Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

eAppendix 1. Phenotypes and Cohort Description

For the discovery phase, we made use of five population based studies.

In the ALSPAC cohort (N= 4336), a prospective pregnancy cohort, when the children were 13 years old, parents completed the Development and Wellbeing Assessment (DAWBA) in an interview setting. The DAWBA is a package of interviews, questionnaires and rating techniques designed to generate ICD-10 and DSM-IV psychiatric diagnoses on 5-17 year olds[1].

In the COGA cohort (N= 1379), an alcohol dependence case-control sample, adult antisocial behaviour was measured using a count of the number of Antisocial Personality Disorder criteria endorsed under Criterion A from the DSM-IV [2].

In the GenerationR study (N= 1420), participants were drawn from a population-based cohort, when the children were between 4 and 10 years old, their teachers were asked to fill out the Teacher Report Form 6-18 (TRF) [3] from which we used the syndrome-oriented Rule-Breaking Behaviour scale.

In the TEDS cohort (N= 2734), a population-based sample, the Antisocial Process Screening Device (APSD) was administered when the children were 12 years old [4].

In the QIMR Berghofer cohort (N= 6531), a population-based sample, childhood conduct disorder was measured retrospectively in adults (at the average age of 30) using DSM-IV criteria for conduct disorder.

For the polygenic risk score analyses and replication phase, three cohorts were available.

In the Finnish CRIME Study (N= 6350), participants were drawn from a forensic cohort and interviewed (at the average age of 29) with the Structured Clinical Interview for DSM-IV-Disorders (SCID), to assess whether or not the prisoner fulfilled criteria for antisocial personality disorder[5].

In the Michigan State University Twin Registry (MSUTR, N= 825), a population-based sample, the Child Behaviour Checklist was administered to mothers to assess the children's (age range 6-10 years) level of antisocial behaviour[6].

In the Yale-Penn cohort (N= 2316), a substance-dependent sample, assessment of DSM-IV Conduct Disorder symptoms was administered in adults (at the average age of 41) via a comprehensive structured interview[7].

eAppendix 2. Meta-analysis and Quality Control.

Sex, age, and the first four principal components from an EIGENSTRAT analysis (to correct for any remaining population stratification) were included as covariates in the GWA analyses in all of the participating cohorts. In addition to the above-mentioned covariates, alcohol dependence case/control status was added as a covariate in the GWAS from the COGA cohort. An additive model was used in all analyses. In the continuous quantitative GWA, linear regressions were performed using imputed dosage genotypes and the above-mentioned covariates, whereas in the Finnish prisoners' cohort a logistic regression was performed. For MSUTR, the R package 'Sandwiches' was used for association analysis, adjusting for family correlation. Further details on the SOP analysis plan are available on the website of BroadABC, http://broadabc.ctglab.nl/.

Quality Control on summary statistics from individual cohorts

Quality control (QC) and meta-analysis of the GWA summary results were performed by two independent analysts (J.J.T. & A.J.), following a strict analysis protocol, which was an adapted version of the protocol from Winkler et al.[8]. First, we performed a format check to verify whether the provided summary file from each contributing cohort was in the correct format (i.e., header present, correct order of columns, etc.). Second, polymorphisms were excluded based on MAF (< 1%), imputation quality (imputation quality score < .6), and missing information (*p*-value, beta or SE). Third, we excluded duplicate polymorphisms. In addition, we compared the meta-analysis results against the 1000 Genomes reference dataset so that SNPs with non-matching alleles (which were not due to strand issues) were excluded. Study-specific Manhattan and Quantile-Quantile (QQ) plots were inspected for systematic bias and population stratification by comparing the distribution of the observed p-values with their expected distribution (for study-specific QQ plots, see Figure S2). The lambda values for

individual cohorts were close to one, indicating that the residual population stratification effect was at most minimal.

eAppendix 3. Gene and Gene-Set Analyses

The statistical software tool MAGMA was employed to perform the gene and gene-set analyses[9]. We utilized the quality-controlled summary statistics of the combined meta-analysis results. The SNP p-values were used as input for MAGMA (which does not require access to the raw genotype data). We tested the accumulated association of multiple SNPs for 18,052 genes, by calculating gene-based test statistics as the mean of the chi-square statistics of all SNPs that reside within a gene, including a window of 50 kb around the gene. The genotype data of the 1,000 Genomes European reference panel[10] were obtained to estimate the Linkage Disequilibrium (LD) between SNPs to account for LD within the genes. Next, we extracted 6213 gene sets from different source databases derived from the NCBI BioSystems database (http://www.ncbi.nlm.nih.gov/Structure/biosystems/docs/biosystems_about.html, accessed 24.3.2016). We then employed MAGMA to perform a competitive gene-set analysis (which tests whether the genes in a gene set are more strongly associated with ASB than other genes in the genome), in which the gene analysis results served as input. The gene-set analysis corrects for gene size and gene density, and accounts for LD between genes using a gene correlation matrix based on the genotype data of the 1,000 Genomes European reference panel.

Gene analyses in MAGMA on both the combined and sex-specific samples yielded no genes that were genome-wide significant ($p<2.8 \times 10^{-6}$) (see Table S3a-c). In the sex-combined analysis, the *CENPI* gene and *DNAH1* gene showed the strongest associations ($p=3.16 \times 10^{-5}$, $p= 6.98 \times 10^{-5}$). *CENPI* is thought to be involved in the response of gonadal tissues to follicle-stimulating hormone[11], whereas *DNAH1* has been previously related to male infertility and Primary Ciliary Dyskinesia[12,13]. The sex-specific gene analyses revealed the strongest associations with the *ACBD6* gene ($p= 1.95 \times 10^{-5}$) and *PMP22* gene ($p= 2.81 \times 10^{-5}$) in females and males, respectively. We conducted the gene-set analysis for the combined, male

and female samples. None of the 6214 gene sets reached significance ($p < 8.0 \times 10^{-6}$), with the 'Reactome cell communication' gene-set showing the strongest association in the combined sample ($p = 3.6 \times 10^{-4}$, Table S3d).

eAppendix 4. Enrichment of Signal in Previously Implicated Genes for Antisocial Behavior

To test for enrichment of signal for antisocial behaviour , we derived 29 genes from the study of Vassos et al. and tested them in the sex-combined and sex-specific samples. None of the traditional candidate genes on antisocial behaviour were significantly associated with our broader concept of antisocial behaviour (Table S4a-c), although the tyrosine hydroxylase gene (TH) in the male sample showed suggestive evidence for association ($p=0.0029$, $p_{corr}=.0841$). The TH gene, responsible for catalyzing the conversion of L-tyrosine to L-DOPA, has been previously related to aggressive social interactions in mice [14]. In addition, repeated exposure to aggressive experience in male mice increased tyrosine hydroxylase and dopamine transporter mRNA levels in another study[15], and the latter gene was also nominally significant in our male samples (SLC6A3, $p=0.028$; $p_{corr}=.812$).

eAppendix 5. Replication

The two female-specific GWS SNPs (chr1: rs2764450, chr11: rs11215217) could not be replicated in the female-specific Yale-Penn sample (N=950, with corresponding p-values of .71 and .54 respectively). However, the statistical power (uncorrected for winner's curse) to replicate in this sample at the level of nominal significance was small: 47% for the most associated SNP (Z = 5.61) with an estimated effect sizes of R^2=.37%. No GWAS results were available for replication on the X chromosome in Yale-Penn. Since the top three SNPs were not available in the non-imputed MSUTR and Finnish Crime cohorts, we selected SNPs in high LD (r2> .6) with the top SNPs utilizing PLINK software, resulting in six SNPs available for replication in both cohorts (see Table S7 for more details). None of the SNPs was significant after correcting for multiple testing, although one SNP (rs12089373, Finnish Crime cohort) yielded a nominal significant p-value (p=.047).

eAppendix 6. Functional Annotation

Functional annotation

We identified all SNPs that had an r2 of 0.1 or higher with the 2 independent lead SNPs of the female-specific METAL output. We used the 1000G phase 3 reference panel to calculate r2. We further filtered on SNPs with a P-value > 0.05. In addition, we only annotated SNPs with MAF ≥ 0.01.

Functional consequences of SNPs on genes for all lead SNPs and SNPs in LD with the lead SNPs were obtained by performing ANNOVAR gene-based annotation using Ensembl genes (build 85). In addition, CADD scores[16], and RegulomeDB[17] scores were annotated to SNPs by matching chromosome, position, reference and alternative alleles. For each SNP eQTLs were extracted from GTEx (44 tissue types)[18], Blood eQTL browser[19] and BIOS gene-level eQTLs[20]. The eQTLs obtained from GTEx were filtered on gene Q-value < 0.05 and eQTLs obtained from the other two databases were filtered on FDR < 0.05.

To test whether the SNPs were functionally active by means of histone modifications, we obtained epigenetic data from the NIH Roadmap Epigenomics Mapping Consortium[21] and ENCODE[22]. For every 200bp of the genome a 15-core chromatin state was predicted by a Hidden Markov Model based on 5 histone marks (i.e. H3K4me3, H3K4me1, H3K27me3, H3K9me3, and H3K36me3) for 127 tissue/cell types[23]. We annotated chromatin states (15 states in total) to SNPs by matching chromosome and position for every tissue/cell type. We computed the minimum state (1: the most active state) and the consensus state (majority of states) across 127 tissue/cell types for each SNP.

Results

Using information on functional consequences and expression quantitative trait loci (eQTLs), three genes were prioritized on chromosome 1 as potential causal genes: ACBD6, LHX4 and MR1 (see regional plot with annotation, Figure S5). The ACBD6 gene did not include exonic

SNPs with a low P-value, yet one of the intronic SNPs (rs10494528, p= 1.5 x 10-7 and in r2= .10 with the lead SNP in this locus) yielded a Combined Annotation Dependent Depletion (CADD) score of 17.6, indicating a possible regulatory function of the gene. eQTL information indicated that rs10494528 influences expression of ACBD6 in the testis (see expression heat plot, Figure S5). The LHX4 gene, which is associated with pituitary hormone deficiency, is mostly expressed in the caudate nucleus and cerebellum. The MR1 (Major Histocompatibility Complex, Class I-Related) gene, was previously associated with dyskinesia and is expressed in lymphocytes. The closest mapped gene on the chr11 locus was NXPE2, yet we didn't find any biological evidence pointing towards this gene. The hits on chromosome 11 in the female-specific analyses are in relatively near distance of the HT3A/B (<1mb) and DRD2 (< 2mb) genes, which are proposed candidate genes for ASB (See regional association plot, Figure 1D).

eAppendix 7. Tissue Expression

Tissue expression of genes

RNA sequencing data of 8,555 tissue samples with 53 unique tissue labels were derived from the GTEx portal v6. Of the 52 genes implicated by either the GWAS or the GWGWAS, 3 were included in the GTEx data. Normalization of the data was performed as described previously[24]. Briefly, genes with RPKM (Reads Per Kilo base Million) value smaller than 0.1 in at least 80% of the samples were removed. The remaining genes were log2 transformed (after using a pseudocount of 1), and finally a zero-mean normalization was applied.

eTable 1. Genotyping, Quality Control, and Imputation Information of the Participating Cohorts

Cohort	Genotyping platform(s)	HWE *P*value	SNP call rate	Sample call rate	Imputation reference set	Imputation software	Association software
ALSPAC	Illumina 550K	>5 x 10-7	>0.95	>0.97	1000G phase 1 v3	MACH	MACH2QTL
COGA	Illumina 1M	>1 x 10-6	>0.95	>0.95	1000G phase 1 v3	IMPUTE	SNPTEST
GENR	Infinium II HumanHap 610 or 660W Quad Arrays	>1 x 10-6	>0.98	>0.975	1000G phase 1 v3	MACH	Plink
TEDS	Affymetrix 6.0	>1 x 10-6	>0.95	>0.98	1000G phase 1 v3	IMPUTE2	SNPTEST
QIMR	Illumina 610 & 670 quad Illumina 370 single & duo Illumina 317 single	>1 x 10-6	>0.95	>0.95	1000G phase 1 v3	MACH / minimac	Merlin-offline
Finnish CRIME Study	Human670-QuadCustom	>1 x 10-3	>0.99	>0.99	NA	NA	NA

MSUTR	Illumina HumanCoreExome v1.1	>1 x 10-5	>0.98	>0.97	NA	NA	NA
Yale-Penn	Illumina HumanOmni-Quad v1.0 Illumina Infinium Human Core Exome miicroarry	>1 x 10-6	≥0.98	≥0.98	1000G phase1 v3	IMPUTE2	R-GEE

HWE= Hardy-Weinberg equilibrium. NA=Not available.

eTable 2. Number of Duplicate Markers and Mismatches, the Genomic Control Values, and Number of Processed Polymorphisms That Were Available After QC

Cohort	Duplicates	Mismatch	GC parameter	Processed Markers
QIMR	None	5109	1.019	7425086
ALSPAC	None	5479	1.008	8113724
GENR	None	7080	1.005	10
TEDS	None	870	0.990	7705607
COGA	2	1	0.994	9222442

QC= Quality Control, GC=Genomic Control

eTable 3. Genes Showing the Strongest Association ($P < 10^{-3}$) With Antisocial Behaviour in the Sex-Combined MAGMA Gene Analysis (N= 16,400)

HGNC Symbol	HGNC ID	CHR	N SNPS	P*
CENPI	2491	X	167	3.16E-05
DNAH1	25981	3	118	6.91E-05
ACSL4	2182	X	61	9.10E-05
SPIC	121599	12	35	0.00013
LIM2	3982	19	27	0.00015
SEMA3G	56920	3	15	0.000154
PSMB3	5691	17	31	0.000175
TADA2B	93624	4	49	0.00028
KDM5A	5927	12	307	0.000347
HOMER2	9455	15	252	0.000375
BDH1	622	3	256	0.000481
IGBP1	3476	X	46	0.000504
CD36	948	7	228	0.000532
C19orf84	147646	19	18	0.000565
PHF7	51533	3	15	0.0006
LY96	23643	8	104	0.000665
DOCK7	85440	1	326	0.000692
UTP20	27340	12	272	0.000814
EHD1	10938	11	64	0.000816
GLYCTK	132158	3	13	0.000819
CEACAM7	1087	19	45	0.000826
HYI	81888	1	7	0.000968

The threshold for significance was Bonferroni corrected at $p<2.8*10-6$.

HGNC= HUGO Gene Nomenclature Committee. CHR=Chromosome. NSNPS=Number of SNPs.

Table 4. Genes Showing the Strongest Association ($P < 10^{-3}$) With Antisocial Behavior in the Female-Specific MAGMA Gene Analysis (N= 8535)

HGNC Symbol	HGNC ID	CHR	N SNPS	P
ACBD6	84320	1	484	1.95E-05
ADGRV1	84059	5	1402	7.65E-05
OSTC	58505	4	39	0.000139
CD151	977	11	32	0.000159
ABRACL	58527	6	50	0.00017
IRG1	730249	13	21	0.00018
POLR2L	5441	11	10	0.000215
VWC2	375567	7	261	0.000237
SPOP	8405	17	74	0.000242
MT4	84560	16	14	0.000257
POP5	51367	12	10	0.00031
NXPH3	11248	17	9	0.000327
CRACR2B	283229	11	11	0.000348
MED29	55588	19	17	0.000352
KCTD18	130535	2	47	0.000365
RNF10	9921	12	127	0.000431
CHIC2	26511	4	52	0.00049
PCSK1N	27344	X	3	0.00053
FLNC	2318	7	53	0.000571
KIAA1429	25962	8	254	0.000572
RHOC	389	1	14	0.0006
ANOS1	3730	X	150	0.00064
DNAJC1	64215	10	323	0.000718
ARHGAP15	55843	2	1374	0.000738
RAB38	23682	11	238	0.00078
DYNLL1	8655	12	79	0.000783
RABGGTB	5876	1	16	0.000817
WDR49	151790	3	241	0.000861
ZNF404	342908	19	17	0.000917
ZNF45	7596	19	68	0.000981
NMNAT3	349565	3	233	0.000984

The threshold for significance was Bonferroni corrected at $p<2.8*10-6$.

HGNC= HUGO Gene Nomenclature Committee. CHR=Chromosome. NSNPS=Number of SNPs.

Table 5. Genes Showing the Strongest Association ($P < 10^{-3}$) With Antisocial Behavior in the Male-Specific MAGMA Gene Analysis (N = 7772)

HGNC Symbol	HGNC ID	CHR	N SNPS	P
PMP22	5376	17	79	2.81E-05
ST13	6767	22	33	2.99E-05
GLP1R	2740	6	183	3.84E-05
XPNPEP3	63929	22	38	4.66E-05
RAB23	51715	6	24	8.04E-05
RBX1	9978	22	14	9.19E-05
TGFB3	7043	14	41	0.00011
NID1	4811	1	181	0.00011
TADA2B	93624	4	43	0.000236
NME2	4831	17	15	0.000249
NDST3	9348	4	637	0.000254
CTSV	1515	9	15	0.000283
OAT	4942	10	66	0.000354
EMC10	284361	19	11	0.000439
LINGO1	84894	15	75	0.000446
ZNF518A	9849	10	74	0.000459
LMO3	55885	12	51	0.000474
FAM171B	165215	2	109	0.000548
LDLR	3949	19	153	0.000566
RPS27L	51065	15	19	0.0007
ZNF329	79673	19	60	0.000742
AK3	50808	9	134	0.000773
NUP93	9688	16	237	0.000857
PEG10	23089	7	15	0.000905
PHC2	1912	1	110	0.000929
KCNQ5	56479	6	1150	0.000946
HCAR3	8843	12	11	0.000977

The threshold for significance was Bonferroni corrected at $p<2.8*10-6$.

HGNC= HUGO Gene Nomenclature Committee. CHR=Chromosome. NSNPS=Number of SNPs.

eTable 6. The 50 Gene Sets Showing the Strongest Association in the Sex-Combined MAGMA Gene-Set Analysis

Gene Set	NGenes	Competitive P
reactome cell cell communication	115	0.0003596
go:0030595 leukocyte chemotaxis	34	0.0004502
go:0005523 tropomyosin binding	13	0.0007121
go:0006084 acetyl-coa metabolic process	30	0.0007307
go:0030427 site of polarized growth	48	0.000805
biocarta il7 pathway	17	0.0009684
panther molecular function neuropeptide	18	0.0010136
go:0030426 growth cone	47	0.0011791
go:0005160 transforming growth factor beta receptor binding	18	0.0012302
reactome signal regulatory protein sirp family interactions	11	0.0012306
go:0050900 leukocyte migration	51	0.0014284
st b cell antigen receptor	40	0.0014959
pc signal regulatory protein (sirp) family interactions	10	0.0015486
pc interactions of the immunoglobulin superfamily (igsf) member proteins	29	0.0016953
go:0008353 rna polymerase subunit kinase activity	11	0.0017244
go:0051250 negative regulation of lymphocyte activation	50	0.0018827
go:0042439 ethanolamine and derivative metabolic process	32	0.0021422
panther biological process cytokine/chemokine mediated immunity	108	0.0021654
st interleukin 4 pathway	26	0.0021679
panther molecular function single-stranded dna-binding protein	23	0.0022061
go:0050890 cognition	765	0.0023966
go:0060326 cell chemotaxis	37	0.0025149
reactome transcription	175	0.0028628
go:0045639 positive regulation of myeloid cell differentiation	31	0.0032747
go:0050866 negative regulation of cell activation	56	0.0033356
go:0002695 negative regulation of leukocyte activation	53	0.0033455
reactome antigen activates b cell receptor leading to generation of second messengers	29	0.0039508
biocarta il17 pathway	17	0.0043007
go:0005913 cell-cell adherens junction	33	0.004389
go:0016049 cell growth	55	0.0044261
go:0009109 coenzyme catabolic process	25	0.0044706
go:0050869 negative regulation of b cell activation	14	0.0044779
go:0007601 visual perception	211	0.0046752
go:0050953 sensory perception of light stimulus	211	0.0046752
go:0050868 negative regulation of t cell activation	41	0.0048581
go:0010884 positive regulation of lipid storage	9	0.0049601
reactome pyruvate metabolism and citric acid tca cycle	36	0.0050238
reactome rna pol ii transcription	97	0.0050703
reactome expra repair	102	0.0052929
pid pdgfra pathway	22	0.0058029

pc pdgfr-alpha signaling pathway	21	0.0060843
pc cell junction organization	51	0.0065199
reactome formation of incision complex in gg ner	19	0.0070958
panther biological process peroxisome transport	14	0.0076914
go:0008334 histone mrna metabolic process	21	0.007742
go:0006099 tricarboxylic acid cycle	22	0.0077486
go:0046356 acetyl-coa catabolic process	22	0.0077486
reactome cleavage of growing transcript in the termination region	42	0.0080788
go:0007613 memory	35	0.0082505

The threshold for significance was Bonferroni corrected at p<8.0*10-6.

NGenes=Number of genes.

eTable 7. Combined (N = 16 400) Enrichment Results Regarding 29 Candidate Genes (Derived From Vassos et al) Previously Related to Antisocial Phenotypes

HGNC Symbol	HGNC ID	CHR	NSNPS	P
OXTR	5021	3	94	0.035
HTR1A	3350	5	3	0.065
APOE	348	19	5	0.123
ESR1	2099	6	1304	0.128
TH	7054	11	22	0.171
DRD3	1814	3	132	0.188
BDNF	627	11	115	0.212
CREB1	1385	2	117	0.220
HTR1B	3351	6	3	0.265
COMT	1312	22	126	0.341
HTR2A	3356	13	239	0.455
TACR1	6869	2	409	0.461
DRD2	1813	11	177	0.482
DRD4	1815	11	11	0.491
AVPR1A	552	12	24	0.522
AR	367	X	122	0.546
SNAP25	6616	20	216	0.604
ABCG1	9619	21	378	0.629
TBX19	9095	1	96	0.659
TPH2	121278	12	301	0.727
DRD1	1812	5	7	0.729

TPH1	7166	11	38	0.757
NOS1	4842	12	449	0.765
MAOA	4128	X	116	0.781
SLC6A3	6531	5	202	0.796
CYP2D6	1565	22	24	0.800
SLC6A4	6532	17	76	0.825
HTR2C	3358	X	496	0.844
ADRA2A	150	10	9	0.885

HGNC= HUGO Gene Nomenclature Committee. CHR=Chromosome. NSNPS=Number of SNPs.

The threshold for significance was Bonferroni corrected at 0.0017.

eTable 8. Female-Specific (N = 8535) Enrichment Results Regarding 29 Candidate Genes (Derived From Vassos et al) Previously Related to Antisocial Phenotypes

HGNC Symbol	HGNC ID	CHR	NSNPS	P
OXTR	5021	3	51	0.053
CREB1	1385	2	90	0.057
TBX19	9095	1	76	0.105
APOE	348	19	5	0.161
TH	7054	11	14	0.174
SLC6A4	6532	17	57	0.223
DRD3	1814	3	114	0.314
TPH2	121278	12	258	0.351
SLC6A3	6531	5	97	0.389
SNAP25	6616	20	187	0.389
CYP2D6	1565	22	16	0.401
HTR2C	3358	X	425	0.440
AR	367	X	86	0.497
TACR1	6869	2	284	0.519
DRD2	1813	11	160	0.537
ESR1	2099	6	1115	0.619
MAOA	4128	X	79	0.678
HTR2A	3356	13	210	0.695
HTR1B	3351	6	2	0.704
ADRA2A	150	10	4	0.734
HTR1A	3350	5	3	0.750

COMT	1312	22	114	0.781
NOS1	4842	12	408	0.794
BDNF	627	11	100	0.801
DRD1	1812	5	5	0.837
ABCG1	9619	21	281	0.847
AVPR1A	552	12	19	0.852
TPH1	7166	11	35	0.900
DRD4	1815	11	3	0.989

HGNC= HUGO Gene Nomenclature Committee. CHR=Chromosome. NSNPS=Number of SNPs.

The threshold for significance was Bonferroni corrected at 0.0017.

eTable 9. Male-Specific (N = 7772) Enrichment Results Regarding 29 Candidate Genes (Derived From Vassos et al) Previously Related to Antisocial Phenotypes

HGNC Symbol	HGNC ID	CHR	NSNPS	P
TH	7054	11	14	0.0029
SLC6A3	6531	5	97	0.0282
COMT	1312	22	114	0.0805
DRD3	1814	3	112	0.178
SNAP25	6616	20	187	0.179
AVPR1A	552	12	19	0.191
TBX19	9095	1	76	0.285
DRD4	1815	11	3	0.344
OXTR	5021	3	51	0.407
DRD1	1812	5	5	0.412
NOS1	4842	12	408	0.444
HTR1B	3351	6	2	0.488
MAOA	4128	X	79	0.528
ABCG1	9619	21	282	0.543
ESR1	2099	6	1114	0.577
DRD2	1813	11	160	0.611
ApoE	348	19	5	0.614
SLC6A4	6532	17	57	0.628
HTR2C	3358	X	425	0.634
CYP2D6	1565	22	16	0.645
ADRA2A	150	10	4	0.646

AR	367	X	86	0.708
CREB1	1385	2	90	0.754
BDNF	627	11	100	0.789
TPH2	121278	12	258	0.822
HTR1A	3350	5	3	0.915
TACR1	6869	2	284	0.949
TPH1	7166	11	35	0.959
HTR2A	3356	13	209	0.961

HGNC= HUGO Gene Nomenclature Committee. CHR=Chromosome. NSNPS=Number of SNPs.

The threshold for significance was Bonferroni corrected at 0.0017.

eTable 10. Replication Test Regarding SNPs in High LD (r^2> 0.6) With the Top 3 SNPs (Chr1: rs2764450, Chr11: rs11215217, ChrX: rs41456347) Available in the Finnish Crime Study and MSUTR

Finnish Crime Study	*SNP*	*BroadABC Beta (A1)*	*BroadABC P*	*Finnish Crime Study OR (A1)*	*Finnish Crime Study P*
Chr1	rs357044	-2.63 (T)	7.46×10^{-6}	1.65 (G)	.24
	rs12089373	-3.10 (T)	7.31×10^{-8}	2.35 (G)	.047
Chr11	rs10891749	2.33 (T)	0.00033	1.02 (A)	.95
	rs11215211	2.65 (A)	1.49×10^{-5}	1.79 (A)	.15
	rs7107688	1.76 (A)	0.0049	1.26 (A)	.51
ChrX	rs7881831	2.67 (T)	3.25×10^{-6}	1.11 (A)	.50
MSUTR	*SNP*	*BroadABC Beta (A1)*	*BroadABC P*	*MSUTR BETA (A1)*	*MSUTR P*
Chr1	rs6425635	3.04 (G)	1.35×10^{-6}	-.084 (G)	.80
ChrX	rs7881831	2.67 (T)	3.25×10^{-5}	-.23 (T)	.13
	rs5911410	2.32 (A)	0.00021	-015 (A)	.31
	rs5911401	2.67 (T)	2.93×10^{-5}	-0.22 (T)	.14

eTable 11. Results of the Combined GWAS Meta-analysis for the Independent* Signals Reaching $P < 10^{-5}$ in the Discovery Stage

SNP (CHR:BP)	A1	A2	FreqA1	Weight	BETA	Zscore	P-value	Direction *
20:11022343	T	C	0.034	16 400	-1,269	-4,987	6.13E-07	-----
1:161203625	D	R	0.377	16 400	3,267	4,767	1.87E-06	+++++
19:28617530	C	G	0.776	16 400	-2,802	-4.75	2.03E-06	-----
22:44814823	A	G	0.987	13666	-0.745	-4,723	2.32E-06	----?
1:214831082	A	G	0.981	16 400	0.897	4,656	3.22E-06	-++++
22:44788714	T	C	0.013	16 400	0.731	4,655	3.23E-06	+++++
6:44486470	T	C	0.242	16 400	2,801	4,627	3.71E-06	+++++
6:20124072	C	G	0.925	13666	1,721	4,624	3.77E-06	++++?
2:142706544	T	C	0.020	16 400	0.919	4,621	3.83E-06	+++++
9:18925517	I	R	0.125	16 400	-2,162	-4,617	3.89E-06	-----
8:130589676	A	G	0.383	16 400	-3,164	-4,603	4.17E-06	---+-
5:174778257	A	G	0.082	13666	1,776	4,589	4.45E-06	++++?
9:18927177	A	C	0.855	16 400	2,285	4,582	4.61E-06	+++++
2:166137272	C	G	0.986	12064	-0.773	-4,572	4.83E-06	-?---
3:44561068	T	C	0.012	12246	0.694	4,543	5.54E-06	+++??
9:18925519	T	G	0.868	16 400	2,167	4,523	6.10E-06	+++++
1:118952620	T	C	0.211	16 400	2,600	4,509	6.51E-06	+++++
4:170198039	T	C	0.870	16 400	2,132	4,479	7.50E-06	+++++
20:13881901	A	G	0.977	16 400	0.940	4,443	8.88E-06	+++++
7:118592423	T	C	0.378	16 400	3,036	4,427	9.54E-06	-++++
2:186178601	A	G	0.112	16 400	1,962	4,405	1.06E-05	+++++
17:65484443	T	C	0.151	16 400	2,223	4,391	1.13E-	+++++

								05
4:157845436	T	C	0.685	16 400	-2,885	-4.39	1.13E-05	+----
2:88358825	C	G	0.311	16 400	2,861	4.37	1.24E-05	+++++
7:46949185	I	R	0.026	16 400	0.983	4,367	1.26E-05	-++-+
1:51480618	D	R	0.308	16 400	2,844	4,355	1.33E-05	+++-+
7:118612692	I	R	0.613	16 400	-2,998	-4,352	1.35E-05	-----
7:46948061	A	T	0.023	16 400	0.913	4,344	1.40E-05	-++-+
9:18926997	A	G	0.895	16 400	1,882	4,344	1.40E-05	+++++
1:33858873	T	C	0.738	16 400	2,698	4.34	1.43E-05	-++++
11:82017936	A	G	0.637	16 400	-2,944	-4,328	1.51E-05	-----
12:83736620	C	G	0.026	16 400	0.974	4,313	1.61E-05	+++++
20:48577475	A	G	0.065	16 400	1,500	4,311	1.62E-05	+++++
1:214825528	A	G	0.012	16 400	-0.663	-4,306	1.66E-05	+----
14:76586835	T	C	0.074	16 400	1,587	4,297	1.73E-05	+++++
3:55222407	A	G	0.978	16 400	-0.891	-4,294	1.75E-05	-----
19:38660115	D	R	0.302	16 400	-2,781	-4,282	1.86E-05	-----
19:51895566	A	G	0.837	16 400	2,235	4.28	1.87E-05	+++++
5:71721068	T	C	0.959	16 400	-1,200	-4.27	1.95E-05	+----
2:58857542	A	G	0.339	16 400	2,856	4,267	1.98E-05	-++++
4:27554040	A	G	0.588	16 400	2,968	4,264	2.01E-05	+++++
15:82199306	A	C	0.924	14980	1,601	4,263	2.02E-05	+++?+
5:14140032	T	C	0.919	16 400	1,648	4,262	2.03E-05	+++++
6:123913570	T	C	0.067	13666	-1,509	-4,259	2.05E-05	----?
9:76715645	T	C	0.049	16 400	1,305	4,259	2.06E-05	-++++
11:105803799	D	R	0.299	16 400	-2,752	-4,249	2.15E-05	-----
X:95654291	C	G	0.987	12246	-0.674	-4,225	2.39E-05	+--??

3:21138757	D	R	0.285	16 400	-2,686	-4,208	2.57E-05	-----
8:16448605	T	C	0.033	16 400	1,059	4.2	2.67E-05	+++++
8:56355418	T	G	0.971	16 400	1,000	4.2	2.67E-05	+++++
3:82479279	T	C	0.564	16 400	-2,937	-4,188	2.82E-05	-----
8:56394915	A	G	0.982	16 400	0.795	4,184	2.86E-05	+++++
3:53603384	A	T	0.089	16 400	-1,680	-4,176	2.97E-05	---+-
1:118933655	I	R	0.211	16 400	2,406	4,174	2.99E-05	+++++
3:174773773	T	C	0.831	16 400	2,209	4,168	3.08E-05	+++++
20:24982422	T	C	0.952	13666	1,256	4,156	3.25E-05	++++?
3:15753502	C	G	0.987	16 400	-0.675	-4,154	3.27E-05	----+
6:106802097	I	R	0.034	12246	1,070	4,152	3.29E-05	+++??
6:44463388	A	G	0.375	16 400	-2,841	-4.15	3.33E-05	-----
20:52115707	A	C	0.676	16 400	2,746	4,149	3.33E-05	+++++
X:94169992	T	C	0.968	13666	-1,029	-4,147	3.37E-05	----?
X:94171676	T	C	0.032	13666	1,029	4,146	3.39E-05	++++?
17:65490250	I	R	0.153	16 400	2,102	4,128	3.66E-05	+++++
10:62354755	T	C	0.988	13666	-0.638	-4,127	3.67E-05	----?
8:103406754	D	R	0.267	16 400	-2,580	-4,124	3.73E-05	-----
3:24744989	T	C	0.983	13666	-0.748	-4,114	3.89E-05	----?
9:114907789	T	C	0.150	16 400	-2,071	-4,102	4.09E-05	-----
6:10893367	I	R	0.361	16 400	2,781	4,096	4.20E-05	+++++
14:91071636	D	R	0.285	16 400	2,607	4,085	4.40E-05	+++++
11:12374101	A	G	0.020	13666	0.809	4,085	4.41E-05	++++?
18:36626487	I	R	0.013	14980	0.646	4,082	4.46E-05	+++?+
7:6158677	C	G	0.964	16 400	1,079	4.08	4.50E-05	+++++
13:39580930	A	G	0.011	14980	0.588	4,076	4.59E-05	+++?+

2:58854064	T	G	0.843	16 400	-2,095	-4,073	4.64E-05	-----
14:35431809	C	G	0.034	16 400	-1,036	-4.07	4.70E-05	-----
8:15930756	T	C	0.114	16 400	1,824	4,066	4.78E-05	+++-+
1:118857528	T	C	0.528	16 400	2,871	4,066	4.79E-05	+++++
7:136457204	A	G	0.118	16 400	-1,852	-4,064	4.83E-05	---+-
7:118923413	T	C	0.545	16 400	2,857	4,057	4.96E-05	+++-+
3:15633771	I	R	0.013	16 400	0.650	4,056	5.00E-05	++++-
15:83503678	I	R	0.080	14980	-1,551	-4,054	5.03E-05	---?-
3:157162127	A	T	0.055	16 400	-1,301	-4,052	5.07E-05	---+-
15:83505262	T	C	0.922	14980	1,539	4,052	5.08E-05	+++?+
22:28043913	C	G	0.985	16 400	0.698	4,045	5.24E-05	+++++
6:10896010	T	C	0.238	16 400	2,433	4,041	5.31E-05	+++++
12:82417539	A	G	0.725	16 400	-2,551	-4,039	5.37E-05	-----
12:121040703	A	T	0.258	16 400	2,497	4,036	5.44E-05	+++-+
14:30202318	A	T	0.044	16 400	1,170	4,033	5.51E-05	+++++
3:81936012	A	G	0.015	16 400	-0.690	-4.03	5.57E-05	-----
18:37595589	C	G	0.964	16 400	1,060	4,028	5.64E-05	+++++
3:119183341	C	G	0.401	16 400	2,791	4,027	5.65E-05	+++++
12:74772005	D	R	0.410	16 400	2,801	4,027	5.66E-05	+++++
3:119191559	I	R	0.385	16 400	2,770	4,025	5.70E-05	+++++
10:54946928	A	G	0.022	16 400	-0.830	-4,018	5.88E-05	-----
4:101922955	A	G	0.047	16 400	-1,204	-4,013	5.99E-05	-----
7:115987538	T	C	0.256	16 400	2,477	4,012	6.02E-05	+++++
11:114674051	C	G	0.106	16 400	1,746	4,009	6.10E-05	+++++
15:25614535	A	C	0.874	14980	1,882	4,008	6.11E-05	-++?-
1:183918820	T	G	0.585	16 400	-2,793	-4,008	6.11E-05	-----

10:10401580	A	G	0.073	14980	-1,476	-4,008	6.12E-05	---?-
8:143088760	D	R	0.259	16 400	2,482	4,008	6.12E-05	+++--
2:85446376	A	G	0.988	13666	-0.622	-4,007	6.15E-05	----?
12:82450048	T	C	0.119	16 400	1,833	4,006	6.16E-05	++++-
8:130624661	A	G	0.510	16 400	2,830	4,003	6.26E-05	+++++
10:13860603	C	G	0.730	16 400	-2,512	-4,002	6.27E-05	-----
9:105185757	A	T	0.935	16 400	-1,398	-4,001	6.30E-05	+----
8:123651639	A	G	0.102	16 400	-1,712	-4,001	6.32E-05	-----
22:33431175	T	C	0.012	12246	0.618	3,998	6.40E-05	+++??
13:93703791	A	G	0.200	16 400	-2,261	-3,996	6.45E-05	-----
2:8796213	D	R	0.711	16 400	-2,559	-3,992	6.54E-05	-----
12:114238211	T	C	0.545	16 400	-2,811	-3,991	6.57E-05	+----
X:100413310	A	G	0.775	13666	-2,356	-3.99	6.62E-05	----?
18:10443693	T	C	0.488	16 400	2,820	3,989	6.63E-05	+++++
2:58721235	T	C	0.194	16 400	2,227	3,983	6.81E-05	-++++
18:36619499	T	C	0.989	14980	-0.600	-3,982	6.85E-05	---?-
11:37518784	T	C	0.205	16 400	2,274	3,981	6.87E-05	+++++
8:15914243	A	G	0.199	16 400	2,247	3.98	6.90E-05	+++-+
5:80101489	A	G	0.837	16 400	-2,078	-3,977	6.99E-05	-----
3:153071132	A	C	0.789	16 400	-2,293	-3,975	7.04E-05	-----
9:86216100	A	G	0.652	16 400	-2,675	-3.97	7.19E-05	-----
7:134190499	T	G	0.568	16 400	-2,780	-3,968	7.24E-05	-+---
18:36625482	I	R	0.012	14980	0.598	3,968	7.25E-05	+++?+
4:32787053	D	R	0.297	16 400	-2,560	-3,961	7.48E-05	-----
5:32922686	T	C	0.308	16 400	2,586	3.96	7.50E-05	+++-+
7:118813757	I	R	0.498	16 400	-2,799	-3,959	7.52E-05	---+-

1:16558838	A	C	0.402	16 400	-2,742	-3,955	7.65E-05	-----
1:233856922	C	G	0.985	16 400	0.671	3,955	7.65E-05	+++++
20:16531772	I	R	0.226	16 400	2,338	3,951	7.78E-05	+++++
3:5594752	I	R	0.128	16 400	1,863	3,946	7.96E-05	+++++
20:19031662	A	T	0.986	16 400	0.660	3,944	8.00E-05	+++++
12:21661642	T	G	0.145	16 400	1,962	3,942	8.09E-05	+++++
19:24474610	T	C	0.212	16 400	2,275	3,939	8.18E-05	+++++
19:50993379	D	R	0.566	16 400	-2,760	-3,938	8.22E-05	-----
10:104779637	T	G	0.988	10644	0.606	3,936	8.29E-05	+?+?+
10:55252741	T	G	0.885	16 400	1,773	3,935	8.32E-05	++++-
8:15220506	T	C	0.885	16 400	1,773	3,935	8.33E-05	+++++
6:139380556	T	C	0.093	16 400	-1,618	-3,934	8.36E-05	-----
3:82502402	T	C	0.240	16 400	2,375	3,933	8.37E-05	+++++
6:89224985	T	C	0.020	16 400	0.769	3,931	8.47E-05	+++++
9:76829180	D	R	0.453	16 400	2,765	3,928	8.56E-05	+++++
5:80287214	A	G	0.509	16 400	-2,776	-3,926	8.64E-05	-----
3:70567224	A	G	0.323	16 400	2,595	3,925	8.66E-05	+++++
11:49983747	D	R	0.496	16 400	-2,775	-3,925	8.69E-05	-----
14:91775889	T	C	0.075	16 400	-1,458	-3,924	8.70E-05	-----
X:93717641	T	C	0.519	13666	-2,769	-3,919	8.89E-05	----?
12:82423772	I	R	0.101	16 400	1,668	3,918	8.92E-05	++++-
16:80319404	A	G	0.053	14980	1,243	3,916	8.99E-05	+++?+
2:155212216	T	C	0.958	13666	1,117	3,915	9.06E-05	++++?
15:94016256	D	R	0.347	14980	2,635	3,914	9.09E-05	+++?+
17:46513678	T	C	0.989	12246	-0.580	-3,914	9.09E-05	---??
5:76843459	D	R	0.259	16 400	2,424	3,914	9.10E-05	+++++

15:25685228	D	R	0.623	14980	2,681	3,912	9.17E-05	+++?+
2:173696015	A	T	0.856	16 400	-1,940	-3,911	9.18E-05	---+-
1:4739425	C	G	0.068	16 400	1,388	3,908	9.30E-05	+++-+
X:108388461	A	T	0.853	13666	-1,958	-3,907	9.34E-05	----?
7:49832310	A	T	0.146	16 400	1,948	3,906	9.40E-05	+++++
10:13847936	T	C	0.436	16 400	2,738	3,905	9.43E-05	+++-+
18:53803843	T	C	0.069	13666	-1,398	-3,904	9.47E-05	----?
6:70792367	T	C	0.065	16 400	-1,359	-3,903	9.49E-05	+----
8:128466046	A	G	0.896	12246	1,685	3,903	9.50E-05	+++??
5:53945997	A	G	0.255	16 400	2,406	3,903	9.51E-05	+++++
15:94213042	A	G	0.213	14980	2,260	3,902	9.53E-05	+++?+
3:82486400	I	R	0.553	16 400	-2,743	-3,902	9.53E-05	-----
X:93728852	A	G	0.543	13666	-2,749	-3,902	9.55E-05	----?
11:1733266	T	C	0.854	16 400	1,946	3,902	9.55E-05	+++-+
18:8211443	D	R	0.328	16 400	-2,590	-3,901	9.58E-05	-----
3:153096430	A	G	0.553	16 400	-2,742	-3.9	9.62E-05	---++
3:54894123	A	G	0.220	16 400	2,284	3.9	9.63E-05	-++++
3:82486401	I	R	0.553	16 400	-2,741	-3,899	9.66E-05	-----
20:24718193	T	C	0.043	13666	-1,122	-3,899	9.67E-05	----?
13:93711456	A	C	0.875	16 400	1,824	3,898	9.71E-05	+++++
4:7048134	T	C	0.505	16 400	2,756	3,898	9.71E-05	+++++
15:59476316	T	C	0.089	12246	-1,571	-3,896	9.76E-05	---??
5:16863628	A	G	0.987	12246	-0.624	-3,894	9.88E-05	---??
10:44892506	A	G	0.547	16 400	2,740	3,893	9.89E-05	+++++
1:112486111	T	C	0.544	16 400	2,742	3,893	9.89E-05	+++-+
4:166829251	A	G	0.945	16 400	-1,256	-3,892	9.93E-	-----

*P-value-informed LD clumping was performed in plink using 0.001 as significance threshold for index SNPs, 0.01 as secondary significance threshold for clumped SNPs, 0.5 as LD r2 threshold, and 250kb as physical distance threshold.*Input order: COGA-ALSPAC-QIMR-GENR-TEDS

eTable 12. Results of the Female-Specific GWAS Meta-analysis for the Independent Signals Reaching $P < 10^{-5}$ in the Discovery Stage

SNP(CHR:BP)	A1	A2	FreqA1	Weight	BETA	Zscore	P-value	Direction *
11:114689701	T	C	0.222	8535	3,292	5,605	2.09E-08	+++++
1:180242092	T	C	0.209	8535	3,138	5,457	4.84E-08	+++++
1:180507318	A	G	0.793	8535	-3,082	-5,374	7.68E-08	-----
1:180503958	I	R	0.208	8535	3,080	5.37	7.89E-08	+++++
1:180245228	I	R	0.791	8535	-3,064	-5,327	1.00E-07	-----
1:180411967	I	R	0.211	8535	3,047	5,283	1.27E-07	+++++
1:227721255	A	G	0.700	4997	3,424	5,282	1.28E-07	?-+++
1:180397485	I	R	0.211	8535	3,042	5,273	1.34E-07	+++++
1:180446708	I	R	0.213	8535	3,046	5,262	1.43E-07	+++++
4:105125350	A	C	0.297	4995	3,154	4,882	1.05E-06	+??+?
2:113371605	T	C	0.215	8535	2,774	4,775	1.80E-06	+++++
7:88760129	T	C	0.185	8535	2,619	4,773	1.81E-06	+++++
13:80701431	D	R	0.149	8535	2,393	4,751	2.02E-06	+++++
7:49849849	A	G	0.734	8535	-2,961	-4,737	2.17E-06	-----
7:155987460	T	C	0.664	8535	-3,150	-4,716	2.41E-06	-----
11:7378221	A	G	0.702	8535	-3,025	-4,676	2.92E-06	-----
3:140058965	D	R	0.482	8535	3,302	4,672	2.98E-06	+++++
3:128701091	C	G	0.792	7266	2,683	4.67	3.01E-06	++?+?
3:140058966	D	R	0.488	8535	3,283	4,644	3.41E-06	+++++
3:167285901	C	G	0.665	8535	-3,098	-4,639	3.50E-06	-----
12:104913623	A	G	0.204	8535	2,625	4,608	4.07E-06	+++++
14:75018880	A	C	0.012	7078	0.703	4,603	4.16E-06	+++?+
X:37918948	D	R	0.019	5809	0.892	4,598	4.27E-	++???

							06	
2:107621847	T	C	0.013	7078	0.728	4,596	4.31E-06	+++?+
2:176732352	A	C	0.315	8535	-3,011	-4,584	4.55E-06	-----
7:88755445	I	R	0.193	8535	2,558	4,579	4.68E-06	+++++
8:112742610	T	C	0.601	8535	3,162	4,566	4.96E-06	+++++
2:59928780	T	C	0.205	8535	2,604	4,563	5.04E-06	+++++
17:48850234	A	G	0.609	8535	-3,143	-4,555	5.25E-06	-+---
11:114670514	T	C	0.256	8535	2,789	4,519	6.22E-06	+++++
1:218708110	A	G	0.229	8535	2,672	4,495	6.95E-06	+++-+
13:80639114	D	R	0.151	8535	2,274	4,493	7.01E-06	+++++
2:113297154	I	R	0.242	8535	2,722	4,492	7.07E-06	+++++
12:77131975	T	G	0.634	8535	3,052	4.48	7.48E-06	+++++
13:80635870	D	R	0.151	8535	2,263	4,472	7.75E-06	+++++
1:180498916	T	C	0.754	8535	-2,721	-4,467	7.95E-06	-----
10:59367194	T	C	0.624	8535	-3,054	-4,457	8.31E-06	-----
16:73475106	A	G	0.300	4997	2,878	4,442	8.90E-06	?++++
4:130513605	A	T	0.348	8535	-2,983	-4,429	9.48E-06	-----
15:68279246	A	G	0.188	8535	2,436	4,408	1.04E-05	+++++
4:116713011	T	C	0.693	8535	-2,861	-4,387	1.15E-05	-----
X:24931797	C	G	0.988	6449	-0.667	-4,383	1.17E-05	--??-
12:9862203	A	G	0.799	8535	-2,485	-4,383	1.17E-05	-----
8:142046065	A	G	0.215	8535	2,540	4,372	1.23E-05	+++++
1:49124886	D	R	0.830	8535	-2,321	-4,369	1.25E-05	--+--
17:48848668	T	C	0.492	8535	-3,083	-4,361	1.29E-05	-----
11:103066685	A	G	0.202	8535	2,472	4,356	1.32E-05	+++++
2:107741093	T	C	0.189	8535	2,411	4,356	1.32E-05	+++-+

13:80701437	D	R	0.133	8535	2,093	4,356	1.33E-05	+++++
4:68096035	A	G	0.262	8535	2,709	4,355	1.33E-05	+++++
9:112751482	T	C	0.361	8535	-2,956	-4,354	1.34E-05	-----
1:232671890	A	G	0.251	8535	2,668	4,351	1.35E-05	++-++
X:23698104	D	R	0.145	7078	2,160	4,332	1.48E-05	+++?+
22:49593443	T	C	0.192	7906	2,408	4,325	1.52E-05	++?++
3:10642207	A	T	0.974	7078	-0.972	-4,325	1.53E-05	---?-
1:214540683	A	G	0.747	8535	-2,656	-4,318	1.58E-05	--+--
4:116709656	I	R	0.691	8535	-2,818	-4,314	1.60E-05	-----
12:28190946	C	G	0.220	8535	2,525	4.31	1.63E-05	+++++
X:86991835	A	G	0.049	7078	1,312	4,309	1.64E-05	+++?+
7:147676385	D	R	0.364	8535	-2,927	-4,302	1.69E-05	-----
17:48843190	I	R	0.355	8535	2,910	4,301	1.70E-05	+++++
14:74988601	A	G	0.180	8535	2,333	4,293	1.77E-05	+++-+
3:140082443	D	R	0.502	8535	3,035	4,292	1.77E-05	+++++
6:22613747	D	R	0.162	4178	2,236	4,292	1.77E-05	+???+
7:36924944	D	R	0.109	8535	-1,881	-4.27	1.96E-05	-----
3:130311041	D	R	0.907	7906	1,757	4,269	1.96E-05	++?++
15:36605335	T	C	0.166	7078	2,243	4,264	2.01E-05	++-?+
1:180480718	I	R	0.252	8535	2,618	4,263	2.02E-05	+++++
5:138055308	T	C	0.368	4997	2,907	4,261	2.03E-05	?++++
9:27121906	T	C	0.746	8535	-2,621	-4,257	2.08E-05	-----
5:150408315	T	C	0.206	8535	2,424	4,241	2.23E-05	+++++
1:180480720	I	R	0.253	8535	2,602	4,233	2.30E-05	+++++
10:36334678	A	G	0.812	8535	-2,340	-4.23	2.33E-05	--+--
21:32961638	A	G	0.203	8535	2,406	4,228	2.36E-05	+++++

5:153796010	A	T	0.422	8535	2,949	4,223	2.41E-05	+++++
9:26753817	A	T	0.220	8535	2,471	4.22	2.44E-05	+++++
17:48836012	I	R	0.509	8535	-2,981	-4,217	2.47E-05	-----
4:58153550	A	G	0.989	6438	-0.635	-4,211	2.54E-05	---??
9:26553737	C	G	0.537	8535	2,967	4,208	2.58E-05	+++++
1:227568960	D	R	0.176	8535	2,268	4,208	2.58E-05	+++++
12:104891353	I	R	0.205	8535	2,401	4,207	2.59E-05	++-+-
20:52077907	A	G	0.494	8535	2,967	4,197	2.70E-05	+++++
4:68098210	I	R	0.259	8535	2,599	4,196	2.72E-05	+++++
X:86993921	T	C	0.047	7078	1,260	4,193	2.75E-05	+++?+
5:150759548	D	R	0.193	8535	-2,339	-4.19	2.79E-05	--+--
13:35368929	D	R	0.412	8535	2,912	4,184	2.87E-05	+++++
7:118579572	D	R	0.606	8535	-2,889	-4.18	2.92E-05	-----
11:130257002	T	G	0.513	7078	2,952	4,176	2.97E-05	+++?+
17:10763574	T	C	0.667	8535	2,781	4,172	3.02E-05	++-++
10:88688049	A	G	0.744	8535	2,571	4,166	3.10E-05	+++++
17:48834023	A	G	0.516	8535	2,943	4,164	3.13E-05	+++++
6:105242004	I	R	0.016	7078	0.743	4,161	3.17E-05	+++?+
13:75951280	T	C	0.673	8535	-2,759	-4,157	3.23E-05	-----
12:42064203	T	C	0.912	7078	1,662	4,156	3.24E-05	+++?+
5:127850375	T	C	0.816	8535	-2,273	-4,152	3.29E-05	-----
12:106376201	A	G	0.189	8535	2,296	4.15	3.33E-05	++++-
20:17843864	T	C	0.687	8535	2,722	4.15	3.33E-05	+++++
6:89954237	A	G	0.809	7906	-2,305	-4,147	3.37E-05	--?--
22:46595692	T	C	0.189	8535	2,290	4,138	3.50E-05	+++++
9:89923639	A	G	0.511	8535	-2,924	-4,136	3.54E-05	-----

7:118612246	D	R	0.606	8535	-2,855	-4,131	3.61E-05	-----
3:64318339	D	R	0.421	8535	2,883	4,129	3.64E-05	+++++
5:17241405	T	C	0.482	8535	-2,917	-4,128	3.66E-05	-----
7:70011689	T	C	0.217	8535	-2,404	-4,128	3.67E-05	-----
13:35370385	D	R	0.404	8535	2,863	4,126	3.69E-05	+++++
2:23873349	A	G	0.237	8535	-2,481	-4,126	3.70E-05	-----
2:211528908	A	G	0.799	8535	-2,336	-4,124	3.73E-05	--+--
1:100205047	T	G	0.047	7078	1,229	4,122	3.76E-05	+++?-
1:180238495	A	G	0.578	8535	2,876	4,118	3.83E-05	+++++
8:112760291	I	R	0.651	8535	2,772	4,114	3.89E-05	+++++
2:239065243	T	C	0.142	7078	2,028	4,111	3.94E-05	+++?+
10:44975510	A	C	0.676	8535	-2,718	-4,107	4.01E-05	----+
20:765937	A	C	0.589	4997	-2,858	-4,107	4.01E-05	?----
5:90193468	T	C	0.651	8535	-2,769	-4,107	4.01E-05	---++
7:52767469	D	R	0.285	8535	-2,622	-4,107	4.01E-05	-----
6:105237327	A	G	0.984	7078	-0.740	-4,106	4.03E-05	---?-
5:27752506	T	C	0.512	8535	-2,900	-4,103	4.09E-05	-----
X:38156584	T	C	0.985	6438	-0.710	-4,102	4.10E-05	--+??
10:81245194	A	G	0.655	4368	-2,757	-4,101	4.12E-05	?-?--
18:57161901	A	G	0.451	8535	2,885	4,099	4.16E-05	+++++
2:208341370	D	R	0.590	8535	2,849	4,097	4.19E-05	++-++
2:86142889	A	T	0.192	7895	2,281	4,095	4.22E-05	++++?
1:15338903	T	G	0.212	8535	2,365	4,094	4.24E-05	+++++
13:75952815	I	R	0.332	8535	2,726	4,093	4.25E-05	+++++
5:138136446	T	C	0.317	4997	2,692	4,093	4.26E-05	?+-++
12:102954326	T	C	0.662	4357	-2,737	-4,093	4.26E-05	?---?

3:130281351	D	R	0.093	7906	-1,681	-4.09	4.31E-05	--?--
8:60546223	A	G	0.191	7906	2,272	4,087	4.36E-05	++?++
10:71524630	T	C	0.283	8535	-2,603	-4,084	4.43E-05	-----
4:29963093	A	G	0.947	6449	1,294	4,083	4.45E-05	++??+
9:27123202	A	G	0.264	8535	2,543	4,082	4.46E-05	+++++
1:227556744	D	R	0.180	8535	2,216	4,081	4.48E-05	++-++
4:109595583	A	T	0.630	8535	2,786	4.08	4.50E-05	+++++
11:86710909	I	R	0.687	8535	-2,673	-4,075	4.59E-05	-----
5:164849859	A	C	0.194	8535	2,277	4,069	4.71E-05	+++++
9:89923256	I	R	0.511	8535	-2,876	-4,069	4.72E-05	-----
10:116470847	A	T	0.587	8535	-2,830	-4,064	4.82E-05	--+--
15:93932133	D	R	0.140	8535	1,995	4,061	4.88E-05	+++++
1:227556746	D	R	0.176	8535	2,183	4,056	5.00E-05	++-++
1:8020833	A	G	0.012	5809	0.629	4,053	5.05E-05	++???
4:95908346	D	R	0.106	7078	1,762	4,053	5.05E-05	+++?+
5:387819	A	G	0.300	4997	2,625	4,052	5.08E-05	?++++
1:227543581	D	R	0.183	8535	2,217	4,051	5.10E-05	++-++
22:17395974	A	C	0.580	4997	-2,826	-4,048	5.17E-05	?----
20:1174157	T	C	0.203	8535	2,297	4,037	5.41E-05	+++++
6:153581600	A	G	0.208	8535	2,317	4,035	5.47E-05	+++++
9:26998333	T	C	0.201	8535	2,283	4,031	5.54E-05	+++++
10:59361978	I	R	0.393	8535	2,782	4,027	5.66E-05	+++++
18:41351195	T	C	0.029	7078	0.959	4,023	5.75E-05	+++?+
5:90195565	I	R	0.347	8535	2,708	4,022	5.78E-05	+++-+
2:107611917	A	G	0.295	8535	2,592	4,021	5.79E-05	++-++
5:90195567	I	R	0.347	8535	2,706	4,019	5.84E-05	+++-+

5:80101489	A	G	0.718	8535	-2,555	-4,017	5.89E-05	-----
10:34154156	A	T	0.062	7078	1,372	4,017	5.89E-05	+++?+
17:48848702	A	G	0.245	8535	2,442	4,013	6.01E-05	+++++
1:245900786	A	G	0.212	8535	2,319	4,012	6.02E-05	+++++
2:199549486	A	G	0.206	7906	-2,291	-4,009	6.11E-05	--?-+
1:76424440	T	C	0.641	8535	-2,719	-4,007	6.16E-05	-----
5:35915250	A	G	0.813	8535	-2,210	-4,006	6.18E-05	-----
16:21022113	A	G	0.768	8535	2,390	4,005	6.21E-05	++-++
6:123275175	T	C	0.265	5624	2,498	4,004	6.22E-05	+?-+?
18:46532474	T	G	0.174	7078	-2,143	-4	6.34E-05	---?-
11:87990315	I	R	0.231	8535	-2,385	-3,999	6.36E-05	-----
15:25398142	T	C	0.434	8535	2,802	3,998	6.40E-05	+++++
8:103787072	A	G	0.611	8535	2,756	3,997	6.42E-05	+++++
5:165737211	C	G	0.809	8535	-2,223	-3,995	6.47E-05	----+
2:19732955	D	R	0.120	8535	-1,831	-3.99	6.61E-05	-----
14:33545545	A	G	0.989	6438	-0.596	-3,987	6.69E-05	---??
13:59661145	D	R	0.196	8535	2,239	3,986	6.71E-05	+++++
18:39152046	A	G	0.448	8535	2,800	3,981	6.86E-05	+++++
5:25932444	T	G	0.208	8535	-2,285	-3.98	6.88E-05	-----
4:66968503	A	T	0.198	8535	2,240	3,979	6.92E-05	+++++
15:99470739	D	R	0.161	4178	2,067	3,976	7.02E-05	+???+
6:52758076	A	G	0.321	4997	2,623	3,974	7.07E-05	?++++
4:78536778	A	C	0.252	8535	2,439	3,972	7.13E-05	+++++
17:11290592	A	T	0.973	7078	-0.912	-3,971	7.16E-05	---?-
2:34043283	D	R	0.351	8535	-2,679	-3.97	7.19E-05	-----
X:90657415	D	R	0.397	7078	2,747	3,969	7.21E-05	+++?+

1:65042248	A	G	0.183	8535	2,169	3,969	7.22E-05	++++-
11:5625490	T	C	0.019	7078	0.764	3,968	7.24E-05	++-?+
2:76807216	T	C	0.693	4997	-2,585	-3,963	7.39E-05	?----
8:112849225	I	R	0.646	8535	2,677	3,958	7.56E-05	+++++
7:89510555	T	C	0.198	8535	-2,231	-3,958	7.56E-05	-----
2:34043285	D	R	0.351	8535	-2,671	-3,958	7.57E-05	-----
20:49757406	T	C	0.489	8535	2,796	3,955	7.66E-05	+++++
1:247941594	A	G	0.192	8535	2,204	3,954	7.70E-05	+++++
11:36331961	T	C	0.300	4997	2,561	3,952	7.74E-05	?++++
6:105240438	D	R	0.103	7078	1,698	3.95	7.80E-05	+++?-
13:35366265	D	R	0.427	8535	2,763	3.95	7.82E-05	+++++
X:24739697	D	R	0.104	7078	1,704	3.95	7.82E-05	+++?-
7:88666164	A	G	0.330	8535	2,626	3,949	7.84E-05	+++++
8:106715359	A	G	0.774	8535	-2,334	-3,948	7.88E-05	-----
3:76340268	A	G	0.193	8535	2,203	3,948	7.88E-05	++-+-
4:109577407	I	R	0.686	8535	2,590	3,947	7.90E-05	+++++
11:114657759	T	C	0.226	8535	-2,336	-3,947	7.90E-05	-----
12:27696460	T	C	0.224	8535	-2,326	-3,947	7.93E-05	-----
15:25379216	I	R	0.291	8535	2,534	3,946	7.95E-05	++-++
21:42204847	D	R	0.189	8535	-2,186	-3,945	7.97E-05	-----
3:73603	A	G	0.605	4997	2,724	3,941	8.12E-05	?++++
5:152232974	T	C	0.311	4997	2,580	3,941	8.13E-05	?++++
17:65487628	T	C	0.241	8535	2,383	3.94	8.13E-05	+++++
7:128520757	A	G	0.260	8535	2,444	3,939	8.20E-05	++-++
9:107664373	T	C	0.216	8535	2,291	3,938	8.22E-05	+++++
5:124089919	T	C	0.692	4997	2,571	3,937	8.24E-05	?++++

1:86063632	A	T	0.191	7895	2,188	3,935	8.33E-05	++++?
3:131593333	T	G	0.793	8535	2,254	3,932	8.41E-05	+++++
8:84784251	D	R	0.492	8535	-2,780	-3,932	8.43E-05	-----
1:75645664	A	G	0.797	8535	-2,237	-3,932	8.43E-05	-----
9:86784852	A	G	0.253	8535	-2,417	-3,931	8.47E-05	-----
2:234685503	A	G	0.180	8535	2,134	3.93	8.51E-05	+++++
10:71381565	T	C	0.982	7078	-0.749	-3,928	8.58E-05	---?-
1:53098710	A	T	0.806	8535	-2,197	-3,928	8.58E-05	-----
11:836008	T	C	0.360	8535	2,665	3,927	8.61E-05	+++++
19:11431252	A	G	0.983	7078	-0.709	-3,925	8.67E-05	---?-
16:56604888	A	C	0.410	8535	2,729	3,923	8.76E-05	++++-
10:86492539	T	C	0.681	8535	-2,585	-3,921	8.80E-05	-----
3:167462868	T	G	0.685	8535	-2,574	-3,919	8.90E-05	-----
22:22069012	A	G	0.071	7078	1,425	3,918	8.91E-05	+++?-
15:25378612	A	G	0.289	8535	2,511	3,918	8.93E-05	++-++
X:87022567	T	C	0.846	7078	-1,999	-3,918	8.93E-05	---?-
13:28675999	D	R	0.220	8535	2,294	3,918	8.95E-05	+++++
2:177631035	A	T	0.019	6438	0.746	3,917	8.95E-05	+++??
10:55042514	D	R	0.272	8535	2,464	3,916	8.99E-05	++-++
9:81730211	A	G	0.245	8535	2,376	3,909	9.27E-05	+++++
21:19713041	D	R	0.183	8535	-2,136	-3,908	9.30E-05	-----
21:25962522	A	T	0.803	8535	-2,195	-3,905	9.42E-05	-----
2:143761463	I	R	0.224	8535	2,300	3,903	9.50E-05	+++++
4:109616156	I	R	0.668	8535	2,600	3,902	9.55E-05	+++++
20:50891056	T	G	0.233	8535	2,331	3.9	9.63E-05	++++-
X:24891558	A	G	0.983	7078	-0.717	-3,899	9.64E-05	---?-

17:11169773	A	G	0.346	4997	2,623	3,899	9.65E-05	?++++
2:76812081	T	C	0.371	8535	-2,664	-3,899	9.67E-05	--+--
8:84783454	D	R	0.491	8535	-2,754	-3,896	9.79E-05	-----
5:89963988	A	C	0.743	7078	-2,408	-3,896	9.79E-05	---?-
2:40680664	C	G	0.186	8535	-2,145	-3,895	9.80E-05	-----
4:105539572	D	R	0.216	8535	2,266	3,895	9.81E-05	++++-
11:12475265	A	G	0.337	4997	2,603	3,893	9.90E-05	?+++-
4:109566972	I	R	0.690	8535	2,547	3,893	9.91E-05	+++++
2:30932550	A	G	0.183	8535	2,129	3,892	9.95E-05	+++++
22:25469345	A	T	0.348	8535	-2,621	-3,891	9.97E-05	----+
2:233905804	T	C	0.488	8535	2,751	3,891	9.98E-05	+++++

*P-value-informed LD clumping was performed in plink using 0.001 as significance threshold for index SNPs, 0.01 as secondary significance threshold for clumped SNPs, 0.5 as LD r2 threshold, and 250kb as physical distance threshold.*Input order: COGA-ALSPAC-QIMR-GENR-TEDS

eTable 13. Results of the Male-Specific GWAS Meta-analysis for the Independent Signals Reaching $P < 10^{-5}$ in the Discovery Stage

SNP	A1	A2	Freq1	Weight	BETA	Zscore	P	Direction *
23:121854298	A	T	0.846	6515	-2,867	-5,616	1.95E-08	---?-
6:82075402	A	T	0.292	7772	-3,290	-5,117	3.11E-07	-----
17:5912544	A	G	0.511	7772	3,415	4.83	1.37E-06	-++++
23:121708160	T	G	0.804	6515	-2,711	-4,825	1.40E-06	---?-
9:134676217	A	T	0.703	7772	-3,051	-4,723	2.32E-06	-----
5:30778215	A	T	0.503	7772	3,323	4,699	2.61E-06	+++++
22:41377326	A	G	0.203	7772	2,642	4,649	3.34E-06	+++++
23:121721640	C	G	0.085	6515	1,830	4,629	3.68E-06	+++?+
1:4666044	A	C	0.213	7772	-2,679	-4,626	3.74E-06	--+--
5:16863628	A	G	0.987	5797	-0.741	-4,592	4.40E-06	?--?-
5:30813302	T	C	0.509	7772	3,246	4,591	4.42E-06	+++++
11:5191872	A	G	0.673	7772	3,031	4.57	4.87E-06	+++++
3:98287344	A	G	0.797	7772	-2,596	-4,566	4.96E-06	-----
17:39670972	A	T	0.976	5797	-0.997	-4,561	5.10E-06	?--?-
5:30782686	A	G	0.606	7772	3,137	4.54	5.63E-06	+++++
3:15751847	A	G	0.813	7054	-2,503	-4,536	5.74E-06	?----
14:55203169	C	G	0.323	7772	-2,996	-4,529	5.92E-06	-----
17:49348564	T	G	0.781	7772	-2,625	-4,489	7.17E-06	-----
1:236199019	T	G	0.370	7772	3,056	4,475	7.64E-06	+++++
1:221254451	A	C	0.192	7054	-2,491	-4,474	7.69E-06	?----
6:123913994	A	C	0.780	7772	2,606	4.45	8.57E-06	+++++
18:36619499	T	C	0.988	5797	-0.678	-4,406	1.05E-05	?--?-
1:95815155	A	G	0.197	7054	2,476	4,401	1.08E-	?+-++

							05	
1:4665232	A	G	0.503	7772	3,065	4,334	1.47E-05	+++++
5:62723814	A	G	0.812	7054	-2,392	-4,332	1.48E-05	?----
6:82423659	A	G	0.809	7054	2,393	4,303	1.68E-05	?++++
18:54689177	A	G	0.263	7772	2,673	4,294	1.75E-05	+++++
9:16449254	A	C	0.024	5797	0.925	4.29	1.79E-05	?++?+
12:121056938	T	C	0.985	5797	-0.743	-4,267	1.98E-05	?--?-
12:114226104	C	G	0.358	7772	-2,889	-4.26	2.05E-05	-----
2:224500613	A	G	0.191	7054	2,367	4,257	2.07E-05	?++++
8:3187251	C	G	0.252	7772	2,611	4,251	2.13E-05	-+-++
1:160975985	T	C	0.815	7054	-2,327	-4,239	2.25E-05	?----
4:169164614	T	G	0.801	7054	-2,390	-4,236	2.28E-05	?----
6:56996688	T	C	0.751	7772	2,589	4,232	2.32E-05	+++++
4:154128948	T	G	0.421	7772	-2,953	-4.23	2.34E-05	-----
13:80604770	T	C	0.287	7772	2,705	4,227	2.37E-05	+++++
2:217753980	T	C	0.769	7772	2,512	4,215	2.50E-05	+++++
11:61879018	A	G	0.429	7772	-2,946	-4,208	2.58E-05	-----
13:40660954	A	G	0.724	7033	-2,654	-4,198	2.70E-05	--?--
14:80199547	A	T	0.630	7772	-2,861	-4,189	2.81E-05	-----
10:126084645	A	G	0.243	7772	2,538	4,187	2.83E-05	+++++
4:181658296	T	C	0.239	7772	2,523	4.18	2.92E-05	+++++
18:55892311	A	C	0.459	6515	-2,934	-4,163	3.14E-05	---?-
13:54826062	T	C	0.247	7772	2,539	4.16	3.18E-05	++-++
8:4906038	T	C	0.806	7054	-2,324	-4,159	3.19E-05	?----
2:43103614	A	C	0.429	7772	-2,904	-4,149	3.34E-05	---+-
13:41676833	A	T	0.509	7772	2,926	4,138	3.50E-05	-++-+

11:14251553	A	G	0.297	7772	-2,672	-4,134	3.57E-05	-----
3:178983584	T	G	0.365	7772	2,812	4,129	3.65E-05	+++-+
2:134590203	A	G	0.204	7772	2,351	4,124	3.72E-05	+++++
3:98431207	T	C	0.632	7772	2,811	4,123	3.73E-05	-++++
17:5891698	A	G	0.372	7772	2,813	4,115	3.86E-05	+++++
6:117855065	A	G	0.390	7772	-2,837	-4,114	3.88E-05	-----
14:49134238	A	C	0.353	7772	-2,777	-4,109	3.97E-05	-----
4:135789780	A	C	0.807	7054	-2,294	-4,107	4.01E-05	?----
9:134677111	A	G	0.281	7772	2,611	4,105	4.04E-05	+++++
19:11243160	A	G	0.316	7772	-2,698	-4,104	4.06E-05	--+--
6:1823732	T	C	0.501	7772	2,901	4,102	4.10E-05	+++++
4:47248308	T	C	0.798	7054	2,328	4,099	4.15E-05	?++++
1:22136245	A	G	0.211	7772	2,363	4,097	4.18E-05	+++++
6:10894255	A	G	0.418	7772	2,854	4,091	4.29E-05	+++++
22:20012962	A	G	0.034	5797	1,053	4,086	4.40E-05	?++?+
9:89712550	A	G	0.814	7054	-2,247	-4,081	4.49E-05	?--+-
18:74709361	T	G	0.393	7772	2,817	4,079	4.52E-05	+++++
23:13529903	T	C	0.210	6515	-2,343	-4,071	4.68E-05	---?-
8:96942953	T	C	0.652	6515	-2,742	-4.07	4.71E-05	---?-
9:38406340	T	C	0.560	7772	-2,857	-4,069	4.72E-05	-----
18:36638417	T	C	0.188	7054	2,247	4,063	4.84E-05	?++-+
8:13730935	C	G	0.307	7772	2,649	4.06	4.90E-05	+++++
4:105441140	T	C	0.324	7772	-2,686	-4.06	4.91E-05	-----
6:23734497	A	G	0.576	7772	-2,835	-4,057	4.98E-05	+----
15:97601511	A	C	0.581	7772	2,827	4,052	5.07E-05	+++++
2:45179238	T	C	0.186	7054	-2,228	-4,051	5.11E-05	?----

15:71100749	T	C	0.215	7772	2,353	4,049	5.14E-05	+++++
5:30839387	T	G	0.282	7772	-2,573	-4,041	5.33E-05	-----
9:79406823	T	C	0.598	7772	2,801	4,039	5.37E-05	+++++
10:97957262	T	C	0.533	7772	-2,847	-4,035	5.45E-05	-----
19:4922958	A	G	0.263	7772	-2,514	-4,035	5.47E-05	--+--
4:146234605	T	G	0.772	6515	-2,395	-4,034	5.48E-05	---?-
3:149006009	A	G	0.387	7772	-2,779	-4,033	5.50E-05	-----
7:83028227	T	C	0.743	7772	2,494	4,033	5.50E-05	+++++
15:88825912	T	C	0.914	6515	-1,599	-4,031	5.55E-05	---?-
18:21392678	A	G	0.648	7772	2,716	4,022	5.77E-05	++-++
2:60552902	T	C	0.197	7054	2,259	4.02	5.81E-05	?++++
12:123168333	A	T	0.426	7772	2,812	4.02	5.82E-05	++-++
13:67426089	A	G	0.797	7772	2,287	4.02	5.82E-05	+++++
2:60517252	A	C	0.194	7054	2,249	4,019	5.86E-05	?++++
6:82414401	T	C	0.806	7054	2,244	4,015	5.95E-05	?++++
11:5182086	A	C	0.523	7772	2,836	4,015	5.95E-05	+++++
23:121719272	C	G	0.376	6515	2,747	4,011	6.05E-05	+++?+
11:79192521	A	G	0.701	7772	-2,595	-4.01	6.06E-05	-----
6:166373748	A	G	0.805	7054	-2,246	-4,008	6.14E-05	?----
3:169968867	A	T	0.650	7772	-2,702	-4,005	6.21E-05	+----
6:70054601	T	C	0.205	7054	2,287	4,004	6.22E-05	?++++
12:114815524	A	T	0.773	7772	2,368	3,995	6.46E-05	-+-++
4:7057037	C	G	0.713	7772	-2,548	-3,984	6.77E-05	-----
3:99275470	A	G	0.213	7772	2,304	3,983	6.82E-05	-++++
5:52924827	A	C	0.208	7772	-2,285	-3,978	6.95E-05	--+--
13:55571705	A	G	0.186	7054	2,189	3,978	6.95E-05	?++++

15:97600216	A	G	0.451	7772	2,796	3,974	7.05E-05	+++++
10:87177256	A	C	0.192	7054	2,211	3,972	7.11E-05	?++++
20:635108	T	C	0.012	5797	0.616	3,971	7.17E-05	?++?+
4:20542485	C	G	0.335	7772	2,649	3,969	7.20E-05	+++++
5:104165126	A	G	0.310	7772	-2,597	-3,969	7.21E-05	+----
14:76439154	T	C	0.203	7772	2,257	3,967	7.28E-05	-++-+
5:1412605	T	C	0.234	6515	-2,375	-3,967	7.28E-05	---?-
19:35351765	A	G	0.375	7772	2,714	3,965	7.35E-05	+++++
7:94287589	A	G	0.862	6515	1,930	3,962	7.42E-05	+++?+
6:102126758	T	G	0.784	7772	2,303	3,955	7.65E-05	+++++
3:102655217	A	G	0.197	7054	2,221	3,953	7.72E-05	?++++
15:82199306	A	C	0.784	7772	2,299	3,952	7.75E-05	+++++
9:79415130	T	C	0.208	7772	-2,268	-3,951	7.78E-05	-----
4:67246329	A	C	0.091	6515	1,608	3,949	7.85E-05	+++?+
4:58693855	T	G	0.497	7772	2,792	3,948	7.88E-05	-++++
3:103824436	A	C	0.787	7772	-2,288	-3,948	7.88E-05	---+-
6:134671134	A	G	0.734	7772	2,467	3,948	7.89E-05	+++++
5:151068513	A	T	0.478	7772	2,786	3,944	8.00E-05	+++++
1:33802817	A	G	0.607	7772	2,724	3,944	8.00E-05	+++++
23:121848501	T	C	0.516	6515	-2,787	-3,944	8.01E-05	---?-
3:98433402	T	C	0.721	7772	2,497	3,939	8.19E-05	+++++
6:74630651	A	G	0.517	7772	-2,783	-3,938	8.20E-05	+----
10:113301953	A	G	0.215	7772	2,286	3,936	8.30E-05	+++++
5:30465845	A	G	0.804	7054	2,210	3,935	8.32E-05	?++++
18:54703519	T	C	0.301	7772	2,551	3,931	8.45E-05	+++++
2:46917358	A	G	0.984	5797	-0.701	-3,929	8.53E-05	?--?-

8:97826658	A	G	0.804	7772	2,206	3,929	8.54E-05	+++++
12:48236550	C	G	0.794	7772	-2,246	-3,925	8.67E-05	-----
11:21412031	T	C	0.227	7772	2,324	3,921	8.82E-05	+++++
18:54674980	A	C	0.605	7772	-2,711	-3,921	8.83E-05	-----
18:65873403	T	C	0.298	7772	-2,536	-3.92	8.85E-05	--+--
10:83104017	A	C	0.201	7772	-2,222	-3,919	8.90E-05	-----
13:55390926	C	G	0.188	7054	2,165	3,917	8.96E-05	?++++
1:213204806	C	G	0.810	7054	-2,175	-3,916	9.02E-05	?----
1:16558838	A	C	0.436	7772	-2,745	-3,915	9.03E-05	-----
17:21738349	T	G	0.303	7033	-2,544	-3,915	9.05E-05	--?--
12:18785821	T	C	0.405	7772	-2,717	-3,914	9.06E-05	-----
22:28051021	A	G	0.014	5797	0.656	3,909	9.25E-05	?++?+
1:160918520	A	G	0.289	7772	-2,503	-3,904	9.47E-05	+-+--
4:27629775	A	T	0.362	7772	-2,652	-3,902	9.55E-05	+----
14:77603593	A	G	0.062	6515	-1,330	-3,899	9.65E-05	---?-
1:171394406	A	G	0.201	7054	2,211	3,899	9.65E-05	?++++
17:15149147	A	C	0.499	7772	2,757	3,899	9.66E-05	++-++
13:29843007	A	C	0.196	7054	-2,185	-3,895	9.82E-05	?----
6:39032835	A	T	0.489	7772	-2,753	-3,894	9.87E-05	+----
18:34066389	A	G	0.617	7772	-2,675	-3,891	9.98E-05	-----

*P-value-informed LD clumping was performed in plink using 0.001 as significance threshold for index SNPs, 0.01 as secondary significance threshold for clumped SNPs, 0.5 as LD r2 threshold, and 250kb as physical distance threshold.*Input order: COGA-ALSPAC-QIMR-GENR-TED

eTable 14. Cohort-Specific *P* Values, β Values, and Allele Frequencies for the 3 SNPs

	GENR (N=702 F; 718 M)			*TEDS N=(1477 F; 1257 M)*			*COGA (N=640 F; 739 M)*			*QIMR (N=3538 F; 2993 M)*			*ALSPAC (N=2271 F; 2065 M)*		
FEMALE top SNPs*	*P*	*BETA*	*AF*	*P*	*BETA*	*AF*	*P*	*BETA*	*AF*	*P*	*BETA*	*AF*	*P*	*BETA*	*AF*
11:11468970, rs11215217 (T) *P= 2.1 x 10^{-8}***	0.0644	0.204	0.060	0.388	0.0631	0.069	0.18	0.202	0.078	3.78E-05	0.168	0.081	0.000820	0.114	0.071
In males:	0.936	0.012	0.080	0.381	-0.0694	0.065	0.647	0.096	0.076	0.408	0.064	0.080	0.871	0.006	0.071
1:180242092, rs2764450 (T) *P= 4.8 x 10^{-8}***	0.0459	0.204	0.068	0.00859	0.207	0.061	0.00626	0.466	0.064	0.0140	0.100	0.057	0.00367	0.105	0.059
In males:	0.58	0.085	0.06	0.334	-	0.063	0.888	0.03	0.0	0.799	-	0.057	0.838	0.008	0.059

	3		9		0.081			1	25		0.021				
MALE top SNPs															
X:121854298, rs41456347 (A) P= 1.95 x 10^{-8**}	0.1218	-0.183	0.876	Missing	Missing	Missing	0.595	-0.0555	0.833	3.74E-06	-0.193	0.853	0.00149	-0.058	0.830
In females:	0.313	0.0710	0.853	Missing	Missing	Missing	0.400	0.0918	0.833	0.740	0.011	0.853	0.0253	-0.057	0.843

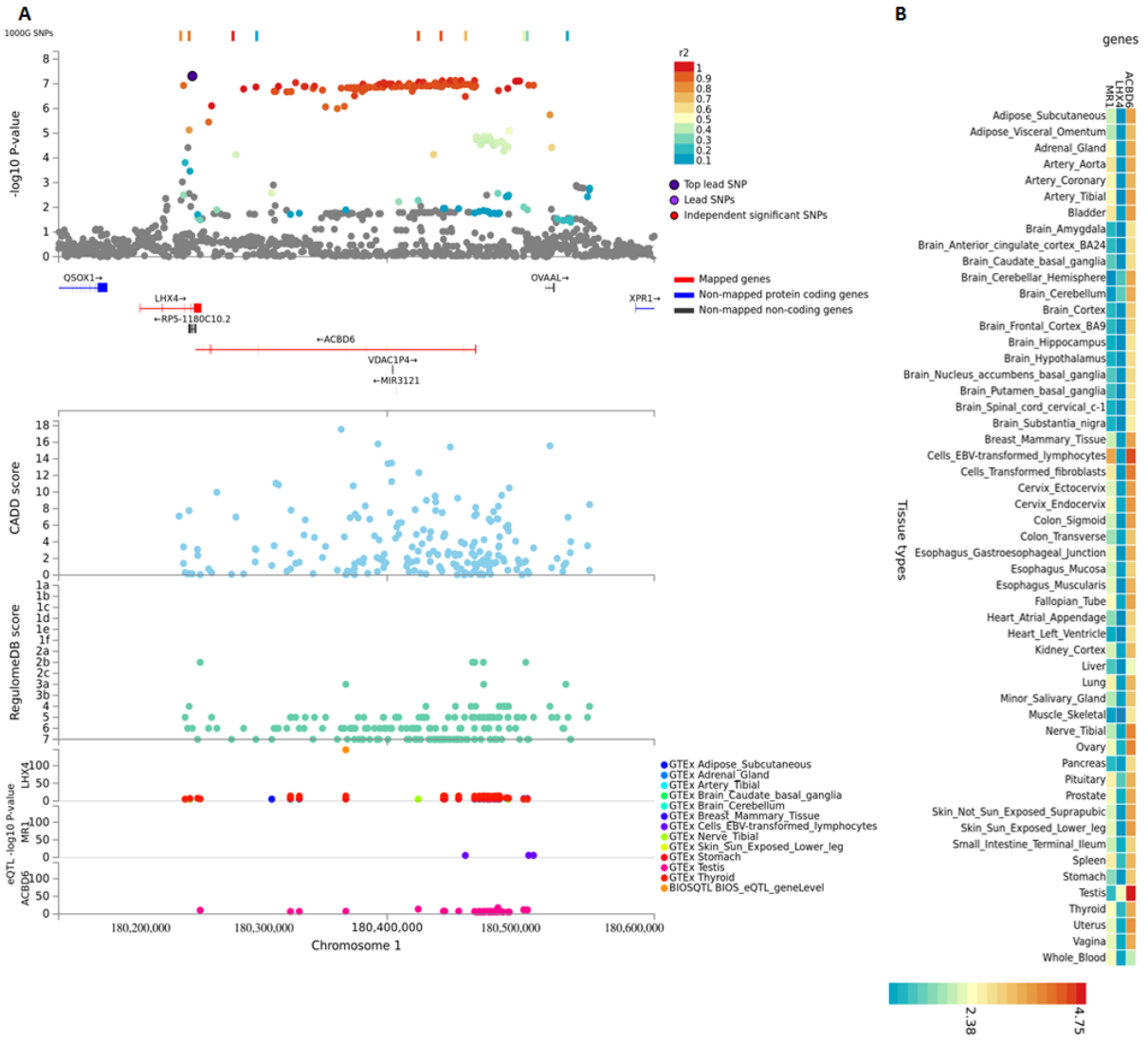
*Build: hg19 **Meta-analytical p-values as derived from the sex-specific analyses. GW= Genome-Wide. AF= Allele Frequency. F= Female. M= Male.

eTable 15. Sign and Fisher Exact Test of Directional Effects Among SNPs of ASB Females With Males (Clumped) and ASB and Educational Attainment (Clumped) for Different *P* Value Thresholds

			Sign test		Fisher's exact test	
Phenotypes	P Threshold	# SNPs	Proportion*	P-value	Odds Ratio	P-value
Males – females	.05	9236	.51	3.1×10^{-12}	1.1	.83
Males – females	.001	206	.52	.56	0.9	1
Males – females	.0001	25	.50	1	NA	NA
*ASB – EA**	.05	31739	.49	1	1.12	1.47×10^{-5}
ASB – EA	.001	2586	.43	.0024	3.26	.0014
ASB – EA	.0001	207	.60	.11	NA	NA

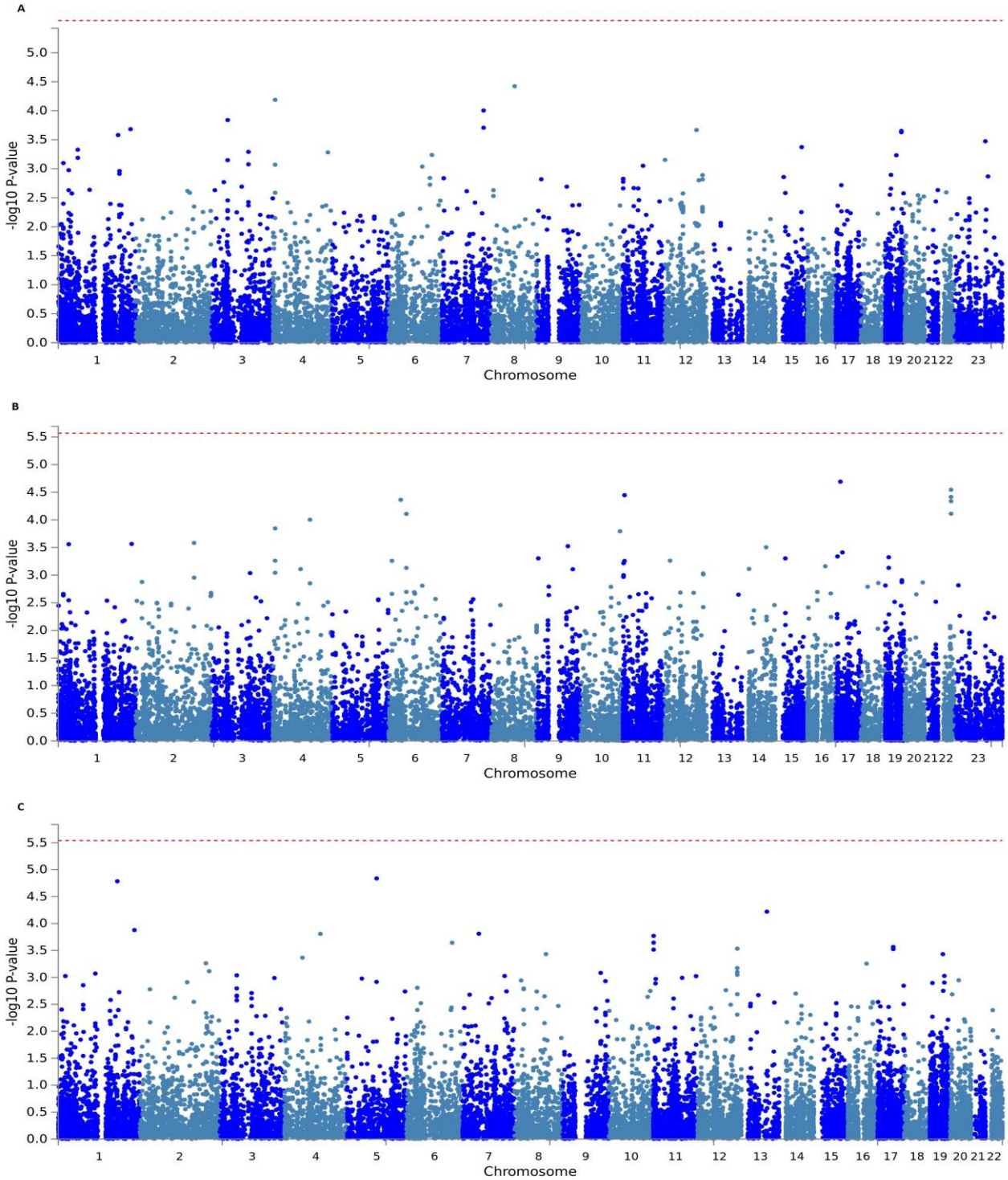
*The expected proportion under the null hypothesis is 0.5. EA= Educational Attainment. # SNPs = Number of SNPs.

eFigure 1. Regional Plot of Chrosomsome 1:180242092 and Heatmap of Gene Expression of Mapped Genes for ASB

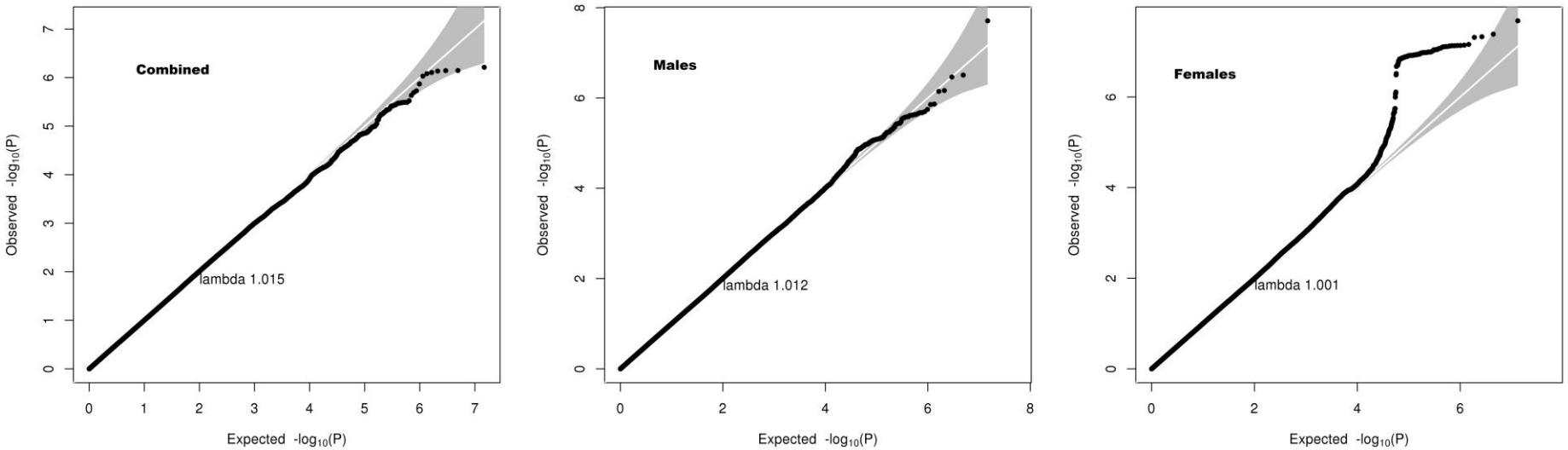


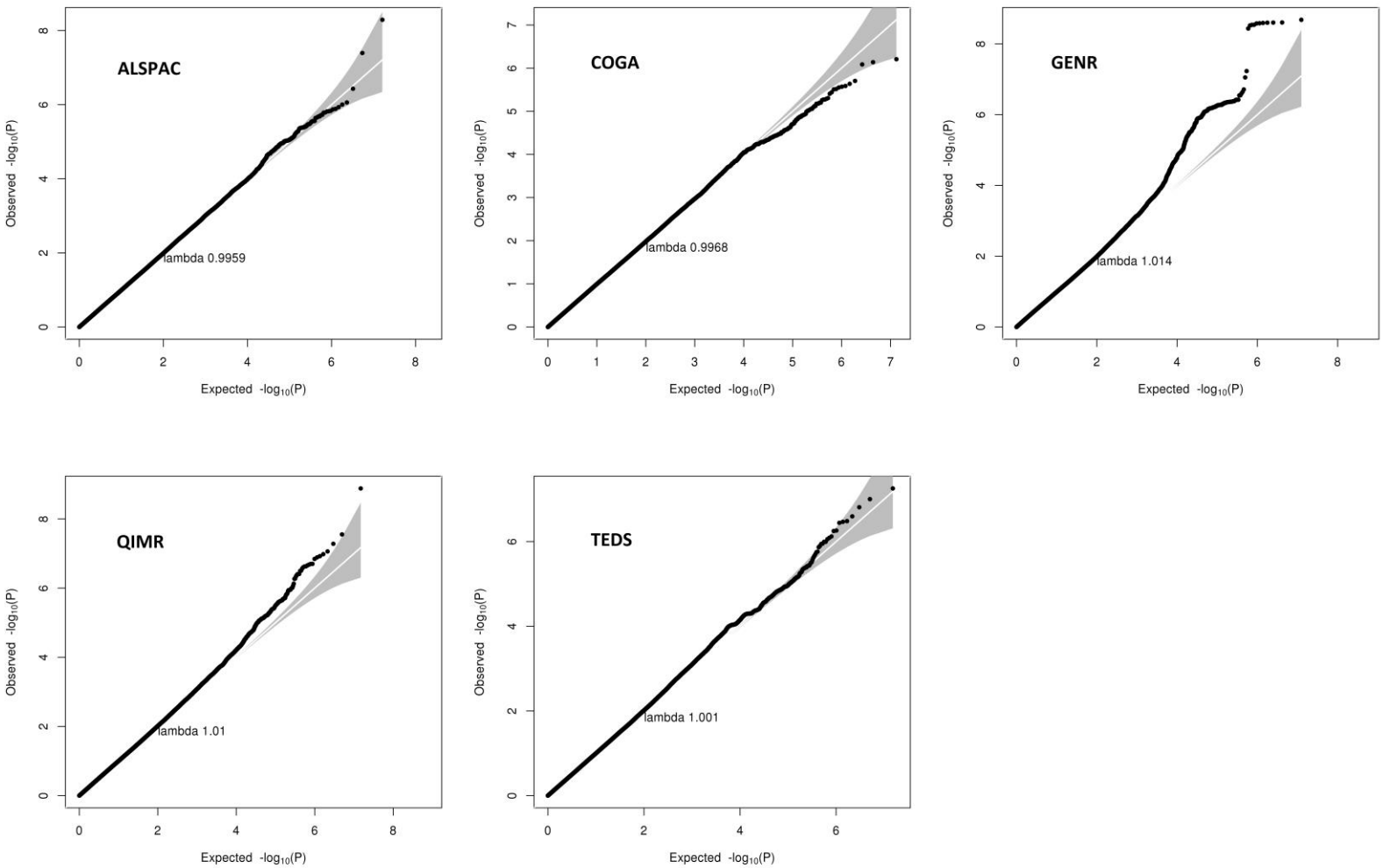
A) Regional plot of chr1:180242092 with functional annotations of SNPs in LD of rs2764450. The plot displays, from the top, GWAS P-value, genes in the locus, CADD score (Combined Annotation Dependent Depletion), RegulomeDB score, expression quantitative trait loci (eQTLs) in different tissue types. B) Heatmap of gene-expression of mapped genes for ASB in 53 tissue types based on GTEx gene expression data. The expression values are log 2 transformed RPKM (Read Per Kilo base per Million) with pseudocount 1. Higher values (red) depict a relatively high expression compared to low values (blue).

eFigure 2. Gene-based genome wide analyses for combined (upper panel, A), male-specific (middle panel, B) and female-specific (lower panel, C) meta-analyses. Negative log10-transformed P-values for each gene are plotted. The threshold for gene-wide statistical significant associations was set at the Bonferroni threshold of P=2.73×10-6.

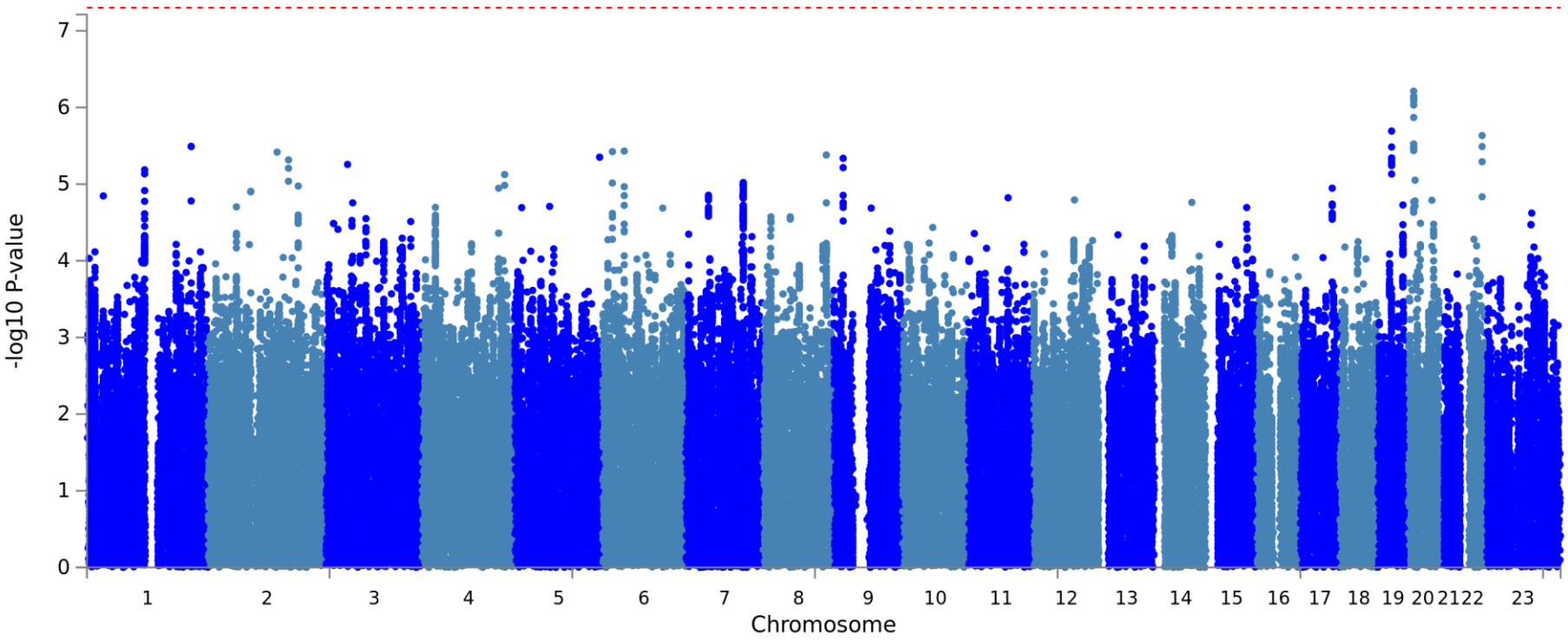


eFigure 3. Quantile-Quantile Plots for Antisocial Behavior Results



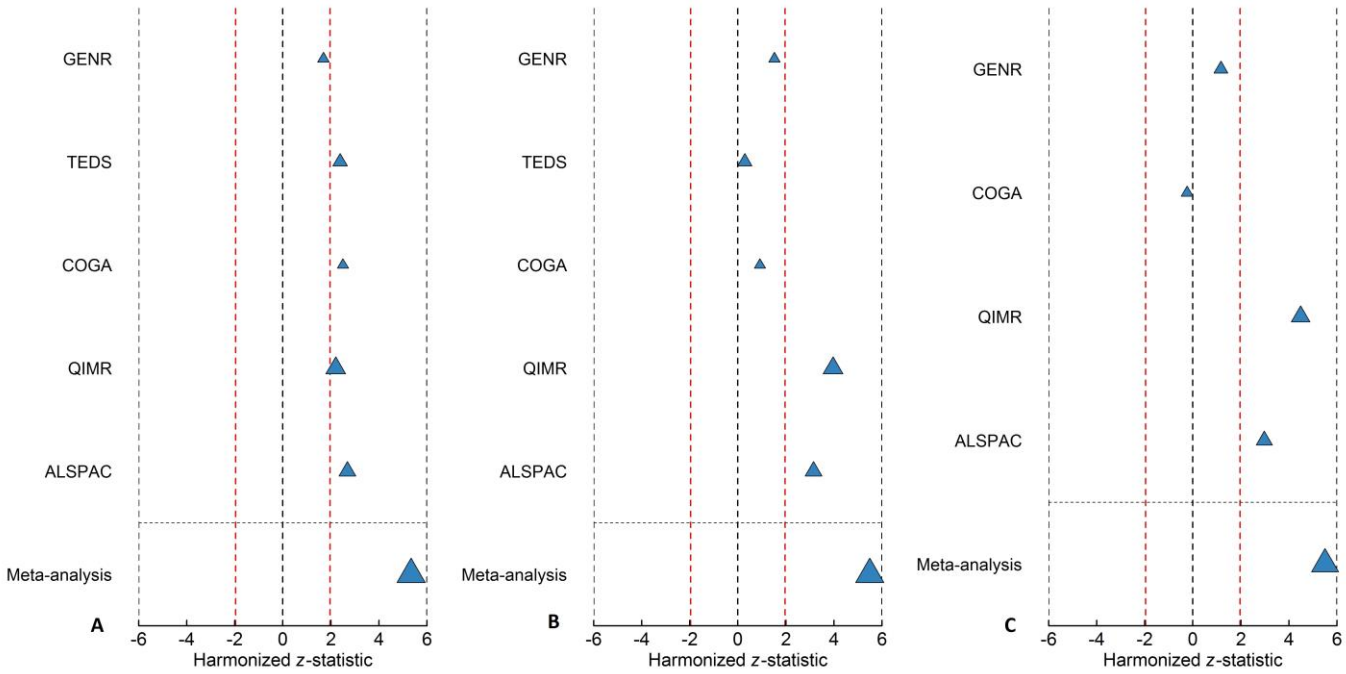


eFigure 4. Manhattan Plot for Antisocial Behavior Results for the Combined Meta-Analyses

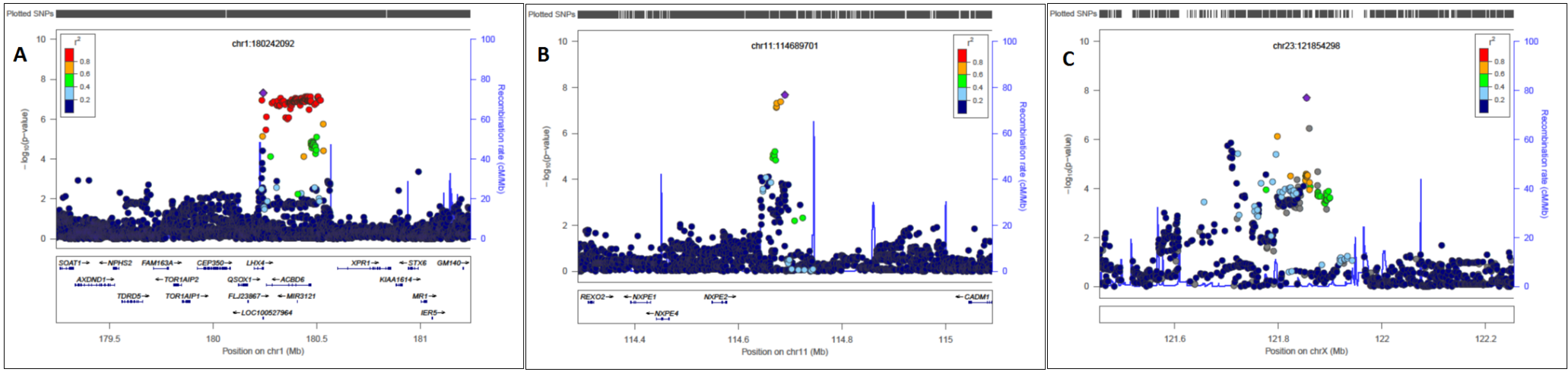


The threshold for genome-wide significance (P < 1.67 ×10-8) is indicated by the red dotted line.

eFigure 5. Forest Plots of the Harmonized z Statistics and Meta-analysis Estimates for the 3 Top SNPs



Combined (upper panel, A), male-specific (middle panel, B) and female-specific (lower panel, C) meta-analyses. Negative log10-transformed P-values for each gene are plotted. The threshold for gene-wide statistical significant associations was set at the Bonferroni threshold of P=2.73×10-6.



Regional association plots generated by LocusZoom, showing the significance of association and the recombination rate. For each SNP (A, chr1:180242092; B, chr11:114689701; C, chr23:121854298), the P-value is plotted against its chromosomal position (hg19), where the colors represent linkage disequilibrium and r2 values with the most significantly associated SNP are shown in purple.

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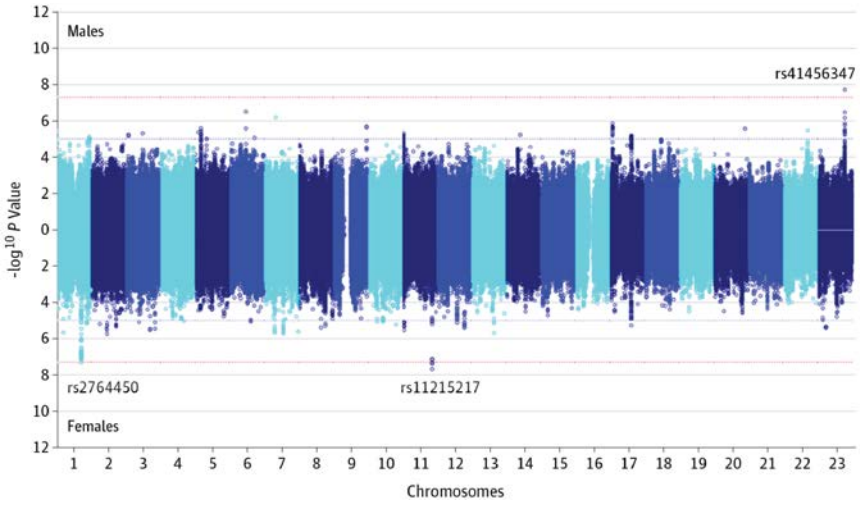

Figure Legend:

Miami Plot Showing P Values of the Single-Nucleotide Polymorphism Associations With Antisocial Behavior in Males and FemalesThe threshold for genome-wide significance ($P < 1.67 \times 10^{-8}$) is indicated by the red dotted line, and the threshold for promising findings ($P < 1.0 \times 10^{-5}$) is indicated by the blue dotted line.

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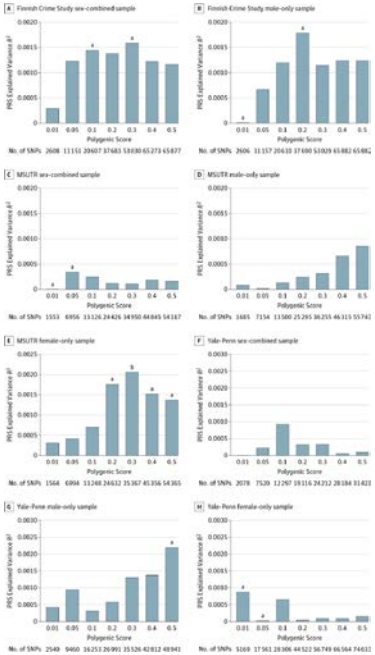

Figure Legend:

Polygenic Risk Scores (PRSs) in the Finnish Crime Study, Michigan State University Twin Registry (MSUTR), and Yale-Penn SamplesThe PRSs for antisocial personality disorder (ASPD) among patients with antisocial behavior (ASB) in the Finnish Crime Study using sex-combined (A) and male-only (B) samples. Summary-summary statistic–based results plotting the explained variance in ASB within the MSUTR (sex combined [C], males only [D], and females only [E]) and Yale-Penn (sex combined [F], males only [G], and females only [H]) samples. The proportion of variance explained (Nagelkerke R^2) was computed by comparison of a full model (covariates plus PRS) score with a reduced model (covariates only). Seven different P value thresholds for selecting risk alleles are denoted by the color of each bar. The number of single-nucleotide polymorphisms (SNPs) per threshold is displayed

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Table 1. Study Design, Sample Sizes, and Phenotypes for Genome-Wide Association Study Cohorts

Sample	Study Design	Antisocial Measure	Total Sample Size (M/F), No.	Age, Mean (SD), y
Discovery samples				
ALSPAC	Prospective pregnancy cohort (family design)	Development and Well-being Assessment, conduct disorder scale	4336 (2065/2271)	13.1 (0.1)
COGA	Alcohol dependence case-control sample (family design)	Count of the number of antisocial personality disorder criteria	1379 (739/640)	43.8 (11.7)
GENR	Population based (family design)	Rule-breaking behavior, Teacher Report Form	1420 (718/702)	6.7 (4.2)
TEDS	Population based (family design)	Antisocial Process Screening Device	2734 (1257/1477)	12.5 (.2)
QIMR	Population based (twin-family design)	Retrospective conduct disorder	6531 (2993/3538)	33.8 (2.4)
Target samples				
Finnish Crime Study	Case-control (prisoners sample)	Structured Clinical Interview for *DSM-IV* disorders	6220 (2536/3684)	56.1 (12.8)
MSUTR	Population based (family design)	Child Behavioral Checklist: conduct problems (reported by mother)	825 (394/431)	8.2 (1.5)
Yale-Penn	Substance-dependent sample	*DSM-IV* conduct disorder criteria	2336 (950/1386)	41.0 (8.2)

Abbreviations: ALSPAC, Avon Longitudinal Study of Parents and Children; COGA, Collaborative Studies on Genetics of Alcoholism; GENR, Generation Rotterdam; MSUTR, Michigan State University Twin Registry; QIMR, Queensland Institute of Medical Research; TEDS, Twins Early Development Study.

Table Title:

Study Design, Sample Sizes, and Phenotypes for Genome-Wide Association Study Cohorts

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Table 2. Genetic Correlation Estimates for 9 Traits With Broad Antisocial Behavior

Phenotype	Sample Size	SNP h2[a]	r_g (SE)[b]	*P* Value
Educational attainment	293 723	0.099	-0.52 (0.18)	.005
Neuroticism	170 911	0.094	0.29 (0.13)	.02
Schizophrenia	150 064	0.576	0.07 (0.15)	.64
Bipolar disorder	17 091	0.516	0.17 (0.20)	.41
Attention-deficit/hyperactivity disorder	9152	0.156	0.002 (0.29)	.99
Age at menarche	87 802	0.207	−0.04 (0.09)	.68
Age at menopause	69 360	0.134	−0.49 (0.19)	.01
Age at first birth	251 151	0.061	−0.43 (0.16)	.008
No. of children ever born	343 072	0.025	0.42 (0.19)	.03

Abbreviations: SNP h2, single-nucleotide polymorphism heritability.

[a] SNP h^2 is the estimation of narrow-sense heritability.

[b] r_g is the genetic correlation and is calculated with the linkage disequilibrium score regression software package using precalculated linkage disequilibrium scores from Finucane et al.[38]

Table Title:

Genetic Correlation Estimates for 9 Traits With Broad Antisocial Behavior