Legends to Supplemental Tables

Table S1: Descriptive table of the cohorts used in Stages 1 and 2. The ancestry and continental analysis group are shown along with genotyping chip type, stage of analysis, age ranges and birth years of samples, number of cases and controls and percentage of males and females within each cohort.

Table S2: SNPs which showed a suggestive association (BF >= 4) in the Stage 1 meta-analyses. "--" indicates that the variant did not pass quality control in that ancestral grouping. The first allele is the effect allele for which the beta applies. Betas, standard errors and p-values are shown for each continental sub-analysis along with the trans-ancestral Bayes' Factor. These SNPs were taken forward to Stage 2.

Table S3: Genetic correlation results from LD score regression in LD Hub using the European sub-analysis of childhood obesity. Trait = the trait compared to childhood obesity. PMID = PubMed ID of the study from with the statistics are derived. Rg = genetic correlation between the trait and childhood obesity. Se = standard error of rg. P = significance of rg.

Table S4: Credible set analysis of the significant loci from the meta-analysis. BF = Bayes factor. Post. Probability is the posterior probability of that particular variant being the

causal variant. Cumulative Post. Probability is the sum of the posterior probabilities after being ranked by Bayes factors.

Table S5: Bayesian colocalization analyses with GTEx v7 for all loci with $\log_{10}$ BF>4. Only significant colocalizations are shown, Tissue = Tissue of the eQTL, Gene = Gene of the eQTL, Chr = Chromosome of variant, Pos = Position of variant, Allele Frequency = Allele Frequency of variant, P Value eQTL = p value of the eQTL in the tissue, rsid = variant name, $\log_{10}$ BF GWAS = Bayes' Factor of the variant in the GWAS, PP.HO.abf = posterior probability of no causal variant, PP.H1.abf = posterior probability of causal variant for trait 1, PP.H2.abf = posterior probability of causal variant for trait 2, PP.H3.abf = posterior probability of two distinct causal variants, PP.H4.abf = posterior probability of one common causal variant.

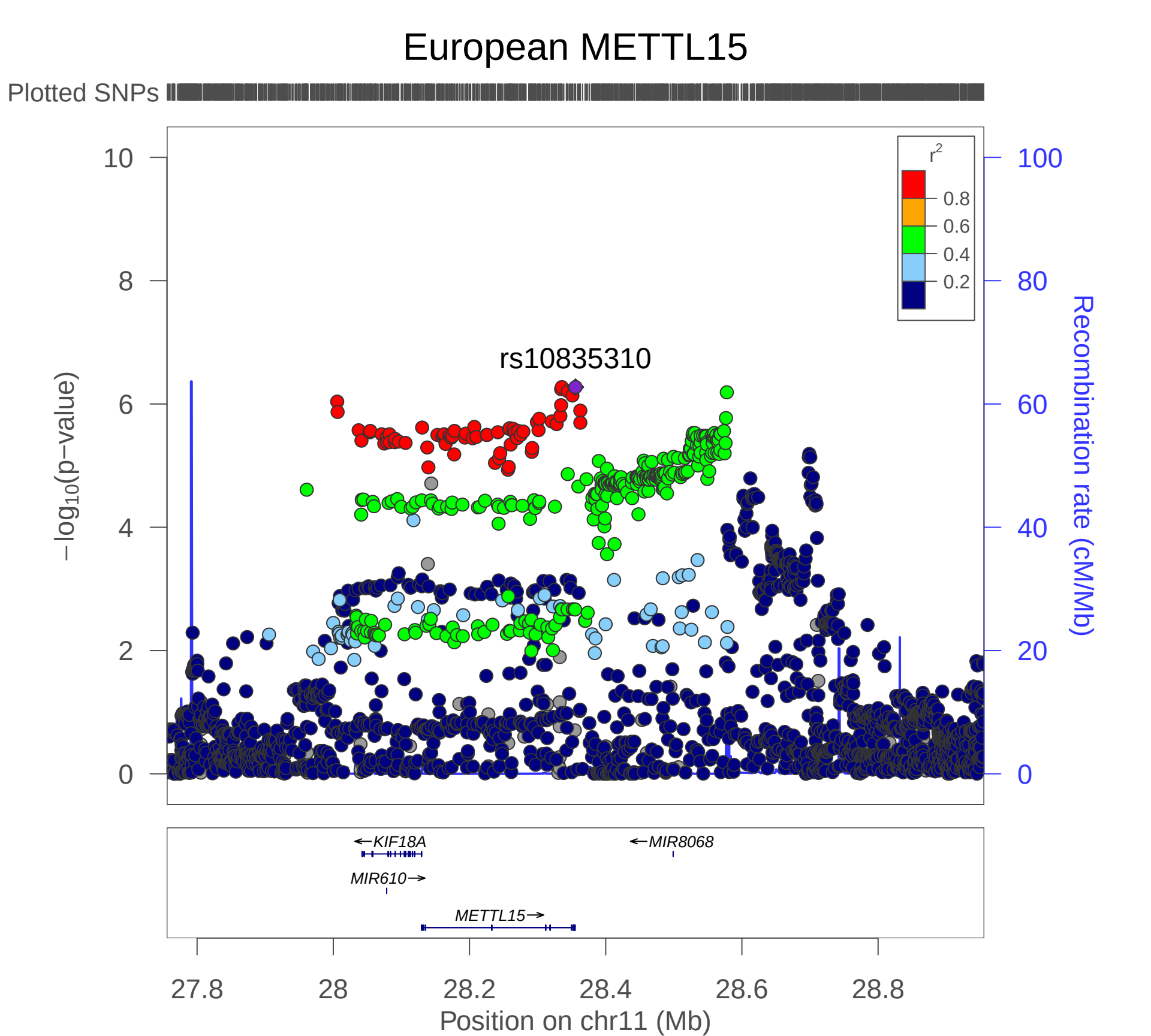
Table S6: Descriptive table of the quality control criteria used by each cohort in the discovery and replication stages. The ancestry and continental analysis group are shown along with genotyping chip type, stage of analysis, exclusionary SNP and sample filters, SNP numbers used in the final analysis and software used by each group.

Legends to Supplemental Figures

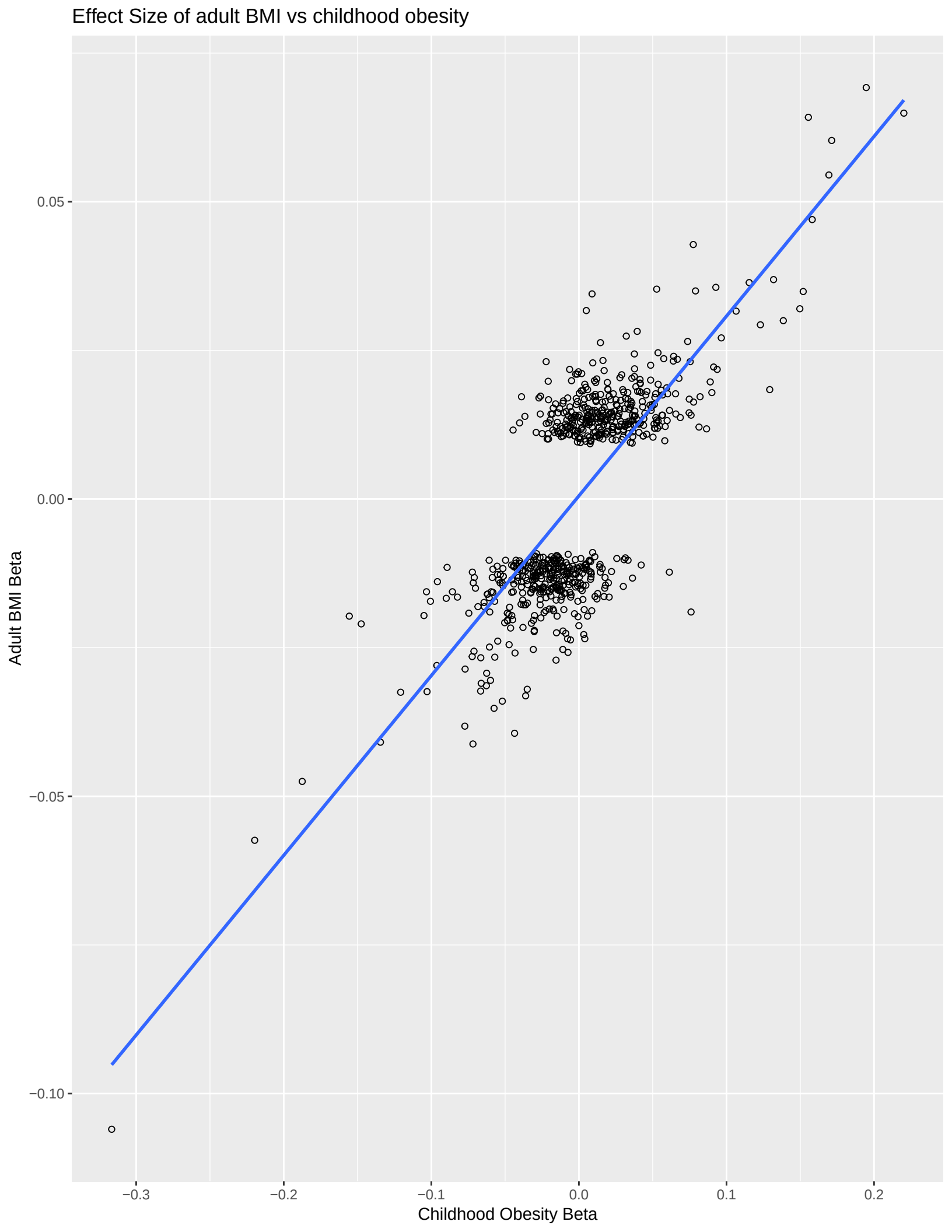
Figure S1: Regional association plot of *METTL15* region centered on rs10835310 in the sex-combined analysis. Linkage disequilibrium is shown according to the main sentinel SNP in European 1000 Genome Project populations.

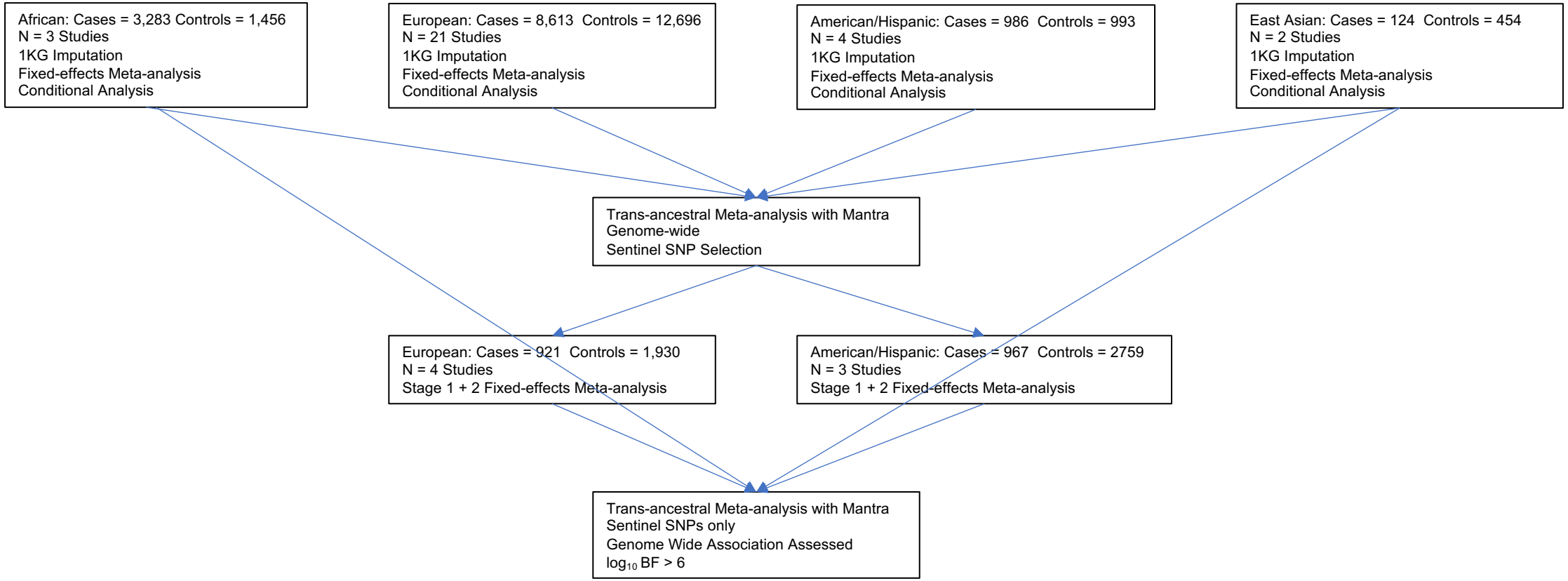
Figure S2: Scatter plot of the betas found in the latest adult BMI meta-analysis vs the corresponding beta's in childhood obesity for all significant variants in the adult BMI meta-analysis. Shown with the linear regression line through the data.

Figure S3: Flowchart of the meta-analysis**.** It shows the particular stage of results that were combined in the trans-ancestral meta-analysis.


European METTL15
Plotted SNPs
rs10835310
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
10
8
6
4
2
0
100
80
60
40
20
0
KIF18A
MIR8068
MIR610
METTL15
27.8
28
28.2
28.4
28.6
28.8
Position on chr11 (Mb)

date:	Tue Dec 12 08:22:02 2017
build:	hg19
display range:	chr11:27755657−28955657 [27755657−28955657]
hilite range:	0 − 0 [0 − 0]
reference SNP:	chr11:28355657
number of SNPs plotted:	2322
min P−value:	5.32E−7 [chr11:28335624]
max P−value:	1E0 [chr11:27767326]


Effect Size of adult BMI vs childhood obesity
Adult BMI Beta
0.05
0.00
−0.05
−0.10
−0.3
−0.2
−0.1
0.0
0.1
0.2
Childhood Obesity Beta


African: Cases = 3,283 Controls = 1,456
N = 3 Studies
1KG Imputation
Fixed-effects Meta-analysis
Conditional Analysis
European: Cases = 8,613 Controls = 12,696
N = 21 Studies
1KG Imputation
Fixed-effects Meta-analysis
Conditional Analysis
American/Hispanic: Cases = 986 Controls = 993
N = 4 Studies
1KG Imputation
Fixed-effects Meta-analysis
Conditional Analysis
East Asian: Cases = 124 Controls = 454
N = 2 Studies
1KG Imputation
Fixed-effects Meta-analysis
Conditional Analysis
Trans-ancestral Meta-analysis with Mantra
Genome-wide
Sentinel SNP Selection
European: Cases = 921 Controls = 1,930
N = 4 Studies
Stage 1 + 2 Fixed-effects Meta-analysis
American/Hispanic: Cases = 967 Controls = 2759
N = 3 Studies
Stage 1 + 2 Fixed-effects Meta-analysis
Trans-ancestral Meta-analysis with Mantra
Sentinel SNPs only
Genome Wide Association Assessed
log10 BF > 6