1715	82.03	13.61	78.74	55.88	142.24	0.87	0.03
		Hip (cm)	1562	101.94	7.50	101.60	64.77	142.24	0.79	0.30	1715	101.41	11.51	99.06	76.20	162.56	0.88	0.11
		WHR (cm/cm)	1562	0.96	0.06	0.96	0.77	1.26	0.58	-0.05	1715	0.81	0.07	0.80	0.63	1.05	0.51	-0.07
FTC	Height, BMI, Weight, WC, WHR	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	120	61.79	15.85	61.79	23.73	75.94	0.30	-0.23
		BMI (kg/m <sup>2</sup> )	NA	NA	NA	NA	NA	NA	NA	NA	108	25.14	3.47	24.59	18.69	35.04	1.00	-0.16
		Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	109	65.74	10.04	65.00	46.50	100.50	0.87	0.33
		Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	109	1.61	0.06	1.61	1.47	1.78	-0.16	1.00
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	120	88.46	11.32	87.58	67.85	135.60	0.85	-0.19
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	120	104.10	9.20	102.20	87.00	135.60	0.82	0.02
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	120	0.85	0.05	0.85	0.74	0.98	0.51	-0.40
FUSION (Cases)	Height, BMI, Weight, WC, WHR	Age (yrs)	623	62.06	7.33	62.41	40.77	77.81	-0.21	-0.18	469	63.66	7.75	64.01	45.00	83.19	-0.21	-0.22
		BMI (kg/m <sup>2</sup> )	623	29.44	4.02	29.14	18.19	43.14	1.00	0.00	469	31.20	5.25	30.71	16.00	47.59	1.00	0.02
		Weight (kg)	623	88.43	13.58	88.00	50.90	144.00	0.89	0.42	469	79.51	14.70	76.90	35.00	125.50	0.91	0.39
		Height (m)	617	1.73	0.06	1.73	1.52	1.97	0.00	1.00	465	1.60	0.06	1.59	1.40	1.76	0.02	1.00
		WC (cm)	620	104.31	10.77	103.25	70.50	144.50	0.86	0.17	465	98.95	12.77	99.00	59.00	134.00	0.86	0.17
		Hip (cm)	620	104.84	7.86	104.50	81.50	140.00	0.72	0.29	464	110.10	11.18	109.00	79.00	145.00	0.84	0.23
		WHR (cm/cm)	620	0.99	0.07	0.99	0.79	1.24	0.52	-0.03	464	0.90	0.07	0.89	0.69	1.21	0.35	0.01

FUSION (Controls)	Height, BMI, Weight, WC, WHR	Age (yrs)	572	63.41	7.62	64.00	46.00	90.91	-0.05	-0.24	599	63.71	7.27	64.75	42.60	89.15	0.05	-0.29
		BMI (kg/m <sup>2</sup> )	572	27.02	3.53	26.78	19.22	51.07	1.00	-0.05	599	27.24	4.15	26.80	17.50	45.90	1.00	-0.12
		Weight (kg)	572	81.40	11.98	80.65	52.10	151.10	0.84	0.46	599	69.99	11.44	68.80	45.70	127.10	0.88	0.33
		Height (m)	569	1.74	0.06	1.74	1.56	1.91	-0.05	1.00	598	1.60	0.06	1.60	1.44	1.79	-0.12	1.00
		WC (cm)	571	96.66	9.88	95.50	72.00	147.00	0.86	0.12	598	86.30	10.67	85.50	64.00	136.00	0.87	0.05
		Hip (cm)	571	100.17	7.14	100.00	81.00	145.00	0.70	0.24	598	102.87	8.76	102.50	83.00	144.00	0.85	0.16
		WHR (cm/cm)	571	0.96	0.06	0.96	0.80	1.12	0.60	-0.06	598	0.84	0.06	0.83	0.67	1.07	0.48	-0.08
GENMETS (Cases)	Height, BMI, Weight, WC, WHR	Age (yrs)	425	49.19	10.42	49.00	30.00	75.00	-0.07	-0.24	423	48.59	10.17	49.00	30.00	74.00	0.04	-0.26
		BMI (kg/m <sup>2</sup> )	425	29.45	3.61	28.86	23.19	47.07	1.00	-0.13	423	25.35	3.15	24.92	17.09	39.04	1.00	-0.16
		Weight (kg)	410	91.16	12.56	91.16	65.00	151.00	0.81	0.47	422	77.62	10.60	77.00	51.00	113.00	0.81	0.45
		Height (m)	410	1.76	0.07	1.76	1.58	1.97	-0.13	1.00	422	1.75	0.07	1.75	1.55	1.96	-0.16	1.00
		WC (cm)	425	104.80	8.74	103.00	94.00	151.00	0.88	0.08	423	92.34	9.31	92.00	65.00	125.00	0.85	0.09
		Hip (cm)	425	104.20	7.08	103.50	87.00	150.00	0.83	0.18	423	97.35	6.07	97.00	76.50	122.00	0.79	0.21
		WHR (cm/cm)	425	1.01	0.04	1.00	0.90	1.17	0.37	-0.14	423	0.95	0.06	0.95	0.75	1.19	0.58	-0.07
GENMETS (Controls)	Height, BMI, Weight, WC, WHR	Age (yrs)	401	48.91	10.15	49.00	30.00	74.00	0.03	-0.27	423	48.59	10.17	49.00	30.00	74.00	0.04	-0.26
		BMI (kg/m <sup>2</sup> )	401	25.41	3.08	24.94	17.09	39.04	1.00	-0.16	423	25.35	3.15	24.92	17.09	39.04	1.00	-0.16
		Weight (kg)	401	78.03	10.33	77.00	54.00	116.00	0.82	0.43	422	77.62	10.60	77.00	51.00	113.00	0.81	0.45
		Height (m)	401	1.75	0.07	1.75	1.55	1.96	-0.16	1.00	422	1.75	0.07	1.75	1.55	1.96	-0.16	1.00
		WC (cm)	401	92.80	8.88	92.00	72.00	125.00	0.85	0.05	423	92.34	9.31	92.00	65.00	125.00	0.85	0.09
		Hip (cm)	401	97.25	5.92	97.00	76.50	122.00	0.78	0.24	423	97.35	6.07	97.00	76.50	122.00	0.79	0.21
		WHR (cm/cm)	401	0.95	0.05	0.95	0.81	1.19	0.58	-0.16	423	0.95	0.06	0.95	0.75	1.19	0.58	-0.07
KORAS3	Height, BMI, Weight, WC, WHR	Age (yrs)	813	52.96	10.09	54.00	25.00	69.00	0.22	-0.33	831	52.09	10.08	53.00	25.00	69.00	0.33	-0.32
		BMI (kg/m <sup>2</sup> )	813	27.69	3.45	27.29	18.73	40.67	1.00	-0.14	829	26.98	4.64	26.40	16.71	45.43	1.00	-0.25
		Weight (kg)	813	83.58	11.46	83.30	59.00	132.50	0.79	0.44	829	69.87	11.88	68.30	42.50	121.80	0.88	0.19
		Height (m)	813	1.74	0.07	1.74	1.51	1.96	-0.14	1.00	830	1.61	0.06	1.61	1.44	1.80	-0.25	1.00
		WC (cm)	812	97.07	9.71	97.00	71.00	137.00	0.84	0.08	827	83.75	11.03	82.50	60.00	132.00	0.87	-0.12
		Hip (cm)	812	103.89	6.45	103.50	81.98	143.01	0.75	0.25	826	104.11	9.31	102.99	78.03	139.53	0.87	-0.01
		WHR (cm/cm)	812	0.93	0.06	0.93	0.74	1.12	0.60	-0.11	826	0.80	0.06	0.80	0.61	1.01	0.52	-0.21
KORAS4	Height, BMI, Weight, WC, WHR	Age (yrs)	884	54.22	8.92	54.00	28.00	72.00	0.13	-0.31	930	53.62	8.80	53.00	25.00	74.00	0.32	-0.27
		BMI (kg/m <sup>2</sup> )	883	27.99	3.91	27.59	18.31	55.11	1.00	-0.13	928	27.49	5.07	26.78	18.21	51.22	1.00	-0.18
		Weight (kg)	883	85.13	12.93	84.00	54.20	192.70	0.83	0.40	929	71.46	13.30	69.60	43.90	142.00	0.90	0.23
		Height (m)	883	1.74	0.07	1.74	1.56	1.95	-0.13	1.00	928	1.61	0.06	1.61	1.44	1.83	-0.18	1.00
		WC (cm)	883	99.01	10.22	98.20	71.50	166.00	0.87	0.06	929	86.65	12.16	85.30	60.20	143.20	0.91	-0.03
		Hip (cm)	883	104.90	7.29	104.20	88.70	172.60	0.80	0.26	929	105.89	10.54	104.60	82.80	198.60	0.89	0.07
		WHR (cm/cm)	883	0.94	0.06	0.94	0.77	1.28	0.60	-0.16	929	0.82	0.06	0.82	0.56	1.06	0.57	-0.11
MICROS	Height, BMI, Weight, WC, WHR	Age (yrs)	475	45.09	15.67	41.97	18.19	87.85	0.28	-0.45	622	45.38	16.41	42.55	18.00	83.88	0.40	-0.52
		BMI (kg/m <sup>2</sup> )	475	26.07	3.96	25.62	18.13	42.75	1.00	-0.07	622	25.28	5.32	24.27	14.03	71.26	1.00	-0.28
		Weight (kg)	468	78.38	13.32	76.90	47.00	127.50	0.86	0.43	612	65.16	13.19	63.00	36.60	169.00	0.91	0.13
		Height (m)	467	1.73	0.07	1.73	1.53	1.95	-0.07	1.00	612	1.61	0.07	1.61	1.40	1.79	-0.28	1.00
		WC (cm)	118	93.55	11.39	93.00	56.00	126.00	0.83	0.03	175	85.07	13.47	82.00	60.00	121.00	0.81	-0.20
		Hip (cm)	118	97.69	9.59	98.00	57.00	118.00	0.52	0.15	175	97.91	15.06	97.00	65.00	198.00	0.69	-0.12
		WHR (cm/cm)	112	1.00	0.19	0.97	0.63	1.53	-0.34	-0.11	169	0.98	0.20	0.96	0.51	1.77	-0.43	0.07
NFBC1966	Height, BMI, Weight, WC, WHR	Age (yrs)	2246	31.00	0.00	31.00	31.00	31.00	NA	NA	2245	31.00	0.00	31.00	31.00	31.00	NA	NA
		BMI (kg/m <sup>2</sup> )	2246	25.17	3.61	24.86	15.32	47.58	1.00	-0.04	2245	24.16	4.68	23.13	15.43	54.35	1.00	-0.10
		Weight (kg)	2246	80.16	12.72	78.70	49.40	150.40	0.89	0.42	2245	65.51	13.24	63.00	29.20	165.40	0.92	0.28
		Height (m)	2246	1.78	0.06	1.78	1.55	2.03	-0.04	1.00	2245	1.65	0.06	1.65	1.05	1.87	-0.10	1.00
		WC (cm)	2246	88.79	9.84	88.00	60.00	149.00	0.90	0.17	2245	78.78	11.93	76.00	51.00	150.00	0.88	0.08
		Hip (cm)	2246	97.43	6.65	97.00	73.00	143.00	0.83	0.34	2245	97.11	8.87	96.00	55.00	149.00	0.87	0.18
		WHR (cm/cm)	2246	0.91	0.06	0.91	0.63	1.16	0.64	-0.08	2245	0.81	0.08	0.79	0.43	1.71	0.51	-0.04
NHS	Height, BMI, Weight, WC, WHR	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	1632	54.81	6.34	56.00	39.00	66.00	0.08	-0.02
		BMI (kg/m <sup>2</sup> )	NA	NA	NA	NA	NA	NA	NA	NA	1595	24.69	4.28	23.74	16.40	52.53	1.00	-0.11
		Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	1595	146.62	26.23	140.00	84.00	310.00	0.91	0.30
		Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	1632	1.64	0.06	1.63	1.50	1.98	-0.11	1.00
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	1632	79.08	10.86	76.20	15.24	134.62	0.79	0.06
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	1632	101.09	9.98	99.06	25.40	162.56	0.79	0.14

		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	1632	0.78	0.10	0.77	0.13	2.90	0.22	-0.05	
NSPHS†	Height, BMI, Weight, Hip	Age (yrs)	309	47.56	20.83	48.00	15.00	87.00	0.31	-0.32	347	46.47	20.60	45.00	14.00	91.00	0.49	-0.40	
		BMI (kg/m <sup>2</sup> )	307	26.75	4.54	26.23	17.78	46.49	1.00	-0.04	340	25.97	5.07	24.98	16.44	46.68	1.00	-0.16	
		Weight (kg)	307	78.42	14.66	77.00	51.00	138.00	0.88	0.42	342	64.99	13.11	63.00	38.00	121.00	0.89	0.29	
		Height (m)	308	1.71	0.07	1.72	1.48	1.89	-0.04	1.00	344	1.58	0.07	1.59	1.40	1.75	-0.16	1.00	
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
		Hip (cm)	307	99.17	14.41	98.00	54.00	184.00	0.78	0.01	339	93.61	13.03	93.00	59.00	149.00	0.86	-0.07	
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NTRNESDA (Cases)	Height, BMI, Weight, WC, WHR	Age (yrs)	526	44.65	11.83	46.00	18.00	74.00	0.28	-0.30	1197	41.63	12.77	42.00	18.00	77.00	0.24	-0.26	
		BMI (kg/m <sup>2</sup> )	526	26.42	4.43	26.01	15.95	50.21	1.00	-0.16	1197	25.41	5.31	24.23	14.61	53.27	1.00	-0.18	
		Weight (kg)	526	87.07	15.22	85.50	51.00	170.00	0.89	0.30	1197	72.44	15.15	70.00	44.00	167.00	0.93	0.18	
		Height (m)	526	1.82	0.07	1.81	1.59	2.07	-0.16	1.00	1197	1.69	0.06	1.69	1.51	1.96	-0.18	1.00	
		WC (cm)	526	96.74	12.82	96.00	67.00	165.00	0.90	0.00	1197	85.86	13.39	84.00	60.00	149.00	0.90	-0.07	
		Hip (cm)	526	104.71	8.18	104.00	83.00	165.00	0.79	0.22	1197	103.82	11.41	102.00	69.00	175.00	0.89	0.03	
		WHR (cm/cm)	526	0.92	0.08	0.92	0.71	1.20	0.66	-0.21	1197	0.83	0.07	0.82	0.66	1.40	0.45	-0.16	
NTRNESDA (Controls)	Height, BMI, Weight, WC, WHR	Age (yrs)	680	47.26	14.45	51.00	18.00	81.00	0.28	-0.30	1106	43.72	13.66	42.00	18.00	78.00	0.24	-0.21	
		BMI (kg/m <sup>2</sup> )	679	25.75	3.47	25.40	17.26	39.19	1.00	-0.12	1101	24.86	4.21	24.09	15.88	47.32	1.00	-0.09	
		Weight (kg)	680	85.01	12.52	83.80	50.10	133.10	0.85	0.42	1105	71.14	12.72	68.80	44.30	150.00	0.91	0.33	
		Height (m)	679	1.82	0.07	1.82	1.61	2.06	-0.12	1.00	1102	1.69	0.06	1.69	1.50	1.92	-0.09	1.00	
		WC (cm)	680	93.60	11.35	93.00	55.00	135.00	0.84	0.07	1106	83.17	11.72	81.00	62.00	149.00	0.84	0.07	
		Hip (cm)	680	104.58	6.54	104.00	84.00	139.00	0.75	0.28	1106	103.52	9.08	103.00	49.00	157.00	0.82	0.20	
		WHR (cm/cm)	680	0.89	0.08	0.89	0.52	1.18	0.62	-0.11	1106	0.80	0.08	0.79	0.62	1.48	0.42	-0.07	
ORCADES	Height, BMI, Weight, WC, WHR	Age (yrs)	332	54.27	15.73	54.66	17.29	93.75	0.29	-0.38	384	53.01	15.68	54.27	17.71	97.62	0.25	-0.38	
		BMI (kg/m <sup>2</sup> )	332	28.08	4.27	27.67	16.97	47.10	1.00	-0.22	384	27.48	5.18	26.60	18.47	47.63	1.00	-0.17	
		Weight (kg)	324	85.76	13.21	84.25	44.40	148.40	0.87	0.28	371	71.06	13.69	69.10	45.60	123.10	0.92	0.22	
		Height (m)	324	1.75	0.07	1.75	1.59	1.99	-0.22	1.00	371	1.61	0.06	1.61	1.38	1.78	-0.17	1.00	
		WC (cm)	324	98.78	12.48	97.80	64.40	147.70	0.91	-0.09	371	89.28	13.62	87.00	62.50	139.10	0.91	-0.04	
		Hip (cm)	324	102.18	9.53	101.40	29.60	180.40	0.73	0.08	371	103.49	11.09	101.50	84.00	198.50	0.79	0.09	
		WHR (cm/cm)	324	0.97	0.15	0.97	0.72	3.25	0.30	-0.12	371	0.86	0.08	0.85	0.47	1.12	0.56	-0.16	
PROCARDIS	Height, BMI, Weight, WC, WHR	Age (yrs)	612	58.28	7.12	59.00	34.00	80.00	-0.07	-0.07	346	60.53	6.96	62.00	33.00	75.00	0.00	-0.15	
		BMI (kg/m <sup>2</sup> )	612	26.95	3.68	26.51	18.51	43.58	1.00	-0.09	346	25.52	4.22	24.66	16.42	41.15	1.00	-0.11	
		Weight (kg)	612	85.40	12.74	84.00	55.00	159.00	0.87	0.41	346	69.92	12.06	68.00	45.00	115.00	0.91	0.31	
		Height (m)	612	1.78	0.06	1.78	1.58	2.06	-0.09	1.00	346	1.66	0.06	1.65	1.49	1.83	-0.11	1.00	
		WC (cm)	612	99.15	9.81	99.00	71.00	141.00	0.86	0.11	346	87.99	11.14	87.00	64.00	126.00	0.84	0.13	
		Hip (cm)	612	101.46	6.54	101.00	85.00	130.00	0.76	0.26	346	101.01	7.88	100.00	84.00	136.00	0.84	0.19	
		WHR (cm/cm)	612	0.98	0.06	0.98	0.77	1.19	0.55	-0.08	346	0.87	0.08	0.86	0.71	1.15	0.45	0.02	
RS1	Height, BMI, Weight, WC, WHR	Age (yrs)	2427	68.13	0.17	67.05	55.01	97.81	-0.55	-0.30	3547	70.32	0.16	69.40	55.00	99.22	0.08	-0.38	
		BMI (kg/m <sup>2</sup> )	2372	25.68	0.06	25.61	14.19	38.19	1.00	-0.05	3372	26.74	0.07	26.31	15.43	59.50	1.00	-0.14	
		Weight (kg)	2375	78.58	0.22	77.80	41.00	122.30	0.81	0.50	3383	69.59	0.19	68.70	40.10	146.50	0.84	0.37	
		Height (m)	2372	1.75	0.00	1.75	1.51	1.98	-0.05	1.00	3372	1.61	0.00	1.62	1.01	1.92	-0.14	1.00	
		WC (cm)	2266	94.33	0.20	94.00	57.00	150.00	0.77	0.14	3205	87.90	0.20	87.00	55.00	143.00	0.72	0.00	
		Hip (cm)	2266	98.56	0.14	97.92	70.09	150.00	0.64	0.32	3202	101.20	0.15	100.00	70.35	160.47	0.77	0.12	
		WHR (cm/cm)	2266	0.96	0.00	0.96	0.56	1.25	0.48	-0.09	3202	0.87	0.00	0.86	0.58	1.31	0.33	-0.08	
SARDINIA	Height, BMI, Weight, WC, WHR	Age (yrs)	1886	44.08	18.10	42.90	14.00	93.90	0.51	-0.46	2419	43.19	17.30	42.10	14.00	101.30	0.55	-0.50	
		BMI (kg/m <sup>2</sup> )	1885	26.15	4.11	25.90	14.90	42.90	1.00	-0.22	2416	24.75	5.03	23.80	13.90	53.30	1.00	-0.31	
		Weight (kg)	1883	72.27	11.71	72.00	34.00	135.00	0.84	0.33	2415	59.17	11.40	57.00	32.00	145.00	0.90	0.11	
		Height (m)	1883	1.66	0.07	1.66	1.44	1.96	-0.22	1.00	2415	1.55	0.06	1.55	1.31	1.78	-0.31	1.00	
		WC (cm)	1886	90.11	11.43	90.00	58.00	134.00	0.91	-0.11	2416	80.66	13.04	78.00	56.00	133.00	0.88	-0.19	
		Hip (cm)	1886	97.24	7.04	97.00	71.00	138.00	0.83	0.17	2415	97.81	9.09	97.00	63.00	142.00	0.87	0.00	
		WHR (cm/cm)	1886	0.92	0.07	0.92	0.57	1.19	0.70	-0.32	2415	0.82	0.09	0.81	0.63	1.43	0.56	-0.30	
SHIP	Height, BMI, Weight, WC, WHR	Age (yrs)	2019	50.88	16.43	52.00	20.00	80.00	0.25	-0.48	2073	48.58	16.02	48.00	20.00	81.00	0.41	-0.48	
		BMI (kg/m <sup>2</sup> )	2019	27.68	4.04	27.41	18.06	48.07	1.00	-0.12	2073	26.92	5.31	26.16	16.10	52.40	1.00	-0.26	
		Weight (kg)	2019	85.06	13.56	83.80	49.90	156.40	0.83	0.40	2073	71.20	13.74	69.20	41.30	133.30	0.89	0.16	
		Height (m)	2019	1.75	0.07	1.75	1.48	1.98	-0.12	1.00	2073	1.63	0.07	1.63	1.42	1.94	-0.26	1.00	

		WC (cm)	2019	95.83	11.68	95.50	67.90	143.50	0.89	-0.06	2073	83.14	12.96	81.50	50.50	129.30	0.91	-0.17
		Hip (cm)	2019	102.84	7.88	102.00	76.80	146.50	0.83	0.14	2073	103.05	11.39	101.90	57.40	148.00	0.92	-0.05
		WHR (cm/cm)	2019	0.93	0.06	0.93	0.71	1.19	0.67	-0.23	2073	0.80	0.06	0.80	0.56	1.36	0.56	-0.26
T2D_WTCCC	Height, BMI, Weight, WC, WHR	Age (yrs)	1085	58.95	9.89	59.00	29.00	96.00	-0.32	-0.17	786	57.85	10.40	59.00	27.00	84.00	-0.30	-0.16
		BMI (kg/m <sup>2</sup> )	1085	30.27	5.37	29.70	18.02	55.91	1.00	-0.01	786	32.56	6.83	31.56	17.91	62.37	1.00	0.01
		Weight (kg)	1085	93.33	17.96	91.00	47.63	161.94	0.91	0.40	786	85.07	19.19	82.56	43.00	155.70	0.93	0.37
		Height (m)	1085	1.75	0.07	1.75	1.50	1.98	-0.01	1.00	786	1.61	0.07	1.61	1.37	1.83	0.01	1.00
		WC (cm)	1085	106.19	13.41	105.00	71.12	167.64	0.86	0.15	786	102.47	15.40	101.55	66.04	152.00	0.84	0.21
		Hip (cm)	1085	108.53	10.90	107.00	78.70	172.00	0.78	0.19	786	114.53	14.66	113.00	76.20	175.00	0.87	0.19
		WHR (cm/cm)	1085	0.98	0.07	0.97	0.74	1.31	0.42	0.01	786	0.90	0.08	0.89	0.69	1.22	0.19	0.08
TwinsUK	Height, BMI, Weight, WC, WHR	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	1479	46.19	12.30	47.55	16.62	76.54	0.15	-0.20
		BMI (kg/m <sup>2</sup> )	NA	NA	NA	NA	NA	NA	NA	NA	1477	25.02	4.80	24.06	13.22	52.71	1.00	-0.12
		Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	1477	66.03	13.00	64.00	35.10	140.90	0.92	0.27
		Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	1479	1.62	0.06	1.63	1.42	1.80	-0.12	1.00
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	1096	78.22	10.30	76.00	53.00	123.00	0.85	0.07
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	1096	100.98	9.90	100.00	69.00	168.00	0.88	0.13
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	1094	0.77	0.06	0.77	0.62	1.29	0.33	-0.03
VIS	Height, BMI, Weight, WC, WHR	Age (yrs)	328	55.95	14.94	57.00	18.00	88.00	0.23	-0.40	467	56.97	15.64	57.00	18.00	93.00	0.30	-0.45
		BMI (kg/m <sup>2</sup> )	328	27.55	3.69	27.49	18.36	40.69	1.00	-0.10	467	27.18	4.50	27.08	17.01	52.02	1.00	-0.20
		Weight (kg)	325	85.56	13.01	84.80	50.90	136.50	0.83	0.47	445	70.99	12.45	69.80	46.60	153.00	0.89	0.26
		Height (m)	325	1.76	0.07	1.76	1.58	2.04	-0.10	1.00	459	1.62	0.07	1.62	1.43	1.91	-0.20	1.00
		WC (cm)	325	98.39	9.75	98.30	72.40	133.10	0.89	0.08	459	94.19	12.82	95.00	65.50	147.40	0.85	-0.16
		Hip (cm)	325	101.82	7.88	101.20	84.10	187.70	0.64	0.18	458	103.37	9.21	103.00	63.20	159.00	0.74	0.15
		WHR (cm/cm)	325	0.97	0.07	0.97	0.51	1.24	0.56	-0.13	458	0.91	0.09	0.91	0.61	1.19	0.49	-0.38
<b>Follow-up Stage</b>																		
<b>In silico follow-up studies</b>																		
BHS	Height, BMI, Weight, WC, WHR	Age (yrs)	536	53.61	17.00	53.90	17.60	91.40	0.14	-0.38	748	53.97	17.02	43.50	17.30	90.50	0.10	-0.43
		BMI (kg/m <sup>2</sup> )	535	26.64	3.61	26.25	15.77	40.12	1.00	-0.09	746	25.51	4.41	24.69	16.82	40.77	1.00	-0.15
		Weight (kg)	536	81.97	12.40	80.50	46.40	127.00	0.84	0.47	746	67.05	11.98	65.20	34.80	109.00	0.90	0.29
		Height (m)	535	1.75	0.07	1.75	1.53	1.99	-0.09	1.00	747	1.62	0.06	1.62	1.35	1.90	-0.15	1.00
		WC (cm)	536	93.76	10.44	93.00	62.80	133.30	0.86	0.05	748	80.88	11.64	78.50	58.65	131.90	0.88	-0.05
		Hip (cm)	536	100.20	7.58	99.40	74.80	136.60	0.82	0.22	748	101.20	9.23	100.00	77.00	138.80	0.88	0.11
		WHR (cm/cm)	536	1.07	0.07	1.07	0.86	1.34	-0.52	0.16	748	1.26	0.11	1.26	0.95	1.56	-0.50	0.21
Corogene	Height, BMI, Weight, WC, WHR	Age (yrs)	2266	59.66	12.83	61.00	25.00	92.00	-0.03	-0.26	1490	62.61	13.47	65.00	25.00	94.00	0.09	-0.30
		BMI (kg/m <sup>2</sup> )	2265	27.39	4.23	26.79	15.95	54.88	1.00	-0.04	1491	26.87	5.21	26.07	13.63	57.68	1.00	-0.14
		Weight (kg)	2265	85.00	14.42	83.50	44.00	170.00	0.89	0.41	1491	70.14	13.88	68.30	36.00	144.00	0.90	0.28
		Height (m)	2267	1.76	0.07	1.76	1.34	2.03	-0.04	1.00	1491	1.62	0.07	1.62	1.05	1.85	-0.14	1.00
		WC (cm)	1122	97.20	11.55	95.50	64.50	142.00	0.90	0.06	942	85.95	12.73	84.00	61.50	142.00	0.91	-0.05
		Hip (cm)	1121	100.48	7.18	100.00	83.00	133.00	0.82	0.24	942	101.67	9.98	100.50	78.50	145.50	0.90	0.07
		WHR (cm/cm)	1121	0.97	0.07	0.96	0.68	1.25	0.64	-0.05	942	0.84	0.07	0.84	0.68	1.20	0.55	-0.17
EGCUT	Height, BMI, Weight, WC, WHR	Age (yrs)	135	40.93	17.81	36.50	18.00	80.00	0.33	-0.55	210	41.03	16.46	39.00	18.00	87.00	0.41	-0.37
		BMI (kg/m <sup>2</sup> )	135	26.03	4.95	25.11	17.30	43.65	1.00	-0.14	210	25.63	6.09	24.02	17.00	48.24	1.00	-0.25
		Weight (kg)	135	83.68	16.41	80.50	50.00	143.00	0.91	0.27	210	70.46	16.22	66.50	40.00	136.00	0.93	0.10
		Height (m)	135	1.79	0.07	1.80	1.58	2.04	-0.14	1.00	210	1.66	0.07	1.66	1.44	1.84	-0.25	1.00
		WC (cm)	135	92.42	14.62	90.00	64.00	147.00	0.87	-0.10	210	82.08	13.98	79.00	46.00	134.00	0.87	-0.15
		Hip (cm)	135	102.40	8.15	101.00	82.00	132.00	0.85	0.13	210	104.30	12.40	101.00	78.00	167.00	0.86	-0.03
		WHR (cm/cm)	135	0.90	0.09	0.90	0.68	1.11	0.67	-0.26	210	0.79	0.08	0.78	0.47	1.17	0.42	-0.23
FHS	Height, BMI, Weight, WC, WHR	Age (yrs)	662	48.20	13.70	46.30	25.60	85.70	0.15	-0.24	880	47.50	13.00	45.00	25.70	85.80	0.19	-0.26
		BMI (kg/m <sup>2</sup> )	632	27.80	4.30	27.20	18.40	46.20	1.00	-0.09	831	27.10	6.10	26.10	16.50	55.00	1.00	-0.12
		Weight (kg)	632	87.10	14.60	85.30	55.30	140.60	0.88	0.39	831	72.30	16.60	68.90	41.70	144.20	0.94	0.22
		Height (m)	632	1.77	0.07	1.77	1.57	2.03	-0.09	1.00	831	1.63	0.06	1.63	1.41	1.96	-0.12	1.00
		WC (cm)	631	99.30	12.50	99.00	44.00	147.00	0.86	0.06	831	92.60	16.90	90.00	27.00	170.00	0.89	-0.01
		Hip (cm)	631	104.20	8.30	104.00	53.00	140.00	0.82	0.27	831	106.80	12.40	104.00	59.00	162.00	0.91	0.10
		WHR (cm/cm)	631	1.00	0.01	1.00	0.40	1.80	0.47	-0.17	831	0.90	0.10	0.90	0.30	1.60	0.52	-0.15

GOOD	Height, BMI, Weight, WC, WHR	Age (yrs)	938	18.90	0.60	18.80	18.00	20.10	0.03	0.01	NA	NA	NA	NA	NA	NA	NA	NA	
		BMI (kg/m <sup>2</sup> )	938	22.40	3.20	21.90	16.10	41.60	1.00	-0.05	NA	NA	NA	NA	NA	NA	NA	NA	NA
		Weight (kg)	938	73.90	11.60	72.00	51.30	127.00	0.88	0.42	NA	NA	NA	NA	NA	NA	NA	NA	NA
		Height (m)	938	1.82	0.07	1.82	1.61	2.03	-0.05	1.00	NA	NA	NA	NA	NA	NA	NA	NA	NA
		WC (cm)	937	78.50	7.20	77.00	63.50	116.00	0.89	0.16	NA	NA	NA	NA	NA	NA	NA	NA	NA
		Hip (cm)	937	92.60	7.90	91.70	57.00	133.00	0.80	0.30	NA	NA	NA	NA	NA	NA	NA	NA	NA
		WHR (cm/cm)	937	0.85	0.05	0.85	0.69	1.39	0.21	-0.19	NA	NA	NA	NA	NA	NA	NA	NA	NA
HBSC	Height, BMI, Weight, WC, WHR	Age (yrs)	737	61.41	2.75	60.80	57.00	69.30	-0.03	-0.15	991	61.55	3.05	60.90	56.70	69.80	-0.10	0.03	
		BMI (kg/m <sup>2</sup> )	736	27.56	4.30	27.01	18.75	68.39	1.00	-0.03	990	27.75	5.06	26.98	14.79	50.10	1.00	-0.09	
		Weight (kg)	737	86.33	14.51	84.50	56.20	213.30	0.92	0.36	990	73.90	13.89	71.70	37.30	133.80	0.93	0.28	
		Height (m)	736	1.77	0.06	1.77	1.59	1.97	-0.03	1.00	990	1.63	0.06	1.63	1.46	1.83	-0.09	1.00	
		WC (cm)	735	100.86	11.47	99.50	73.50	141.50	0.92	0.11	989	91.22	13.04	89.90	62.50	142.50	0.91	0.07	
		Hip (cm)	735	101.43	6.74	100.70	86.00	129.50	0.88	0.30	988	104.31	9.48	103.05	81.30	148.50	0.88	0.14	
		WHR (cm/cm)	735	0.99	0.07	0.99	0.78	1.19	0.68	-0.10	988	0.87	0.08	0.87	0.68	1.14	0.54	-0.03	
NHS	Height, BMI, Weight, WC, WHR	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	2196	53.81	6.64	55.00	39.00	65.00	0.02	-0.06	
		BMI (kg/m <sup>2</sup> )	NA	NA	NA	NA	NA	NA	NA	NA	2162	26.54	5.41	25.51	17.01	54.87	1.00	-0.05	
		Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	2162	157.26	33.90	150.00	90.00	338.00	0.93	0.25	
		Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	2196	1.64	0.07	1.63	1.35	1.83	-0.05	1.00	
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	2196	83.32	13.26	81.28	15.24	139.70	0.85	0.10	
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	2196	104.04	12.03	101.60	30.48	177.80	0.82	0.15	
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	2196	0.80	0.12	0.79	0.17	3.33	0.28	-0.01	
RS-II	Height, BMI, Weight, WC, WHR	Age (yrs)	973	64.48	7.59	61.89	55.14	93.95	-0.13	-0.22	1156	65.04	8.33	62.03	55.12	95.33	-0.03	-0.31	
		BMI (kg/m <sup>2</sup> )	971	26.92	3.36	26.72	16.78	40.52	1.00	-0.10	1151	27.52	4.45	26.89	16.66	50.12	1.00	-0.06	
		Weight (kg)	972	83.32	11.58	82.20	54.00	126.80	0.85	0.44	1151	72.77	12.74	71.10	36.20	150.00	0.90	0.38	
		Height (m)	971	1.76	0.06	1.76	1.57	2.03	-0.10	1.00	1153	1.63	0.06	1.63	1.42	1.90	-0.06	1.00	
		WC (cm)	878	99.03	10.21	98.65	70.00	198.60	0.82	0.09	1037	89.89	11.62	89.00	62.00	145.00	0.86	0.10	
		Hip (cm)	878	101.82	5.93	101.30	86.50	163.20	0.75	0.25	1037	104.13	8.69	103.00	82.00	154.00	0.86	0.20	
		WHR (cm/cm)	878	0.97	0.07	0.97	0.58	1.95	0.54	-0.08	1037	0.86	0.08	0.86	0.60	1.18	0.45	-0.05	
SORBS	Height, BMI, Weight, WC, WHR	Age (yrs)	371	48.10	16.70	48.10	18.10	82.10	0.39	-0.43	536	48.00	15.90	48.60	18.00	88.40	0.49	-0.54	
		BMI (kg/m <sup>2</sup> )	371	27.20	4.00	26.80	19.00	43.90	1.00	-0.24	536	26.90	5.50	26.20	15.40	47.40	1.00	-0.32	
		Weight (kg)	371	85.40	12.70	84.00	58.00	139.00	0.85	0.30	536	72.10	14.00	70.00	43.00	126.00	0.92	0.07	
		Height (m)	371	1.77	0.07	1.77	1.58	1.95	-0.24	1.00	536	1.64	0.07	1.64	1.44	1.82	-0.32	1.00	
		WC (cm)	371	96.80	12.10	97.00	72.00	137.00	0.89	-0.15	536	87.40	14.00	86.00	59.00	139.00	0.91	-0.24	
		Hip (cm)	371	102.30	6.70	101.00	86.00	139.00	0.83	0.15	536	105.10	10.30	103.00	85.00	146.00	0.92	-0.08	
		WHR (cm/cm)	371	0.90	0.10	1.00	0.70	1.20	0.66	-0.34	536	0.80	0.10	0.80	0.60	1.10	0.58	-0.33	
WGHS	Height, BMI, Weight, WC, WHR	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	20529	54.74	7.06	53.02	38.71	89.89	-0.02	-0.07	
		BMI (kg/m <sup>2</sup> )	NA	NA	NA	NA	NA	NA	NA	NA	20167	25.72	4.83	24.72	14.23	59.58	1.00	-0.06	
		Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	20297	69.48	13.79	67.13	38.56	158.76	0.92	0.32	
		Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	20363	1.64	0.06	1.65	1.30	2.01	-0.06	1.00	
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	20529	88.88	14.32	86.36	38.10	170.18	0.77	0.12	
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	20529	106.33	12.07	104.14	50.80	193.04	0.79	0.17	
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	20529	0.83	0.08	0.83	0.33	1.93	0.35	0.00	
YFS	Height, BMI, Weight, WC, WHR	Age (yrs)	1123	37.55	5.06	39.00	30.00	45.00	0.13	-0.12	1320	37.57	5.01	39.00	30.00	45.00	0.11	-0.06	
		BMI (kg/m <sup>2</sup> )	908	26.76	4.29	26.11	17.54	49.35	1.00	0.04	1081	25.32	5.03	24.34	16.56	58.82	1.00	-0.06	
		Weight (kg)	908	86.56	15.65	85.00	54.00	166.00	0.91	0.45	1083	69.82	14.55	67.00	42.00	166.00	0.94	0.29	
		Height (m)	911	1.80	0.07	1.80	1.57	2.03	0.04	1.00	1084	1.66	0.06	1.66	1.45	1.89	-0.06	1.00	
		WC (cm)	913	94.42	12.00	93.25	68.15	151.60	0.93	0.20	1086	83.51	12.59	81.25	60.00	145.90	0.91	0.08	
		Hip (cm)	913	99.84	7.67	99.40	82.40	132.25	0.83	0.39	1086	99.83	9.80	98.25	77.00	164.10	0.87	0.20	
		WHR (cm/cm)	913	0.94	0.07	0.94	0.78	1.19	0.71	-0.07	1086	0.83	0.07	0.83	0.59	1.24	0.56	-0.09	
De-novo genotyped follow-up studies																			
BCG	Height, BMI, Weight, WC, WHR	Age (yrs)	361	25.02	0.76	25.00	23.17	27.25	-0.01	0.02	318	25.01	0.76	25.00	23.08	26.75	-0.01	0.03	
		BMI (kg/m <sup>2</sup> )	359	25.08	3.91	24.76	15.84	41.78		-0.06	314	25.23	5.35	23.83	16.97	47.85		-0.12	
		Weight (kg)	360	78.97	13.12	78.00	45.00	127.00	0.91	0.36	316	67.66	14.52	64.25	42.00	141.00	0.93	0.23	

		Height (m)	359	1.77	0.06	1.77	1.53	1.96	-0.06		315	1.64	0.06	1.64	1.46	1.80	-0.12	
		WC (cm)	358	82.53	8.83	81.95	61.30	116.10	0.92	0.10	314	73.42	11.35	71.00	51.50	121.50	0.93	0.07
		Hip (cm)	360	98.92	7.46	98.50	78.70	129.15	0.85	0.24	316	102.03	10.30	101.10	70.30	144.45	0.89	0.14
		WHR (cm/cm)	358	0.83	0.05	0.83	0.71	1.02	0.58	-0.13	313	0.72	0.06	0.71	0.61	0.96	0.58	-0.04
BPPP	Height, BMI, Weight, WC, WHR	Age (yrs)	1631	49.28	15.95	51.11	19.06	76.39	0.16	-0.34	1808	49.18	16.03	51.32	18.76	76.80	0.31	-0.34
		BMI (kg/m <sup>2</sup> )	1644	23.70	3.43	23.37	13.97	43.95	1.00	0.13	1818	21.29	3.83	20.80	13.39	49.85	1.00	0.03
		Weight (kg)	1644	83.99	13.09	82.95	47.50	168.10	0.96	0.37	1818	69.80	12.95	68.20	43.00	165.50	0.97	0.24
		Height (m)	1644	1.77	0.07	1.77	1.58	2.00	0.13	1.00	1819	1.64	0.06	1.64	1.42	1.87	0.03	1.00
		WC (cm)	1644	94.80	11.29	94.00	66.00	145.00	0.88	0.00	1819	83.74	12.11	82.00	60.00	162.00	0.90	-0.06
		Hip (cm)	1644	100.12	6.59	100.00	80.00	138.00	0.83	0.26	1819	100.89	8.91	100.00	80.00	178.00	0.90	0.10
		WHR (cm/cm)	1644	0.95	0.08	0.94	0.74	1.23	0.63	-0.20	1819	0.83	0.07	0.82	0.64	1.46	0.57	-0.17
BWHS	Height, BMI, Weight, WC, WHR	Age (yrs)	NA	NA	NA	NA	NA	NA	NA	NA	4269	68.89	5.51	69.00	59.00	80.00	-0.06	-0.21
		BMI (kg/m <sup>2</sup> )	NA	NA	NA	NA	NA	NA	NA	NA	3941	27.61	5.01	26.86	15.25	58.83		-0.10
		Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	3947	69.57	13.05	67.90	37.40	145.10	0.90	0.31
		Height (m)	NA	NA	NA	NA	NA	NA	NA	NA	3942	1.59	0.06	1.59	1.35	2.00	-0.10	
		WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	3924	86.22	12.19	84.80	56.40	147.85	0.84	0.06
		Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	3927	105.12	10.35	103.60	78.15	162.45	0.89	0.14
		WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	3930	0.82	0.07	0.81	0.58	1.20	0.37	-0.05
DESIR	Height, BMI, Weight, WC, WHR	Age (yrs)	2253	47.28	10.05	46.57	30.07	65.82	0.26	-0.30	2283	47.33	10.03	46.91	30.13	65.50	0.27	-0.28
		BMI (kg/m <sup>2</sup> )	2253	25.46	3.36	25.10	16.70	45.40	1.00	-0.12	2281	23.97	4.11	23.20	15.40	53.60	1.00	-0.19
		Weight (kg)	2253	75.91	10.93	75.00	46.00	140.00	0.85	0.42	2281	61.03	10.52	59.00	37.00	127.00	0.90	0.24
		Height (m)	2253	1.73	0.07	1.72	1.50	1.96	-0.12	1.00	2281	1.60	0.06	1.60	1.41	1.83	-0.19	1.00
		WC (cm)	2249	89.73	9.61	89.00	63.00	133.00	0.87	0.04	2274	76.94	10.35	75.00	55.00	125.00	0.87	-0.05
		Hip (cm)	2249	97.47	6.45	96.81	61.16	133.33	0.78	0.26	2274	97.12	8.74	96.20	68.97	160.26	0.83	0.08
		WHR (cm/cm)	2249	0.92	0.06	0.92	0.71	1.21	0.60	-0.18	2274	0.79	0.07	0.78	0.54	1.06	0.48	-0.17
DIAGEN	Height, BMI, Weight, WC, WHR	Age (yrs)	830	60.96	13.47	60.00	22.00	96.00	-0.14	-0.35	991	62.05	15.00	61.00	18.00	97.00	0.00	-0.35
		BMI (kg/m <sup>2</sup> )	830	27.66	4.00	27.05	18.94	44.64	1.00	0.02	991	27.99	6.00	26.98	15.63	61.71	1.00	-0.04
		Weight (kg)	830	84.73	13.96	83.00	50.00	137.00	0.85	0.51	991	74.00	16.98	71.00	40.00	182.00	0.91	0.34
		Height (m)	830	1.75	0.07	1.75	1.50	1.96	0.02	1.00	991	1.62	0.07	1.62	1.41	1.92	-0.04	1.00
		WC (cm)	812	101.38	11.23	101.00	74.00	142.00	0.81	0.15	965	93.67	15.32	92.00	28.00	150.00	0.82	0.03
		Hip (cm)	812	104.09	7.65	104.00	81.00	131.00	0.67	0.28	964	106.99	13.34	105.00	59.00	175.00	0.85	0.12
		WHR (cm/cm)	812	0.97	0.07	0.97	0.76	1.20	0.58	-0.06	964	0.87	0.08	0.87	0.28	1.16	0.31	-0.11
EGCUT	Height, BMI, Weight, WC, WHR	Age (yrs)	1891	42.97	18.43	41.00	18.00	101.00	0.28	-0.38	1888	44.77	17.45	43.50	18.00	101.00	0.41	-0.39
		BMI (kg/m <sup>2</sup> )	1891	26.29	4.61	25.68	15.90	55.50	1.00	-0.12	1888	26.18	5.60	25.12	11.51	53.15	1.00	-0.18
		Weight (kg)	1891	83.75	15.37	82.00	46.00	168.00	0.90	0.33	1888	71.33	15.24	69.00	28.00	150.00	0.93	0.18
		Height (m)	1891	1.79	0.07	1.78	1.52	2.03	-0.12	1.00	1888	1.65	0.06	1.65	1.40	1.90	-0.18	1.00
		WC (cm)	1891	92.94	13.70	92.00	52.00	162.00	0.85	0.00	1888	83.98	14.33	82.00	50.00	150.00	0.87	-0.08
		Hip (cm)	1891	102.00	9.61	101.00	53.00	197.00	0.72	0.18	1888	103.50	11.77	102.00	55.00	160.00	0.86	0.04
		WHR (cm/cm)	1891	0.91	0.09	0.90	0.53	1.36	0.55	-0.17	1888	0.81	0.08	0.80	0.58	1.45	0.49	-0.17
EPIC-Norfolk	Height, BMI, Weight, WC, WHR	Age (yrs)	9084	59.08	9.30	59.00	39.00	79.00	0.06	-0.23	9400	58.57	9.34	58.00	39.00	77.00	0.09	-0.26
		BMI (kg/m <sup>2</sup> )	9084	26.49	3.28	26.21	16.13	49.06	1.00	-0.05	9400	26.15	4.23	25.49	15.23	58.69	1.00	-0.11
		Weight (kg)	9084	80.31	11.40	79.40	44.60	160.00	0.84	0.49	9400	67.75	11.64	66.00	36.00	139.20	0.89	0.35
		Height (m)	9084	1.74	0.07	1.74	1.39	2.00	-0.05	1.00	9400	1.61	0.06	1.61	1.29	2.00	-0.11	1.00
		WC (cm)	9073	95.72	9.73	95.10	61.00	180.00	0.84	0.15	9398	82.08	10.70	80.60	56.00	141.30	0.85	0.04
		Hip (cm)	9069	102.73	6.35	102.20	80.00	145.80	0.80	0.30	9391	103.32	9.01	102.00	39.00	160.00	0.88	0.18
		WHR (cm/cm)	9068	0.93	0.06	0.93	0.61	1.74	0.56	-0.05	9391	0.79	0.06	0.79	0.60	1.87	0.40	-0.12
FINRISK	Height, BMI, Weight, WC, WHR	Age (yrs)	3997	50.39	13.75	50.00	25.00	74.00	0.25	-0.37	3906	47.59	12.88	48.00	25.00	74.00	0.40	-0.35
		BMI (kg/m <sup>2</sup> )	3897	27.04	3.96	26.58	14.70	48.39	1.00	-0.13	3890	26.31	5.02	25.45	14.69	53.28	1.00	-0.21
		Weight (kg)	3897	83.10	13.07	81.60	40.50	150.00	0.83	0.39	3890	69.24	13.17	67.10	37.10	137.80	0.89	0.21
		Height (m)	3898	1.75	0.07	1.76	1.34	2.04	-0.13	1.00	3890	1.62	0.06	1.62	1.39	1.92	-0.21	1.00
		WC (cm)	3997	95.05	11.33	94.50	64.50	149.00	0.88	0.01	3906	81.83	12.34	80.00	58.00	133.50	0.91	-0.07
		Hip (cm)	3997	102.04	6.83	101.50	76.50	146.50	0.80	0.27	3906	101.77	9.19	100.50	69.50	159.00	0.88	0.07
		WHR (cm/cm)	3997	0.93	0.07	0.93	0.68	1.20	0.71	-0.18	3906	0.80	0.07	0.79	0.60	1.38	0.66	-0.18

FUSION T2D (Cases)	Height, BMI, Weight, WC, WHR	Age (yrs)	728	58.28	9.04	59.00	28.00	82.00	-0.12	-0.14	498	61.19	7.98	61.00	34.36	89.00	-0.12	-0.14
		BMI (kg/m <sup>2</sup> )	728	30.20	5.03	29.70	19.40	52.97	1.00	0.02	498	31.60	5.79	30.86	17.85	53.45	1.00	0.00
		Weight (kg)	728	92.48	17.20	90.00	42.20	167.00	0.89	0.43	498	81.23	16.10	78.90	48.00	143.50	0.93	0.35
		Height (m)	728	1.75	0.07	1.75	1.39	1.96	0.02	1.00	498	1.60	0.06	1.60	1.41	1.80	0.00	1.00
		WC (cm)	728	105.52	13.23	104.00	73.00	160.00	0.89	0.16	496	98.76	13.89	98.00	62.00	142.50	0.85	0.18
		Hip (cm)	728	106.28	9.73	105.00	74.00	164.00	0.85	0.24	496	110.73	11.74	109.00	84.00	147.50	0.91	0.16
		WHR (cm/cm)	728	0.99	0.07	0.99	0.72	1.23	0.56	0.02	496	0.89	0.07	0.89	0.61	1.15	0.31	0.12
		FUSION T2D (Controls)	Height, BMI, Weight, WC, WHR	Age (yrs)	1863	56.45	8.14	56.10	41.30	75.10	0.08	-0.15	1833	57.23	8.31	56.80	40.99	75.20
		BMI (kg/m <sup>2</sup> )	1863	26.81	3.94	26.40	15.78	93.00	1.00	0.04	1833	27.02	4.80	26.20	17.21	57.20	1.00	-0.14
		Weight (kg)	1863	82.27	12.92	81.00	46.50	146.60	0.86	0.50	1833	70.70	12.86	68.80	42.80	153.80	0.90	0.27
		Height (m)	1863	1.75	0.06	1.75	1.53	1.95	0.04	1.00	1833	1.62	0.06	1.62	1.32	1.81	-0.14	1.00
		WC (cm)	1859	95.94	10.57	95.00	56.60	155.00	0.86	0.22	1829	86.99	12.26	85.00	58.00	150.00	0.86	0.03
		Hip (cm)	1859	100.45	6.97	100.00	76.00	145.00	0.78	0.33	1829	102.53	9.55	101.00	72.00	150.50	0.88	0.09
		WHR (cm/cm)	1859	0.95	0.07	0.95	0.56	1.89	0.57	0.04	1829	0.85	0.07	0.84	0.47	1.29	0.52	-0.03
HUNT	Height, BMI, Weight, WC, WHR	Age (yrs)	2387	63.64	14.44	67.00	20.00	97.00	-0.03	-0.37	2477	66.52	14.21	71.00	20.00	92.00	0.05	-0.45
		BMI (kg/m <sup>2</sup> )	2387	27.02	3.64	26.60	16.30	45.60	1.00	0.01	2477	28.15	5.09	27.60	14.70	48.50	1.00	-0.10
		Weight (kg)	2387	82.51	12.94	81.50	43.40	139.00	0.85	0.50	2477	72.77	13.88	71.50	31.00	135.00	0.89	0.32
		Height (m)	2387	1.75	0.07	1.75	1.49	1.98	0.01	1.00	2477	1.61	0.06	1.61	1.37	1.84	-0.10	1.00
		WC (cm)	2380	94.74	9.88	94.00	69.00	136.00	0.80	0.15	2457	87.60	12.60	87.00	60.00	139.00	0.86	0.00
		Hip (cm)	2380	102.99	6.47	102.00	83.00	136.00	0.76	0.30	2456	105.61	10.55	104.00	80.00	150.00	0.88	0.07
		WHR (cm/cm)	2380	0.92	0.06	0.92	0.73	1.25	0.53	-0.04	2456	0.83	0.06	0.82	0.64	1.22	0.49	-0.10
		Inter99	Height, BMI, Weight, WC, WHR	Age (yrs)	3165	46.56	7.85	45.17	29.92	61.12	0.11	-0.22	3332	45.85	7.98	45.06	29.69	61.35
		BMI (kg/m <sup>2</sup> )	3165	26.82	4.02	26.32	16.73	56.90	1.00	-0.06	3331	25.81	5.09	24.68	14.93	55.75	1.00	-0.08
		Weight (kg)	3165	85.74	14.11	84.00	53.00	183.00	0.88	0.41	3331	71.07	14.68	68.50	36.80	159.30	0.93	0.30
		Height (m)	3165	1.79	0.07	1.79	1.54	2.07	-0.06	1.00	3332	1.66	0.06	1.66	1.29	1.88	-0.08	1.00
		WC (cm)	3165	93.20	11.03	92.00	53.00	180.00	0.89	0.14	3332	80.44	12.42	78.00	53.00	146.00	0.90	0.09
		Hip (cm)	3165	101.50	8.01	101.00	76.00	165.00	0.80	0.27	3332	100.60	11.35	99.00	63.00	174.00	0.89	0.14
		WHR (cm/cm)	3165	0.92	0.06	0.91	0.61	1.64	0.58	-0.07	3332	0.80	0.06	0.79	0.60	1.10	0.45	-0.03
KORA 2	Height, BMI, Weight, WC, WHR	Age (yrs)	1867	49.56	14.17	50.00	25.00	74.00	0.25	-0.45	1824	48.70	13.88	49.00	25.00	74.00	0.36	-0.40
		BMI (kg/m <sup>2</sup> )	1852	27.06	3.60	26.84	17.54	46.38	1.00	-0.15	1796	26.18	4.77	25.39	16.81	50.50	1.00	-0.26
		Weight (kg)	1852	81.71	12.00	80.20	45.20	150.00	0.83	0.43	1796	67.87	12.09	66.20	37.50	122.90	0.90	0.19
		Height (m)	1857	1.74	0.07	1.74	1.33	1.98	-0.15	1.00	1817	1.61	0.07	1.61	1.34	1.88	-0.26	1.00
		WC (cm)	1857	94.73	10.42	94.00	64.00	165.00	0.86	-0.03	1800	81.53	11.53	80.00	51.00	132.00	0.88	-0.16
		Hip (cm)	1857	102.77	7.09	102.50	78.00	143.00	0.77	0.21	1800	101.22	10.41	100.00	74.50	153.00	0.87	-0.02
		WHR (cm/cm)	1857	0.92	0.07	0.92	0.63	1.18	0.59	-0.25	1800	0.80	0.06	0.80	0.57	1.06	0.44	-0.26
		KORA 3	Height, BMI, Weight, WC, WHR	Age (yrs)	631	41.39	13.72	37.00	25.00	74.00	0.23	-0.38	693	41.15	12.88	38.00	25.00	74.00
		BMI (kg/m <sup>2</sup> )	626	26.59	3.43	26.21	17.59	40.99	1.00	-0.15	678	25.26	4.74	24.17	16.89	49.31	1.00	-0.25
		Weight (kg)	626	82.42	11.52	81.20	52.30	132.00	0.83	0.41	678	66.83	12.26	64.20	43.60	125.20	0.91	0.18
		Height (m)	630	1.76	0.07	1.76	1.55	2.00	-0.15	1.00	690	1.63	0.06	1.63	1.42	1.80	-0.25	1.00
		WC (cm)	630	92.99	9.32	92.00	70.50	127.00	0.85	-0.03	679	79.41	11.51	76.50	59.00	131.50	0.89	-0.14
		Hip (cm)	630	102.97	6.21	102.50	86.00	125.00	0.78	0.24	679	101.43	9.61	100.00	79.00	144.50	0.89	0.03
		WHR (cm/cm)	630	0.90	0.06	0.90	0.76	1.10	0.58	-0.26	679	0.78	0.06	0.77	0.63	1.05	0.52	-0.28
KORA 4	Height, BMI, Weight, WC, WHR	Age (yrs)	714	43.51	15.00	38.00	25.00	74.00	0.32	-0.47	788	42.19	13.96	37.00	25.00	74.00	0.29	-0.43
		BMI (kg/m <sup>2</sup> )	711	26.80	3.61	26.44	16.32	42.37	1.00	-0.23	775	26.01	5.05	25.33	15.84	49.15	1.00	-0.23
		Weight (kg)	711	83.12	11.64	82.40	52.30	136.50	0.83	0.35	775	68.97	13.32	67.10	41.10	137.00	0.90	0.20
		Height (m)	714	1.76	0.07	1.76	1.55	1.96	-0.23	1.00	783	1.63	0.07	1.63	1.39	1.89	-0.23	1.00
		WC (cm)	714	94.94	10.01	94.20	65.40	134.20	0.89	-0.11	775	82.50	11.99	80.90	60.20	141.50	0.91	-0.11
		Hip (cm)	714	104.27	6.54	103.85	87.10	136.20	0.82	0.19	775	103.87	9.89	102.50	82.10	146.20	0.91	0.04
		WHR (cm/cm)	714	0.91	0.06	0.91	0.72	1.07	0.62	-0.34	775	0.79	0.06	0.79	0.62	0.98	0.55	-0.26
		METSIM	Height, BMI, Weight, WC, WHR	Age (yrs)	8167	57.50	7.01	57.00	45.00	74.00	0.03	-0.26	NA	NA	NA	NA	NA	NA
		BMI (kg/m <sup>2</sup> )	8167	27.26	4.16	26.66	16.18	55.54	1.00	-0.04	NA	NA	NA	NA	NA	NA	NA	NA
		Weight (kg)	8167	84.39	14.00	83.00	43.00	174.00	0.87	0.41	NA	NA	NA	NA	NA	NA	NA	NA
		Height (m)	8167	1.76	0.06	1.76	1.47	2.03	-0.04	1.00	NA	NA	NA	NA	NA	NA	NA	NA
		WC (cm)	8166	98.71	11.47	97.00	66.00	167.00	0.88	0.14	NA	NA	NA	NA	NA	NA	NA	NA
		Hip (cm)	8165	101.31	7.10	100.50	72.00	160.00	0.78	0.30	NA	NA	NA	NA	NA	NA	NA	NA

		WHR (cm/cm)	8165	0.97	0.07	0.97	0.76	1.44	0.69	-0.05	NA	NA	NA	NA	NA	NA	NA	NA
NFBC1986	Height, BMI, Weight, WC, WHR	Age (yrs)	2642	16.00	NA	16.00	16.00	16.00	NA	NA	2728	16.00	NA	16.00	16.00	16.00	NA	NA
		BMI (kg/m <sup>2</sup> )	2634	21.54	3.98	20.77	11.07	44.66	1.00	-0.12	2718	21.00	3.57	20.46	10.36	46.94	1.00	-0.22
		Weight (kg)	2637	64.92	12.70	62.60	35.10	140.60	0.89	0.35	2721	57.23	9.90	55.40	34.70	123.20	0.88	0.26
		Height (m)	2634	1.74	0.08	1.74	1.46	1.98	-0.12	1.00	2719	1.65	0.07	1.65	1.32	1.98	-0.22	1.00
		WC (cm)	2627	75.94	9.22	73.80	48.00	129.20	0.87	0.19	2707	72.16	8.37	70.20	56.50	162.00	0.85	0.08
		Hip (cm)	2628	91.72	7.63	90.50	58.50	130.00	0.85	0.29	2718	93.06	7.17	92.00	42.00	161.50	0.81	0.20
		WHR (cm/cm)	2622	0.83	0.05	0.82	0.52	1.23	0.52	-0.03	2704	0.77	0.05	0.77	0.43	1.57	0.45	-0.08
OBB	Height, BMI, Weight, WC, WHR	Age (yrs)	745	41.10	5.50	42.00	29.00	53.00	0.10	-0.08	724	41.30	6.30	41.00	30.00	53.00	0.04	-0.03
		BMI (kg/m <sup>2</sup> )	745	26.70	3.90	26.20	15.30	46.20	1.00	-0.07	724	26.70	3.90	26.20	15.30	46.20	1.00	-0.12
		Weight (kg)	745	84.80	13.80	83.10	44.70	172.10	0.87	0.42	724	69.20	13.10	66.50	43.50	127.90	0.92	0.29
		Height (m)	745	1.78	0.07	1.78	1.50	2.03	-0.07	1.00	724	1.65	0.07	1.65	0.83	1.82	-0.12	1.00
		WC (cm)	745	93.60	11.40	92.00	61.00	186.00	0.86	0.13	724	81.30	11.20	79.00	60.00	146.00	0.87	0.06
		Hip (cm)	745	101.30	7.00	100.00	69.00	129.00	0.81	0.30	724	101.00	9.70	100.00	64.00	156.00	0.87	0.07
		WHR (cm/cm)	745	0.92	0.08	0.92	0.73	1.98	0.57	-0.08	724	0.80	0.07	0.79	0.66	1.33	0.40	-0.07
R58	Height, BMI, Weight, WC, WHR	Age (yrs)	683	45.30	0.36	45.42	44.25	46.00	-0.03	0.01	657	45.33	0.34	45.42	44.25	46.00	-0.02	-0.01
		BMI (kg/m <sup>2</sup> )	683	27.26	4.11	26.69	18.06	43.05	1.00	-0.05	657	27.64	5.47	26.50	14.34	1.42	1.00	-0.08
		Weight (kg)	683	85.54	14.14	84.00	55.60	145.00	0.83	0.44	657	71.97	15.10	69.30	40.00	127.00	0.91	0.26
		Height (m)	683	1.76	0.07	1.76	1.58	1.98	-0.05	1.00	657	1.63	0.06	1.63	1.42	1.83	-0.08	1.00
		WC (cm)	649	97.50	10.92	96.10	65.40	142.80	0.82	0.19	632	85.87	12.88	84.25	56.20	125.30	0.89	0.11
		Hip (cm)	649	104.86	7.06	104.20	87.10	142.90	0.75	0.33	632	105.54	11.31	103.95	79.20	149.50	0.90	0.12
		WHR (cm/cm)	649	0.93	0.06	0.93	0.71	1.17	0.62	-0.02	632	0.81	0.06	0.81	0.58	1.05	0.49	0.05

\* Study contributed only for Waist circumference

~ Study contributed only for Waist circumference

† Study contributed only for Hip circumference



## Supplementary Table 9: Study-specific genotyping platforms, imputation methods, SNP quality control, and software for statistical analysis

Cohort	Genotyping					Imputation				Association analyses					
	Platform	Genotype calling	MAF	Inclusion criteria Call rate*	p for HWE	SNPs that met QC criteria	Software	MAF	Inclusion criteria Imputation quality	SNPs in meta-analysis	λ			Software	
<b>Discovery Stage</b>															
ADVANCE (Cases)**	Illumina 550k	BeadStudio	none	≥ 98.5%	> 10 <sup>-3</sup>	543,985	BIMBAM	>0%	none	NA	NA	NA	NA	SNPTEST	
ADVANCE (Controls)**	Illumina 550k	BeadStudio	none	≥ 98.5%	> 10 <sup>-3</sup>	543,985	BIMBAM	>0%	none	NA	NA	NA	NA	SNPTEST	
AGES Reykjavik~	Illumina Human370CNV	BeadStudio	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	308,340	MACH	>0%	r2-hat ≥ 0.30	NA	NA	NA	NA	ProbABEL	
Amish	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	338,598	MACH	>0%	rsqr>=0	2,291,092	1.033	1.019	1.059	MIMAP	
ARIC	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	≥ 1%	≥90%	>10 <sup>-6</sup>	685,812	MACH v1.0.16	NOTE: SNPs used for imputation had: HWE p>1e-05, MAF>0.01, and were >95% complete			2,511,301	NA	1.009	1.007	ProbABEL
B58C (T1DGC)	Illumina HumanHap 550 V.1	ILLUMINUS	> 0%	none	none	539,458	MACH	>0%	r2-hat ≥ 0.30	2,507,988	NA	1.009	0.997	ProbABEL	
B58C (WTCCC)	Affymetrix GeneChip Human Mapping 500K	CHIAMO	>0%	none	none	392,575	IMPUTE	>0%	proper-info ≥ 0.40	2,448,428	NA	1.01	1.005	SNPTEST	
BRIGHT	Affymetrix GeneChip Human Mapping 500K	CHIAMO	≥5%	≥ 95%	> 10 <sup>-6</sup>	387,666	IMPUTE	>0%	proper-info ≥ 0.40	2,429,136	NA	1.009	0.993	SNPTEST	
CHS	Illumina 370-CNV	BeadStudio		>97%	> 10 <sup>-5</sup>	306,655	BimBam	>0%	≥ 0.30	2,191,645	NA	1.034	1.007	R	
CoLauS	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥ 1%	≥ 70%	> 10 <sup>-7</sup>	390,631	IMPUTE	>0%	r2-hat ≥ 0.30	2,479,491	NA	1.008	1.004	QUICKTEST	
deCODE	Illumina HumanHap300 or HumanHapCNV370	BeadStudio	≥ 1%	≥ 96%	> 10 <sup>-6</sup>	290,447	IMPUTE	>0%	proper-info ≥ 0.40	2,453,316	0.999	1.006	1	SNPTEST	
DGI (Cases)	Affymetrix 500K Array Set	BRLMM	> 5%	≥ 95%	> 10 <sup>-6</sup>	347,010	MACH	≥1%	r2-hat ≥ 0.30	2,394,620	1.029	1.037	1.041	MACH2QTL	
DGI (Controls)	Affymetrix 500K Array Set	BRLMM	> 5%	≥ 95%	> 10 <sup>-6</sup>	347,010	MACH	≥1%	r2-hat ≥ 0.30	2,359,151	1.029	1.024	1.01	MACH2QTL	
EGCUT	Illumina Beadarray Human370CNV	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	299,484	IMPUTE	≥ 1%	proper-info ≥ 0.40	2,429,620	NA	1.033	1.008	SNPTEST	
EPIC-Obesity Study	Affymetrix GeneChip Human Mapping 500K	BRLMM	≥ 1%	≥ 90%	> 10 <sup>-6</sup>	397,438	IMPUTE	>0%	proper-info ≥ 0.40	2,420,624	NA	0.998	1.017	SNPTEST	
ERF (EUROSPAN)	Illumina 318K, 370K, Affymetrix 250K	BRLMM, BeadStudio	>0.5%	> 95%	> 10 <sup>-6</sup>	NA	MACH	>0%	r2-hat ≥ 0.30	2,463,910	1.028	1.009	1.017	ProbABEL	
Fenland	Affymetrix SNPs.0	BRLMM	≥ 1%	≥ 90%	> 10 <sup>-6</sup>	362,055	IMPUTE	>0%	proper-info ≥ 0.40	2,407,059	NA	1.008	1.009	SNPTEST	
FHS (Cases)	Illumina 1Million GeneChip	BeadStudio	≥1%	≥ 98%	> 10 <sup>-6</sup>	874,830	MACH	≥1%	r2-hat ≥ 0.30	2,473,344	1.024	1.002	1.046	SAS	
FHS (Controls)	Illumina 1Million GeneChip	BeadStudio	≥1%	≥ 98%	> 10 <sup>-6</sup>	874,830	MACH	≥1%	r2-hat ≥ 0.30	2,470,979	1.002	1.01	0.982	SAS	
FRAM	Affymetrix 500K	BRLMM	≥ 1%	≥ 97%	> 10 <sup>-6</sup>	378,163	MACH v1.0.15	>1%	RATIO>= 0.3	2,511,291	1.014	1.011	1.008	R	
	Affymetrix 50K supplemental														
FTC	Illumina HumanHap 318K	BeadStudio	≥ 1%	≥ 90%	> 10 <sup>-6</sup>	304,582	MACH	>0%	r2-hat ≥ 0.30	2,273,661	NA	NA	1.005	ProbABEL	
FUSION (Cases)	Illumina Infinium™ II HumanHap300 BeadChip	BeadStudio	> 1%	≥ 90%	≥ 10 <sup>-6</sup>	315,635	MACH	> 5%	r2-hat ≥ 0.30	2,466,546	1.08	0.993	1.006	MACH2QTL	
FUSION (Controls)	Illumina Infinium™ II HumanHap300 BeadChip	BeadStudio	> 1%	≥ 90%	≥ 10 <sup>-6</sup>	315,635	MACH	> 5%	r2-hat ≥ 0.30	2,466,546	1.112	1.002	1.027	MACH2QTL	
GENMETS (Cases)	Illumina HumanHap 610K	ILLUMINUS	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	555,388	MACH	>0%	r2-hat ≥ 0.30	2,482,249	NA	1.006	1.02	ProbABEL	
GENMETS (Controls)	Illumina HumanHap 610K	ILLUMINUS	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	555,388	MACH	>0%	r2-hat ≥ 0.30	2,482,698	NA	1.016	1.011	ProbABEL	
KORA S3	Affymetrix 500K	BRLMM	none	none	none	490,032	MACH v1.0.9	≥1%	r2-hat ≥ 0.30	2,415,072	NA	0.995	0.997	MACH2QTL	
KORA S4	Affymetrix 6.0	Birdseed	none	none	none	909,622	IMPUTE v0.4.2	≥1%	proper-info ≥ 0.40	2,480,938	NA	0.997	1.009	SNPTEST	
MICROS	ILLUMINA318K	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	318,237	MACH 1.0	>0%	r2-hat ≥ 0.30	2,396,452	0.996	0.988	0.999	ProbABEL	
NFBC1966	Illumina HumanCNV-370DUO Analysis BeadChip	Illumina BeadStudio	≥ 5%	≥ 95%	> 10 <sup>-4</sup>	328,007	IMPUTE	>0%	proper-info ≥ 0.40	2,460,379	NA	1.02	0.991	SNPTEST	
NHS	Illumina HumanHap550	Illumina BeadStudio	≥ 1%	≥ 90%	none	510,073	MACH	≥ 1%	r2-hat ≥ 0.30	2,520,546	NA	NA	0.996	MACH2QTL	
NSPHS †	ILLUMINA318K	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	318,236	MACH 1.0	>0%	r2-hat ≥ 0.30	NA	NA	NA	NA	ProbABEL	
NTRNESDA (Cases)	Perlegen - Affymetrix gene chip 600K	Proprietary Perlegen	>1%	≥ 95%	none	435,291	IMPUTE	≥1%	proper-info ≥ 0.40	2,490,448	NA	1.004	0.987	SNPTEST	
NTRNESDA (Controls)	Perlegen - Affymetrix gene chip 600K	Proprietary Perlegen	>1%	≥ 95%	none	435,291	IMPUTE	≥1%	proper-info ≥ 0.40	2,489,532	NA	1.009	1.002	SNPTEST	
ORCADES	ILLUMINA318K	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	318,235	MACH 1.0	>0%	r2-hat ≥ 0.30	2,434,147	0.993	0.99	0.99	ProbABEL	
PROCARDIS	HumanHap300 BeadChips	Illumina BeadStudio 2.0	> 5%	≥ 95%	>5x10 <sup>-7</sup>	~820k	IMPUTE	>0%	proper-info ≥ 0.40	2,580,770	NA	1.01	1.007	SNPTEST	
RS1	Illumina / HumanHap 550K V.3 ADHumanHap 550 V.3 DUO;	BeadStudio Genecall	≥ 1%	≥ 97.5%	> 10 <sup>-6</sup>	512,349	MACH	≥1%	(O/E)o2 ratio ≥ 0.1 r2-hat ≥ 0.30	2,488,215	NA	1.006	1.039	MACH2QTL	
SARDINIA	Affymetrix 500K and Affymetrix 10K	BRLMM	≥ 5%	≥ 90%	> 10 <sup>-6</sup>	356,359	MACH	>0%	r2-hat ≥ 0.30	2,251,689	1.163	1.11	1.104	Merlin	
SHIP	Affymetrix Human SNP Array 6.0	Birdseed V2	≥ 0%	≥ 0%	≥ 0%	869,224	IMPUTE v0.5.0	>0%	proper-info ≥ 0.40	2,609,015	NA	1.01	1.003	SNPTEST v1.1.5 ; nforSense	
T2D_WTCCC	Affymetrix GeneChip Human Mapping 500K	CHIAMO	>5%	≥ 95%	> 10 <sup>-6</sup>	387,667	IMPUTE	>0%	proper-info ≥ 0.40	2,425,374	NA	1.008	1.001	SNPTEST	
TwinsUK	Illumina / HumanHap 300 & 550	ILLUMINUS	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	295,702	IMPUTE	≥1%	proper-info ≥ 0.40	2,460,943	NA	NA	1.004	SNPTEST	
VIS	ILLUMINA318K	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	317,465	MACH 1.0	>0%	r2-hat ≥ 0.30	2,423,222	0.993	0.99	0.985	ProbABEL	
<b>Follow-up Stage</b>															
<b>In silico follow-up studies</b>															
BHS	Illumina Human 610-Quad	ILLUMINUS	≥ 1%	≥ 95%	> 5.7x10 <sup>-7</sup>	549,294	MACH	≥1%	r2-hat ≥ 0.30	664	NA	NA	NA	R	
Corogene	Illumina BeadChip Human 610-Quad	ILLUMINUS	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	554,988	MACH	≥1%	r2-hat ≥ 0.30	663	NA	NA	NA	PLINK	

EGCUT	Illumina Beadarray Human370CNV	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	316,924	IMPUTE	≥ 1%	proper-info ≥ 0.30	662	NA	NA	NA	SNPtest
FHS	Illumina 1Million GeneChip	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	874,830	MACH-1.0.16	≥ 1%	r2-hat ≥ 0.30	665	NA	NA	NA	SAS
GOOD	Illumina Infinium HumanHap 610K	BeadStudio	≥ 1%	≥ 98%	> 10 <sup>-6</sup>	521,160	MACH	>0%	r2-hat ≥ 0.30	664	NA	NA	NA	MACH2QTL
HBCS	Illumina custom made BeadChip Human 670-Quad	Illuminus	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	533491	MACH	≥ 1%	r2-hat ≥ 0.30	663	NA	NA	NA	PLINK
NHS	Affymetrix Genome-Wide Human 6.0 array	Birdseed calling algorithm v2	≥ 2%	≥ 98%	> 10 <sup>-4</sup>	704,409	MACH	≥ 2%	r2-hat ≥ 0.30	392	NA	NA	NA	ProbABEL
RS-II	Illumina / HumanHap 550 V.3 DUO; Illumina / HumanHap 610 QUAD	Genomestudio GeneCall	≥ 1%	≥ 97.5%	> 10 <sup>-6</sup>	466,389	MACH V.1.05	≥ 1%	(O/E)σ2 ratio ≥ 0.1 r2-hat ≥ 0.30	664	NA	NA	NA	MACH2QTL
SORBS	500K Affymetrix GeneChip (250K Sty and 250K Nsp arrays, Affymetrix, Inc) and Affymetrix Genome-Wide Human SNP Array 6.0	BRLMM algorithm (Affymetrix, Inc) for 500K and Birdseed Algorithm for Genome-Wide Human SNP Array 6.0	≥ 1%	≥ 95%	> 10 <sup>-4</sup>	378,513	IMPUTE	>1%	proper-info > 0.40	650	NA	NA	NA	SNPTEST
WGHS	Illumina HumanHap300 Duo "+"	Beadstudio v 3.3	NA	≥ 90%	> 10 <sup>-6</sup>	339,596	MACH	>0%	r2-hat ≥ 0.30	663	NA	NA	NA	R
YFS	Illumina custom made BeadChip Human 670-Quad	Illuminus	≥ 1%	≥ 95%	> 10 <sup>-6</sup>	546,674	MACH	≥ 1%	r2-hat ≥ 0.30	663	NA	NA	NA	PLINK
<b>De-novo follow-up studies</b>														
BCG	KASPAR (Kbiosciences)	NA		> 90%	> 10 <sup>-3</sup>	NA	NA	NA	NA	NA	NA	NA	NA	STATA 10
BPPP	1.iPLEX™ Sequenom MassARRAY®	NA		≥ 95%	> 10 <sup>-6</sup>	NA	NA	NA	NA	NA	NA	NA	NA	PLINK
BWHHS	KASPAR (Kbiosciences)	NA		>90%	> 10 <sup>-3</sup>	NA	NA	NA	NA	NA	NA	NA	NA	STATA 10
DESIR	SNPkex, Applied biosystems, Foster City, CA, USA	NA		≥ 95%	> 10 <sup>-6</sup>	NA	NA	NA	NA	NA	NA	NA	NA	R
DIAGEN	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 88%	> .005	NA	NA	NA	NA	NA	NA	NA	NA	Merlin
EGCUT	Custom TaqMan® SNP Genotyping Assays (Applied Biosystems, Warrington, UK)	NA		≥ 90%	> 10 <sup>-3</sup>	NA	NA	NA	NA	NA	NA	NA	NA	PLINK
EPIC-Norfolk	1. Custom TaqMan® SNP Genotyping Assays (Applied Biosystems, Warrington, UK) 2. Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 95%	> 10 <sup>-6</sup>	NA	NA	NA	NA	NA	NA	NA	NA	SAS
FINRISK	iPLEX™ Sequenom MassARRAY®	NA		≥ 95%	> 10 <sup>-6</sup>	NA	NA	NA	NA	NA	NA	NA	NA	PLINK
FUSION T2D (Cases)	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 94%	>.03	NA	NA	NA	NA	NA	NA	NA	NA	Merlin
FUSION T2D (Controls)	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 94%	>.03	NA	NA	NA	NA	NA	NA	NA	NA	Merlin
HUNT2	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 92%	> .005	NA	NA	NA	NA	NA	NA	NA	NA	Merlin
Inter99	Kbioscience allele-specific PCR (KASPar) (Kbioscience, Hoddesdon, UK)	NA		≥ 95%	> 10 <sup>-6</sup>	NA	NA	NA	NA	NA	NA	NA	NA	R
KORA2	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 90%	> =.001	NA	NA	NA	NA	NA	NA	NA	NA	R
KORA3	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 90%	> =.001	NA	NA	NA	NA	NA	NA	NA	NA	R
KORA4	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 90%	> =.001	NA	NA	NA	NA	NA	NA	NA	NA	R
METSIM	Sequenom MassARRAY® system ((Sequenom, San Diego, USA)	NA		≥ 94%	> .005	NA	NA	NA	NA	NA	NA	NA	NA	Merlin
NFBC1986	SNPkex, Applied biosystems, Foster City, CA, USA	NA		≥ 95%	≥ 10 <sup>-6</sup>	NA	NA	NA	NA	NA	NA	NA	NA	R
OBB	Custom TaqMan® SNP Genotyping Assays (Applied Biosystems, Warrington, UK)	NA		≥ 90%	> 10 <sup>-3</sup>	NA	NA	NA	NA	NA	NA	NA	NA	SNPTEST
R58	Custom TaqMan® SNP Genotyping Assays (Applied Biosystems, Warrington, UK)	NA		≥ 90%	> 10 <sup>-3</sup>	NA	NA	NA	NA	NA	NA	NA	NA	SNPTEST

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

\*\* Study contributed only for Waist circumference

~Study contributed only for Waist circumference

† Study contributed only for Hip circumference

**Supplementary Table 10: SNPs with  $P < 1.00E-05$  in the WHR discovery analysis beyond those already given in Table 1, which were used in pathway analyses.**

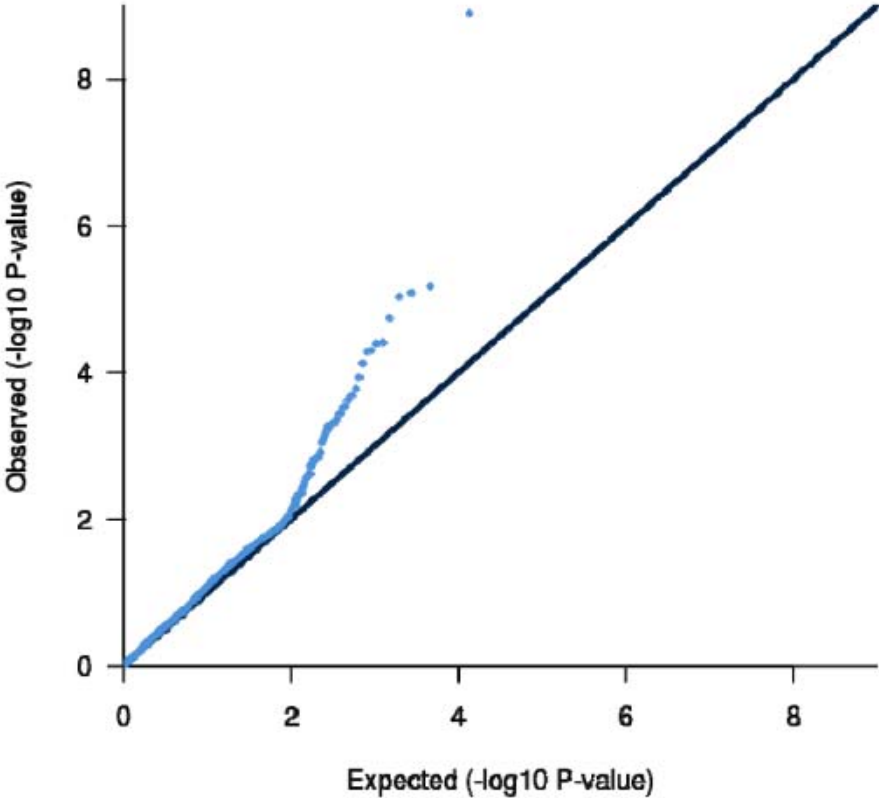
SNP	Chr	Position (b36)	Nearest gene	Effect Allele <sup>a</sup>	EAF <sup>b</sup>	Discovery P	Discovery Beta
rs2148150	1	119,373,580	WARS2	G	0.297	1.17E-09	0.034
rs4580892	6	127,451,575	RSPO3	T	0.294	2.35E-09	0.032
rs6701231	1	119,297,184	TBX15	G	0.633	4.13E-09	0.029
rs987763	6	127,323,240	RSPO3	C	0.413	2.37E-07	0.026
rs11154370	6	127,209,284	RSPO3	T	0.958	4.40E-07	0.068
rs1034207	6	127,379,392	RSPO3	C	0.917	8.62E-07	0.063
rs402443	8	60,080,758	TOX	A	0.918	1.01E-06	0.044
rs4959406	6	6,729,139	LY86	A	0.544	1.04E-06	0.034
rs4785963	16	4,424,397	DNAJA3	A	0.272	1.41E-06	0.026
rs2494192	1	217,815,884	SLC30A10	G	0.806	1.51E-06	0.029
rs13226446	7	116,675,397	ST7	G	0.931	1.64E-06	0.048
rs16863031	1	168,337,451	KIFAP3	A	0.080	1.89E-06	0.044
rs9756317	3	53,063,855	SFMBT1	C	0.095	2.27E-06	0.039
rs17185996	1	119,410,255	WARS2	C	0.855	2.43E-06	0.033
rs12502605	4	25,640,626	C4orf52	C	0.817	2.57E-06	0.029
rs758801	3	52,511,348	STAB1	C	0.136	2.68E-06	0.036
rs3768	12	123,065,792	ZNF664	C	0.192	2.80E-06	0.031
rs2997447	1	26,260,010	TRIM63	G	0.214	2.91E-06	0.029
rs4646404	17	17,360,924	PEMT	G	0.349	3.07E-06	0.027
rs7251505	19	38,494,382	LOC80054	G	0.102	3.21E-06	0.040
rs164637	3	52,240,255	TWF2	G	0.057	3.46E-06	0.051
rs1687721	10	27,984,392	MKX	T	0.444	3.67E-06	0.022
rs2301573	3	130,788,609	PLXND1	T	0.906	3.68E-06	0.038
rs646984	6	32,684,570	HLA-DRB1	C	0.381	3.93E-06	0.025
rs1010553	3	52,515,813	STAB1	C	0.535	4.45E-06	0.022
rs7258031	19	38,578,194	PEPD	T	0.333	5.10E-06	0.023
rs11238863	10	43,927,432	CXCL12	G	0.803	5.51E-06	0.028
rs13395694	2	66,062,304	MEIS1	A	0.141	6.18E-06	0.033
rs7522839	1	119,344,378	TBX15	G	0.061	6.82E-06	0.056
rs4708871	6	160,889,086	LPA	T	0.959	6.85E-06	0.095
rs10919298	1	168,330,968	KIFAP3	T	0.573	9.24E-06	0.022
rs1930538	1	168,597,397	LOC284688	T	0.725	9.88E-06	0.024

P-values and beta-coefficients (per change of WHR increasing allele) for WHR association in the discovery meta-analysis (up to 77,167 subjects) for the 32 SNPs with discovery  $P < 1.00E-05$  beyond those 16 SNPs already given in **Table 1** (HapMap  $r^2 < 0.2$ ). These were used in the PANTHER and GRAIL analysis (details see **Supplementary Note**).

<sup>a</sup> WHR increasing allele on the forward strand; <sup>b</sup> Effect allele frequency; <sup>c</sup> Only 34,531 subjects in the discovery analysis

**Supplementary Table 11: uploaded as .xls**

**Supplementary Figure 1: Copy-Number-Variation analyses:** QQ plot for the *P*-values of the association of 6,018 CNV tagging SNPs with WHR. *P*-value are GC corrected.



## SUPPLEMENTARY NOTE

### ***Testing for gender difference***

For each SNP, the pooled men-specific beta estimate  $b_m$  was tested for difference from the women-specific beta estimate  $b_w$  using the T-statistic

$$(b_m - b_w) / (\text{se}_m^2 + \text{se}_w^2 - 2 \cdot \text{corr}(b_m, b_w) \cdot \text{se}_m \cdot \text{se}_w)$$

with  $\text{se}_m$  and  $\text{se}_w$  being the standard errors of  $b_m$  or  $b_w$ . The correlation between the sex-specific beta estimates was estimated using the sex-specific beta estimates across all SNPs in the discovery studies and approximated by zero in the replication studies.

### ***Percentage of variance explained***

We computed the percentage of the variance of the analyzed trait WHR that is explained by one SNP based on the SNP's effect size from the BMI-adjusted RAW phenotype analyses in the follow-up studies' meta-analysis (beta), the average effect allele frequency (EAF), and related the effect size to the variance (var) of the age- and BMI-adjusted WHR in KORA-S3 (n=3996) according to Rosner B<sup>6</sup>. Hence, this percentage computed as  $2 \cdot \text{EAF} \cdot (1 - \text{EAF}) \cdot (\text{beta}^2 / \text{var})$  represents the portion of the age- and BMI-adjusted WHR variance explained by one SNP in a population like KORA.

### ***Evaluation of potential sources of heterogeneity***

We found low between-study heterogeneity for 12 of the 14 SNP associations with WHR ( $I^2 < 30\%$ ) but moderate heterogeneity at the *GRB14* ( $I^2 = 41\%$ ) and the *LYPLAL1* locus ( $I^2 = 53\%$ ).

The heterogeneity disappeared in men-only analyses ( $I^2 = 4\%$  and  $22\%$ ), which is in line with the fact that these two SNPs showed association mainly in

women (**Table 2**) and that heterogeneity can only appear when association is present. However, the fact that the  $I^2$  values only slightly reduced when restricting to women ( $I^2 = 37\%$  or  $43\%$ , respectively) indicates that sex does not fully explain the heterogeneity.

In order to investigate the sources of this heterogeneity, we checked whether the  $I^2$  values differed between studies with mean age of subjects  $> 50$  years versus mean age  $\leq 50$  years, or between studies with more Northern European origin of study subjects (Finland, Sweden, United Kingdom, Estonia) versus more Central/Southern (Netherlands, France, Germany, Austria, Croatia, Italy) excluding studies from the U.S.A.. We found no differences of  $I^2$  values across strata. Therefore, in our data, the source of heterogeneity of these two loci associations with WHR remains elusive.

### ***BMI as modifier of the SNP association with WHR***

In a substantial subset of our follow-up data (N up to 32,127), we investigated whether BMI modified the SNP-association with WHR by adding a SNP\*BMI interaction term to the linear regression model. We only found evidence of BMI interaction ( $P$  of interaction  $> 0.004 = 0.05/14$ ) at the *LY86* locus ( $P=9.5 \times 10^{-5}$ ) with higher WHR association estimates among obese compared to normal subjects: e.g. for individuals with BMI of  $40 \text{ kg/m}^2$ , the increase in WHR per effect allele was 0.111 (on the same scale as in **Table 1**) as compared to -0.039 for subjects with a BMI of  $20 \text{ kg/m}^2$ .

### ***PANTHER analysis***

For the pathway analysis we selected 680 SNPs from the discovery WHR meta-analysis with  $P < 1 \times 10^{-5}$  and that had genotype information (typed or imputed)

in more than 50% of the discovery individuals, which resulted in 48 independent SNP according to an  $r^2 < 0.2$  of Hap Map CEU including our 14 WHR loci per definition. **Supplementary Table 10** shows the WHR associations of those 32 SNPs that are not already given in **Table 1**. We defined a 0.2 cM interval centered on the SNP based on the Oxford CEU recombination map and selected all genes (identified by Entrez gene IDs) that overlapped with the interval. Genes mapping to the MHC region were excluded due to high density of related genes in that region. For intervals with no overlapping genes we included the nearest gene to the index SNP regardless of the distance.

Of these 95 selected genes, 89 were included in the PANTHER database of 25,431 genes and this subset was tested for correlation with 240 biological processes classified in the database<sup>7</sup>.

For each biological process, the difference between the observed fraction of genes in the WHR associated regions and what was expected by chance was tested using a Fisher exact test. To adjust for potential bias in the selection of genes and for testing of the many biological processes, we constructed 2,500 random sets of 48 autosomal SNPs that were matched to the original SNP set on frequency, distance to the nearest gene and size of the nearest gene. For each random set of SNPs, we repeated the process of selecting genes and testing for correlation with all the 240 biological processes. Based on the results from the 2,500 simulated sets, we adjusted the original  $P$  value associated with each biological process in two ways: First, we calculated an adjusted  $P$  value,  $P_{adj-I}$ , for each biological process separately as the fraction of simulated sets that produced a  $P$  value for the same process that was equal or lower than the original  $P$  value. Second, we calculated a further adjusted  $P$  value (adjusting for the 240 biological processes tested),  $P_{adj-II}$ ,

as the fraction of simulated sets that produced a  $P$  value for any process that was equal or lower than the original  $P$  value.

### **Summary of Literature Research on Genes nearest to the 14 WHR loci**

1. **Chromosome 1p12:** T-box 15 (***TBX15***) is a transcription factor that has been reported to be up-regulated in subcutaneous fat compared to intra-abdominal adipocytes, with expression levels closely correlated with the pattern of fat distribution (WHR) as well as overall obesity (BMI)<sup>8</sup>. ***TBX15*** may be involved in embryonic development, pattern specification, adipocyte development, and specific adipose depot development underlying variation in fat distribution.<sup>8</sup> Further, ***TBX15*** is implicated in Cousin syndrome, an autosomal recessive disorder characterized by congenital dwarfism, facial dysmorphism, and skeletal anomalies,<sup>9</sup>, phenotypes largely supported by animal models<sup>10,11</sup>. ***WARS2*** is a mitochondrial tryptophanyl-tRNA synthetase.

2. **Chromosome 1q24.3:** Dynamin 3 (***DNM3***) is a member of the dynamin family of enzymes that are important for interactions between the cell membrane and actin cytoskeleton<sup>12</sup>. Dominant negative mutations in transfected dynamin enzymes promote GLUT6 and GLUT8 glucose transporters to the cell surface in cultured rat adipocytes *in vitro*<sup>13</sup>. Phosphatidylinositol glycan anchor biosynthesis, class C (***PIGC***) encodes a subunit of the enzyme that transfers N-acetylglucosamine to phosphatidylinositol, the first step of glycosylphosphatidylinositol (GPI) lipid anchor biosynthesis. GPI anchors many proteins to the cell membrane<sup>14,15</sup>. Fas ligand (***FASLG***) interacts with FAS to triggers apoptosis in some cell types<sup>16</sup>. Additional nearby genes include ***C1orf105*** and ***C1orf9***.

3. **Chromosome 1q41:** rs4846567 lies in an intergenic region and is more than 330 kb away from the two nearest known genes. ***LYPLAL1*** encodes the



lysophospholipase-like 1 protein, which is thought to act as a triglyceride lipase and is reported to be up-regulated in subcutaneous adipose tissue of obese subjects<sup>17</sup>. Solute carrier family 30, member 10 (**SLC30A10**) belongs to a family of membrane transporters involved in intracellular zinc homeostasis and is expressed in brain and liver<sup>18</sup>. Family member *SLC30A8* is a type 2 diabetes risk-locus<sup>19</sup>.

4. **Chromosome 2q24.3:** Growth factor receptor-bound protein 14 (**GRB14**) is a member of a family of SH2-containing adaptors and binds directly to the insulin receptor<sup>20,21</sup>. *Grb14*-deficient mice exhibit enhanced body weight, mainly explained by increased lean mass on normal diet<sup>22</sup>, improved glucose homeostasis despite lower circulating insulin levels, and enhanced insulin signaling in liver and skeletal muscle<sup>23</sup>. *Grb14* expression is increased in adipose tissue of insulin-resistant animal models and type 2 diabetic human patients,<sup>24</sup> suggesting that *Grb14* may modulate insulin sensitivity. Cordon-bleu protein-like 1 (**COBLL1**) may be involved in neural tube formation<sup>25</sup>. The WHR signal is distinct from a locus previously associated with smoking initiation and current smoking (rs4423615,  $D'=0.01$ ,  $r^2<.01$ , HapMap CEU)<sup>26</sup>.

5. **Chromosome 3p21.1:** Nischarin is encoded by **NISCH** and interacts with insulin receptor substrate 4<sup>27</sup>, which is phosphorylated by the insulin receptor tyrosine kinase upon receptor stimulation in kidney cells<sup>28</sup> but has also been reported to play a redundant role in insulin receptor signaling<sup>29</sup>. Other nearby genes include troponin C type 1 (**TNNC1**), semaphoring 3G (**SEMA3G**), which is highly expressed in adipocytes<sup>30</sup>, stablin 1 (**STAB1**), which is a scavenger receptor that plays a role in intracellular trafficking<sup>31</sup>, 5'-nucleotidase domain containing 2 (**NT5DC2**), PHD finger protein 7 (**PHF7**), *BRCA1* associated protein-1 (**BAP1**), which helps regulate cell growth and proliferation<sup>32</sup>, hypothetical protein (**LOC440957**), polybromo 1 (**PBRM1**), glycerate kinase (**GLYCTK**), and dynein axonemal heavy chain 1 (**DNAH1**). *Mdhc7*

null male mice (homologous to *DNAH1*) are infertile due to decreased sperm motility<sup>33</sup>.

6. **Chromosome 3p14.1:** SNP rs6795735 is located upstream of zinc-dependent protease ***ADAMTS9***. It is a member of the *ADAMTS* family, a group of genes encoding metalloproteases that lack transmembrane domains and are secreted into the extracellular matrix<sup>34</sup>. *ADAMTS9* is associated with type 2 diabetes<sup>5</sup>, possibly mediated through decreased insulin sensitivity of peripheral tissues<sup>35</sup>. The index SNP is also located in noncoding RNA ***BC040632*** and within 400 bp of the start of microRNA-***548a-2***.

7. **Chromosome 5q35.2:** Cytoplasmic polyadenylation element binding protein ***CPEB4*** promotes polyadenylation-induced translation. CPEB nucleates a complex of factors that regulate polyadenylation elongation through a deadenylating enzyme and mediate many processes including germ-cell development, cell division and cellular senescence and synaptic plasticity<sup>36</sup>. Other nearby protein-coding genes include ***C5orf47*** and ***HMP19***.

8. **Chromosome 6p25.1:** The closest known protein-coding gene is lymphocyte antigen 86 (***LY86***), which plays a role in recognition of lipopolysaccharide via the Toll-like receptor pathway when bound as a heterodimer with RP105. It has been associated with asthma and has been suggested to play a role along with RP105 in autoimmune diseases<sup>37,38</sup>. The lead SNP (rs1294421) is closely correlated ( $r^2=0.9845$ ) with a 2,832 bp CNV at the *LY86* locus, CNVR2760.1. The closest transcripts to this CNV are noncoding RNA *BC039678* (12 kb centromeric) and *LY86* (87 kb centromeric).

9. **Chromosome 6p21.1:** Multiple variants and mutations in vascular endothelial growth factor A (***VEGFA***) are risk factors for diabetic retinopathy<sup>19,39,40</sup>. Variants in *VEGFA* have been nominally associated with T2D.<sup>5</sup> *VEGFA* is proposed as a key

mediator of adipogenesis and angiogenesis<sup>41</sup>, is highly expressed in adipose tissue, and has increased expression during adipocyte differentiation<sup>42-45</sup>. VEGFA serum concentrations are elevated in overweight and obese patients compared with lean subjects<sup>46</sup> and decrease after weight loss following bariatric surgery, behaving similarly to other hormones related to adipose mass, such as leptin and insulin<sup>47</sup>.

10. **Chromosome 6q22.33:** R-spondin 3 homolog (**RSPO3**) encodes a secreted protein that regulates beta-catenin signaling<sup>48</sup>. RSPO3 promotes angiogenesis and vascular development<sup>49</sup>. *Rspo3* knockout mice die due to defects in placental development<sup>50</sup>, and *Rspo3* is required for *Vegf* expression and endothelial cell proliferation<sup>49</sup>. *Rspo3* has also been shown to be an oncogene in mouse mammary epithelial cells<sup>51</sup>. rs9491696 is also located within 160kb of ring finger 146 (**RNF146**) and enoyl Coenzyme A hydratase domain containing 1 (**ECHDC1**), and near to previously identified breast cancer susceptibility variant rs2180341<sup>52</sup>. **ECHDC1** encodes for a protein that shares the enoyl-Coenzyme A hydratase domain with trifunctional protein (HADHA), which is an enzyme involved in fatty acid oxidation<sup>53</sup> that is expressed highly in adipocyte<sup>30</sup>.

11. **Chromosome 7p15.2:** The index SNP rs1055144 is more than 300 kb from the nearest known protein-coding gene, the transcription factor nuclear factor (erythroid-derived 2)-like 3 (**NFE2L3**). rs1055144 is located within the exon of spliced ESTs (e.g. **BX116657**) and <20 kb from a set of unspliced ESTs (e.g. AA553656, corresponding to Contig27623\_RC). rs1055144 is also upstream of hypothetical protein **LOC646588**, and >100 kb from microRNA-**148a**, which can repress the DNA methyltransferase DNMT3B<sup>54</sup>.

12. **Chromosome 12p11.23:** **SSPN** encodes sarcospan, a member of the dystrophin-glycoprotein complex, which links the subsarcolemmal cytoskeleton and the extracellular matrix of muscle cells. **ITPR2** is inositol 1,4,5-triphosphate receptor,

type 2, an intracellular calcium release channel. Mice lacking both *Itpr2* and *Itpr3* exhibited impaired calcium signaling, secretion defects, hypoglycemia and lean body type<sup>55</sup>.

13. **Chromosome 12q13.13:** The index SNP is located between ***HOXC13*** and ***HOXC12*** of the ***HOXC*** gene cluster. This cluster encodes homeobox transcription factors important for the spatial distribution of cells during embryonic development. rs1443512 is also near to noncoding RNA ***HOTAIR*** which has been shown to repress transcription of the ***HOXD*** gene cluster in *trans*<sup>56</sup>.

14. **Chromosome 22q12.1:** The index SNP is located within the 3' untranslated region of ***ZNRF3***, which encodes zinc and ring finger 3. ***KREMEN1*** is a kringle-domain containing transmembrane protein that functions as a receptor for DKK1, forms a complex with low-density lipoprotein receptor-related protein 6 (LRP6), and regulates Wnt/beta-catenin signaling<sup>57</sup>. ***KREMEN1*** also interacts with R-Spondin 1 (RSPO1)<sup>58</sup>. Double null *Kremen1/Kremen2* mice show increased bone volume compared to wild type<sup>59</sup>. Nearby genes also include ***C22orf31***.

### **Copy-Number-Variations analyses**

We examined SNPs known to provide robust tags with high LD for Copy-Number-Variations (CNVs) in European-descent samples by combining four catalogues of CNV- tag SNPs (CtS): (i) 261 CtS's ( $r^2 > 0.8$ ) generated at the Broad Institute by typing HapMap samples on the Affymetrix 6.0 array<sup>60</sup>; (ii) 2,174 multiethnic CtS's ( $r^2 > 0.8$ , of which 1,168 are polymorphic in CEU) recently made available by the Genomic Structural Variation consortium and based largely on typing 450 HapMap samples on a custom-made Agilent 105K array capable of genotyping ~3,320 CNVs in CEU<sup>22</sup>; (iii) 3,113 SNPs (listed in **Supplementary Table 11**) selected to tag each of the 856 CNVs in the HapMap 3 catalog across all HapMap 3

populations (where the CNV was present) with the 856 CNVs generated using Affymetrix 6.0 and Illumina 1M array and available at <http://hapmap.ncbi.nlm.nih.gov/>; (iv) 2,905 CtS's, generated on a custom-made Agilent 105K array<sup>22</sup>, but using ~19,000 samples (all European-descent, 3,000 controls and 2,000 cases for each of 8 diseases) typed by the Wellcome Trust Case Control Consortium<sup>61</sup> Taken together these lists comprise a total of 6018 CtS's for which we had WHR discovery results in our meta-analysis, but the list was not further cropped to exclude SNPs that are tagging the same CNV.

When focusing our discovery analysis on these 6018 CtS's, we found higher associations than expected by chance (**Supplementary Figure 1**). Specifically, the strongest association with a CtS was the rs1294421, which is among our 14 WHR associations, near *LY86* ( $P = 6.1 \times 10^{-9}$ ). Two further SNPs, rs11710394 (near *SFMBT1*) and rs2802329 (near *PDIK1L*) were borderline significant ( $P = 1.6 \times 10^{-5}$  and  $8.4 \times 10^{-5}$ ).

### **Expression QTL analyses**

It was our aim to identify *cis*-eQTL that was coincident with the WHR signal: (1) We looked for interesting *cis*-eQTL signals (unadjusted  $P$  of WHR SNP association with transcript expression  $< 1.0 \times 10^{-5}$ ) for transcripts that mapped within 1 Mb of the lead WHR SNPs and were expressed in  $> 5\%$  of the samples. (2) For each transcript with an interesting *cis*-eQTL, we checked whether there was a nearby SNP with a more convincing association with expression of that transcript (*transcript peak SNP*). If the WHR signal and the *cis* eQTL were coincident, one would expect the  $P$  for the WHR SNP association with the transcript expression to be equally small as the  $P$  for the transcript peak SNP. (3) If there was a transcript peak SNP different from the WHR SNP, but in high LD ( $r^2 > 0.7$ ) with the WHR SNP, this was another indication for the

WHR signal and the *cis*-eQTL signal being coincident. (4) We performed mutual conditional analyses computing the association of the WHR SNP adjusted for the transcript peak SNP and vice versa. If the association of the transcript peak SNP disappeared ( $P>0.05$ ) by adjusting on the WHR SNP, this was the final indication for the WHR signal and the *cis*-eQTL signal being coincident, i.e. that the WHR SNP signal was mediated through the respective gene and that the transcript was probably implicated in the WHR modulation.

**Lymphocytes:** Publicly available eQTL GWA data from lymphocytes as described previously<sup>62</sup> were utilized. Briefly, peripheral blood lymphocytes were transformed into lymphoblastoid cell lines for 206 families of European descent, totaling 830 parents and offspring. Using extracted RNA, gene expression was assessed with the Affymetrix HG-U133 Plus 2.0 chip and the Illumina Sentrix Human Expression BeadChip. Genotyping was conducted using the Illumina Human1M Beadchip and Illumina HumanHap300K Beadchip and imputation performed based on HapMap and 1000 Genomes Project. SNPs were tested for *cis* associations with genes within 1 Mb of the lead SNP.

**Liver, subcutaneous fat, and omental fat from Massachusetts General Hospital:** Liver tissue (N=955), abdominal subcutaneous adipose tissue (SAT, N=610), and omental fat tissue (N=740) was available from 518 Caucasian bariatric surgery patients and 437 patients post mortem at the Massachusetts General Hospital (MGH, Boston, MA) as described previously<sup>63</sup>. RNA was isolated from the tissues and gene expression was measured using a custom Agilent 44,000 microarray composed of 39,280 oligonucleotide probes. Genotyping was conducted using the Affymetrix 500K and Illumina 650K platforms followed by imputation based on HapMap. Each SNP was tested for *cis* associations with genes within 1Mb of lead WHR SNP using an ANOVA analysis. P-values were adjusted for the ~10,000 tests performed.

**Blood and subcutaneous adipose tissue from deCODE:** deCODE eQTL analyses were done on 23,720 transcripts in abdominal SAT (N=603) and whole blood (N=745) as described previously<sup>64</sup>. SAT samples (5-10 cm<sup>3</sup>) were removed through a 3 cm incision at the bikini line. Analyses were based on genotypes from the Illumina 317K or 370K chip and HapMap based imputation. Analysis was done by regressing the mean logarithm ( $\log_{10}$ ) expression ratio (MLR) on the number of effect alleles per person controlling for age, sex (for whole blood also for differential cell count) for each SNP. *P*-values were adjusted for multiple testing using permutation and adjusted for relatedness of the individuals by dividing the  $\text{Chi}^2$  statistics by the adjustment factors 1.063 and 1.078 for adipose tissue and blood, respectively.

#### ***Differential gene expression between abdominal and gluteal fat***

For 73 individuals (29 with and 44 without metabolic syndrome), both gluteal adipose tissue and abdominal adipose tissue samples were successfully extracted at the Oxford Centre for Diabetes, Endocrinology and Metabolism as part of the MoIOBB study. Subcutaneous abdominal fat tissue was taken from the abdominal wall at the level of the umbilicus; gluteal fat tissue was taken from the upper outer quadrant of the buttock.

Total RNA was extracted with TRIreagent (SIGMA-ALDRICH) from the fat biopsies. For six of the subjects, twice the amount of RNA was extracted from each sample, and the RNA was split into two aliquots before labelling (i.e. each of six gluteal, and six abdominal, samples was run in technical replicate). Labelled RNA was hybridized onto Affymetrix Human Genome U133 Plus 2.0 gene-expression microarrays (hgu133plus2 arrays), washed, stained, and scanned for fluorescence intensity indicative of gene expression level. One sample was hybridized to each array. Quality control checks were performed on the basis of signal intensities,

background intensity, expression of control genes and spike-ins, as well as spatial representation of the intensities on each array. After outlying arrays had been removed, there remained data from 54 abdominal fat samples (4 in technical duplicate), and 65 gluteal fat samples (5 in technical duplicate); 49 subjects (20 subjects with metabolic syndrome and 29 without) had both gluteal and abdominal samples remaining in the analysis.

The majority of the probes on the hgu133plus2 arrays were collected into 17,726 non-overlapping probe sets according to ENTREZG annotations; with a single probe set for each gene. The mapping is contained in a chip-definition file (CDF, [http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/genomic\\_curated\\_CDF.asp](http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/genomic_curated_CDF.asp)). The rationale and design criteria behind such CDFs is given by Dai et al<sup>65</sup>. All arrays (both gluteal and abdominal sample-derived) were preprocessed concurrently using GeneChip robust multi-array analysis (GCRMA) resulting in a summarized expression measure for each probe set. Gene-specific expression summaries were averaged across technical replicates of a sample. We then filtered the data, retaining only those probe sets that were annotated to an autosomal location, and also showed a mean intensity above 4 arbitrary units of  $\log_2(\text{intensity})$  in at least 10% of individuals. Of the 20 genes, 19 had probes available on the array and four of these were not detected above background, leaving 15 genes to be analysed.

To investigate whether genes are differentially expressed between abdominal and gluteal fat samples, we fitted a linear mixed model using the R package 'Maanova'. We fitted tissue (abdominal versus gluteal fat), Metabolic Syndrome case-control status, gender, and plate as fixed effects, and subject (sample donor) as a random effect. The P-values from the F-test were adjusted for multiple testing using



the false discovery rate<sup>66</sup> across the 15 tested genes and considered significant if the adjusted P-value of the F test was <0.05.

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