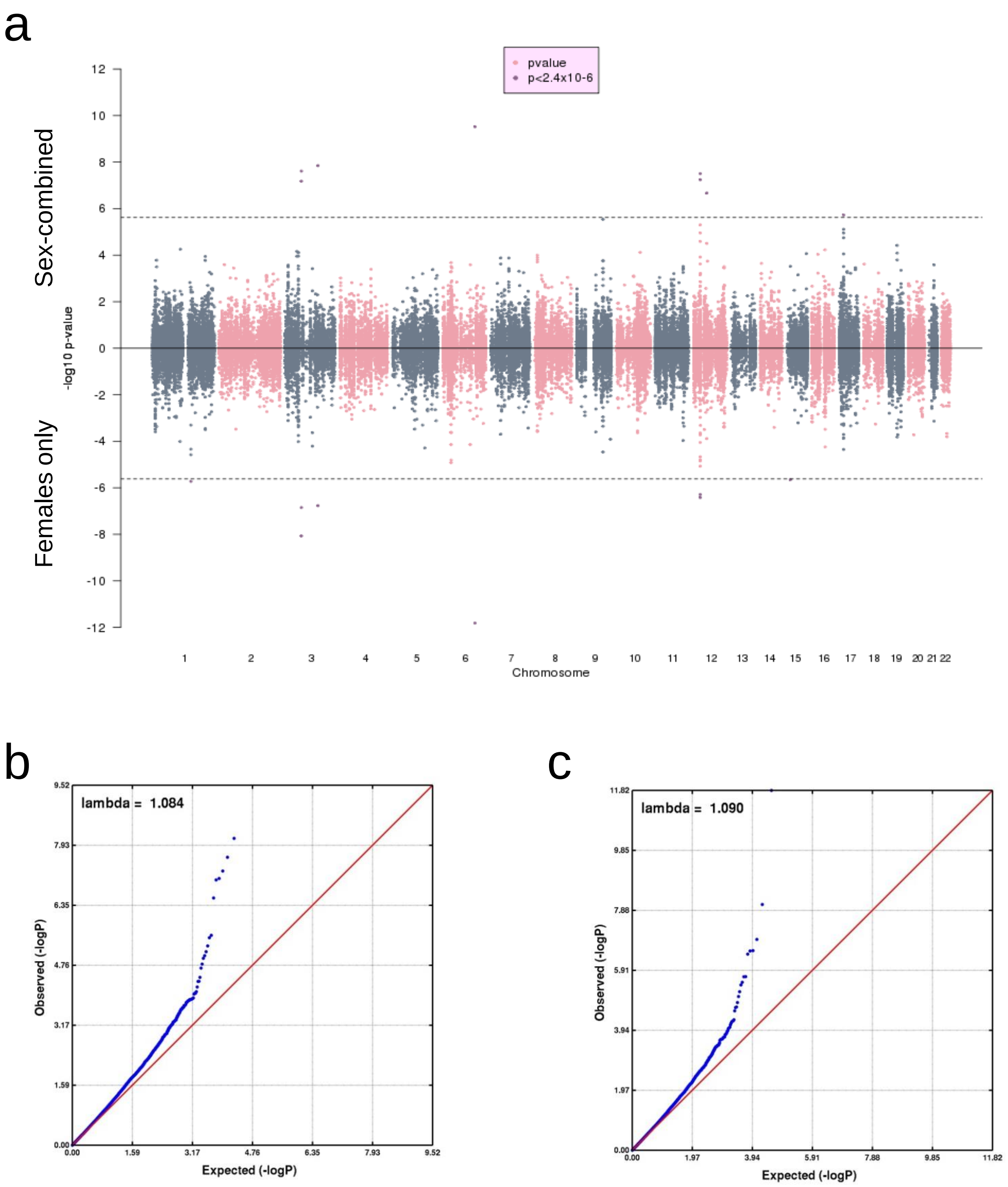
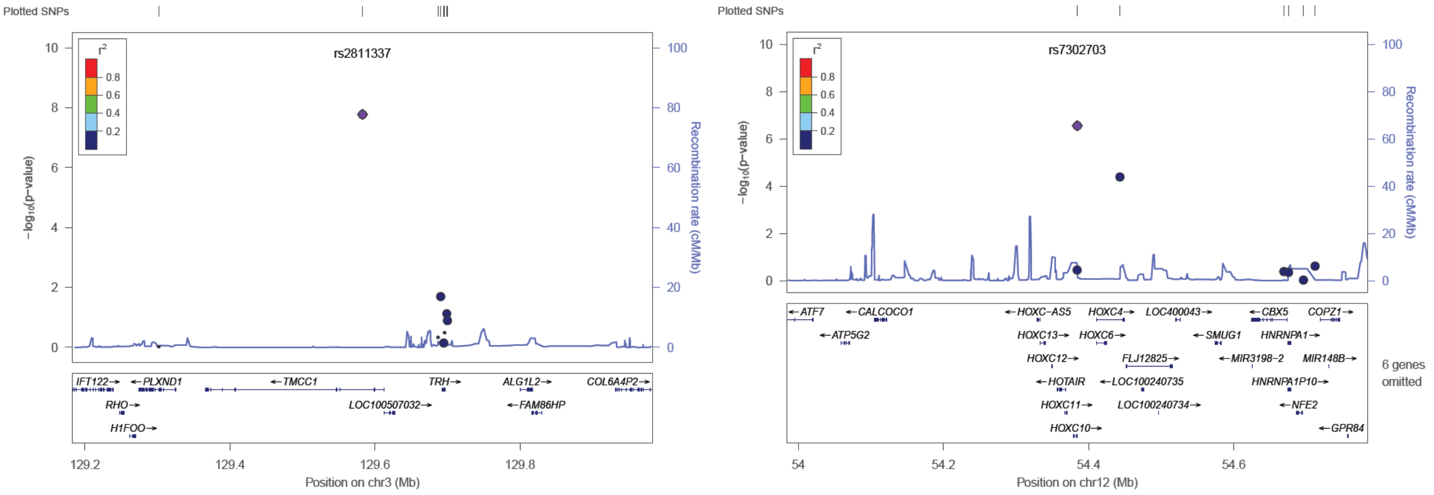
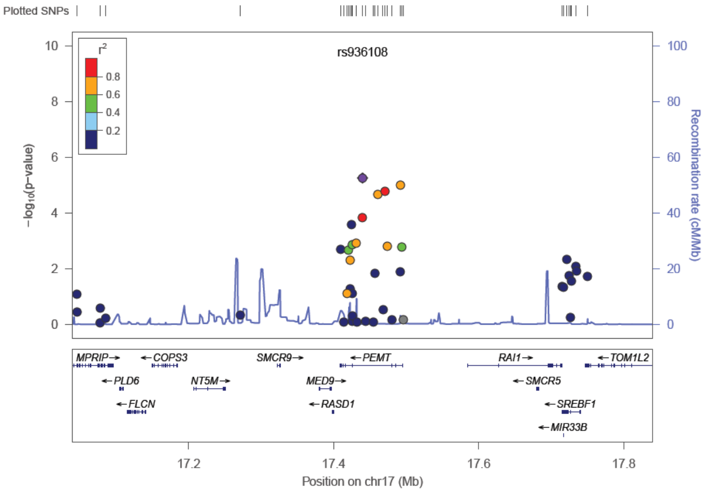


Supplementary Figure 1. (a) Array-wide association results for waist-to-hip ratio adjusted for BMI (WHRadjBMI) among sex-combined (top half) and females (bottom half). *P*-values are shown along the y-axis and location along the chromosomes are shown along the x-axis. The dotted line indicates the array-wide significance threshold of 2.4x10^{-6}. (b) Quantile-quantile plot of observed sex-combined association *P*-values for WHRadjBMI against expected *P*-values. (c) Quantile-quantile plot of observed female-only association *P*-values for WHRadjBMI against expected *P*-values.

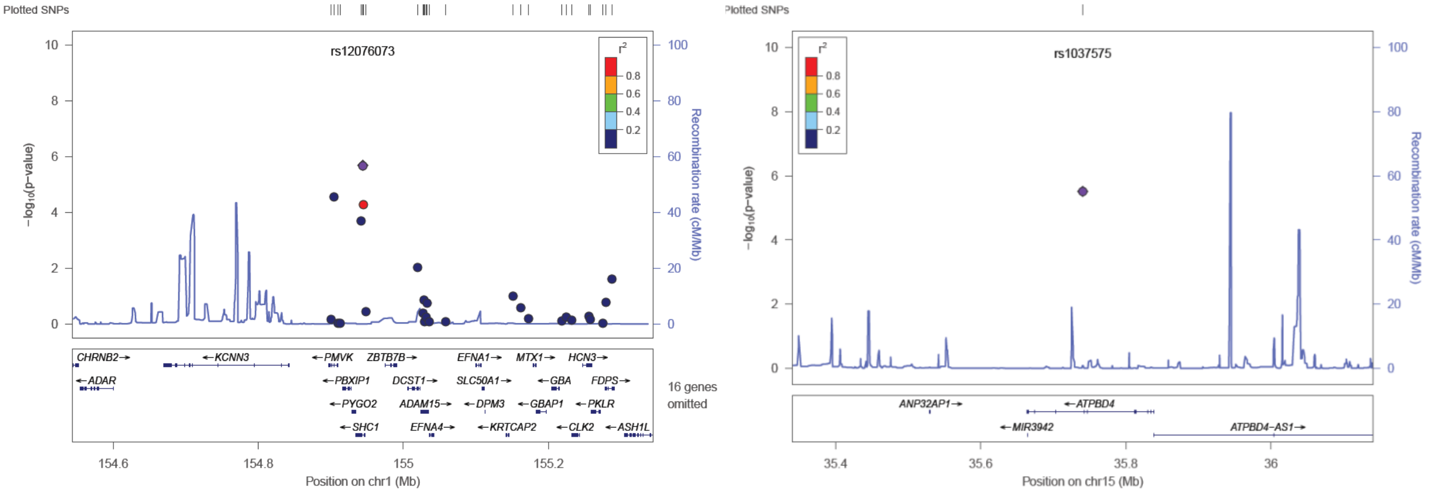


3q.21.3 loci (sex combined meta-analysis)

12q13.13 loci (sex combined meta-analysis)



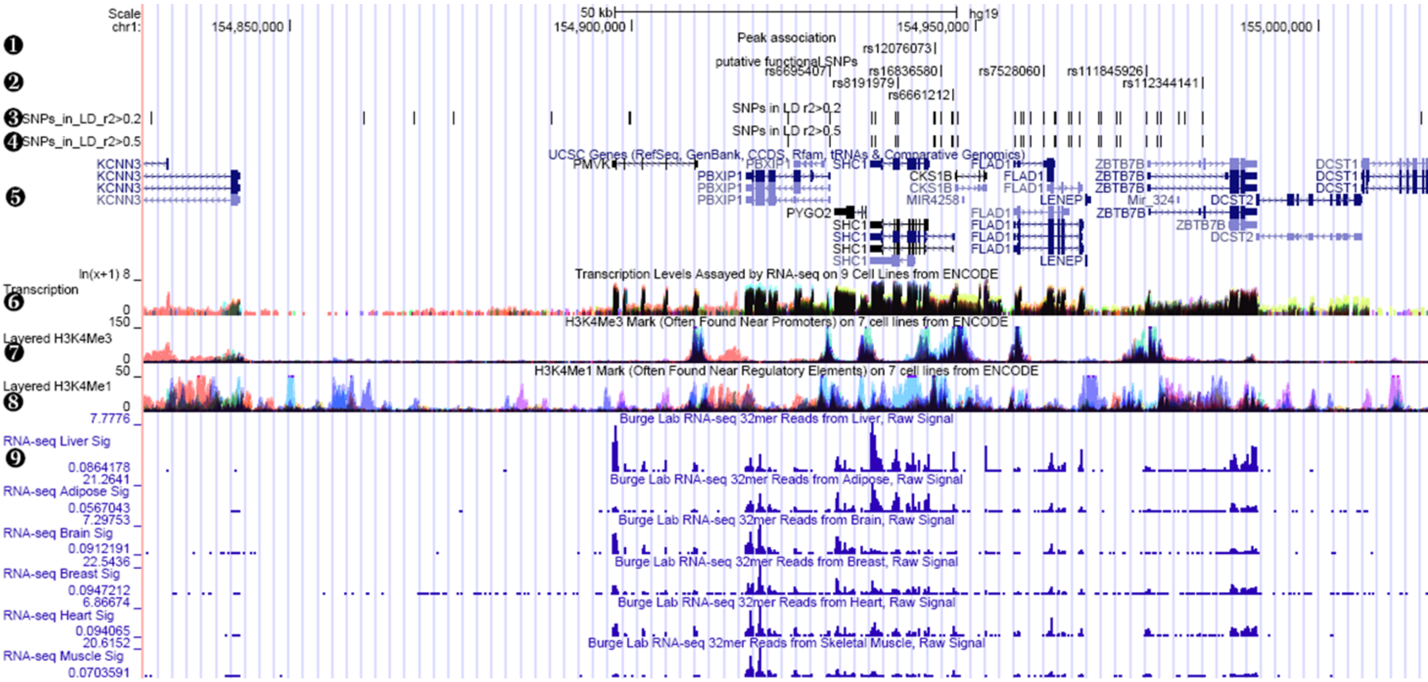
17p11.2 loci (sex combined meta-analysis)



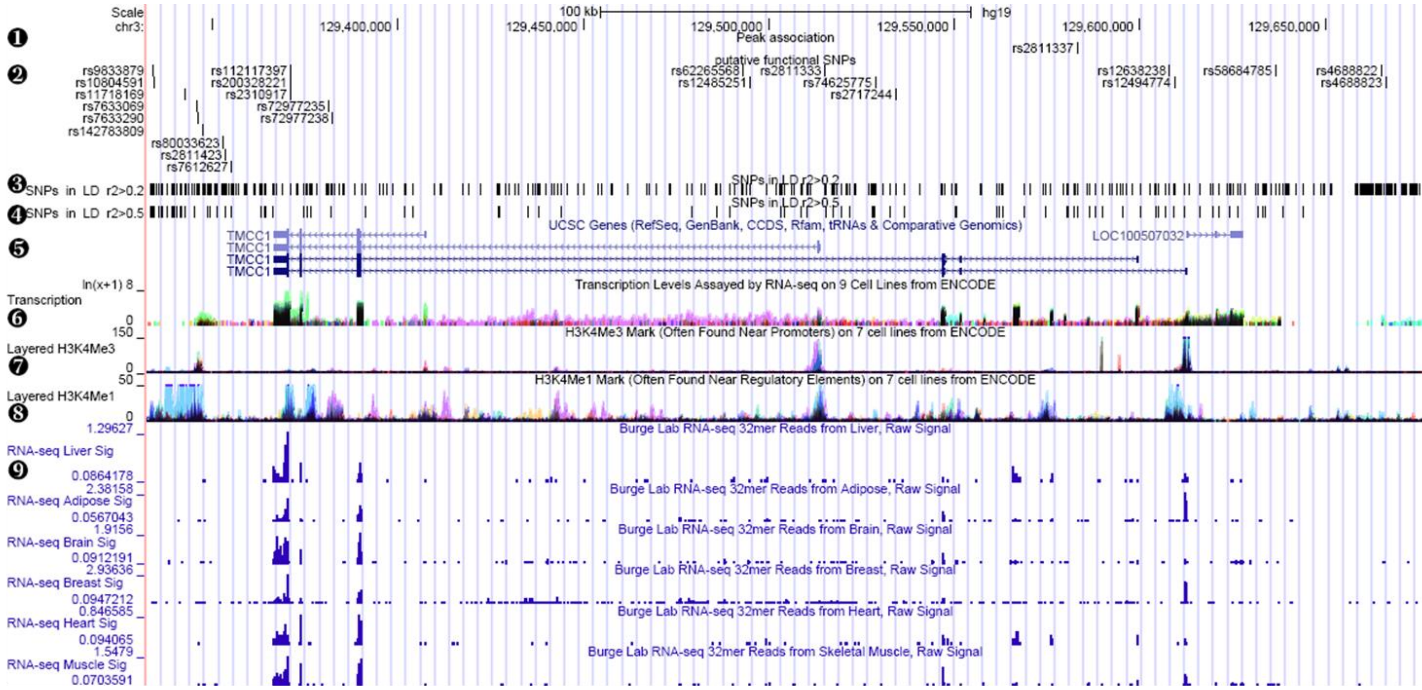
1q21.3 loci (female only meta-analysis)

15q14 loci (female only meta-analysis)

Supplementary Figure 2. Regional association plots with the WHRadjBMI phenotype for five novel loci detected among up to 51,990 European descendants. The -log10 of *P*-values (left y-axis) are plotted against the SNP genomic position based on NCBI build 37 (x-axis). The peaks in the blue line show the estimated recombination rate from the 1000 Genomes Project European populations release March 2012 (right y-axis). The novel SNP for each loci is denoted with a purple diamond; the remaining SNPs are colored to reflect the approximate r^2 correlation with the novel SNP (shown in the upper right legend).

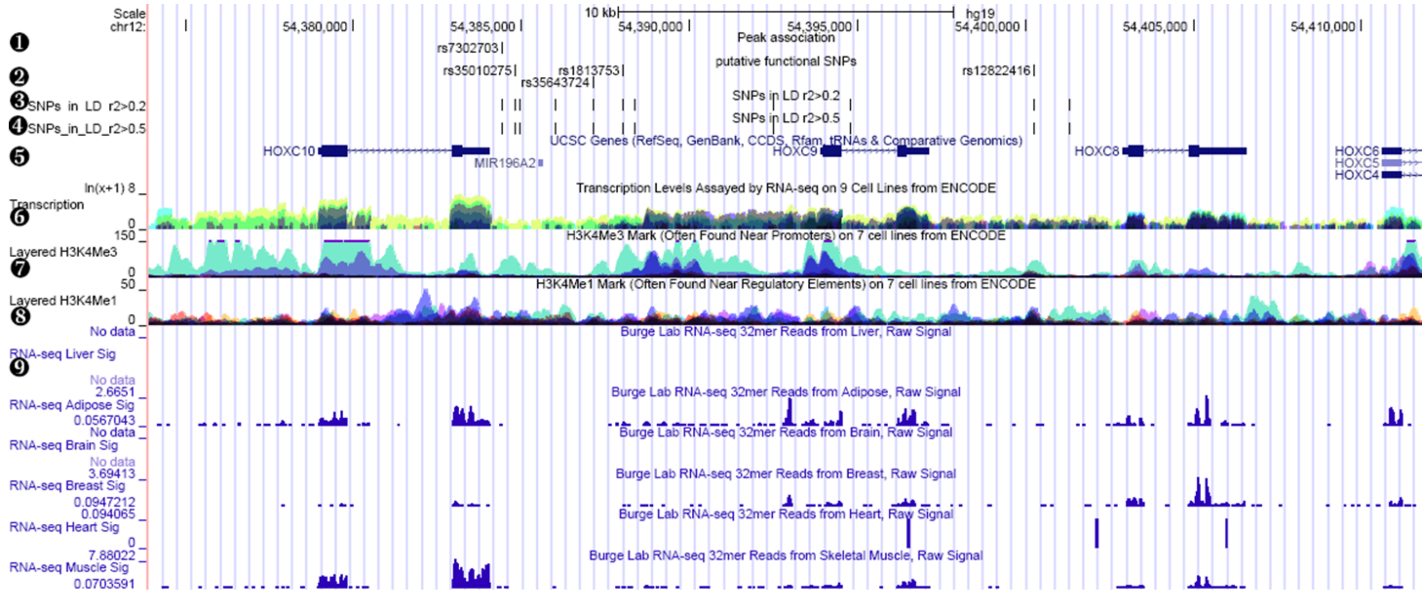


Supplementary Figure 3a. Genomic context of signal found in chromosome 1 locus.

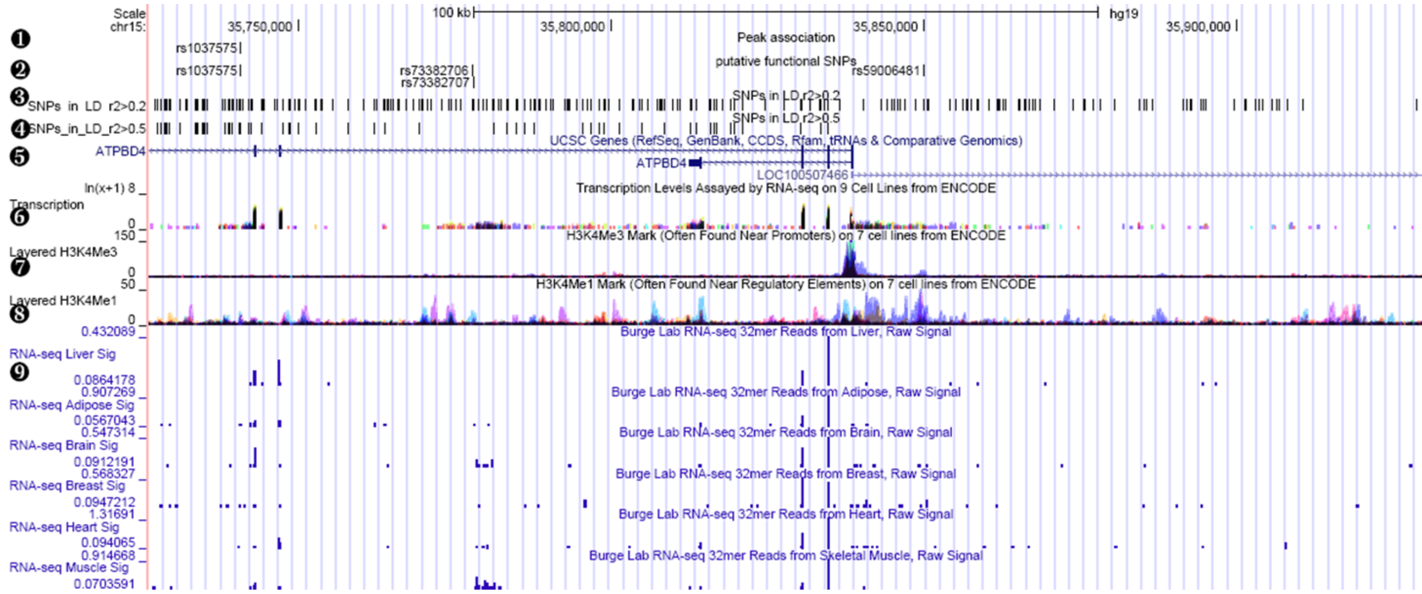


Supplementary Figure 3b. Genomic context of signal found in chromosome 3 locus.

Supplementary Figures 3a-e. Genomic context of novel loci reported in this study. 1a) Chromosome 1 locus, 1b) Chromosome 3 locus, 1c) Chromosome 12 locus, 1d) Chromosome 15 locus, 1e) Chromosome 17 locus. Data is visualised using the UCSC human genome browser and custom track data, presented in the following order: ❶ Sentinel SNP representing the strongest association, ❷ SNPs with strongest evidence of functional impact (score <4). ❸ Extended LD region (SNPs in LD with Sentinel SNP (r^2 LD>0.2)), ❹ Core LD region (SNPs in LD with Sentinel SNP (r^2 LD>0.5)), ❺ Known human gene transcripts, ❻ ENCODE: RNA-seq assayed in 9 human cell lines, (Red:GM12878 (lymphoblastoid cell line), Orange:H1-hESC (embryonic stem cells), Yellow:HeLa-S3 (Cervical carcinoma), Green:HepG2 (hepatocellular carcinoma), light blue:HSMM (skeletal muscle myoblasts), darker blue: HUVEC (umbilical vein endothelial cells), violet:K562(Leukemia), magenta:NHEK (Epidemal keratinocytes), Pink:NHLF (lung fibroblasts) ❼ ENCODE: H3K4Me3 histone marks representing probable promoter activity in 7 human cell lines (Red:GM12878, Orange:H1-hESC, light blue:HSMM, darker blue: HUVEC, violet:K562, magenta:NHEK, Pink:NHLF), ❽ ENCODE: H3KMe1 histone marks presenting probable regulatory enhancer activity in 7 human cell lines (as in 7), ❾ RNA-seq across 6 tissues (Adipose, Brain, Breast, Heart, Liver, Muscle) from the Burge lab.

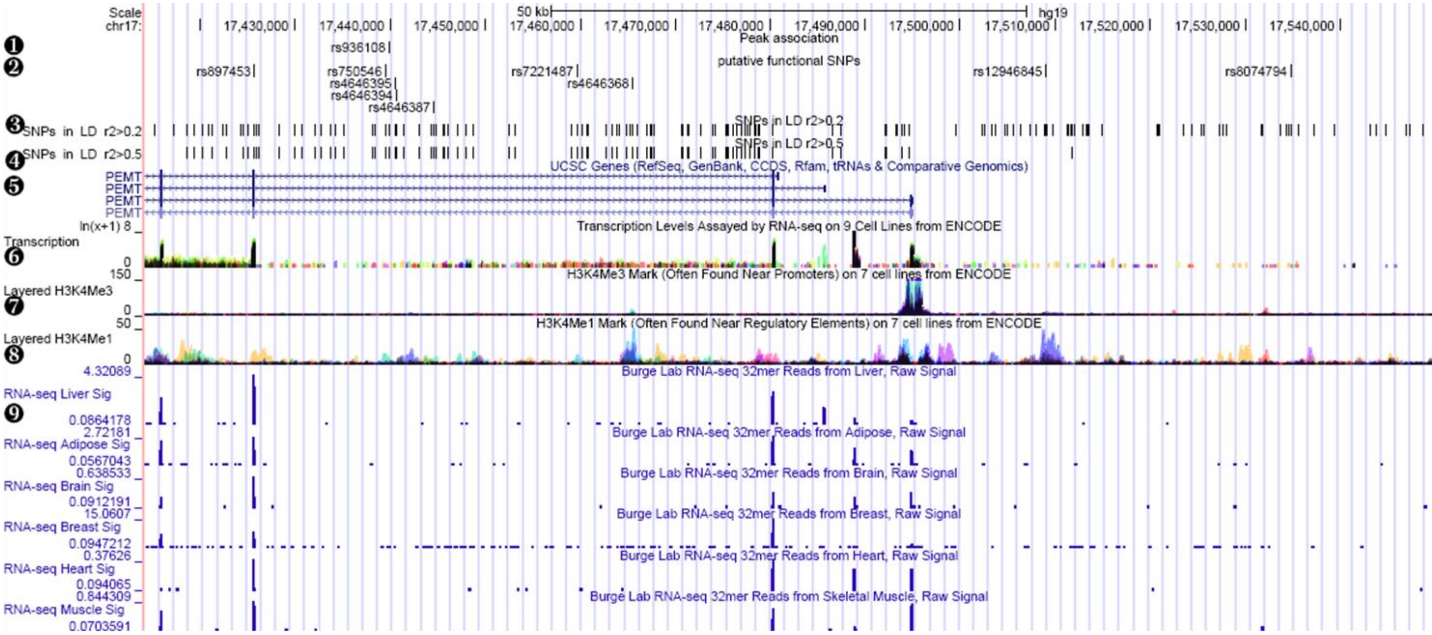


Supplementary Figure 3c. Genomic context of signal found in chromosome 12 locus.



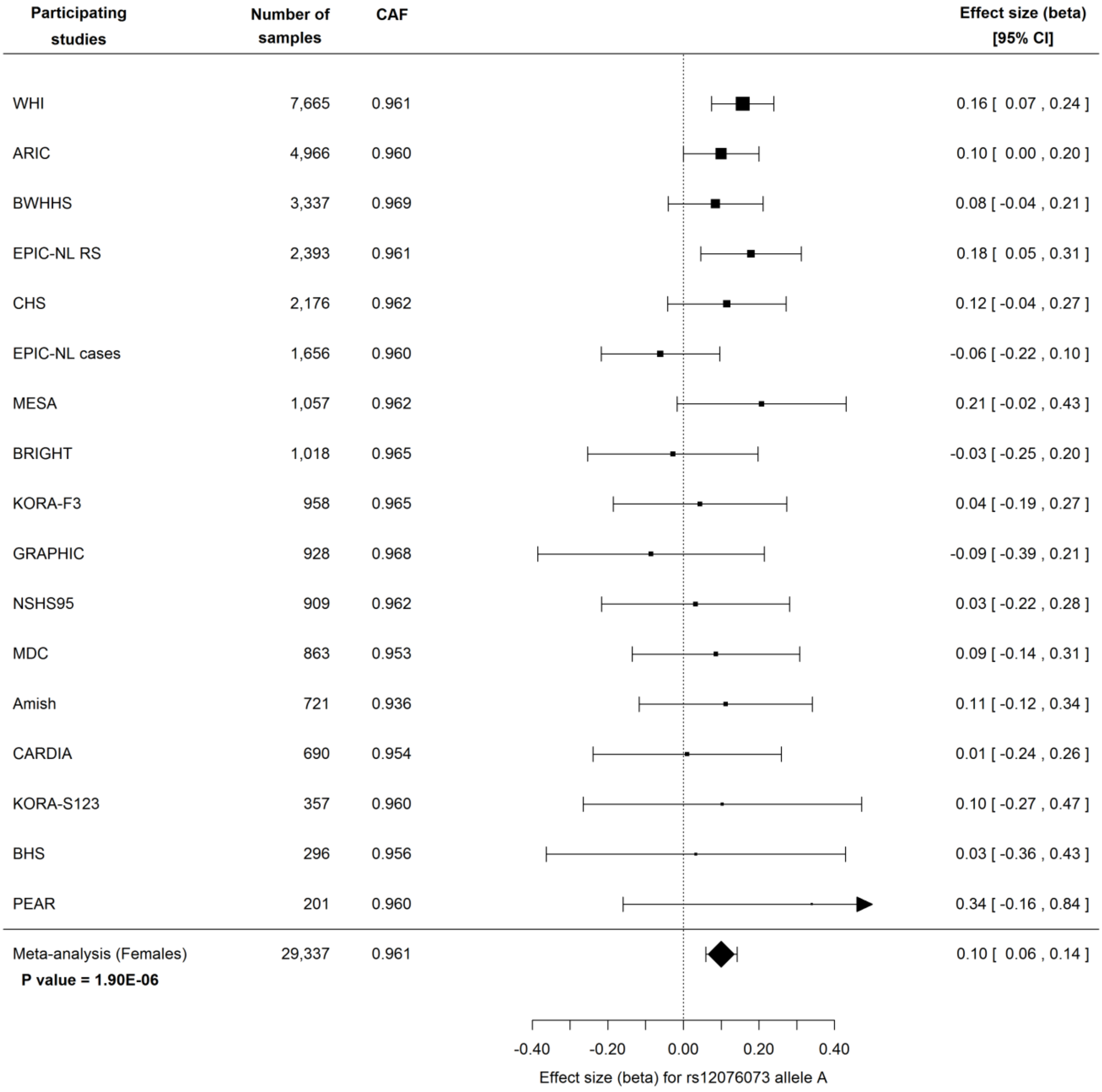
Supplementary Figure 3d. Genomic context of signal found in chromosome 15 locus.

Supplementary Figures 3a-e. Genomic context of novel loci reported in this study. 1a) Chromosome 1 locus, 1b) Chromosome 3 locus, 1c) Chromosome 12 locus, 1d) Chromosome 15 locus, 1e) Chromosome 17 locus. Data is visualised using the UCSC human genome browser and custom track data, presented in the following order: ❶ Sentinel SNP representing the strongest association, ❷ SNPs with strongest evidence of functional impact (score <4). ❸ Extended LD region (SNPs in LD with Sentinel SNP (r^2 LD>0.2)), ❹ Core LD region (SNPs in LD with Sentinel SNP (r^2 LD>0.5)), ❺ Known human gene transcripts, ❻ ENCODE: RNA-seq assayed in 9 human cell lines, (Red:GM12878 (lymphoblastoid cell line), Orange:H1-hESC (embryonic stem cells), Yellow:HeLa-S3 (Cervical carcinoma), Green:HepG2 (hepatocellular carcinoma), light blue:HSMM (skeletal muscle myoblasts), darker blue: HUVEC (umbilical vein endothelial cells), violet:K562(Leukemia), magenta:NHEK (Epidemal keratinocytes), Pink:NHLF (lung fibroblasts) ❼ ENCODE: H3K4Me3 histone marks representing probable promoter activity in 7 human cell lines (Red:GM12878, Orange:H1-hESC, light blue:HSMM, darker blue: HUVEC, violet:K562, magenta:NHEK, Pink:NHLF), ❽ ENCODE: H3KMe1 histone marks presenting probable regulatory enhancer activity in 7 human cell lines (as in 7), ❾ RNA-seq across 6 tissues (Adipose, Brain, Breast, Heart, Liver, Muscle) from the Burge lab.



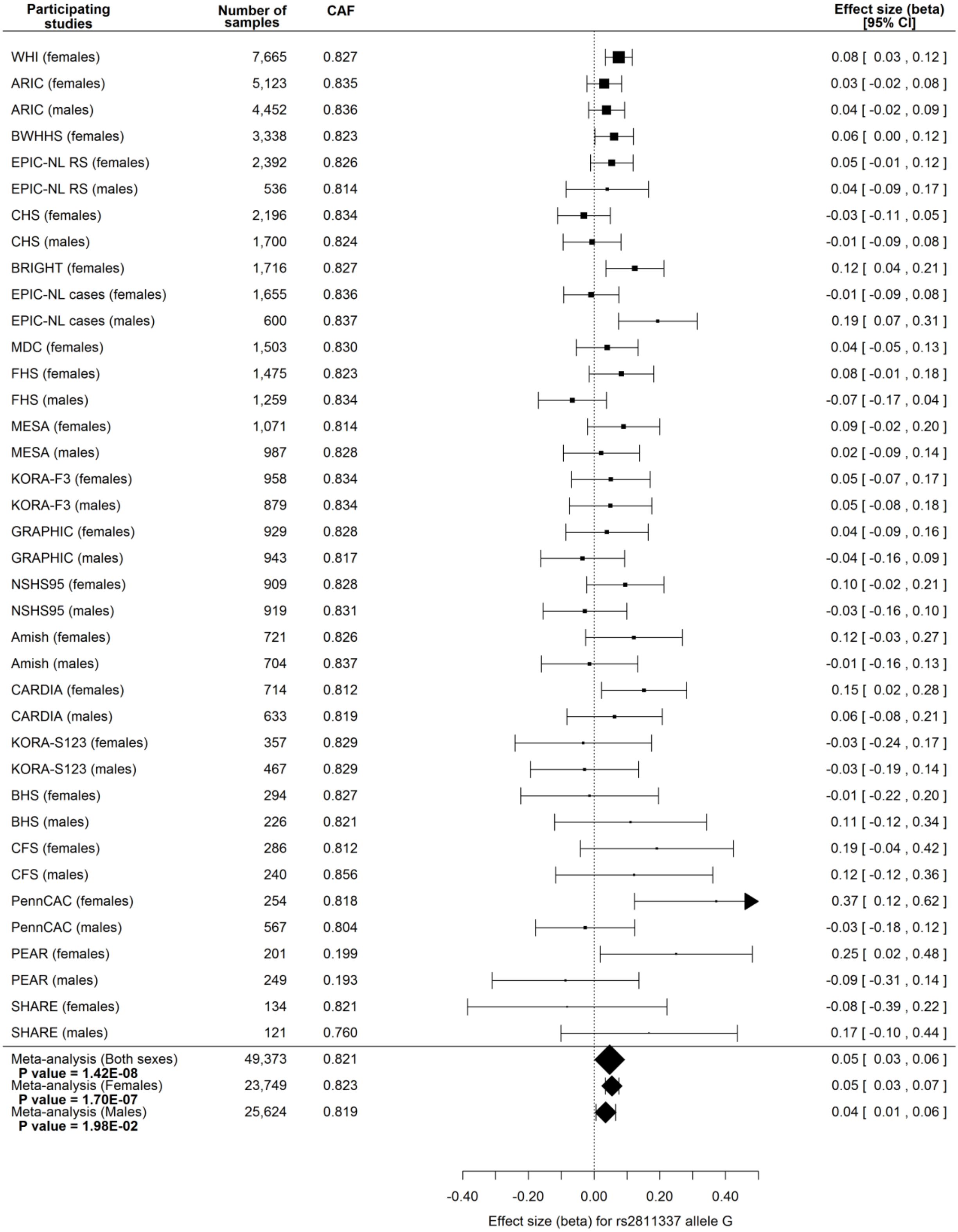
Supplementary Figure 3e. Genomic context of signal found in chromosome 17 locus.

Supplementary Figures 3a-e. Genomic context of novel loci reported in this study. 1a) Chromosome 1 locus, 1b) Chromosome 3 locus, 1c) Chromosome 12 locus, 1d) Chromosome 15 locus, 1e) Chromosome 17 locus. Data is visualised using the UCSC human genome browser and custom track data, presented in the following order: ❶ Sentinel SNP representing the strongest association, ❷ SNPs with strongest evidence of functional impact (score <4). ❸ Extended LD region (SNPs in LD with Sentinel SNP (r^2 LD>0.2)), ❹ Core LD region (SNPs in LD with Sentinel SNP (r^2 LD>0.5)), ❺ Known human gene transcripts, ❻ ENCODE: RNA-seq assayed in 9 human cell lines, (Red:GM12878 (lymphoblastoid cell line), Orange:H1-hESC (embryonic stem cells), Yellow:HeLa-S3 (Cervical carcinoma), Green:HepG2 (hepatocellular carcinoma), light blue:HSMM (skeletal muscle myoblasts), darker blue: HUVEC (umbilical vein endothelial cells), violet:K562(Leukemia), magenta:NHEK (Epidemal keratinocytes), Pink:NHLF (lung fibroblasts) ❼ ENCODE: H3K4Me3 histone marks representing probable promoter activity in 7 human cell lines (Red:GM12878, Orange:H1-hESC, light blue:HSMM, darker blue: HUVEC, violet:K562, magenta:NHEK, Pink:NHLF), ❽ ENCODE: H3KMe1 histone marks presenting probable regulatory enhancer activity in 7 human cell lines (as in 7), ❾ RNA-seq across 6 tissues (Adipose, Brain, Breast, Heart, Liver, Muscle) from the Burge lab.



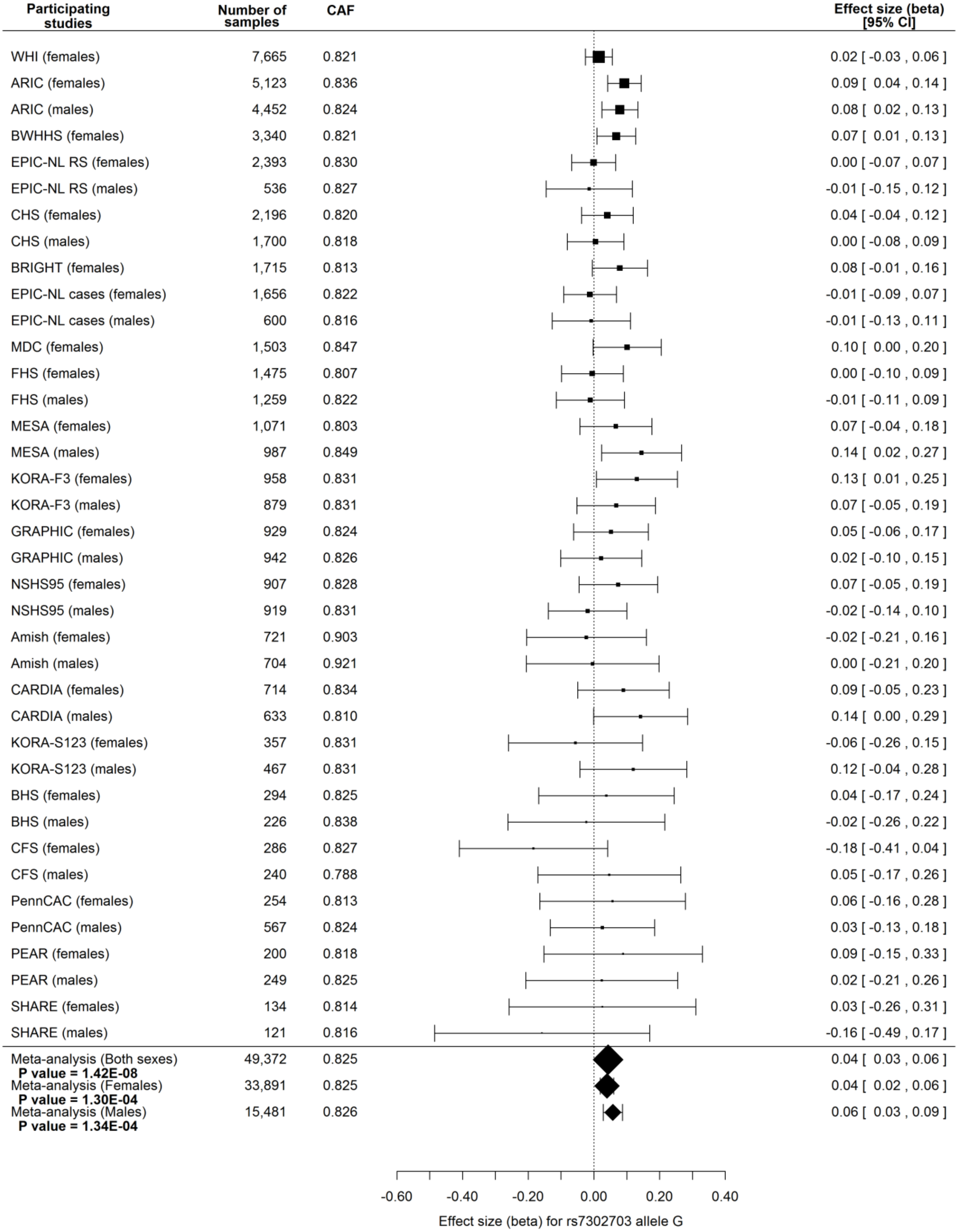
Participating studies	Number of samples	CAF	Effect size (beta) [95% CI]
WHI	7,665	0.961	0.16 [0.07 , 0.24]
ARIC	4,966	0.960	0.10 [0.00 , 0.20]
BWHHS	3,337	0.969	0.08 [-0.04 , 0.21]
EPIC-NL RS	2,393	0.961	0.18 [0.05 , 0.31]
CHS	2,176	0.962	0.12 [-0.04 , 0.27]
EPIC-NL cases	1,656	0.960	-0.06 [-0.22 , 0.10]
MESA	1,057	0.962	0.21 [-0.02 , 0.43]
BRIGHT	1,018	0.965	-0.03 [-0.25 , 0.20]
KORA-F3	958	0.965	0.04 [-0.19 , 0.27]
GRAPHIC	928	0.968	-0.09 [-0.39 , 0.21]
NSHS95	909	0.962	0.03 [-0.22 , 0.28]
MDC	863	0.953	0.09 [-0.14 , 0.31]
Amish	721	0.936	0.11 [-0.12 , 0.34]
CARDIA	690	0.954	0.01 [-0.24 , 0.26]
KORA-S123	357	0.960	0.10 [-0.27 , 0.47]
BHS	296	0.956	0.03 [-0.36 , 0.43]
PEAR	201	0.960	0.34 [-0.16 , 0.84]
Meta-analysis (Females) **P value = 1.90E-06**	29,337	0.961	0.10 [0.06 , 0.14]

Supplementary Figure 4a. Forest plot for the association between rs12076073 (in *SHC1*, chromosome 1) and waist-to-hip ratio adjusted for BMI among for each female component of the 17 cohorts contributing to the inverse variance weighted fixed-effect meta-analysis oriented on the A allele. Abbreviations. CAF: Coded allele frequency; CI: Confidence interval



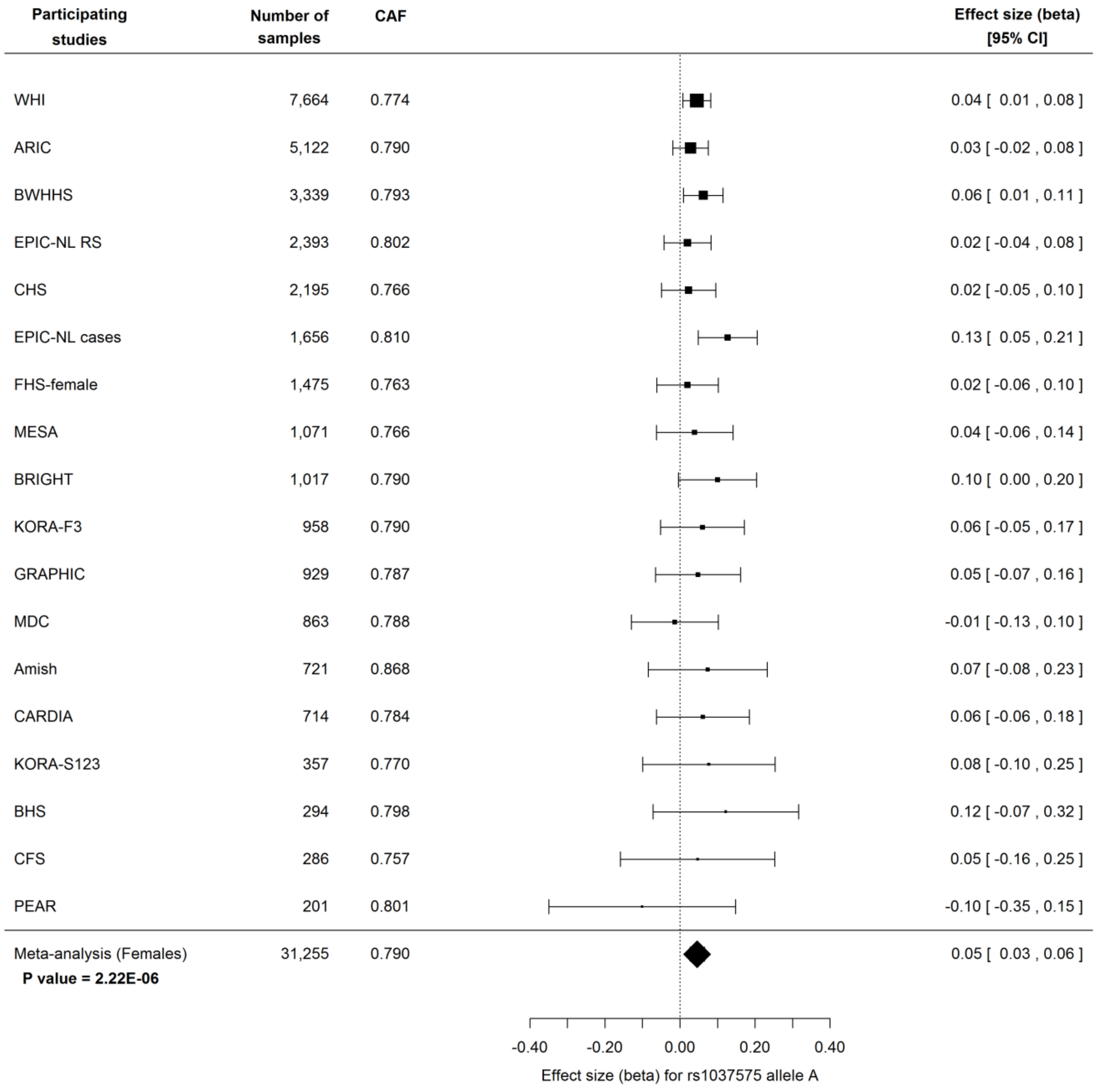
Participating studies	Number of samples	CAF	Effect size (beta) [95% CI]
WHI (females)	7,665	0.827	0.08 [0.03 , 0.12]
ARIC (females)	5,123	0.835	0.03 [-0.02 , 0.08]
ARIC (males)	4,452	0.836	0.04 [-0.02 , 0.09]
BWHHS (females)	3,338	0.823	0.06 [0.00 , 0.12]
EPIC-NL RS (females)	2,392	0.826	0.05 [-0.01 , 0.12]
EPIC-NL RS (males)	536	0.814	0.04 [-0.09 , 0.17]
CHS (females)	2,196	0.834	-0.03 [-0.11 , 0.05]
CHS (males)	1,700	0.824	-0.01 [-0.09 , 0.08]
BRIGHT (females)	1,716	0.827	0.12 [0.04 , 0.21]
EPIC-NL cases (females)	1,655	0.836	-0.01 [-0.09 , 0.08]
EPIC-NL cases (males)	600	0.837	0.19 [0.07 , 0.31]
MDC (females)	1,503	0.830	0.04 [-0.05 , 0.13]
FHS (females)	1,475	0.823	0.08 [-0.01 , 0.18]
FHS (males)	1,259	0.834	-0.07 [-0.17 , 0.04]
MESA (females)	1,071	0.814	0.09 [-0.02 , 0.20]
MESA (males)	987	0.828	0.02 [-0.09 , 0.14]
KORA-F3 (females)	958	0.834	0.05 [-0.07 , 0.17]
KORA-F3 (males)	879	0.834	0.05 [-0.08 , 0.18]
GRAPHIC (females)	929	0.828	0.04 [-0.09 , 0.16]
GRAPHIC (males)	943	0.817	-0.04 [-0.16 , 0.09]
NSHS95 (females)	909	0.828	0.10 [-0.02 , 0.21]
NSHS95 (males)	919	0.831	-0.03 [-0.16 , 0.10]
Amish (females)	721	0.826	0.12 [-0.03 , 0.27]
Amish (males)	704	0.837	-0.01 [-0.16 , 0.13]
CARDIA (females)	714	0.812	0.15 [0.02 , 0.28]
CARDIA (males)	633	0.819	0.06 [-0.08 , 0.21]
KORA-S123 (females)	357	0.829	-0.03 [-0.24 , 0.17]
KORA-S123 (males)	467	0.829	-0.03 [-0.19 , 0.14]
BHS (females)	294	0.827	-0.01 [-0.22 , 0.20]
BHS (males)	226	0.821	0.11 [-0.12 , 0.34]
CFS (females)	286	0.812	0.19 [-0.04 , 0.42]
CFS (males)	240	0.856	0.12 [-0.12 , 0.36]
PennCAC (females)	254	0.818	0.37 [0.12 , 0.62]
PennCAC (males)	567	0.804	-0.03 [-0.18 , 0.12]
PEAR (females)	201	0.199	0.25 [0.02 , 0.48]
PEAR (males)	249	0.193	-0.09 [-0.31 , 0.14]
SHARE (females)	134	0.821	-0.08 [-0.39 , 0.22]
SHARE (males)	121	0.760	0.17 [-0.10 , 0.44]
Meta-analysis (Both sexes) **P value = 1.42E-08**	49,373	0.821	0.05 [0.03 , 0.06]
Meta-analysis (Females) **P value = 1.70E-07**	23,749	0.823	0.05 [0.03 , 0.07]
Meta-analysis (Males) **P value = 1.98E-02**	25,624	0.819	0.04 [0.01 , 0.06]

Supplementary Figure 4b. Forest plot for the association between rs2811337 (in *TMCC1*, chromosome 3) and waist-to-hip ratio adjusted for BMI among for each of the 21 cohorts contributing to the inverse variance weighted fixed-effect meta-analysis oriented on the G allele. Effect estimates for each study, denoted by a square, is shown stratified by female and male participants when applicable, with sex-combined, female only, and male only meta-analysis estimates shown as diamonds. Abbreviations. CAF: Coded allele frequency; CI: Confidence interval

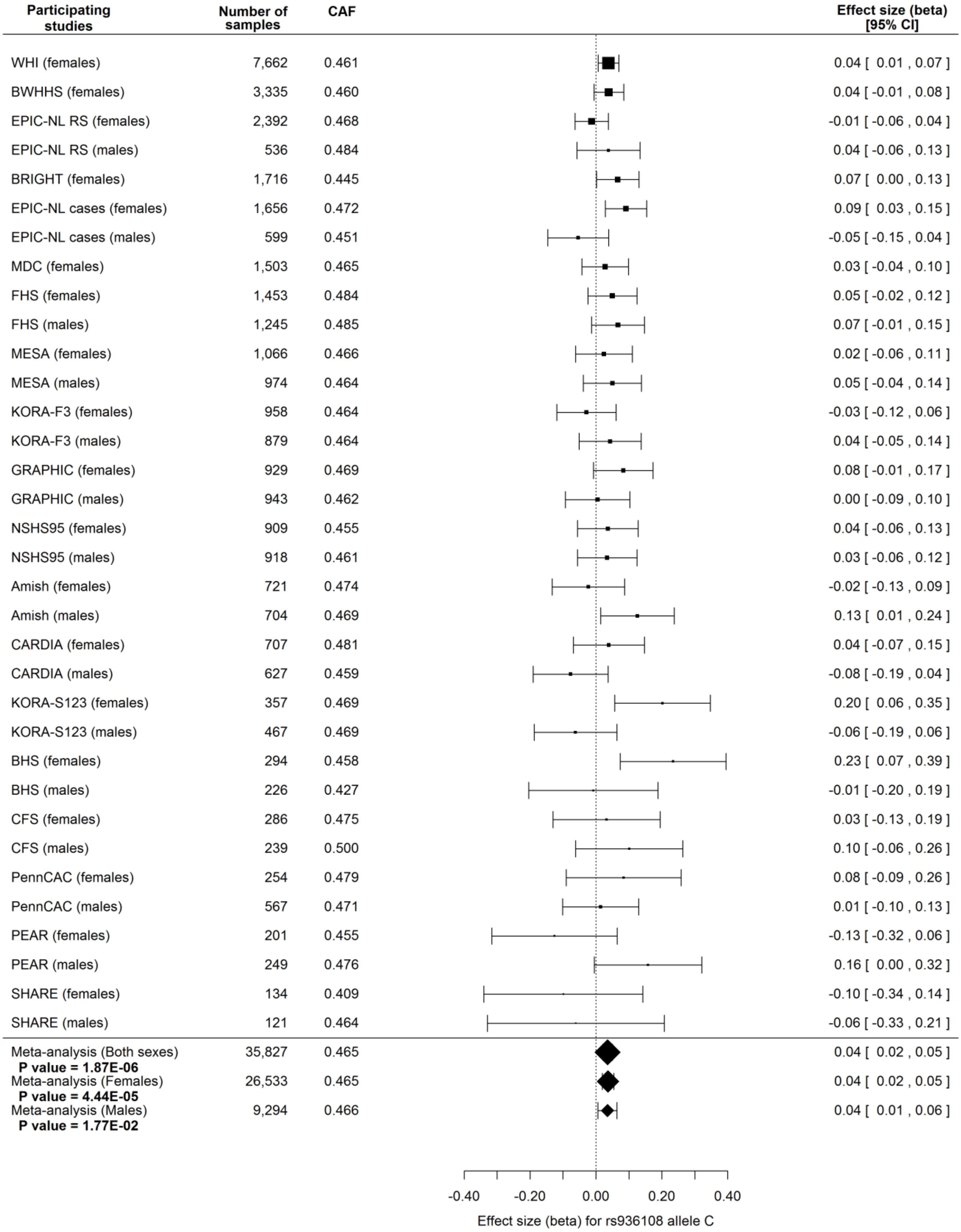


Participating studies	Number of samples	CAF	Effect size (beta) [95% CI]
WHI (females)	7,665	0.821	0.02 [-0.03 , 0.06]
ARIC (females)	5,123	0.836	0.09 [0.04 , 0.14]
ARIC (males)	4,452	0.824	0.08 [0.02 , 0.13]
BWHHS (females)	3,340	0.821	0.07 [0.01 , 0.13]
EPIC-NL RS (females)	2,393	0.830	0.00 [-0.07 , 0.07]
EPIC-NL RS (males)	536	0.827	-0.01 [-0.15 , 0.12]
CHS (females)	2,196	0.820	0.04 [-0.04 , 0.12]
CHS (males)	1,700	0.818	0.00 [-0.08 , 0.09]
BRIGHT (females)	1,715	0.813	0.08 [-0.01 , 0.16]
EPIC-NL cases (females)	1,656	0.822	-0.01 [-0.09 , 0.07]
EPIC-NL cases (males)	600	0.816	-0.01 [-0.13 , 0.11]
MDC (females)	1,503	0.847	0.10 [0.00 , 0.20]
FHS (females)	1,475	0.807	0.00 [-0.10 , 0.09]
FHS (males)	1,259	0.822	-0.01 [-0.11 , 0.09]
MESA (females)	1,071	0.803	0.07 [-0.04 , 0.18]
MESA (males)	987	0.849	0.14 [0.02 , 0.27]
KORA-F3 (females)	958	0.831	0.13 [0.01 , 0.25]
KORA-F3 (males)	879	0.831	0.07 [-0.05 , 0.19]
GRAPHIC (females)	929	0.824	0.05 [-0.06 , 0.17]
GRAPHIC (males)	942	0.826	0.02 [-0.10 , 0.15]
NSHS95 (females)	907	0.828	0.07 [-0.05 , 0.19]
NSHS95 (males)	919	0.831	-0.02 [-0.14 , 0.10]
Amish (females)	721	0.903	-0.02 [-0.21 , 0.16]
Amish (males)	704	0.921	0.00 [-0.21 , 0.20]
CARDIA (females)	714	0.834	0.09 [-0.05 , 0.23]
CARDIA (males)	633	0.810	0.14 [0.00 , 0.29]
KORA-S123 (females)	357	0.831	-0.06 [-0.26 , 0.15]
KORA-S123 (males)	467	0.831	0.12 [-0.04 , 0.28]
BHS (females)	294	0.825	0.04 [-0.17 , 0.24]
BHS (males)	226	0.838	-0.02 [-0.26 , 0.22]
CFS (females)	286	0.827	-0.18 [-0.41 , 0.04]
CFS (males)	240	0.788	0.05 [-0.17 , 0.26]
PennCAC (females)	254	0.813	0.06 [-0.16 , 0.28]
PennCAC (males)	567	0.824	0.03 [-0.13 , 0.18]
PEAR (females)	200	0.818	0.09 [-0.15 , 0.33]
PEAR (males)	249	0.825	0.02 [-0.21 , 0.26]
SHARE (females)	134	0.814	0.03 [-0.26 , 0.31]
SHARE (males)	121	0.816	-0.16 [-0.49 , 0.17]
Meta-analysis (Both sexes) **P value = 1.42E-08**	49,372	0.825	0.04 [0.03 , 0.06]
Meta-analysis (Females) **P value = 1.30E-04**	33,891	0.825	0.04 [0.02 , 0.06]
Meta-analysis (Males) **P value = 1.34E-04**	15,481	0.826	0.06 [0.03 , 0.09]

Supplementary Figure 4c. Forest plot for the association between rs7302703 (downstream of *HOXC10*, chromosome 12) and waist-to-hip ratio adjusted for BMI among for each of the 21 cohorts contributing to the inverse variance weighted fixed-effect meta-analysis oriented on the G allele. Effect estimates for each study, denoted by a square, is shown stratified by female and male participants when applicable, with sex-combined, female only, and male only meta-analysis estimates shown as diamonds. Abbreviations. CAF: Coded allele frequency; CI: Confidence interval



Supplementary Figure 4d. Forest plot for the association between rs1037575 (in *ATPBD4,* chromosome 15) and waist-to-hip ratio adjusted for BMI among for each female component of the 18 cohorts contributing to the inverse variance weighted fixed-effect meta-analysis oriented on the A allele. Abbreviations. CAF: Coded allele frequency; CI: Confidence interval



Supplementary Figure 4e. Forest plot for the association between rs936108 (in *PEMT*, chromosome 17) and waist-to-hip ratio adjusted for BMI among for each of the 19 cohorts contributing to the inverse variance weighted fixed-effect meta-analysis oriented on the C allele. Effect estimates for each study, denoted by a square, is shown stratified by female and male participants when applicable, with sex-combined, female only, and male only meta-analysis estimates shown as diamonds. Abbreviations. CAF: Coded allele frequency; CI: Confidence interval