Multi-ancestry genome-wide association study identifies new asthma susceptibility loci that co-localize with immune cell enhancer histone marks

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*A full list of co-authors names appears in the main paper

Supplementary Information

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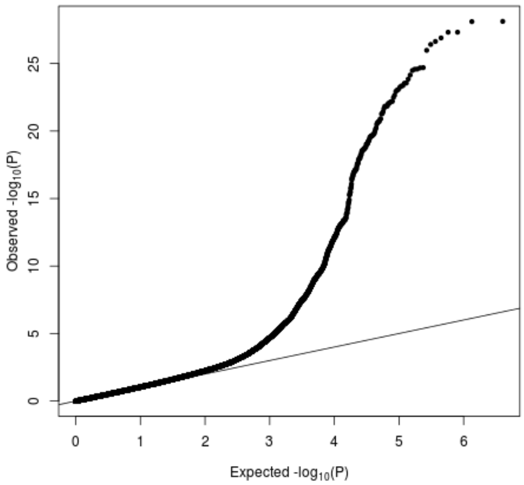
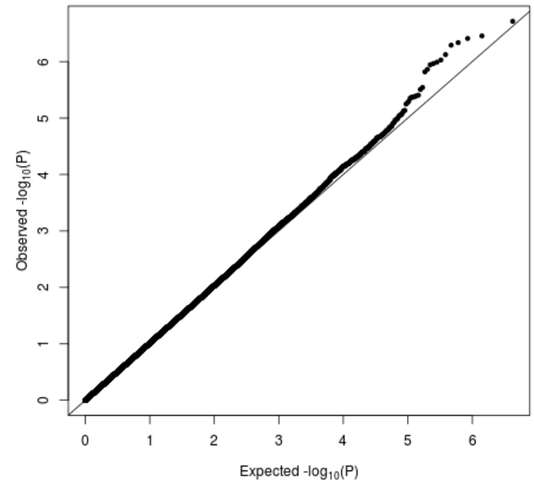
Supplementary Figures

Supplementary Figure 1. Quantile-quantile (QQ) plots for the ancestry-specific and multi-ancestry meta-analyses of asthma. QQ plots of P_{random} or P_{fixed} values for all SNPs passing QC in a least two-thirds of studies.

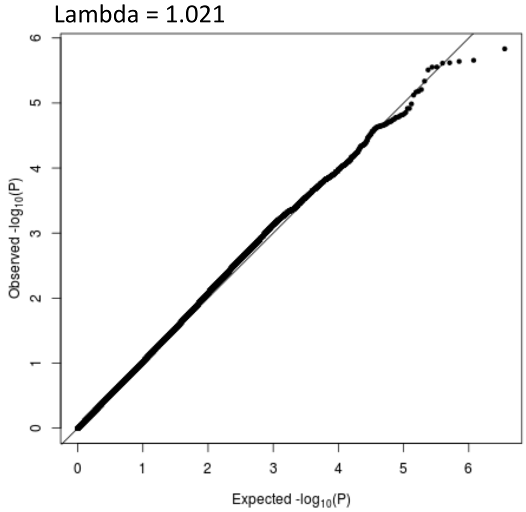
European ancestry (P_{random})
56 studies (19,954 cases, 107,715 controls)
Lambda = 1.031



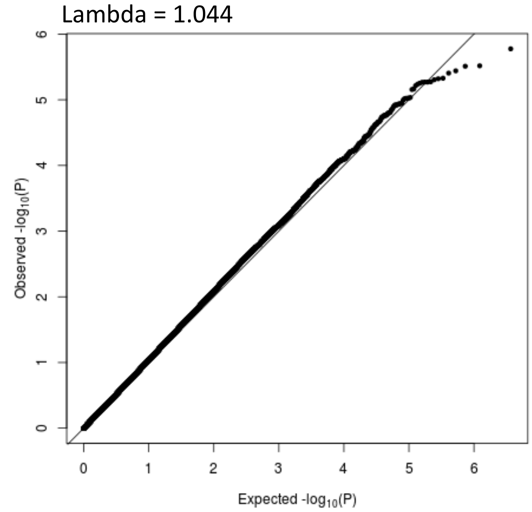
African ancestry (P_{fixed})
7 studies (2,149 cases, 6,055 controls)
Lambda = 1.014



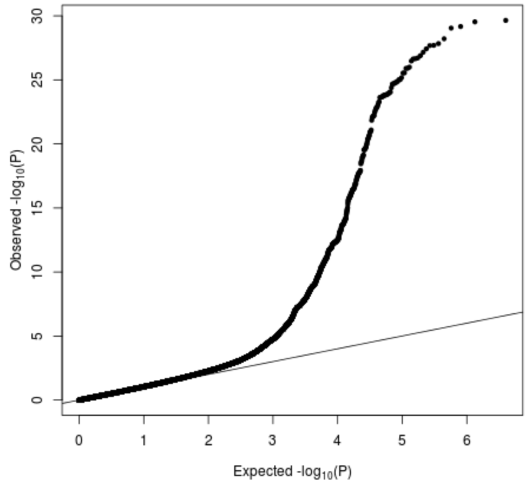
Japanese (P_{fixed})
2 studies (1,239 cases, 3,976 controls)
Lambda = 1.021



Latino (P_{fixed})
One study (606 cases, 792 controls)
Lambda = 1.044



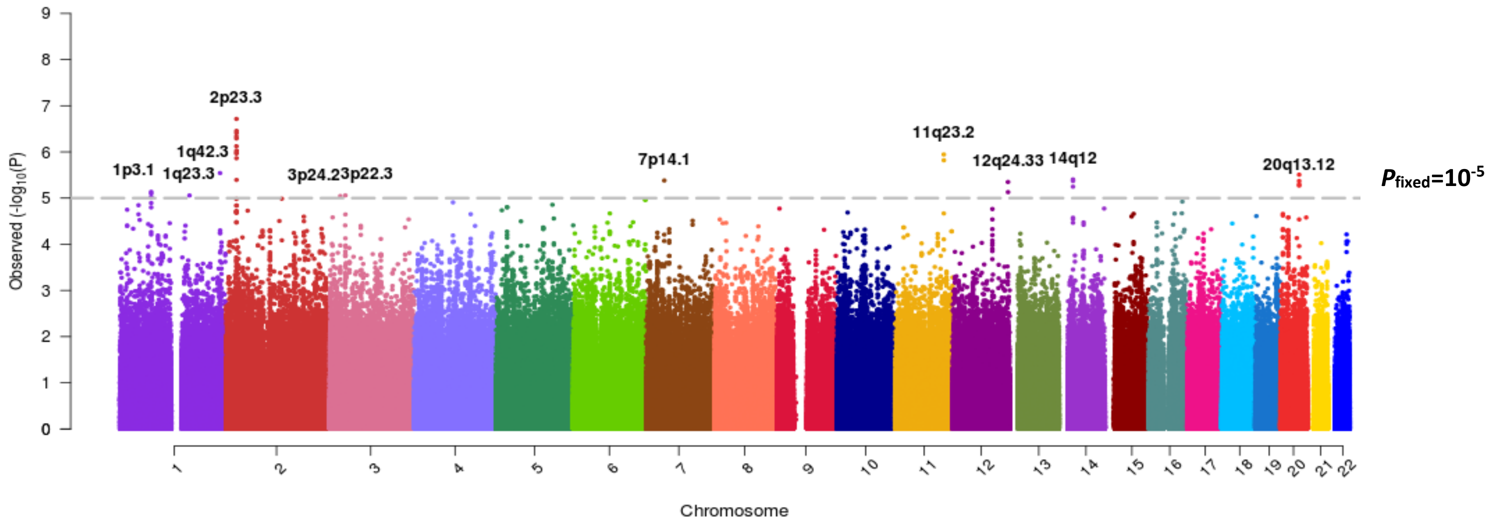
Multi-ancestry (P_{random})
66 studies (23,948 cases, 118,538 controls)
Lambda = 1.046



Supplementary Figure 2. Manhattan plots for each meta-analysis in African ancestry, Japanese and Latino populations.

The -log10 *Pfixed* values for all SNPs passing QC in at least two-thirds of studies have been plotted; the dashed horizontal line corresponds to a *P*-value threshold of 10^{-5}

African ancestry



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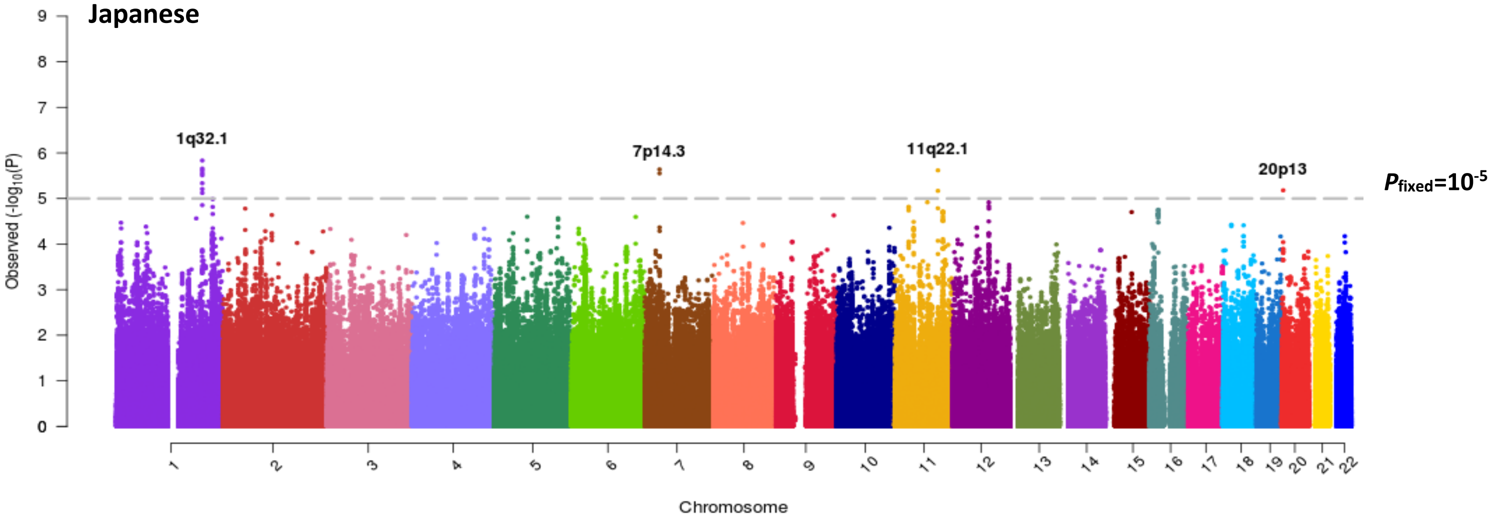
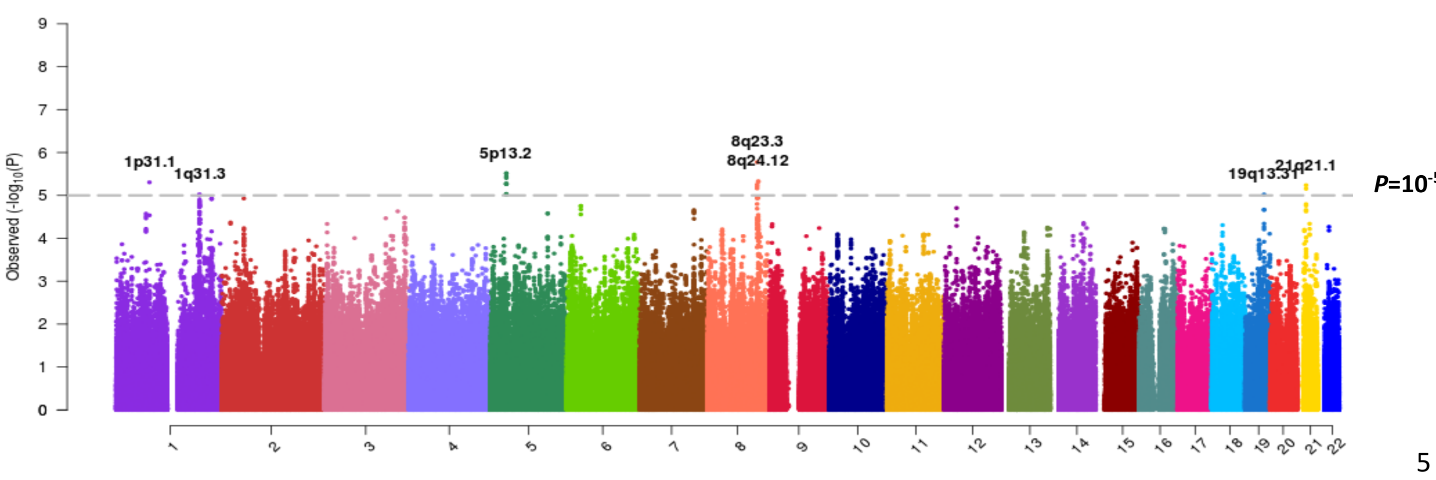


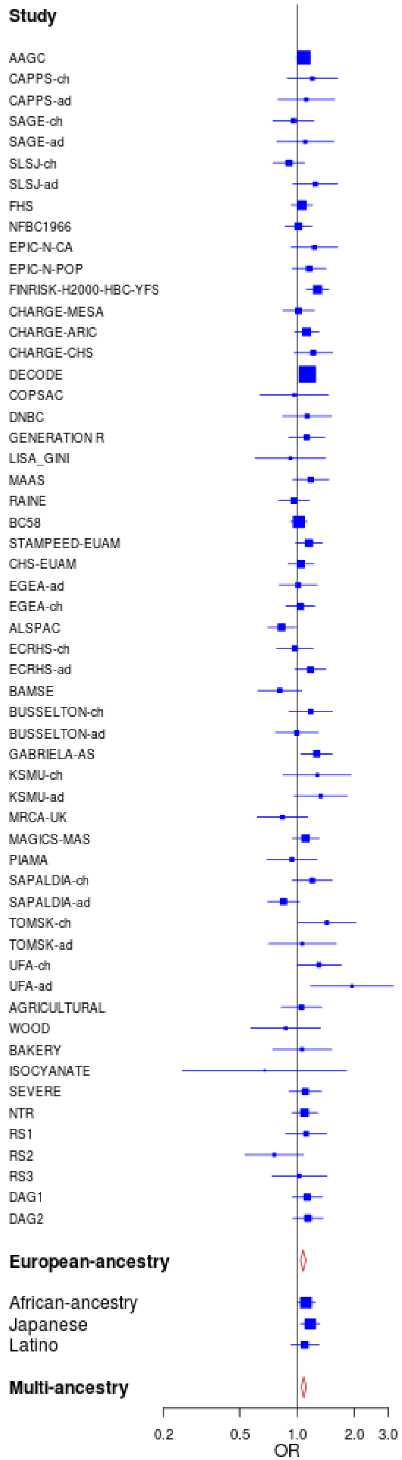
Latino



Supplementary Figure 3. Forest Plots of the lead SNPs at the 18 genome-wide significant loci
(nine loci harbouring new signals for asthma followed by nine known asthma loci, as shown in Table 1)

Odds-ratio (OR) and 95% Confidence Intervals (CI) are plotted by study and by population. European ancestry and multi-ancestry random-effects meta-analysis results are plotted as a diamond.

5q31.3, rs7705042



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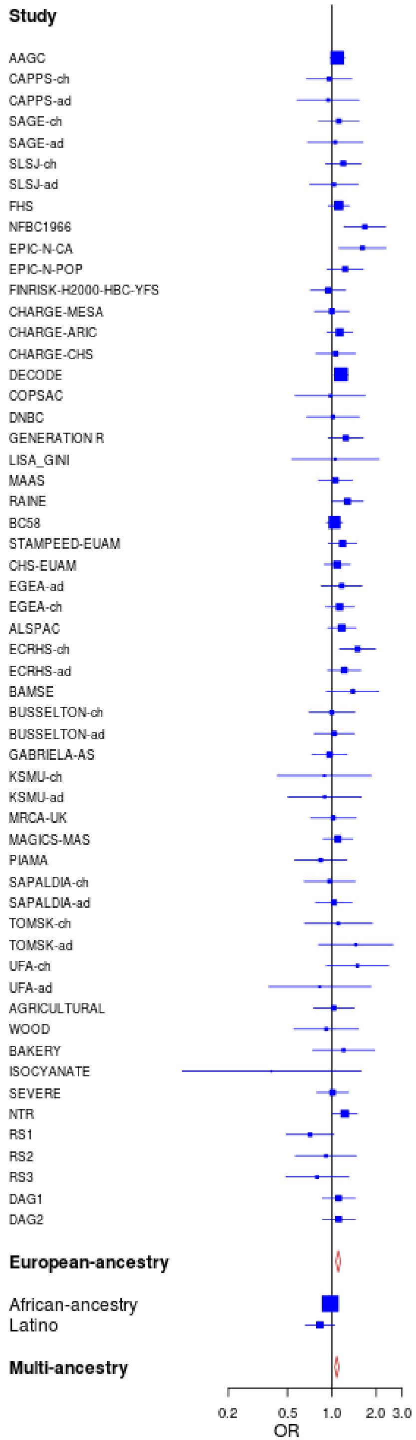

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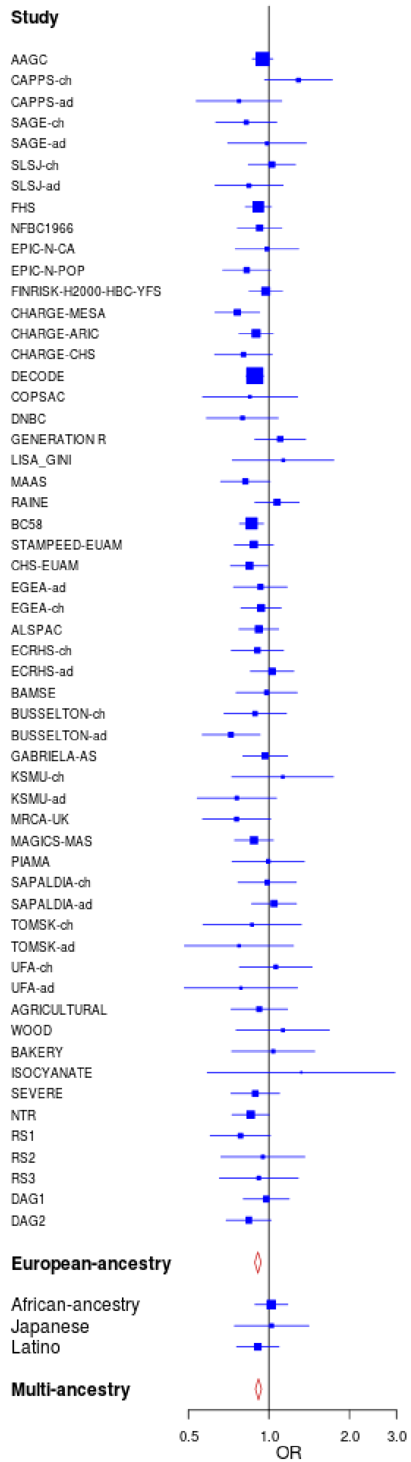

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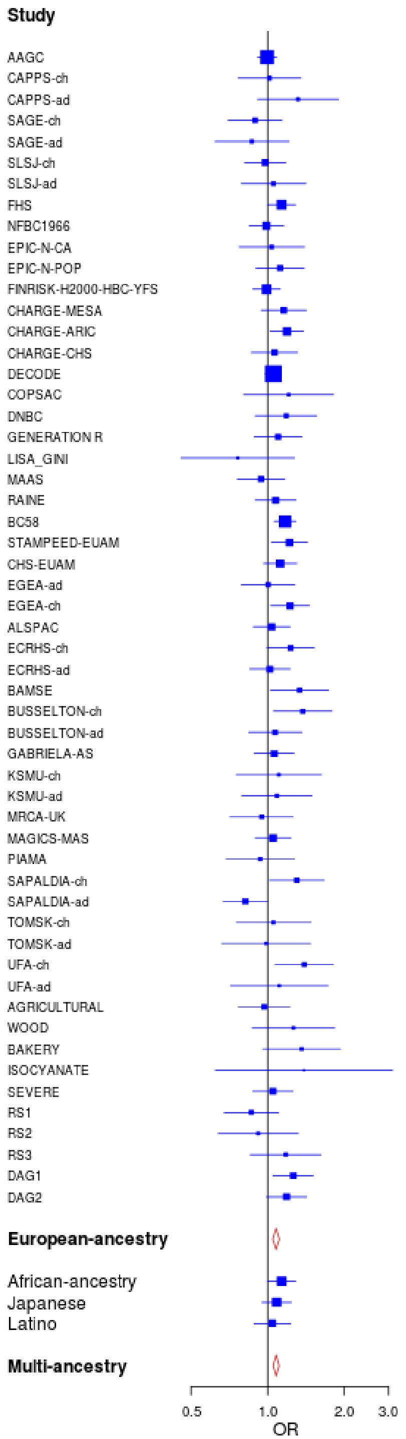

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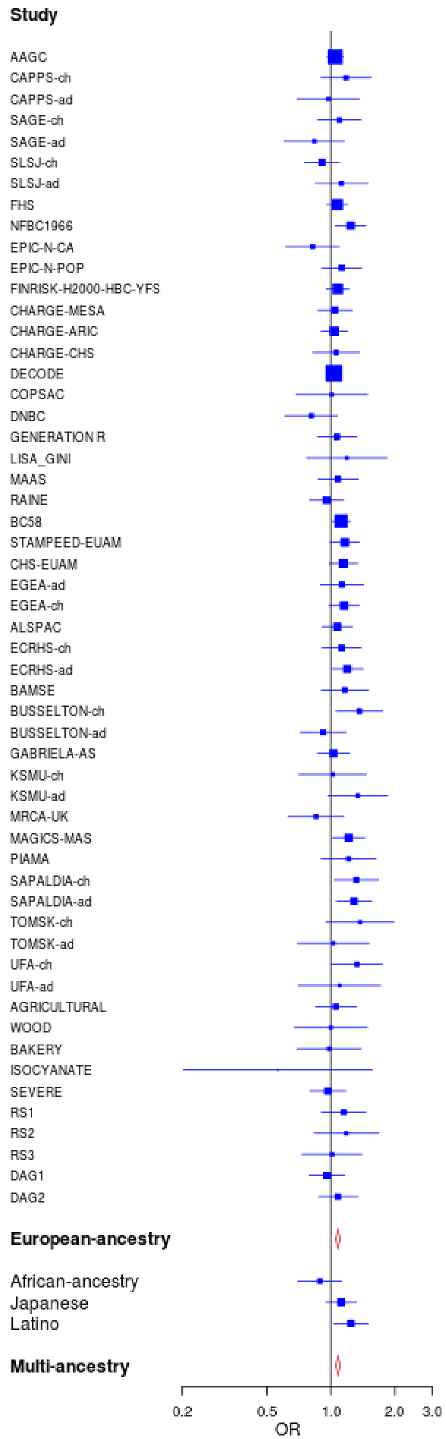

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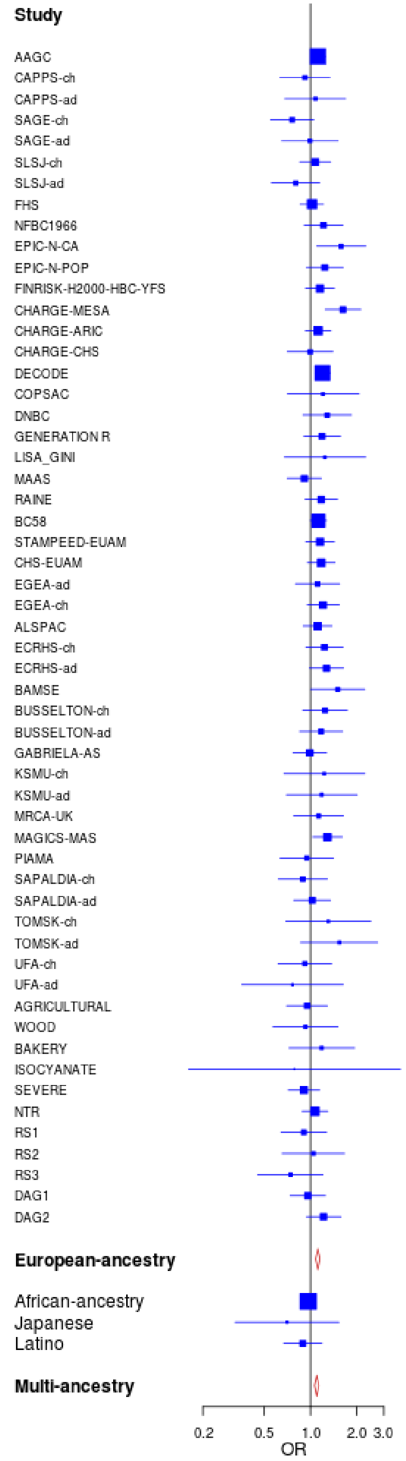

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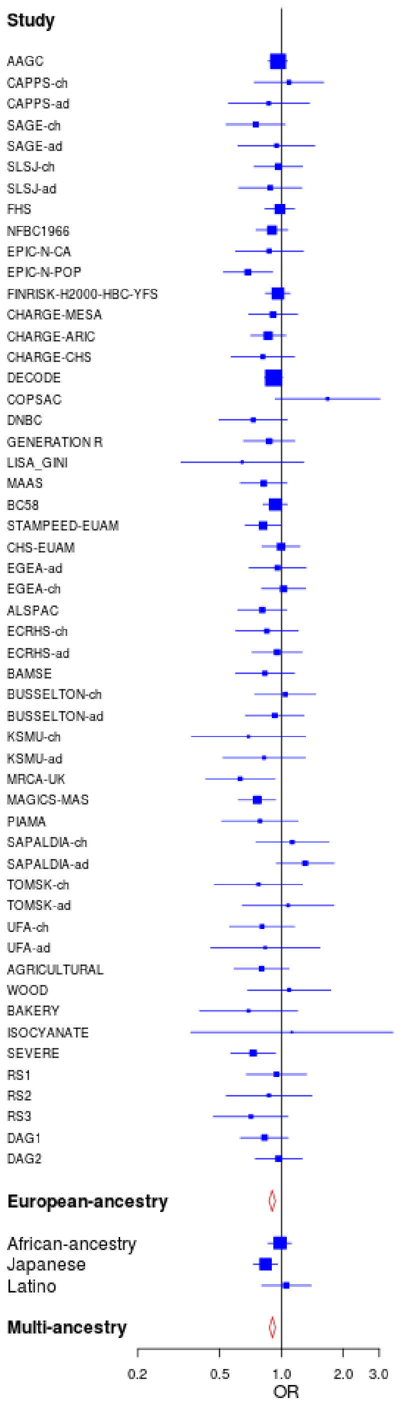

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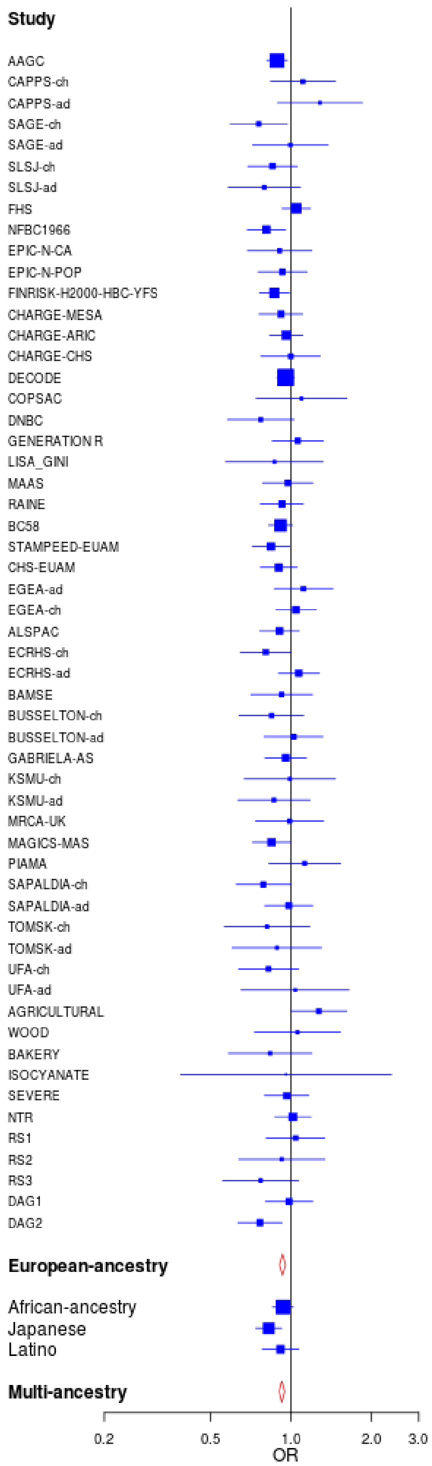

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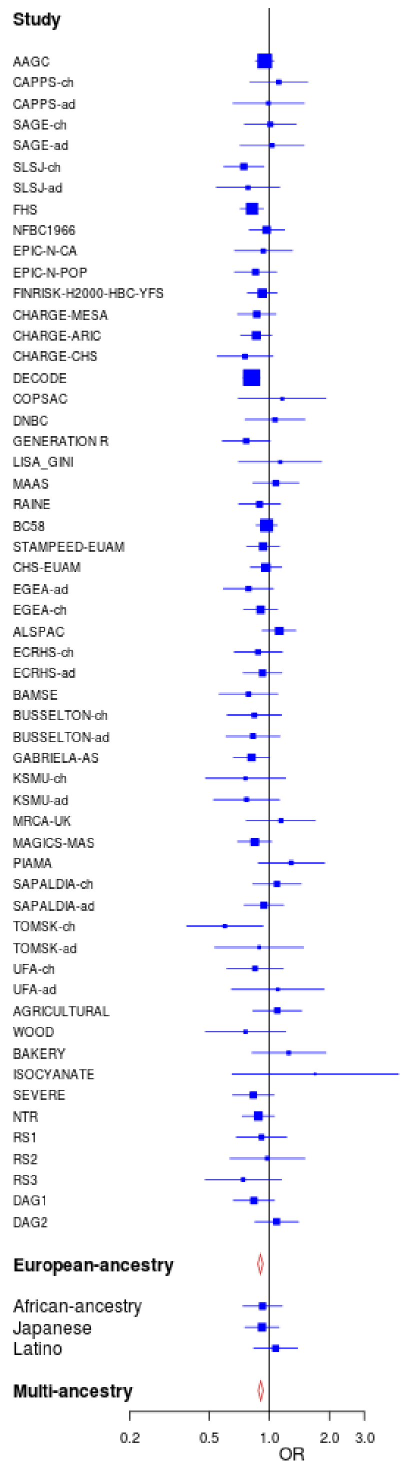

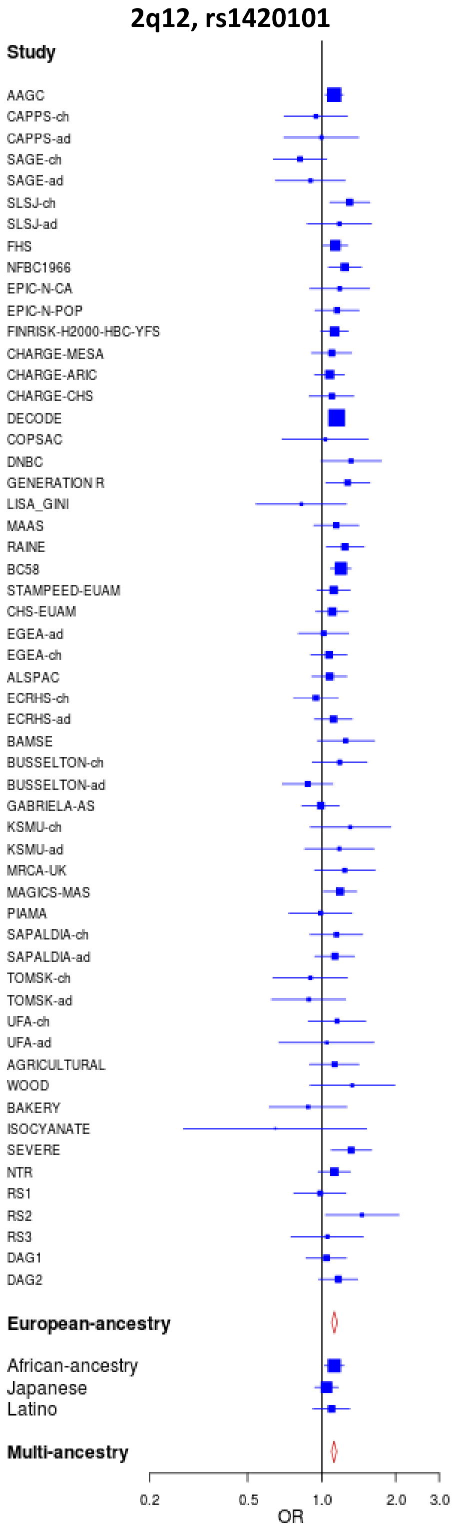
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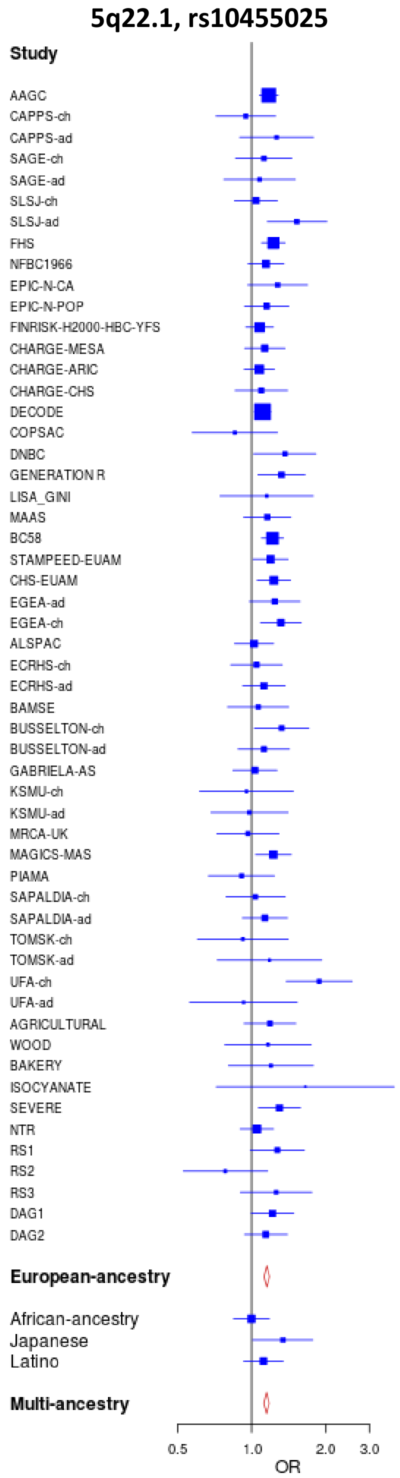
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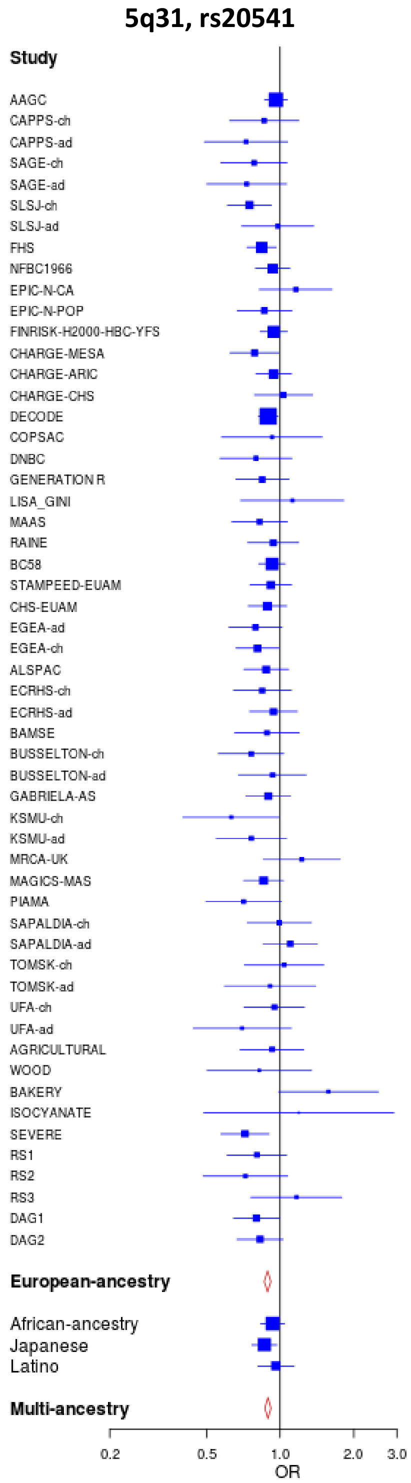
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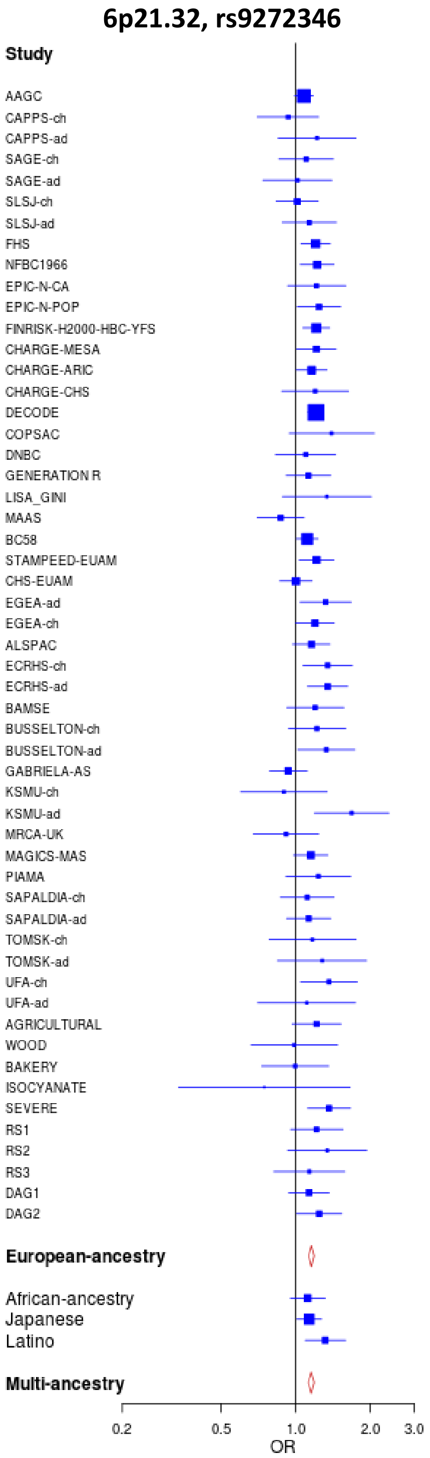
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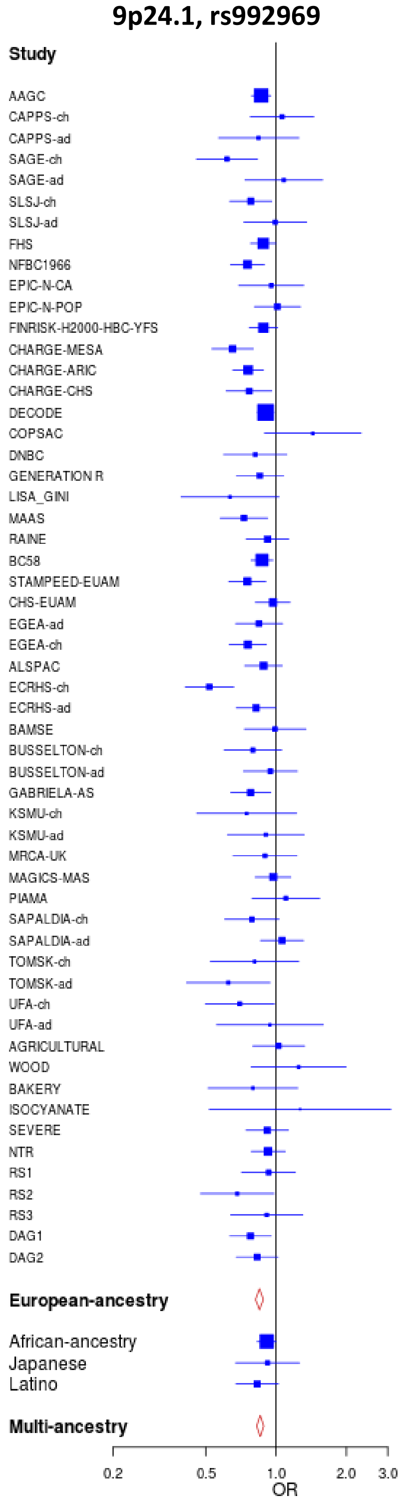
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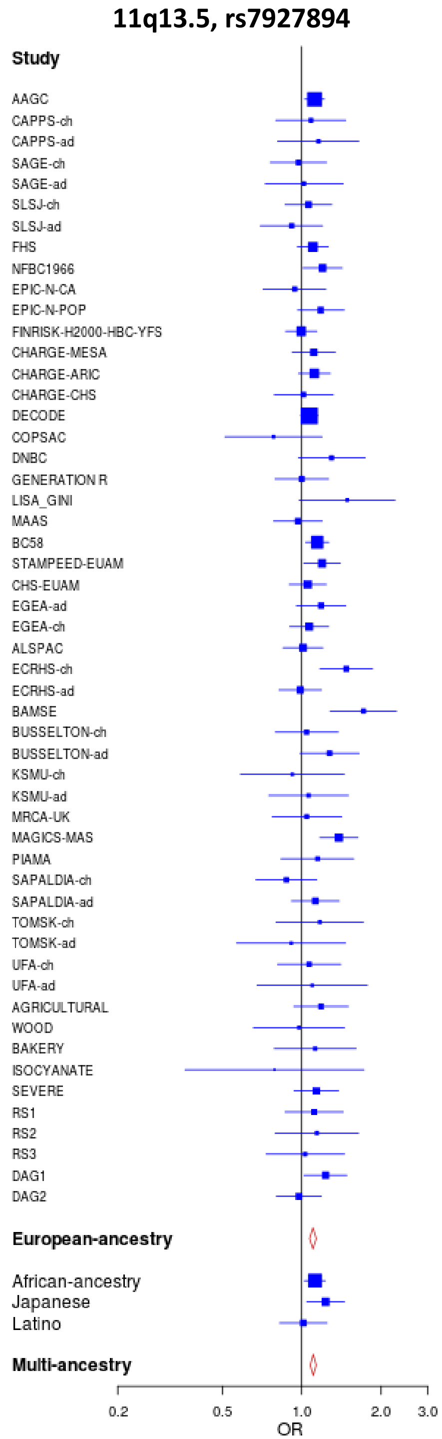
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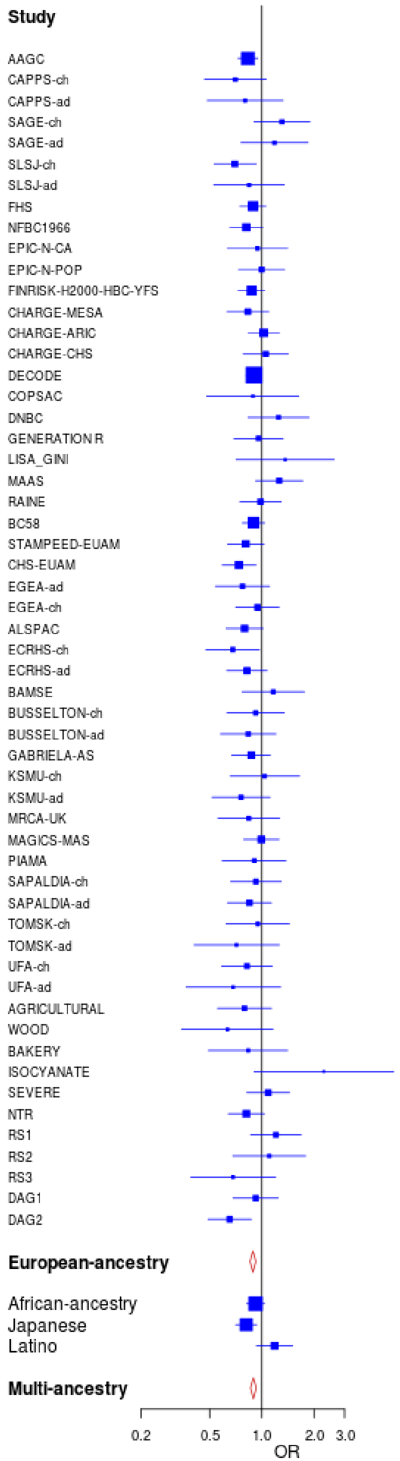

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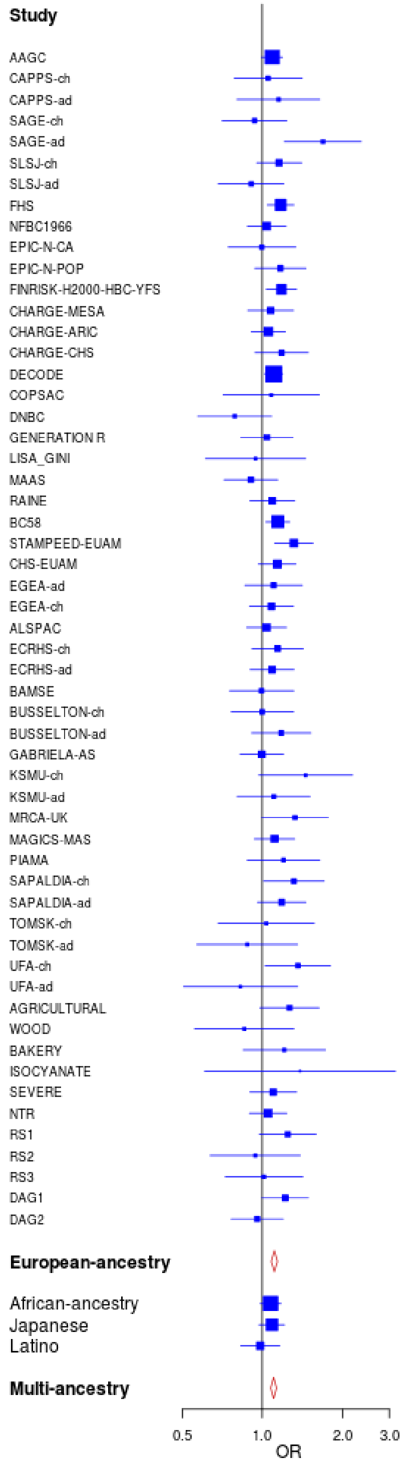
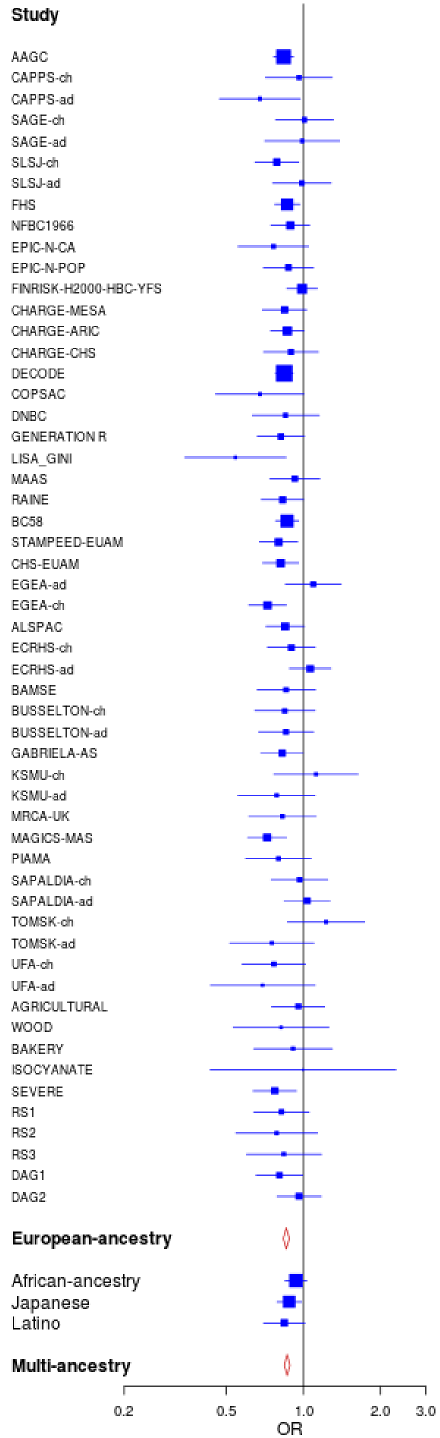
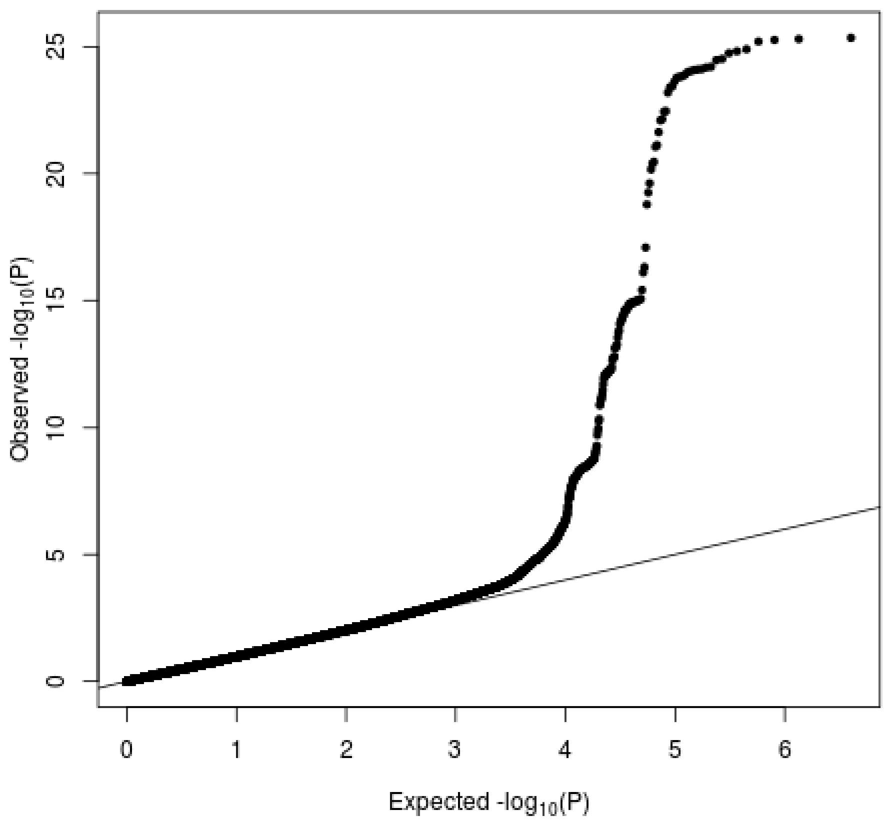


17q12-21, rs2952156



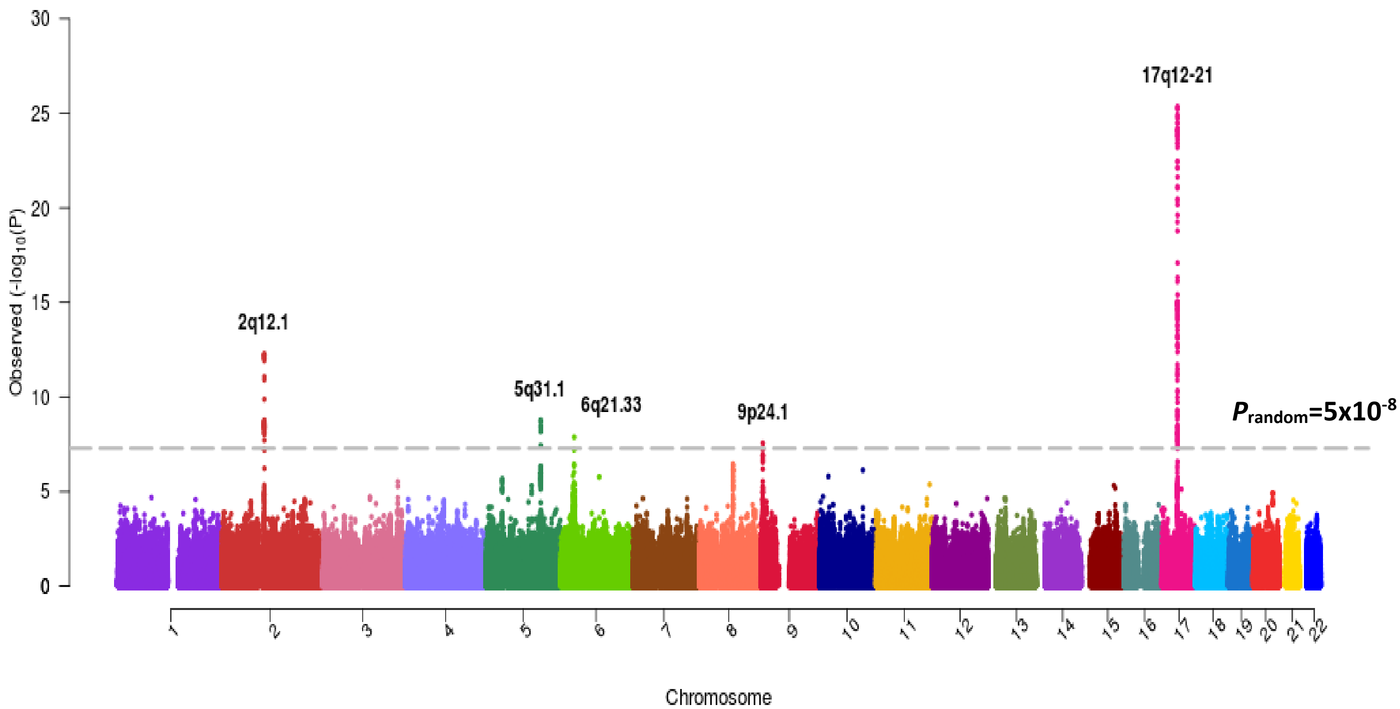
Supplementary Figure 4. Quantile-quantile (QQ) plot for the meta-analysis of pediatric asthma
QQ plots of P_{random} values for all SNPs passing QC in at least two-thirds of the studies (27 studies; 8,976 cases, 18,399 controls)

Lambda = 0.951



Supplementary Figure 5. Manhattan plot for the meta-analysis of pediatric asthma

The -log10 *Prandom* values for all SNPs passing QC in at least two-thirds of pediatric studies have been plotted; the dashed horizontal line corresponds to a P_{random} threshold of $5\mathrm{x}10^{-8}$

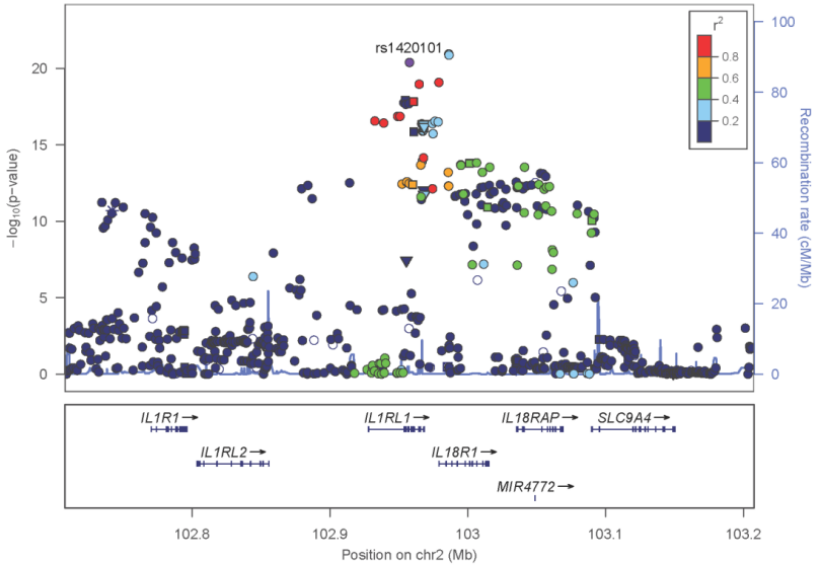


Supplementary Figure 6. Regional plots for the nine known asthma loci reaching genome-wide significance

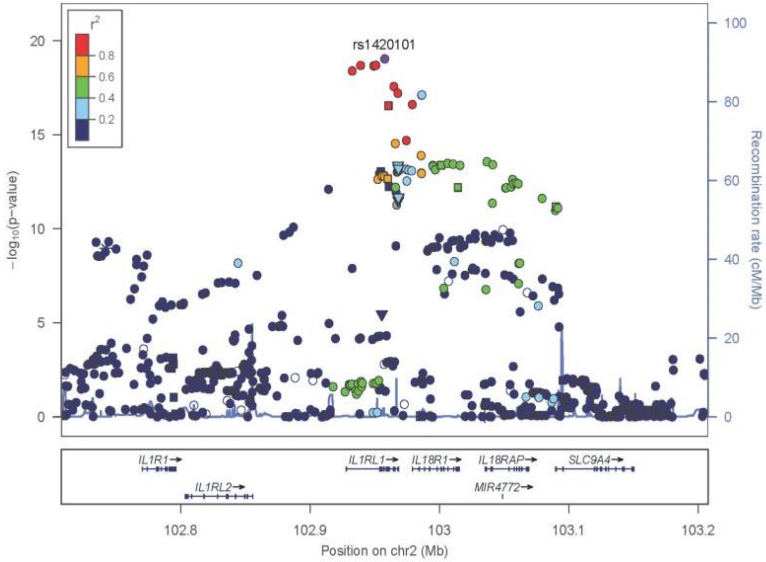
The x axis presents physical distance in megabase (build 37.3) and the Y axis presents $-\log10P_{random}$ values for association statistics in either the multi-ancestry or European ancestry meta-analysis using Locus Zoom. The rs ID is shown for the lead SNP in the region (purple diamond). For remaining SNPs the color indicates r^2 with the lead SNP.

2q12 – rs1420101

Multi-ancestry



European-ancestry



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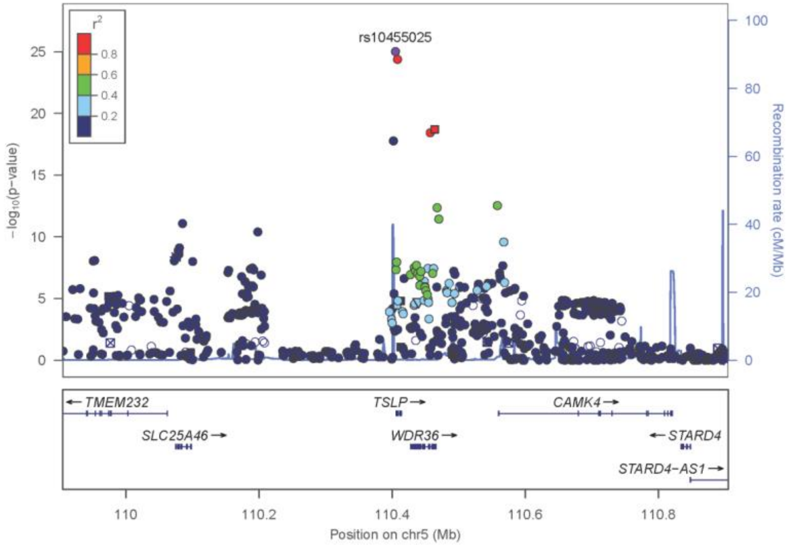

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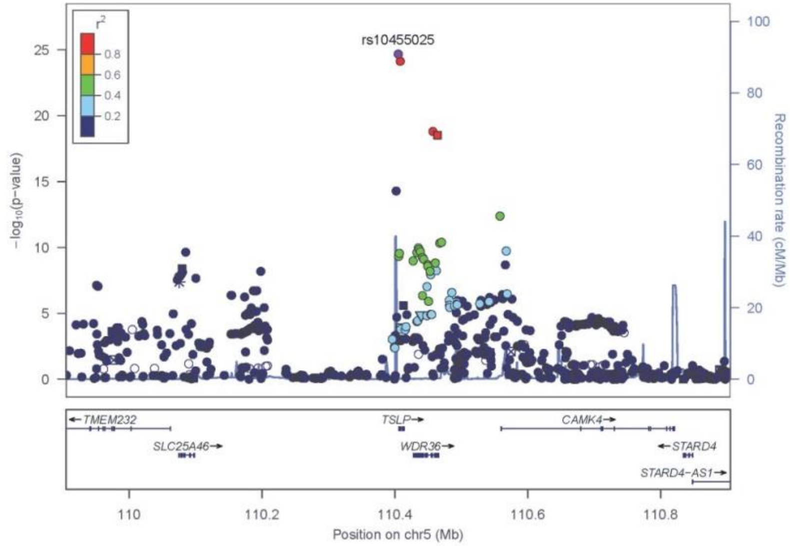

5q31 – rs20541

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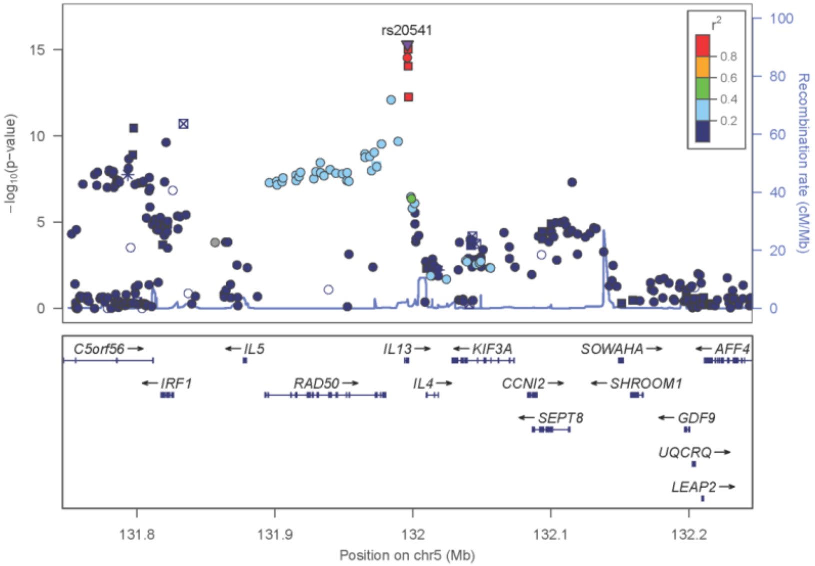

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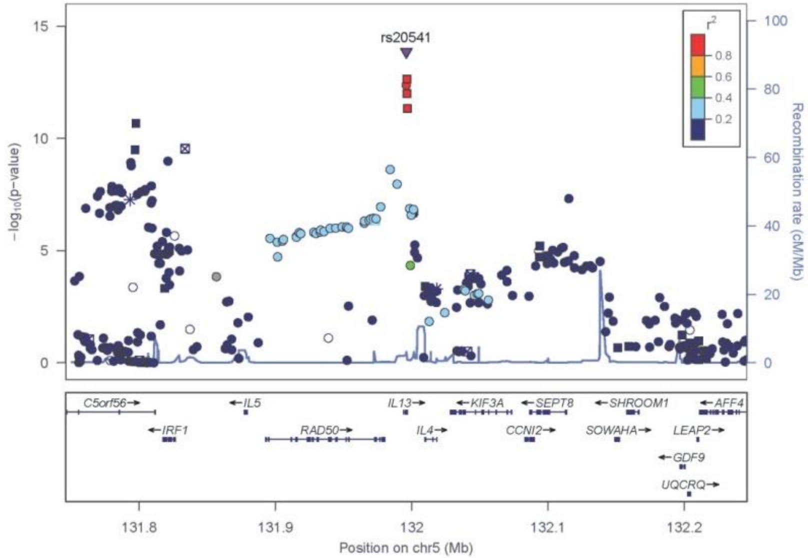
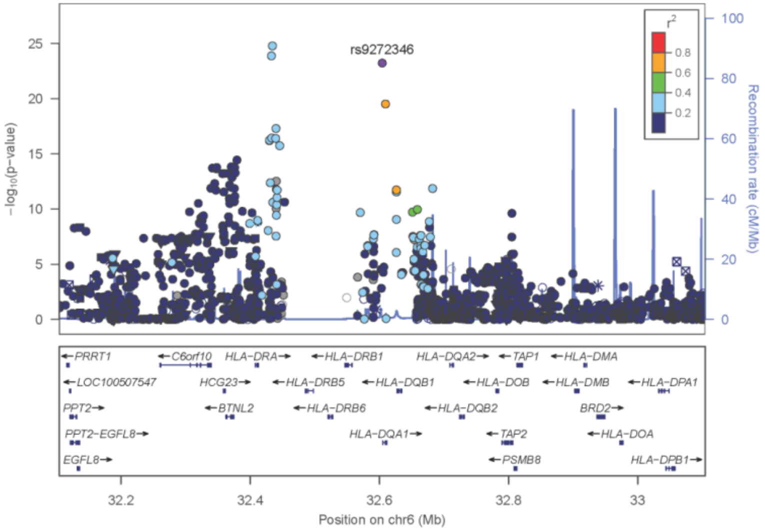


6p21.32 – rs9272346

Multi-ancestry



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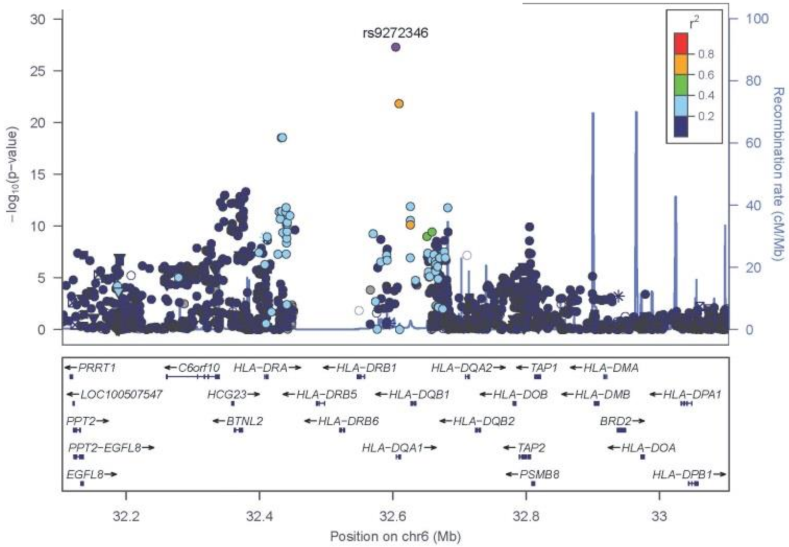
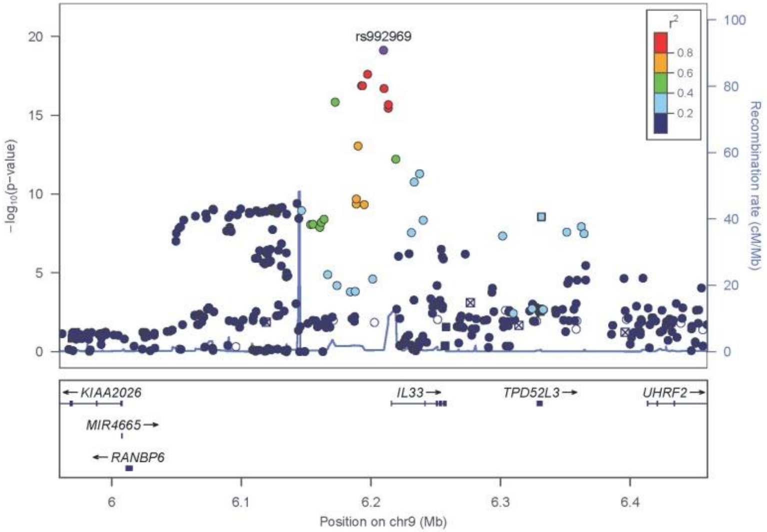


9p24.1 – rs992969

Multi-ancestry



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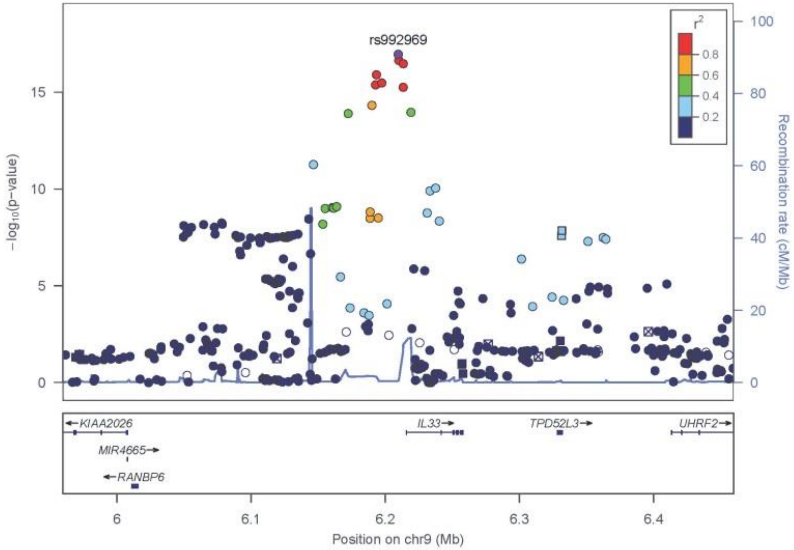
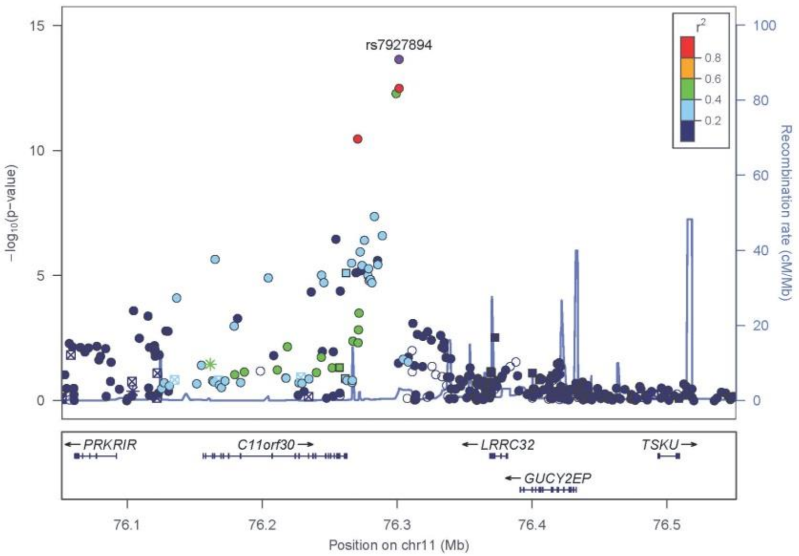


11q13.5 – rs7927894

Multi-ancestry



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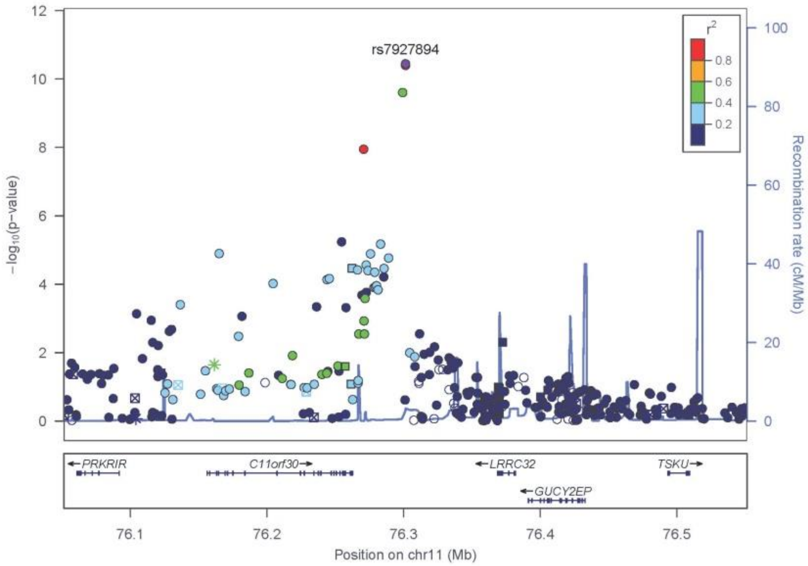

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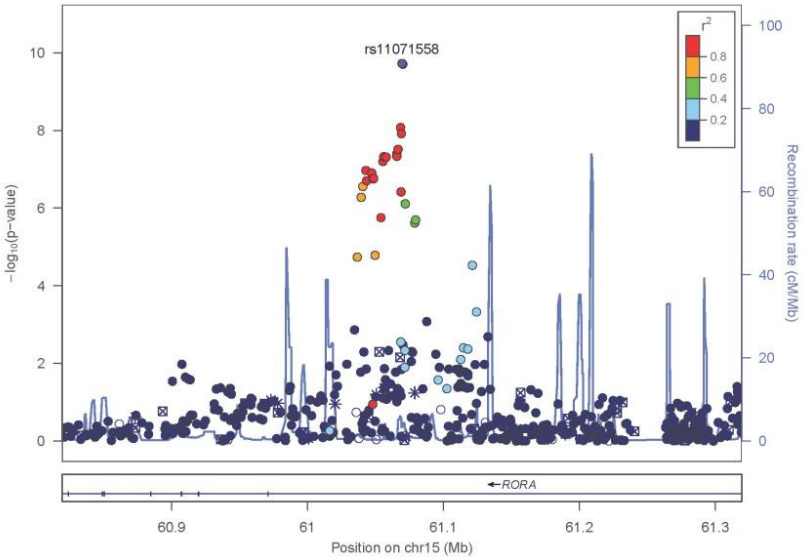
Multi-ancestry



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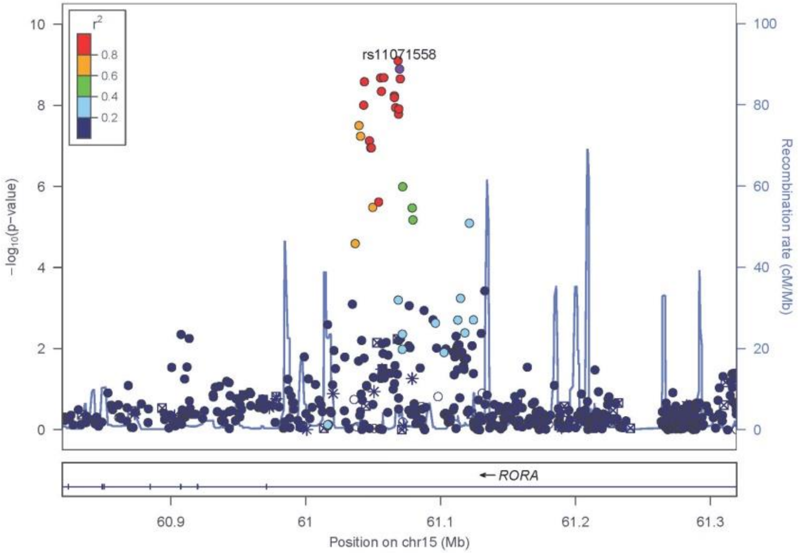

15q22.33 – rs2033784

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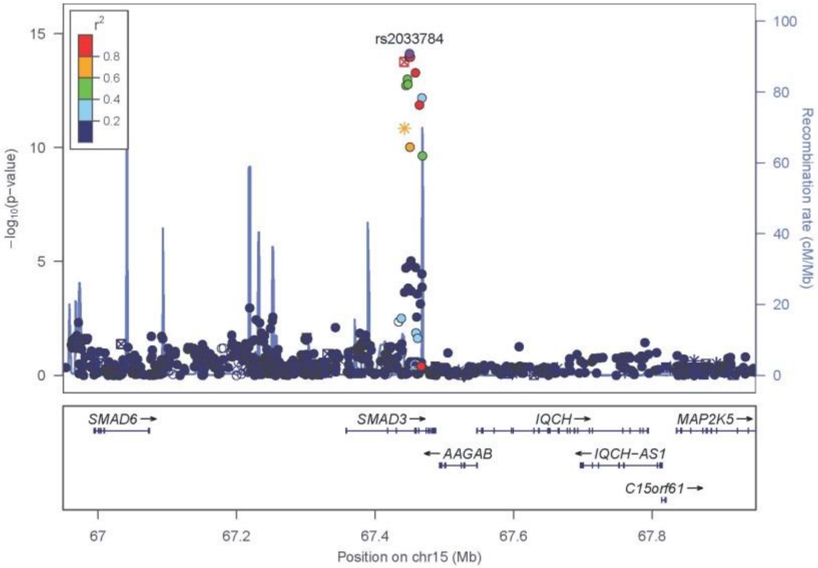

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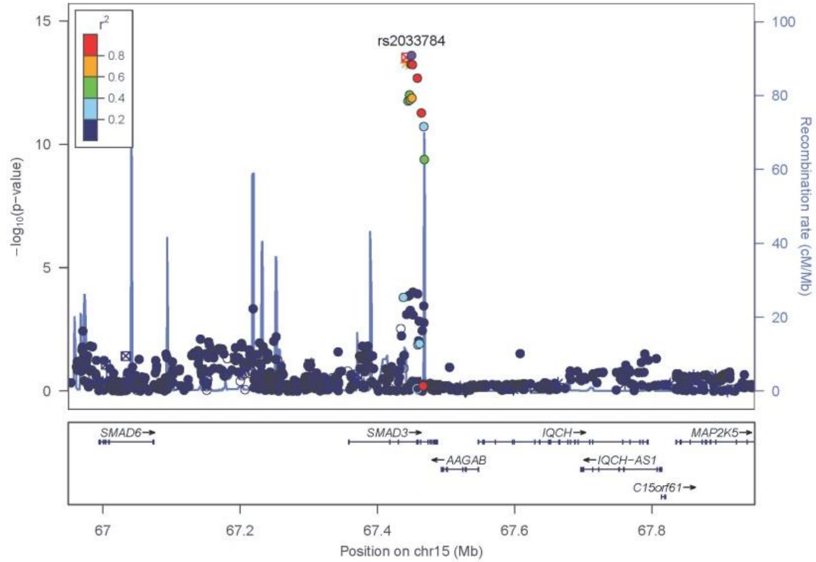
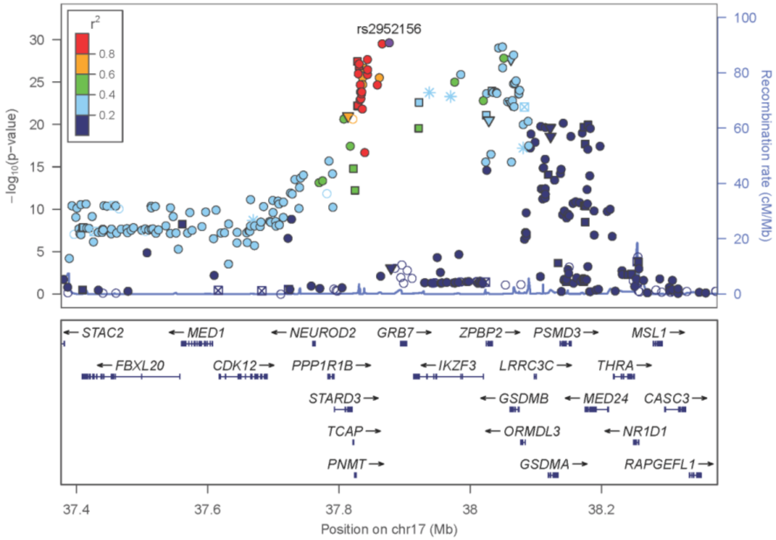
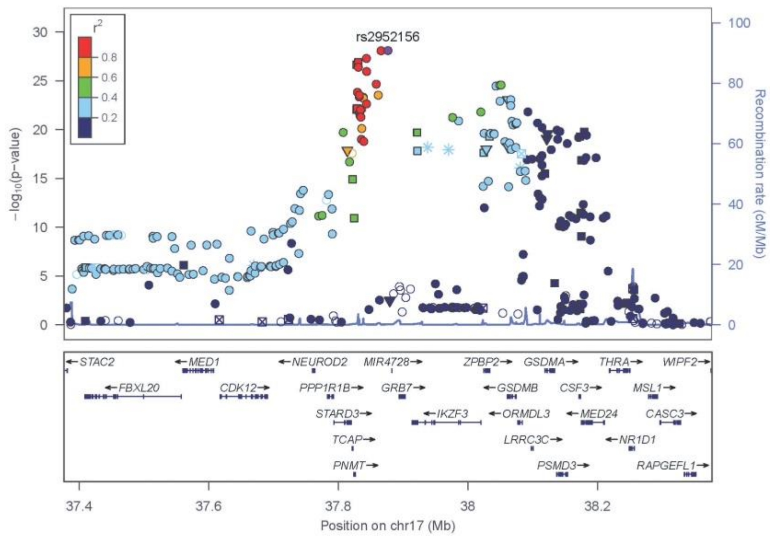


17q12-21 – rs2952156

Multi-ancestry



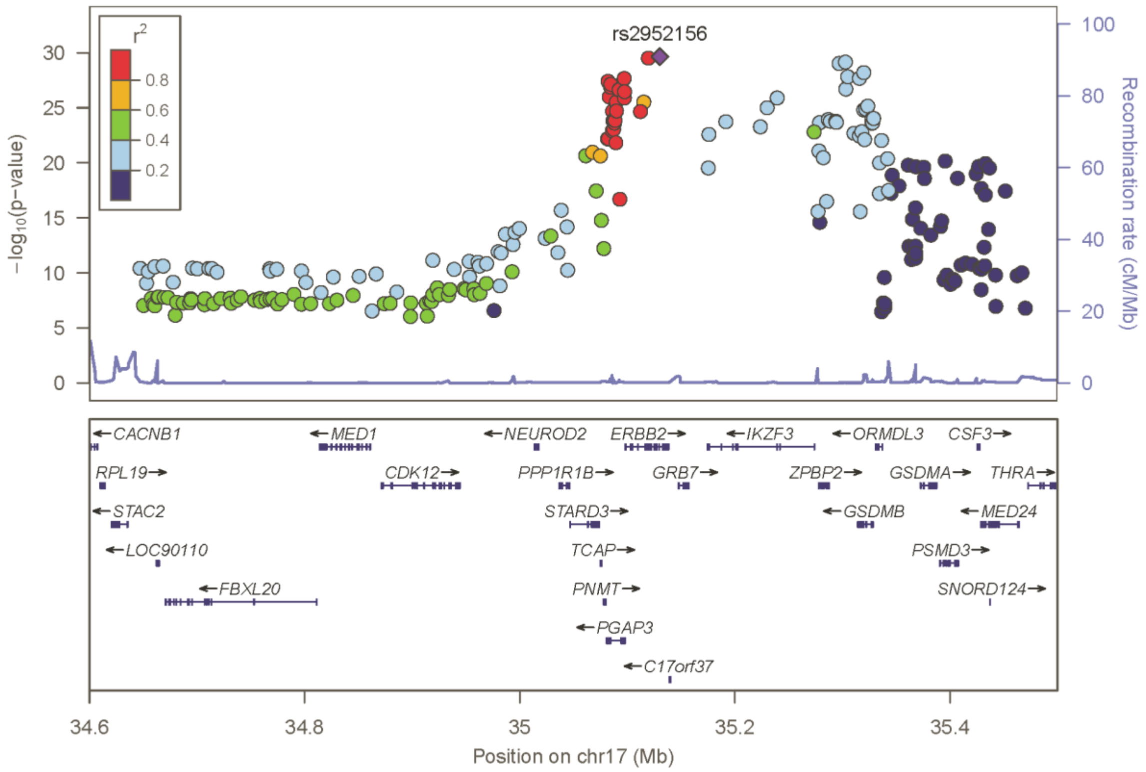
European-ancestry



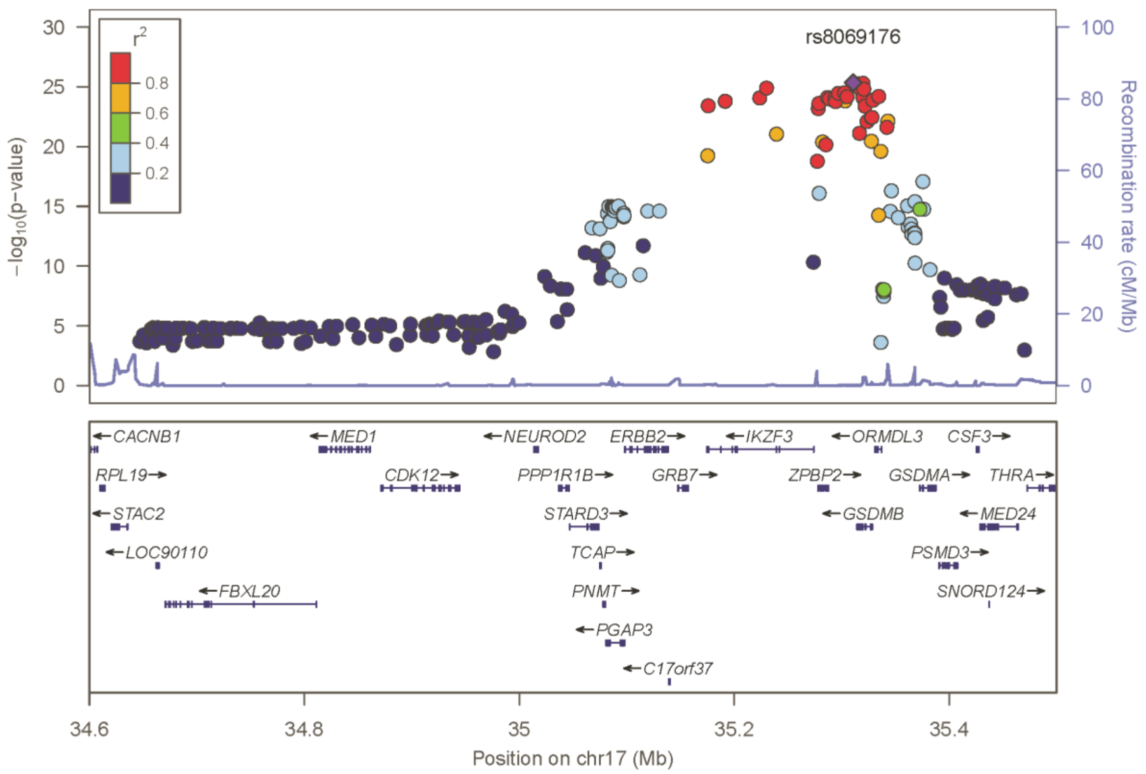
Supplementary Figure 7. Regional plots for the 17q12-21 locus in multi-ancestry and pediatric subgroup meta-analyses

The x axis presents physical distance in megabase (build 37.3) and the Y axis presents −log10P_{random} values for association statistics in either the multi-ancestry or pediatric subgroup meta-analysis using LocusZoom (see URLs). The rs ID is shown for the lead SNP in the region (purple diamond). For remaining SNPs the color indicates r^2 with the lead SNP.

Multi-ancestry meta-analysis



Pediatric subgroup meta-analysis



Supplementary Tables

Supplementary Table 1. Description and study design of the studies included in the meta-analysis

Consortium Name	Study Name	Study Abbreviation	Ancestry	Country of Residence	Study Design	Number of cases	Number of controls	Pediatric samples (P)[a]
Australian Asthma Genetics Consortium (AAGC)	Australian Asthma Genetics Consortium	AAGC	European	Australia	Population-based and case-control studies	2,110	3,857	
ALLERGEN	Canadian Asthma Primary Prevention Study (childhood onset)	CAPPS-ch	European	Canada	High-risk birth cohort	266	156	P
ALLERGEN	Canadian Asthma Primary Prevention Study (adult onset)	CAPPS-ad	European	Canada	High-risk birth cohort	94	250	
ALLERGEN	Study of Asthma Genes and the Environment (childhood onset)	SAGE-ch	European	Canada	Population-based birth cohort	257	267	P
ALLERGEN	Study of Asthma Genes and the Environment (adult onset)	SAGE-ad	European	Canada	Population-based birth cohort	96	402	
ALLERGEN	Saguenay-Lac-Saint Jean Study (childhood onset)	SLSJ-ch	European	Canada	Family study	373	390	P
ALLERGEN	Saguenay-Lac-Saint Jean Study (adult onset)	SLSJ-ad	European	Canada	Family study	213	223	
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	Framingham Heart Study	FHS	European	USA	Population-based cohort	797	6,463	
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	Northern Finland Birth Cohort 1966	NFBC1966	European	Finland	Population-based birth cohort	364	3,502	
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	EPIC-Norfolk obese cases	EPIC-N-CA	European	UK	Case Cohort	123	910	
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	EPIC-Norfolk population based	EPIC-N-POP	European	UK	Case Cohort	216	2,005	
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	FINRISK + Health 2000 (H2000) +Helsinki Birth Cohort (HBC) + Young Finns Study (YFS)	FINRISK-H2000-HBC-YFS	European	Finland	Population-based studies	555	6,923	
Candidate Gene Association Resource (CARe) Consortium	Atherosclerosis Risk in Communities Study (ARIC)	ARIC-AFAM	African	USA	Population-based study	148	1,087	
Candidate Gene Association Resource (CARe) Consortium	Corornary Artery Risk Development in Young Adults (CARDIA)	CARDIA	African	USA	Population-based study	106	318	
Candidate Gene Association Resource (CARe) Consortium	Jackson Heart Study (JHS)	JHS	African	USA	Population-based study	344	1,321	
Candidate Gene Association Resource (CARe) Consortium	Multi-Ethnic Study of Atherosclerosis (MESA)	MESA-AFAM	African	USA	Population-based study	294	2,275	

Consortium Name	Study Name	Study Abbreviation	Ancestry	Country of Residence	Study Design	Number of cases	Number of controls	Pediatric samples (P)[a]
Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE)	Multi-Ethnic Study of Atherosclerosis (MESA)	MESA-EUAM	European	USA	Population-based cohort	267	2,381	P (for part of the data)
Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE)	Atherosclerosis Risk in Communities Study (ARIC)	ARIC-EUAM	European	USA	Population-based cohort	453	9,713	
Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE)	Cardiovascular Health Study (CHS)	CHS	European	USA	Population-based cross sectional study	179	3,058	
deCODE Genetics	deCODE Genetics	deCODE	European	Iceland	Case-control study	1,675	33,408	
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Cophenhagen Study on Asthma in Childdhood	COPSAC	European	Denmark	High-risk birth cohort	70	240	P
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Danish National Birth Cohort	DNBC	European	Denmark	Population-based birth cohort	113	850	P
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	GENERATION R	GENERATION R	European	The Netherlands	Population-based birth cohort	201	1,749	P
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	LISA Plus & GINI Plus (German Infant Nutritional Intervention Program) Birth Cohorts	LISA-GINI	European	Germany	Population-based birth cohort	49	999	P
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Manchester Asthma and Allergy Study	MAAS	European	UK	Population-based birth cohort	317	545	P
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Western Australian Pregnancy (Raine) Cohort	RAINE	European	Australia	Population-based birth cohort	328	870	P
B58C	British 1958 Birth Cohort	B58C	European	UK	Population-based birth cohort	986	5,505	
EVE	CAG/CSGA/SARP-EUAM	STAMPEED-EUAM	European	USA	Case-control study	843	580	
EVE	Children'Health Study (CHS) Hispanic White	CHS-LAT	Latino	USA	Case-control study	606	792	P
EVE	CAG/CSGA/SARP-AFAM	STAMPEED-AFAM	African	USA	Case-control study	644	451	
EVE	Genomic Research on Asthma in the African Diaspora	GRAAD	African	USA	Case-control study	464	471	
EVE	Study of Asthma Phenotypes and Pharmacogenomics Interactions by Race Ethnicity	SAPPHIRE	African	USA	Case-control study	149	132	
EVE	Children'Health Study (CHS) Non-Hispanic white	CHS-EUAM	European	USA	Case-control study	643	959	P
Japanese Adult Asthma Research Consortium (JAARC)	Japanese Childhood Onset Asthma in Adult Asthma research	JCOAAD	Japenese	Japan	Case-control study	301	3,304	P

Consortium Name	Study Name	Study Abbreviation	Ancestry	Country of Residence	Study Design	Number of cases	Number of controls	Pediatric samples (P)[a]
Japan Pediatric Asthma Consortium (JPAC)	Japan Pediatric Asthma Consortium	JPAC	Japenese	Japan	Case-control study	938	672	P
GABRIEL	Epidemiological study on the Genetics and Environment of Asthma (childhood-onset asthma)	EGEA-ch	European	France	Family study	482	598	P
GABRIEL	Epidemiological study on the Genetics and Environment of Asthma (adult-onset asthma)	EGEA-ad	European	France	Family study	194	654	
GABRIEL	Avon Longitudinal Study of Parents and Children	ALSPAC	European	United Kingdom	Population-based birth cohort	607	609	P
GABRIEL	European Community Respiratory Health Survey (childhood-onset asthma)	ECRHS-ch	European	Mutliple European Countries	Population-based cohort	279	620	P
GABRIEL	European Community Respiratory Health Survey (adult-onset asthma)	ECRHS-ad	European	Mutliple European Countries	Population-based cohort	385	926	
GABRIEL	Barn Allergy Milieu Stockholm Epidemiology	BAMSE	European	Sweden	Population-based birth cohort	239	246	P
GABRIEL	Busselton study (childhood-onset asthma)	BUSSELTON-ch	European	Australia	Population-based study	188	390	P
GABRIEL	Busselton study (adult-onset asthma)	BUSSELTON-ad	European	Australia	Population-based study	210	419	
GABRIEL	Gabriel Advanced Surveys	GABRIELA-AS	European	Austria,Germany, Switzerland	Cross-sectional population-based study	841	851	P
GABRIEL	Kursk State Medical University study (childhood-onset asthma)	KSMU-ch	European	Russia	Case-control study	112	116	P
GABRIEL	Kursk State Medical University study (adult-onset asthma)	KSMU-ad	European	Russia	Case-control study	179	161	
GABRIEL	Medical Research Council Asthma UK Center in Allergic Mechanisms of Asthma (MRCA-UK)	MRCA-UK	European	UK	Family study	177	399	P
GABRIEL	German Multicentre Asthma Genetics in Childhood Study (MAGICS) and Multicentre Allergy Study (MAS)	MAGICS-MAS	European	Germany	Case-control study	630	572	P
GABRIEL	The Prevention and Incidence of Asthma and Mite Allergy birth cohort study	PIAMA	European	The Netherlands	Population-based birth cohort	172	187	P
GABRIEL	Swiss study on Air Pollution And Lung Disease in Adults (childhood-onset asthma)	SAPALDIA-ch	European	Switzerland	Population-based cohort	237	356	P
GABRIEL	Swiss study on Air Pollution And Lung Disease in Adults (adult-onset asthma)	SAPALDIA-ad	European	Switzerland	Population-based cohort	371	557	
GABRIEL	TOMSK study (childhood-onset asthma)	TOMSK-ch	European	Russia	Family study	197	91	P

Consortium Name	Study Name	Study Abbreviation	Ancestry	Country of Residence	Study Design	Number of cases	Number of controls	Pediatric samples (P)[a]
GABRIEL	TOMSK study (adult-onset asthma)	TOMSK-ad	European	Russia	Family study	62	331	
GABRIEL	UFA region study (childhood-onset asthma)	UFA-ch	European	Russia	Case-control study	269	209	P
GABRIEL	UFA region study (adult-onset asthma)	UFA-ad	European	Russia	Case-control study	61	139	
GABRIEL	Industrial Cohorts / Agricultural exposures	AGRICULTURAL	European	Mutliple European Countries	Industrial cohort	256	427	
GABRIEL	Industrial Cohorts / Wood exposure	WOOD	European	Mutliple European Countries	Industrial cohort	112	107	
GABRIEL	Industrial Cohorts / Wheat and amylase exposures (bakers)	BAKERY	European	Mutliple European Countries	Industrial cohort	136	127	
GABRIEL	Industrial Cohorts / Isocyanate exposure	ISOCYANATE	European	Mutliple European Countries	Industrial cohort	25	37	
GABRIEL	Severe asthma study	SEVERE	European	United Kingdom	Case-control study	290	974	
Netherlands Twin Registry (NTR)	The Netherlands Twin Register	NTR	European	The Netherlands	Twin Registry (Population-based/Families)	451	2,416	
Rotterdam Study (RS)	Rotterdam Study 1	RS1	European	The Netherlands	Population-based cohort study	143	4,662	
Rotterdam Study (RS)	Rotterdam Study 2	RS2	European	The Netherlands	Population-based cohort study	67	1,616	
Rotterdam Study (RS)	Rotterdam Study 3	RS3	European	The Netherlands	Population-based cohort study	79	1,727	
Dutch Asthma Genetics Consortium (DAGC)	Dutch Asthma GWAS 1 Family-Based	DAG1	European	The Netherlands	Family study	463	469	
Dutch Asthma Genetics Consortium (DAGC)	Dutch Asthma GWAS 2 Case-Control	DAG2	European	The Netherlands	Case-control study	452	517	

[a]Pediatric asthma is defined as asthma onset ≤ 16 years of age

Supplementary Table 2. Information on genotyping methods, imputation, and statistical analysis by study

Details and references for each study can be found in the Supplementary Note

Consortium Name	Study Name	Study Abbreviation	Genotyping platform	Imputation software	Reference panel used for imputation	Statistical method used for analysis	Software used for analysis
Australian Asthma Genetics Consortium (AAGC)	Australian Asthma Genetics Consortium	AAGC	Ilumina 370K,610K	IMPUTE2	HapMap3 (Feb 2009 release), 1000 Genomes (CEU, Mar 2010 release) but only HapMap2 SNPs provided to TAGC	Cochran-Mantel-Haenszel (CMH) test with two strata corresponding to the 610K and 370K arrays	PLINK v1.07
ALLERGEN	Canadian Asthma Primary Prevention Study (childhood onset)	CAPPS-ch	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic Regression (robust variance to account for family dependence)	Stata V11
ALLERGEN	Canadian Asthma Primary Prevention Study (adult onset)	CAPPS-ad	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK
ALLERGEN	Study of Asthma Genes and the Environment (childhood onset)	SAGE-ch	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic Regression (robust variance to account for family dependence)	Stata V11
ALLERGEN	Study of Asthma Genes and the Environment (adult onset)	SAGE-ad	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK
ALLERGEN	Saguenay-Lac-Saint Jean Study (childhood onset)	SLSJ-ch	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic Regression (robust variance to account for family dependence)	Stata V10
ALLERGEN	Saguenay-Lac-Saint Jean Study (adult onset)	SLSJ-ad	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic Regression (robust variance to account for family dependence)	Stata V10
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	Framingham Heart Study	FHS	Affymetrix 5.0	MACH 1.0	HapMap2 CEU, r22	GEE model	GWAF (R package)
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	Northern Finland Birth Cohort 1966	NFBC1966	Illumina CNV370 Duo	IMPUTE	HapMap2 CEU, r21	Logistic regression	QUICKTEST v0.94
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	EPIC-Norfolk obese cases	EPIC-N-CA	Affymetrix 500K	IMPUTE	HapMap2 CEU, r21	Logistic regression	SNPTEST 1.1.5
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	EPIC-Norfolk population based	EPIC-N-POP	Affymetrix 500K	IMPUTE	HapMap2 CEU, r21	Logistic regression	SNPTEST 1.1.5
Analysis in Population-based Cohorts of Asthma Traits (APCAT)	FINRISK + Health 2000 (H2000) +Helsinki Birth Cohort (HBC) + Young Finns Study (YFS) analyzed together	FINRISK	Illumina Human610- Quad; Affymetrix 6.0	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK v1.07
		Health 2000	IlluminaHuman610-Quad; Illumina 370K	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK v1.07
		Helsinki Birth Cohort	Illumina 670K	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK v1.07
		Young Finns Syudy	Illumina 670K	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK v1.07

Consortium Name	Study Name	Study Abbreviation	Genotyping platform	Imputation software	Reference panel used for imputation	Statistical method used for analysis	Software used for analysis
Candidate Gene Association Resource (CARe) Consortium	Atherosclerosis Risk in Communities Study (ARIC)	ARIC-AFAM	Affymetrix 6.0	MACH 1.0	HapMap2 CEU and YRI, r22	Logistic regression	PLINK v1.07
Candidate Gene Association Resource (CARe) Consortium	Corornary Artery Risk Development in Young Adults (CARDIA)	CARDIA	Affymetrix 6.0	MACH 1.0	HapMap2 CEU and YRI, r22	Logistic regression	PLINK v1.07
Candidate Gene Association Resource (CARe) Consortium	Jackson Heart Study (JHS)	JHS	Affymetrix 6.0	MACH 1.0	HapMap2 CEU and YRI, r22	Logistic regression	PLINK v1.07
Candidate Gene Association Resource (CARe) Consortium	Multi-Ethnic Study of Atherosclerosis (MESA)	MESA-AFAM	Affymetrix 6.0	IMPUTE2	HapMap2 (all populations), r22	Additive model using GEE to account for familial correlation	GWAF (R package)
Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE)	Multi-Ethnic Study of Atherosclerosis (MESA)	MESA-EUAM	Affymetrix 6.0	IMPUTE2	HapMap2 CEU, r24	Logistic regression (frequentist association test)	SNPTEST v2.2.0
Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE)	Atherosclerosis Risk in Communities Study (ARIC)	ARIC-EUAM	Affymetrix 6.0	MACH 1.0	Hapmap2 CEU, r22	Logistic regression	ProbABEL v.0.1-3
Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE)	Cardiovascular Health Study (CHS)	CHS	Illumina 370K CNV	BIMBAM	HapMap CEU, r22	Logistic regression with robust SE estimates	R
decCODE Genetics	deCODE Genetics	deCODE	Illumina HumanHap300 or HumanHapCNV370	IMPUTE	HapMap2 CEU, r22	Logistic regression	SNPTEST v2
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Cophenhagen Study on Asthma in Childdhood	COPSAC	Illumina 550K	MACH 1.0	HapMap2 CEU, r22	Logistic regression	SNPTEST v2.2.0
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Danish National Birth Cohort	DNBC	Illumina 660K	MACH 1.0	HapMap2 CEU, r22	Logistic regression	PLINK v1.07 MACH2DAT
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	GENERATION R	GENERATION R	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic regression	GRIMP
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	LISA Plus & GINI Plus (German Infant Nutritional Intervention Program) Birth Cohorts	LISA-GINI	Affymetrix 5.0 and 6.0	IMPUTE2	Hapmap2, r22	Logistic regression	SNPTEST v2.2.0
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Manchester Asthma and Allergy Study	MAAS	Illumina Human610-Quad	IMPUTE2	HapMap 3 + 1,000 Genomes	Logistic regression	SNPTEST v2.4.0
Early Genetics and Lifecourse Epidemiology (EAGLE) Consortium	Western Australian Pregnancy (Raine) Cohort	RAINE	Illumina 660K	MACH 1.0., Minimac	HapMap2 r22	Logistic regression	SNPTEST v2.2.0

Consortium Name	Study Name	Study Abbreviation	Genotyping platform	Imputation software	Reference panel used for imputation	Statistical method used for analysis	Software used for analysis
B58C	British 1958 Birth Cohort	B58C	Illumina 550K and Illumina Human 610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	ProbABEL 0.1-3 (palogist)
EVE	CAG/CSGA/SARP-EUAM	STAMPEED-EUAM	Illumina 1Mv1	MACH 1.0	HapMap2 CEU, r21	Logistic regression	R
EVE	Children'Health Study (CHS) Hispanic White	CHS-LAT	Illumina 550K and Illumina Human610-Quad	MACH 1.0	HapMap2 CEU+ASN, r21	Logistic regression	R
EVE	CAG/CSGA/SARP-AFAM	STAMPEED-AFAM	Illumina 1Mv1	MACH 1.0	HapMap2 CEU+YRI, r21	Logistic regression	R
EVE	Genomic Research on Asthma in the African Diaspora	GRAAD	Illumina 650K	MACH 1.0	HapMap2 CEU+YRI+ASN, r21	T-test	R
EVE	Study of Asthma Phenotypes and Pharmacogeneomics Interactions by Race Ethnicity	SAPPHIRE	Affymetrix 5.0, 6.0 and mapping 500k array	MACH 1.0	HapMap2 CEU+YRI, r21	Logistic regression	R
EVE	Children'Health Study (CHS) Non-Hispanic white	CHS-EUAM	Illumina 550K and Illumina Human 610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	R
Japanese Adult Asthma Research Consortium (JAARC)	Japanese Childhood Onset Asthma in Adult Asthma research	JCOAAD	Illumina 550K and Illumina Human610-Quad	MACH 1.0	HapMap2 JPT+CHB, r21	Logistic regression	MACH2DAT
Japan Pediatric Asthma Consortium (JPAC)	Japan Pediatric Asthma Consortium	JPAC	Illumina 550K and Illumina Human610-Quad	MACH 1.0	HapMap2 JPT+CHB, r21	Logistic regression	MACH2DAT
GABRIEL	Epidemiological study on the Genetics and Environment of Asthma (childhood-onset asthma)	EGEA-ch	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression (robust variance to account for family dependence)	Stata V10
GABRIEL	Epidemiological study on the Genetics and Environment of Asthma (adult-onset asthma)	EGEA-ad	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression (robust variance to account for family dependence)	Stata V10
GABRIEL	Avon Longitudinal Study of Parents and Children	ALSPAC	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	European Community Respiratory Health Survey (childhood-onset asthma)	ECRHS-ch	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	European Community Respiratory Health Survey (adult-onset asthma)	ECRHS-ad	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Barn Allergy Milieu Stockholm Epidemiology	BAMSE	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Busselton study (childhood-onset asthma)	BUSSELTON-ch	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Busselton study (adult-onset asthma)	BUSSELTON-ad	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r21	Logistic regression	Stata V10

Consortium Name	Study Name	Study Abbreviation	Genotyping platform	Imputation software	Reference panel used for imputation	Statistical method used for analysis	Software used for analysis
GABRIEL	Gabriel Advanced Surveys	GABRIELA-AS	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Kursk State Medical University study (childhood-onset asthma)	KSMU-ch	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Kursk State Medical University study (adult-onset asthma)	KSMU-ad	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Medical Research Council Asthma UK Center in Allergic Mechanisms of Asthma (MRCA-UK)	MRCA-UK	Illumina Sentrix Human-1 and Sentrix HumanHap300	MACH 1.0	Hapmap2 CEU, r21	Logistic regression (robust variance to account for family dependence)	Stata V10
GABRIEL	German Multicentre Asthma Genetics in Childhood Study (MAGICS) and Multicentre Allergy Study (MAS)	MAGICS-MAS	Illumina Sentrix HumanHap300 (MAGICS) Illumina Human610-Quad (MAS)	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	The Prevention and Incidence of Asthma and Mite Allergy birth cohort study	PIAMA	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Swiss study on Air Pollution And Lung Disease in Adults (childhood-onset asthma)	SAPALDIA-ch	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Swiss study on Air Pollution And Lung Disease in Adults (adult-onset asthma)	SAPALDIA-ad	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	TOMSK study (childhood-onset asthma)	TOMSK-ch	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression (robust variance to account for family dependence)	Stata V10
GABRIEL	TOMSK study (adult-onset asthma)	TOMSK-ad	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression (robust variance to account for family dependence)	Stata V10
GABRIEL	UFA region study (childhood-onset asthma)	UFA-ch	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	UFA region study (adult-onset asthma)	UFA-ad	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Industrial Cohorts / Agricultural exposures	AGRICULTURAL	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Industrial Cohorts / Wood exposure	WOOD	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Industrial Cohorts / Wheat and amylase exposures (bakers)	BAKERY	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Industrial Cohorts / Isocyanate exposure	ISOCYANATE	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
GABRIEL	Severe asthma study	SEVERE	Illumina Human610-Quad	MACH 1.0	Hapmap2 CEU, r21	Logistic regression	Stata V10
Netherlands Twin Registry (NTR)	The Netherlands Twin Register	NTR	Illumina 660K, Illumina Omni Express 1 mil, Affymetrix Perlegen and Affymetrix 6.0	IMPUTE2	HapMap2 CEU, r24	Logistic regression	PLINK v1.07

Consortium Name	Study Name	Study Abbreviation	Genotyping platform	Imputation software	Reference panel used for imputation	Statistical method used for analysis	Software used for analysis
Rotterdam Study (RS)	Rotterdam Study 1	RS1	Illumina 550K	MACH 1.0	HapMap2 CEU, r22	Logistic regression	MACH2DAT (GRIMP)
Rotterdam Study (RS)	Rotterdam Study 2	RS2	Illumina 550K and Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic regression	MACH2DAT (GRIMP)
Rotterdam Study (RS)	Rotterdam Study 3	RS3	Illumina Human610-Quad	MACH 1.0	HapMap2 CEU, r22	Logistic regression	MACH2DAT (GRIMP)
Dutch Asthma Genetics Consortium (DAGC)	Dutch Asthma GWAS 1 Family-Based	DAG1	Illumina 317K	BEAGLE	Hapmap2 CEU, r22	Logistic regression	PLINK v1.07
Dutch Asthma Genetics Consortium (DAGC)	Dutch Asthma GWAS 2 Case-Control	DAG2	Illumina 370 Duo	BEAGLE	Hapmap2 CEU, r22	Logistic regression	PLINK v1.07

Supplementary Table 3. Effect sizes of the lead SNPs in ancestry-specific and multi-ancestry meta-analyses

The lead SNPs belong to the 18 loci that are genome-wide significant ($P_{random} \leq 10^{-8}$) in European-ancestry and/or multi-ancestry meta-analyse (as shown in Table 1)

				EUROPEAN ANCESTRY (56 studies)					AFRICAN ANCESTRY (7 studies)				JAPANESE (2 studies)				LATINOS (1 study)			MULTTI-ANCESTRY (66 studies)				
Region[a]	SNP	Position	Allele (R/E)[c]	EAF[d]	OR (95% CI)[e]	P_{random}[f]	P_{fixed}[g]	P_{het}[h]	EAF	OR (95% CI)[e]	P_{fixed}[g]	P_{het}[h]	EAF	OR (95% CI)[e]	P_{fixed}[g]	P_{het}[h]	EAF	OR (95% CI)[e]	P[i]	OR (95% CI)[e]	P_{random}[f]	P_{fixed}[g]	P_{het}[h]	P_{ethnic}[j]
New asthma susceptibility loci																								
5q31.3	rs7705042	141,492,419	C/A	0.63	1.08 (1.05-1.11)	1.6×10^{-6}	8.5×10^{-10}	0.07	0.77	1.12 (1.0-1.24)	0.04	0.39	0.63	1.17 (1.05-1.31)	5.5×10^{-3}	0.98	0.67	1.10 (0.93-1.3)	0.27	1.09 (1.06-1.12)	7.9×10^{-9}	3.1×10^{-12}	0.11	0.53
6p22.1	rs1233578	28,712,247	A/G	0.13	1.11 (1.07-1.15)	5.3×10^{-9}	5.3×10^{-9}	0.82	0.41	0.98 (0.90-1.07)	0.65	0.73		NA	NA	NA	0.15	0.83 (0.66-1.05)	0.12	1.09 (1.05-1.12)	5.9×10^{-7}	5.9×10^{-7}	0.56	0.003
6q15	rs2325291	90,986,686	G/A	0.33	0.91 (0.89-0.93)	8.6×10^{-13}	8.6×10^{-13}	0.78	0.12	1.02 (0.89-1.17)	0.78	0.49	0.03	1.02 (0.74-1.41)	0.88	0.69	0.30	0.91 (0.76-1.09)	0.30	0.91 (0.89-0.94)	2.2×10^{-12}	2.2×10^{-12}	0.8	0.39
12q13.3	rs167769	57,503,775	C/T	0.4	1.08 (1.05-1.11)	1.6×10^{-7}	5.5×10^{-9}	0.19	0.14	1.14 (1.0-1.29)	0.05	0.71	0.21	1.09 (0.95-1.24)	0.22	0.18	0.37	1.04 (0.89-1.23)	0.60	1.08 (1.05-1.11)	3.9×10^{-9}	4.6×10^{-10}	0.31	0.87
17q21.33	rs17637472	47,461,433	G/A	0.39	1.08 (1.05-1.11)	3.3×10^{-9}	3.3×10^{-9}	0.56	0.08	0.91 (0.77-1.09)	0.32	0.13	0.13	1.12 (0.95-1.32)	0.18	0.58	0.22	1.24 (1.03-1.5)	0.02	1.08 (1.05-1.11)	6.6×10^{-9}	1.1×10^{-9}	0.35	0.12
New signals at loci previously assosiated with asthma in ancestry-specific populations																								
6p21.33	rs3131064	30,763,893	T/C	0.14	1.12 (1.08-1.16)	2.6×10^{-10}	2.6×10^{-10}	0.54	0.25	0.97 (0.87-1.07)	0.53	0.98	0.01	0.70 (0.32-1.53)	0.37	NA	0.09	0.89 (0.67-1.19)	0.44	1.10 (1.06-1.13)	2.6×10^{-8}	1.9×10^{-8}	0.46	0.02
10p14	rs2589561	9,046,645	A/G	0.82	0.90 (0.87-0.94)	1.4×10^{-8}	1.4×10^{-8}	0.78	0.86	0.99 (0.87-1.12)	0.83	0.74	0.81	0.84 (0.73-0.96)	9.8×10^{-3}	0.60	0.89	1.06 (0.80-1.39)	0.69	0.91(0.88-0.94)	3.5×10^{-9}	3.5×10^{-9}	0.82	0.25
Asthma signals previously reported for asthma plus hay fever																								
8q21.13	rs12543811	81,278,885	G/A	0.66	0.93 (0.91-0.95)	3.5×10^{-8}	3.0×10^{-8}	0.47	0.59	0.93 (0.85-1.02)	0.12	0.72	0.38	0.82 (0.74-0.92)	7.6×10^{-4}	0.71	0.52	0.91 (0.78-1.07)	0.25	0.92 (0.9-0.95)	1.1×10^{-10}	1.1×10^{-10}	0.54	0.24
16p13.13	rs17806299	11,199,980	G/A	0.2	0.90 (0.88-0.93)	2.1×10^{-10}	2.1×10^{-10}	0.51	0.06	0.94 (0.78-1.13)	0.50	0.20	0.09	0.92 (0.76-1.12)	0.40	0.78	0.11	1.08 (0.84-1.39)	0.56	0.91 (0.88-0.94)	2.7×10^{-10}	2.7×10^{-10}	0.49	0.58
Knwon asthma loci																								
2q12	rs1420101	102,957,716	C/T	0.37	1.12 (1.10-1.15)	9.1×10^{-20}	9.1×10^{-20}	0.63	0.33	1.12 (1.03-1.23)	0.01	0.59	0.42	1.04 (0.94-1.16)	0.44	0.05	0.27	1.09 (0.92-1.3)	0.31	1.12 (1.09-1.15)	3.9×10^{-21}	3.9×10^{-21}	0.61	0.64
5q22.1	rs10455025	110,404,999	A/C	0.34	1.15 (1.12-1.18)	2.0×10^{-25}	2.0×10^{-25}	0.53	0.09	1.0 (0.84-1.18)	0.99	0.55	0.04	1.34 (1.01-1.77)	0.04	0.85	0.25	1.11 (0.93-1.34)	0.25	1.15 (1.12-1.18)	9.4×10^{-26}	9.4×10^{-26}	0.57	0.27
5q31	rs20541	131,995,964	A/G	0.79	0.89 (0.86-0.91)	1.4×10^{-14}	1.4×10^{-14}	0.73	0.82	0.93 (0.83-1.04)	0.21	0.43	0.69	0.86 (0.77-0.97)	0.01	0.58	0.56	0.96 (0.81-1.14)	0.63	0.89 (0.87-0.92)	5.0×10^{-16}	5.0×10^{-16}	0.77	0.62
6p21.32	rs9272346	32,604,372	G/A	0.56	1.16 (1.13-1.19)	4.8×10^{-28}	2.4×10^{-28}	0.46	0.51	1.11 (1.02-1.21)	0.02	4E-03	0.53	1.13 (1.01-1.27)	0.03	0.90	0.69	1.32 (1.09-1.59)	4×10^{-3}	1.16 (1.12-1.19)	5.7×10^{-24}	8.2×10^{-32}	0.14	0.43
9p24.1	rs992969	6,209,697	A/G	0.75	0.85 (0.82-0.88)	1.1×10^{-17}	4.3×10^{-29}	0.008	0.70	0.91 (0.83-1.0)	0.05	0.60	0.97	0.92 (0.67-1.26)	0.59	0.66	0.83	0.83 (0.67-1.02)	0.08	0.86 (0.83-0.88)	7.2×10^{-20}	3.3×10^{-30}	0.02	0.53
11q13.5	rs7927894	76,301,316	C/T	0.37	1.10 (1.07-1.13)	3.5×10^{-11}	3.2×10^{-12}	0.38	0.35	1.12 (1.02-1.23)	0.01	0.86	0.13	1.23 (1.05-1.45)	0.01	0.88	0.24	1.01 (0.82-1.25)	0.89	1.10 (1.08-1.13)	2.2×10^{-14}	2.2×10^{-14}	0.56	0.48
15q22.2	rs11071558	61,069,421	A/G	0.14	0.89 (0.85-0.92)	1.9×10^{-10}	8.3×10^{-11}	0.44	0.32	0.92 (0.83-1.01)	0.08	0.21	0.23	0.81 (0.71-0.93)	2.6×10^{-3}	0.07	0.12	1.18 (0.93-1.5)	0.18	0.89 (0.86-0.92)	1.3×10^{-9}	3.1×10^{-12}	0.19	0.06
15q22.33	rs2033784	67,449,660	A/G	0.3	1.11 (1.08-1.14)	2.5×10^{-14}	2.5×10^{-14}	0.75	0.44	1.07 (0.98-1.17)	0.11	0.51	0.40	1.09 (0.97-1.21)	0.14	0.24	0.36	0.98 (0.83-1.16)	0.83	1.10 (1.08-1.13)	7.4×10^{-15}	7.4×10^{-15}	0.76	0.48
17q12-21	rs2952156	37,876,835	A/G	0.7	0.86 (0.84-0.88)	7.6×10^{-29}	7.6×10^{-29}	0.55	0.60	0.94 (0.85-1.03)	0.17	0.36	0.51	0.88 (0.79-0.98)	0.02	0.37	0.57	0.84 (0.7-1.02)	0.07	0.87 (0.84-0.89)	2.2×10^{-30}	2.2×10^{-30}	0.52	0.35

[a]Cytogenetic position of the chromosomal region harboring the lead SNP

[b]Genes coding for proteins; the gene where eventually the lead SNP lies is first indicated followed by the previous gene and next gene

[c] R=reference allele /E=effect allele. [d]EAF = Effect allele frequency

[e]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele under a random-effects model (European ancestry and multi-ancestry meta-analyses) or fixed-effects model (African ancestry and Japanese meta-analysis) or in the Latino GWAS

[f]P_{random} is P-value for test of association between SNP and asthma under a random-effects model

[g]P_{fixed} is P-value for test of association between SNP and asthma under a fixed-effects model

[h]P_{het} is the P-value for test of heterogeneity across studies with the use of Cochran's Q test

[i]P for test of association between SNP and asthma in the Latino GWAS

[j]P_{ethnic} for test of heterogeneity between ancestry-specific effect sizes

NA= the SNP did not pass QC in the Japanese studies

Supplementary Table 4. SNPs with $P_{random} \leq 10^{-8}$ in the European ancestry meta-analysis

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
2	rs1465325	102,734,551	A/G	0.17	0.88 (0.85-0.92)	5.09×10^{-10}	0.88 (0.85-0.91)	3.68×10^{-14}	0.12	100%
2	rs1465324	102,735,612	G/A	0.18	0.89 (0.86-0.93)	2.71×10^{-9}	0.89 (0.86-0.92)	7.69×10^{-13}	0.16	100%
2	rs12328681	102,736,867	G/T	0.18	0.89 (0.86-0.93)	2.83×10^{-9}	0.89 (0.86-0.92)	7.19×10^{-13}	0.15	100%
2	rs10172039	102,738,785	C/A	0.18	0.89 (0.86-0.93)	2.72×10^{-9}	0.89 (0.86-0.92)	7.39×10^{-13}	0.15	100%
2	rs12619383	102,741,718	A/G	0.17	0.88 (0.85-0.92)	1.67×10^{-9}	0.88 (0.85-0.91)	5.95×10^{-14}	0.09	100%
2	rs12620132	102,742,115	A/G	0.17	0.88 (0.85-0.92)	1.12×10^{-9}	0.88 (0.85-0.91)	3.88×10^{-14}	0.09	100%
2	rs13392285	102,744,338	C/A	0.18	0.89 (0.86-0.92)	4.72×10^{-10}	0.89 (0.86-0.91)	2.12×10^{-13}	0.19	100%
2	rs13387400	102,750,020	G/A	0.17	0.88 (0.85-0.92)	1.16×10^{-9}	0.88 (0.85-0.91)	4.37×10^{-14}	0.09	100%
2	rs1558641	102,765,865	G/A	0.17	0.88 (0.85-0.92)	7.85×10^{-9}	0.88 (0.85-0.91)	6.20×10^{-14}	0.05	100%
2	rs1558640	102,765,878	G/A	0.17	0.88 (0.85-0.92)	4.12×10^{-9}	0.88 (0.85-0.91)	4.73×10^{-14}	0.06	100%
2	rs871657	102,771,341	C/T	0.18	0.89 (0.85-0.93)	9.31×10^{-9}	0.88 (0.86-0.91)	9.67×10^{-14}	0.07	100%
2	rs2287048	102,773,999	C/T	0.17	0.88 (0.85-0.92)	2.45×10^{-9}	0.88 (0.85-0.91)	3.50×10^{-14}	0.06	100%
2	rs1997502	102,844,249	A/G	0.65	1.09 (1.06-1.13)	6.51×10^{-9}	1.09 (1.06-1.12)	3.20×10^{-10}	0.26	96%
2	rs10189629	102,879,464	C/A	0.14	0.85 (0.81-0.89)	2.16×10^{-10}	0.85 (0.82-0.89)	1.49×10^{-15}	0.02	98%
2	rs11692065	102,883,975	C/T	0.14	0.85 (0.81-0.89)	1.47×10^{-10}	0.85 (0.82-0.89)	1.21×10^{-15}	0.02	98%
2	rs11674302	102,887,128	T/C	0.14	0.85 (0.81-0.89)	8.05×10^{-11}	0.85 (0.82-0.89)	7.92×10^{-16}	0.03	98%
2	rs11690644	102,914,214	A/G	0.14	0.84 (0.8-0.88)	7.74×10^{-13}	0.84 (0.81-0.87)	6.93×10^{-20}	0.03	96%
2	rs950880	102,932,562	C/A	0.38	1.12 (1.09-1.15)	3.95×10^{-19}	1.12 (1.09-1.15)	3.95×10^{-19}	0.55	100%
2	rs13001325	102,939,036	C/T	0.38	1.12 (1.09-1.15)	2.02×10^{-19}	1.12 (1.09-1.15)	2.02×10^{-19}	0.55	100%
2	rs12479210	102,949,161	C/T	0.38	1.12 (1.09-1.15)	2.14×10^{-19}	1.12 (1.09-1.15)	2.14×10^{-19}	0.57	100%
2	rs13019081	102,950,822	A/C	0.38	1.12 (1.09-1.15)	1.99×10^{-19}	1.12 (1.09-1.15)	1.99×10^{-19}	0.57	100%
2	rs17026974	102,952,360	G/A	0.29	1.1 (1.08-1.13)	2.30×10^{-13}	1.1 (1.08-1.13)	2.30×10^{-13}	0.62	100%
2	rs3771180	102,953,617	G/T	0.14	0.84 (0.8-0.88)	1.11×10^{-13}	0.84 (0.81-0.87)	1.47×10^{-20}	0.04	100%
2	rs13431828	102,954,653	C/T	0.14	0.84 (0.8-0.88)	9.10×10^{-14}	0.84 (0.81-0.87)	1.14×10^{-19}	0.07	100%
2	rs13408661	102,955,082	G/A	0.14	0.84 (0.8-0.88)	1.33×10^{-13}	0.84 (0.81-0.87)	5.52×10^{-20}	0.05	100%
2	rs873022	102,955,683	G/T	0.29	1.11 (1.08-1.13)	1.57×10^{-13}	1.11 (1.08-1.13)	1.57×10^{-13}	0.63	100%
2	rs3771177	102,955,860	G/T	0.29	1.11 (1.08-1.13)	1.53×10^{-13}	1.11 (1.08-1.13)	1.53×10^{-13}	0.64	100%
2	rs10173081	102,957,348	C/T	0.14	0.84 (0.8-0.88)	1.43×10^{-13}	0.84 (0.81-0.87)	6.85×10^{-20}	0.05	100%
2	rs3732129	102,957,532	T/C	0.29	1.1 (1.08-1.13)	1.61×10^{-13}	1.1 (1.08-1.13)	1.61×10^{-13}	0.65	100%
2	rs1420101	102,957,716	C/T	0.37	1.12 (1.1-1.15)	9.08×10^{-20}	1.12 (1.1-1.15)	9.08×10^{-20}	0.63	100%
2	rs12905	102,960,007	G/A	0.29	1.1 (1.08-1.13)	2.21×10^{-13}	1.1 (1.08-1.13)	2.21×10^{-13}	0.66	100%
2	rs12712142	102,960,584	C/A	0.40	1.12 (1.09-1.15)	2.87×10^{-17}	1.12 (1.09-1.15)	3.93×10^{-19}	0.39	98%
2	rs2160203	102,960,824	A/G	0.24	0.89 (0.86-0.92)	5.89×10^{-13}	0.89 (0.86-0.92)	5.89×10^{-13}	0.67	89%
2	rs13017455	102,964,742	C/T	0.39	1.12 (1.09-1.15)	2.66×10^{-18}	1.12 (1.09-1.15)	3.12×10^{-19}	0.43	100%
2	rs12469506	102,965,871	C/T	0.30	1.12 (1.09-1.15)	2.86×10^{-15}	1.12 (1.09-1.15)	2.86×10^{-15}	0.52	96%
2	rs1921622	102,966,067	G/A	0.53	1.09 (1.07-1.12)	6.14×10^{-13}	1.09 (1.07-1.12)	6.14×10^{-13}	0.50	100%
2	rs10208293	102,966,310	G/A	0.28	0.88 (0.85-0.92)	8.00×10^{-10}	0.88 (0.86-0.91)	9.42×10^{-19}	0.00	100%
2	rs10197862	102,966,549	A/G	0.14	0.84 (0.8-0.88)	1.17×10^{-12}	0.84 (0.81-0.88)	2.23×10^{-19}	0.03	100%
2	rs1861245	102,966,906	C/T	0.38	0.9 (0.87-0.93)	5.33×10^{-12}	0.9 (0.88-0.93)	4.06×10^{-15}	0.18	100%
2	rs13424006	102,967,236	T/C	0.39	0.89 (0.87-0.92)	9.42×10^{-14}	0.89 (0.87-0.92)	2.59×10^{-18}	0.15	100%
2	rs6751967	102,967,413	T/C	0.39	0.89 (0.87-0.92)	9.01×10^{-14}	0.89 (0.87-0.92)	2.40×10^{-18}	0.15	100%
2	rs6749114	102,967,587	A/C	0.39	0.89 (0.87-0.92)	8.61×10^{-14}	0.89 (0.87-0.92)	2.98×10^{-18}	0.16	100%
2	rs11123923	102,967,844	C/A	0.39	1.12 (1.09-1.15)	6.03×10^{-18}	1.12 (1.09-1.15)	1.59×10^{-19}	0.40	100%
2	rs4988955	102,967,928	A/G	0.39	0.89 (0.87-0.92)	7.24×10^{-14}	0.89 (0.87-0.92)	3.32×10^{-18}	0.17	100%
2	rs4988956	102,968,007	G/A	0.39	0.89 (0.87-0.92)	4.41×10^{-14}	0.89 (0.87-0.92)	2.00×10^{-18}	0.17	100%
2	rs4988957	102,968,075	T/C	0.39	0.89 (0.87-0.92)	7.22×10^{-14}	0.89 (0.87-0.92)	2.55×10^{-18}	0.16	100%
2	rs10204137	102,968,212	A/G	0.39	0.89 (0.86-0.92)	3.08×10^{-12}	0.89 (0.87-0.92)	1.49×10^{-16}	0.13	91%
2	rs4988958	102,968,285	T/C	0.39	0.89 (0.87-0.92)	7.07×10^{-14}	0.89 (0.87-0.92)	2.43×10^{-18}	0.16	100%
2	rs10192157	102,968,356	C/T	0.39	0.89 (0.87-0.92)	6.33×10^{-14}	0.89 (0.87-0.92)	2.90×10^{-18}	0.17	100%
2	rs10206753	102,968,362	T/C	0.39	0.89 (0.86-0.92)	2.16×10^{-12}	0.89 (0.87-0.92)	1.29×10^{-16}	0.14	91%
2	rs7603730	102,974,371	A/C	0.39	0.89 (0.87-0.92)	6.72×10^{-14}	0.89 (0.87-0.92)	1.97×10^{-18}	0.16	100%
2	rs12998521	102,974,417	G/T	0.39	1.12 (1.09-1.15)	1.98×10^{-15}	1.12 (1.09-1.15)	6.77×10^{-18}	0.33	98%
2	rs10170583	102,974,764	G/A	0.39	0.89 (0.87-0.92)	2.81×10^{-13}	0.89 (0.87-0.92)	2.71×10^{-18}	0.12	100%
2	rs10176664	102,976,172	G/A	0.38	0.89 (0.87-0.92)	7.43×10^{-14}	0.89 (0.87-0.92)	1.90×10^{-18}	0.16	100%
2	rs3755276	102,978,459	C/T	0.38	0.89 (0.87-0.92)	8.01×10^{-14}	0.89 (0.87-0.92)	1.96×10^{-18}	0.15	100%
2	rs2287037	102,979,028	C/T	0.39	1.12 (1.09-1.15)	2.41×10^{-17}	1.12 (1.09-1.15)	1.19×10^{-19}	0.36	100%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
2	rs3771172	102,985,812	C/T	0.29	1.11 (1.08-1.14)	1.24×10^{-14}	1.11 (1.08-1.14)	1.24×10^{-14}	0.48	100%
2	rs3771171	102,985,950	T/C	0.29	1.11 (1.08-1.14)	1.05×10^{-13}	1.11 (1.08-1.14)	2.01×10^{-14}	0.42	96%
2	rs2160202	102,986,154	G/A	0.29	1.11 (1.08-1.14)	1.12×10^{-13}	1.11 (1.08-1.14)	2.00×10^{-14}	0.42	96%
2	rs3771166	102,986,222	G/A	0.38	0.89 (0.86-0.91)	7.64×10^{-18}	0.89 (0.86-0.91)	1.31×10^{-19}	0.38	95%
2	rs1974675	102,986,375	G/A	0.38	0.89 (0.86-0.91)	7.47×10^{-18}	0.89 (0.86-0.91)	1.26×10^{-19}	0.38	95%
2	rs10439410	102,990,788	G/T	0.49	0.92 (0.89-0.94)	1.49×10^{-9}	0.92 (0.9-0.94)	2.21×10^{-11}	0.22	100%
2	rs6758936	102,991,369	G/A	0.49	0.92 (0.89-0.94)	1.24×10^{-9}	0.92 (0.9-0.94)	2.29×10^{-11}	0.23	100%
2	rs2041739	102,994,333	C/T	0.49	0.92 (0.89-0.94)	9.48×10^{-10}	0.92 (0.9-0.94)	2.32×10^{-11}	0.25	100%
2	rs17027037	102,994,884	A/G	0.29	1.11 (1.08-1.14)	4.15×10^{-14}	1.11 (1.08-1.14)	4.15×10^{-14}	0.51	100%
2	rs2080289	102,995,020	G/A	0.29	1.11 (1.08-1.14)	4.61×10^{-14}	1.11 (1.08-1.14)	4.61×10^{-14}	0.52	100%
2	rs10208196	102,996,345	G/A	0.49	0.92 (0.89-0.94)	9.18×10^{-10}	0.92 (0.9-0.94)	2.56×10^{-11}	0.26	100%
2	rs11683700	102,996,805	C/T	0.29	1.11 (1.08-1.14)	7.04×10^{-14}	1.11 (1.08-1.14)	6.65×10^{-14}	0.47	96%
2	rs3213732	102,998,279	A/G	0.49	0.92 (0.89-0.94)	8.97×10^{-10}	0.92 (0.9-0.94)	2.38×10^{-11}	0.25	100%
2	rs6760621	102,999,952	T/C	0.49	0.92 (0.89-0.94)	2.94×10^{-10}	0.92 (0.89-0.94)	3.53×10^{-11}	0.36	91%
2	rs1035130	103,001,402	C/T	0.29	1.11 (1.08-1.14)	4.15×10^{-14}	1.11 (1.08-1.14)	4.15×10^{-14}	0.53	100%
2	rs6706002	103,006,104	A/G	0.49	0.92 (0.89-0.94)	8.57×10^{-10}	0.92 (0.9-0.94)	2.17×10^{-11}	0.25	100%
2	rs4851570	103,006,387	A/G	0.29	1.11 (1.08-1.14)	3.27×10^{-14}	1.11 (1.08-1.14)	3.27×10^{-14}	0.52	100%
2	rs6749014	103,006,448	C/T	0.49	0.92 (0.89-0.94)	1.15×10^{-9}	0.92 (0.9-0.94)	4.83×10^{-11}	0.29	95%
2	rs4851004	103,009,537	C/T	0.49	0.92 (0.89-0.94)	4.45×10^{-10}	0.92 (0.9-0.94)	1.82×10^{-11}	0.29	100%
2	rs2287034	103,010,588	C/A	0.29	1.11 (1.08-1.14)	3.58×10^{-14}	1.11 (1.08-1.14)	3.58×10^{-14}	0.61	100%
2	rs2287033	103,011,237	T/C	0.49	0.92 (0.89-0.94)	4.12×10^{-10}	0.92 (0.9-0.94)	1.78×10^{-11}	0.29	100%
2	rs4851005	103,011,552	C/T	0.38	1.09 (1.06-1.12)	5.40×10^{-9}	1.09 (1.06-1.12)	8.91×10^{-11}	0.26	100%
2	rs1135354	103,014,302	T/G	0.29	1.11 (1.08-1.14)	6.31×10^{-13}	1.11 (1.08-1.14)	6.31×10^{-13}	0.52	91%
2	rs1420094	103,015,687	C/T	0.49	0.92 (0.89-0.94)	3.82×10^{-10}	0.92 (0.9-0.94)	1.54×10^{-11}	0.29	100%
2	rs17027087	103,015,918	C/T	0.29	1.11 (1.08-1.14)	4.18×10^{-14}	1.11 (1.08-1.14)	4.18×10^{-14}	0.57	100%
2	rs6710528	103,016,142	C/T	0.49	0.92 (0.89-0.94)	9.76×10^{-10}	0.92 (0.9-0.94)	1.83×10^{-11}	0.23	100%
2	rs3732124	103,018,052	C/T	0.49	0.92 (0.89-0.94)	7.18×10^{-10}	0.92 (0.9-0.94)	1.55×10^{-11}	0.24	100%
2	rs4851571	103,019,000	C/T	0.49	0.92 (0.89-0.94)	7.45×10^{-10}	0.92 (0.9-0.94)	1.74×10^{-11}	0.25	100%
2	rs4851572	103,019,031	G/A	0.49	0.92 (0.89-0.94)	7.46×10^{-10}	0.92 (0.9-0.94)	1.72×10^{-11}	0.25	100%
2	rs6710034	103,023,678	G/A	0.49	0.92 (0.89-0.94)	3.29×10^{-10}	0.92 (0.9-0.94)	1.32×10^{-11}	0.29	100%
2	rs10203558	103,027,640	T/C	0.49	0.92 (0.89-0.94)	3.27×10^{-10}	0.92 (0.9-0.94)	1.31×10^{-11}	0.29	100%
2	rs10200952	103,027,651	A/C	0.49	0.91 (0.89-0.94)	1.77×10^{-10}	0.92 (0.89-0.94)	2.53×10^{-11}	0.37	91%
2	rs1420105	103,035,119	T/C	0.49	0.92 (0.89-0.94)	2.25×10^{-10}	0.92 (0.9-0.94)	7.94×10^{-12}	0.28	100%
2	rs2293224	103,035,779	T/C	0.49	0.92 (0.89-0.94)	4.45×10^{-10}	0.92 (0.9-0.94)	1.32×10^{-11}	0.27	100%
2	rs6743516	103,036,335	A/G	0.49	0.92 (0.89-0.94)	4.31×10^{-10}	0.92 (0.9-0.94)	1.36×10^{-11}	0.27	100%
2	rs3771156	103,036,677	C/T	0.29	1.11 (1.08-1.14)	2.67×10^{-14}	1.11 (1.08-1.14)	2.67×10^{-14}	0.53	100%
2	rs1420100	103,037,002	C/A	0.49	0.92 (0.89-0.94)	4.22×10^{-10}	0.92 (0.9-0.94)	1.50×10^{-11}	0.28	100%
2	rs3771155	103,037,826	A/G	0.49	0.92 (0.89-0.94)	3.77×10^{-10}	0.92 (0.9-0.94)	1.06×10^{-11}	0.27	100%
2	rs10206291	103,038,863	T/C	0.49	0.92 (0.89-0.94)	4.23×10^{-10}	0.92 (0.9-0.94)	1.44×10^{-11}	0.28	100%
2	rs885088	103,039,044	A/G	0.49	0.92 (0.89-0.94)	3.95×10^{-10}	0.92 (0.9-0.94)	1.36×10^{-11}	0.28	100%
2	rs3771154	103,039,360	C/T	0.49	0.92 (0.89-0.94)	4.33×10^{-10}	0.92 (0.9-0.94)	1.36×10^{-11}	0.27	100%
2	rs6759479	103,040,047	A/C	0.49	0.92 (0.89-0.94)	5.05×10^{-10}	0.92 (0.9-0.94)	1.93×10^{-11}	0.27	100%
2	rs887972	103,040,945	G/A	0.30	1.11 (1.08-1.14)	4.25×10^{-12}	1.11 (1.08-1.14)	4.25×10^{-12}	0.60	89%
2	rs887971	103,041,167	T/C	0.30	1.11 (1.08-1.14)	3.79×10^{-14}	1.11 (1.08-1.14)	3.79×10^{-14}	0.60	100%
2	rs3755266	103,042,712	G/A	0.49	0.92 (0.89-0.94)	2.05×10^{-10}	0.92 (0.9-0.94)	1.49×10^{-11}	0.33	100%
2	rs7559845	103,046,214	T/G	0.49	0.92 (0.89-0.94)	3.01×10^{-10}	0.92 (0.9-0.94)	1.54×10^{-11}	0.31	100%
2	rs2310300	103,049,074	A/G	0.49	0.92 (0.89-0.94)	1.10×10^{-10}	0.92 (0.9-0.94)	1.09×10^{-11}	0.35	100%
2	rs11681718	103,051,144	A/G	0.29	1.1 (1.07-1.13)	6.61×10^{-13}	1.1 (1.07-1.13)	4.62×10^{-13}	0.46	100%
2	rs4851582	103,051,558	T/C	0.29	1.1 (1.07-1.13)	6.39×10^{-13}	1.1 (1.07-1.13)	4.56×10^{-13}	0.46	100%
2	rs3755265	103,052,816	C/A	0.49	0.92 (0.89-0.94)	4.67×10^{-10}	0.92 (0.9-0.94)	1.90×10^{-11}	0.29	100%
2	rs2058659	103,054,556	G/A	0.49	0.92 (0.9-0.94)	1.64×10^{-10}	0.92 (0.9-0.94)	1.93×10^{-11}	0.36	100%
2	rs17027166	103,055,420	G/A	0.29	1.1 (1.07-1.13)	5.74×10^{-13}	1.1 (1.07-1.13)	5.74×10^{-13}	0.48	100%
2	rs13021177	103,056,493	A/G	0.49	0.92 (0.9-0.94)	4.09×10^{-10}	0.92 (0.9-0.94)	2.26×10^{-11}	0.31	100%
2	rs10490204	103,056,534	A/C	0.29	1.1 (1.08-1.13)	2.35×10^{-13}	1.1 (1.08-1.13)	2.35×10^{-13}	0.50	100%
2	rs17027179	103,057,159	C/T	0.29	1.1 (1.07-1.13)	3.90×10^{-13}	1.1 (1.07-1.13)	3.90×10^{-13}	0.48	100%
2	rs10490203	103,059,237	T/G	0.29	1.1 (1.07-1.13)	3.57×10^{-13}	1.1 (1.07-1.13)	3.57×10^{-13}	0.48	100%
2	rs3771150	103,060,851	G/A	0.29	1.1 (1.07-1.13)	3.93×10^{-13}	1.1 (1.07-1.13)	3.93×10^{-13}	0.49	100%
2	rs11123928	103,061,286	G/A	0.34	1.08 (1.06-1.12)	6.75×10^{-9}	1.08 (1.06-1.12)	6.75×10^{-9}	0.51	96%
2	rs7597017	103,062,116	A/G	0.34	1.08 (1.06-1.12)	6.54×10^{-9}	1.08 (1.06-1.12)	6.54×10^{-9}	0.51	96%
2	rs17027230	103,079,330	C/T	0.29	1.1 (1.07-1.13)	2.36×10^{-12}	1.1 (1.07-1.13)	7.82×10^{-13}	0.43	98%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
2	rs4851011	103,089,678	C/T	0.29	1.1 (1.07-1.13)	1.02×10^{-11}	1.1 (1.07-1.13)	1.59×10^{-12}	0.40	98%
2	rs17027255	103,090,127	C/T	0.29	1.1 (1.07-1.13)	6.90×10^{-12}	1.1 (1.07-1.13)	1.61×10^{-12}	0.42	98%
2	rs17027258	103,091,540	A/G	0.29	1.1 (1.07-1.13)	7.72×10^{-12}	1.1 (1.07-1.13)	1.60×10^{-12}	0.41	98%
5	rs17446534	110,079,450	T/C	0.09	1.14 (1.09-1.18)	4.02×10^{-9}	1.14 (1.09-1.18)	4.02×10^{-9}	0.82	100%
5	rs244923	110,080,363	T/C	0.91	0.88 (0.84-0.92)	6.96×10^{-9}	0.88 (0.84-0.92)	6.96×10^{-9}	0.79	98%
5	rs381661	110,085,098	C/T	0.90	0.86 (0.82-0.9)	2.19×10^{-10}	0.86 (0.82-0.9)	2.19×10^{-10}	0.88	96%
5	rs6893213	110,198,114	C/T	0.08	1.15 (1.1-1.21)	6.22×10^{-9}	1.16 (1.11-1.21)	7.99×10^{-11}	0.28	98%
5	rs1837253	110,401,872	T/C	0.74	1.16 (1.12-1.21)	4.94×10^{-15}	1.16 (1.12-1.19)	1.06×10^{-21}	0.06	96%
5	rs10455025	110,404,999	A/C	0.34	1.15 (1.12-1.18)	2.03×10^{-25}	1.15 (1.12-1.18)	2.03×10^{-25}	0.53	98%
5	rs3806932	110,405,675	A/G	0.45	0.92 (0.9-0.95)	4.51×10^{-10}	0.92 (0.9-0.95)	2.49×10^{-10}	0.45	100%
5	rs3806933	110,406,742	C/T	0.45	0.92 (0.9-0.95)	2.70×10^{-10}	0.92 (0.9-0.95)	1.42×10^{-10}	0.45	100%
5	rs1898671	110,408,002	C/T	0.34	1.15 (1.12-1.18)	7.12×10^{-25}	1.15 (1.12-1.18)	7.12×10^{-25}	0.50	100%
5	rs7723819	110,427,347	G/A	0.47	0.92 (0.89-0.94)	1.00×10^{-9}	0.92 (0.89-0.94)	3.05×10^{-12}	0.26	100%
5	rs1993465	110,433,098	A/G	0.46	0.92 (0.9-0.94)	2.32×10^{-10}	0.92 (0.9-0.94)	1.10×10^{-11}	0.36	100%
5	rs6859041	110,435,231	G/A	0.47	0.92 (0.89-0.94)	1.02×10^{-10}	0.92 (0.89-0.94)	4.71×10^{-12}	0.36	100%
5	rs10038177	110,436,450	C/T	0.47	0.92 (0.89-0.94)	1.37×10^{-10}	0.92 (0.89-0.94)	4.63×10^{-12}	0.35	100%
5	rs10045255	110,438,357	A/G	0.47	0.92 (0.89-0.94)	2.03×10^{-10}	0.92 (0.89-0.94)	2.85×10^{-12}	0.32	100%
5	rs1379300	110,441,439	T/C	0.47	0.92 (0.89-0.94)	5.58×10^{-10}	0.92 (0.89-0.94)	4.96×10^{-12}	0.29	100%
5	rs10038058	110,443,281	A/G	0.47	0.92 (0.89-0.94)	7.49×10^{-10}	0.92 (0.89-0.94)	4.20×10^{-12}	0.27	100%
5	rs2112541	110,449,346	T/C	0.47	0.92 (0.89-0.94)	1.92×10^{-9}	0.92 (0.9-0.94)	5.00×10^{-12}	0.23	100%
5	rs10060003	110,449,357	A/G	0.47	0.92 (0.89-0.95)	2.50×10^{-9}	0.92 (0.9-0.94)	5.54×10^{-12}	0.23	100%
5	rs10051830	110,452,845	G/A	0.46	0.92 (0.9-0.95)	6.16×10^{-9}	0.92 (0.9-0.94)	2.72×10^{-11}	0.23	100%
5	rs17624673	110,457,158	C/T	0.33	1.14 (1.11-1.17)	1.51×10^{-19}	1.14 (1.11-1.17)	9.65×10^{-23}	0.32	98%
5	rs7702774	110,460,851	G/T	0.47	0.92 (0.89-0.94)	1.43×10^{-9}	0.92 (0.9-0.94)	6.66×10^{-12}	0.26	100%
5	rs4530809	110,462,230	A/G	0.37	0.93 (0.9-0.95)	5.53×10^{-9}	0.93 (0.9-0.95)	5.53×10^{-9}	0.84	98%
5	rs1043828	110,464,008	T/C	0.34	1.13 (1.1-1.17)	3.01×10^{-19}	1.13 (1.11-1.16)	1.48×10^{-22}	0.31	100%
5	rs1438673	110,467,499	C/T	0.51	0.91 (0.88-0.93)	4.52×10^{-11}	0.9 (0.88-0.92)	2.50×10^{-16}	0.12	100%
5	rs6594499	110,470,137	C/A	0.51	0.9 (0.88-0.93)	3.84×10^{-11}	0.9 (0.88-0.92)	6.30×10^{-16}	0.15	96%
5	rs2162893	110,558,064	A/G	0.62	0.9 (0.88-0.93)	3.95×10^{-13}	0.9 (0.88-0.93)	3.95×10^{-13}	0.64	91%
5	rs10057913	110,566,175	G/A	0.88	1.13 (1.08-1.17)	2.00×10^{-9}	1.13 (1.08-1.17)	2.00×10^{-9}	0.77	98%
5	rs1457115	110,567,598	C/T	0.45	1.08 (1.06-1.11)	1.78×10^{-10}	1.08 (1.06-1.11)	1.78×10^{-10}	0.94	98%
5	rs11950562	131,652,529	A/C	0.45	0.93 (0.9-0.95)	1.65×10^{-9}	0.93 (0.9-0.95)	1.65×10^{-9}	0.63	100%
5	rs10058074	131,686,146	G/A	0.45	0.93 (0.91-0.95)	3.89×10^{-9}	0.93 (0.91-0.95)	3.89×10^{-9}	0.53	100%
5	rs4705938	131,694,077	T/C	0.45	0.93 (0.9-0.95)	3.97×10^{-9}	0.93 (0.9-0.95)	3.25×10^{-9}	0.46	100%
5	rs17622208	131,717,050	G/A	0.45	0.93 (0.9-0.95)	1.02×10^{-9}	0.93 (0.9-0.95)	1.02×10^{-9}	0.51	100%
5	rs1023518	131,793,772	G/T	0.27	1.09 (1.06-1.12)	1.16×10^{-9}	1.09 (1.06-1.12)	1.16×10^{-9}	0.59	100%
5	rs3857440	131,794,069	G/A	0.27	1.09 (1.06-1.12)	1.61×10^{-9}	1.09 (1.06-1.12)	1.61×10^{-9}	0.57	100%
5	rs11745587	131,796,922	G/A	0.36	1.09 (1.06-1.11)	3.19×10^{-10}	1.09 (1.06-1.11)	3.19×10^{-10}	0.54	98%
5	rs6894249	131,797,547	A/G	0.39	1.09 (1.06-1.12)	2.15×10^{-11}	1.09 (1.06-1.12)	2.15×10^{-11}	0.48	96%
5	rs17622656	131,820,997	G/A	0.38	0.91 (0.88-0.94)	1.00×10^{-9}	0.91 (0.89-0.94)	1.94×10^{-11}	0.26	96%
5	rs736801	131,833,599	C/T	0.38	0.91 (0.88-0.94)	2.86×10^{-10}	0.91 (0.89-0.94)	8.51×10^{-12}	0.29	96%
5	rs2158177	131,984,058	A/G	0.18	1.13 (1.09-1.18)	2.36×10^{-9}	1.13 (1.09-1.17)	6.18×10^{-11}	0.26	96%
5	rs1295686	131,995,843	T/C	0.78	0.89 (0.87-0.92)	4.11×10^{-13}	0.89 (0.87-0.92)	4.11×10^{-13}	0.57	100%
5	rs20541	131,995,964	A/G	0.79	0.89 (0.86-0.91)	1.36×10^{-14}	0.89 (0.86-0.91)	1.36×10^{-14}	0.73	98%
5	rs1295685	131,996,445	A/G	0.78	0.89 (0.86-0.92)	2.24×10^{-13}	0.89 (0.86-0.92)	1.21×10^{-13}	0.45	98%
5	rs848	131,996,500	A/C	0.79	0.89 (0.86-0.92)	1.01×10^{-12}	0.89 (0.86-0.92)	2.60×10^{-13}	0.41	96%
5	rs847	131,996,669	T/C	0.79	0.89 (0.86-0.92)	4.66×10^{-12}	0.89 (0.86-0.92)	8.53×10^{-13}	0.38	98%
6	rs16901847	28,375,851	G/A	0.19	1.1 (1.06-1.13)	9.42×10^{-9}	1.1 (1.06-1.13)	9.42×10^{-9}	0.79	100%
6	rs7765989	28,400,295	T/C	0.18	1.1 (1.06-1.13)	9.61×10^{-9}	1.1 (1.06-1.13)	9.61×10^{-9}	0.78	100%
6	rs16894116	28,414,967	G/T	0.18	1.1 (1.06-1.13)	9.27×10^{-9}	1.1 (1.06-1.13)	9.27×10^{-9}	0.75	100%
6	rs1233578	28,712,247	A/G	0.13	1.11 (1.07-1.15)	5.32×10^{-9}	1.11 (1.07-1.15)	5.32×10^{-9}	0.82	100%
6	rs3130117	30,508,956	G/A	0.11	1.12 (1.08-1.17)	9.09×10^{-9}	1.12 (1.08-1.17)	9.09×10^{-9}	0.59	100%
6	rs3132610	30,544,401	A/G	0.11	1.12 (1.08-1.17)	8.07×10^{-9}	1.12 (1.08-1.17)	8.07×10^{-9}	0.65	100%
6	rs9262143	30,652,781	C/T	0.11	1.12 (1.08-1.17)	5.97×10^{-9}	1.12 (1.08-1.17)	5.97×10^{-9}	0.67	100%
6	rs3132584	30,688,427	G/T	0.18	1.1 (1.07-1.14)	4.06×10^{-10}	1.1 (1.07-1.14)	4.06×10^{-10}	0.77	100%
6	rs8233	30,692,965	G/A	0.18	1.11 (1.07-1.14)	3.03×10^{-10}	1.11 (1.07-1.14)	3.03×10^{-10}	0.76	100%
6	rs3095330	30,693,633	A/G	0.17	1.12 (1.08-1.15)	5.73×10^{-10}	1.12 (1.08-1.15)	5.73×10^{-10}	0.78	89%
6	rs3095329	30,693,816	A/G	0.18	1.11 (1.07-1.14)	3.07×10^{-10}	1.11 (1.07-1.14)	3.07×10^{-10}	0.77	100%
6	rs3094127	30,697,447	A/G	0.18	1.11 (1.07-1.14)	2.67×10^{-10}	1.11 (1.07-1.14)	2.67×10^{-10}	0.77	100%
6	rs1064627	30,698,541	A/G	0.18	1.11 (1.07-1.14)	4.59×10^{-10}	1.11 (1.07-1.14)	4.59×10^{-10}	0.74	98%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
6	rs1059612	30,708,955	C/T	0.12	1.13 (1.08-1.17)	1.56×10^{-9}	1.13 (1.08-1.17)	1.56×10^{-9}	0.60	100%
6	rs2284174	30,713,580	T/C	0.16	1.11 (1.07-1.15)	9.37×10^{-10}	1.11 (1.07-1.15)	9.37×10^{-10}	0.68	100%
6	rs3129973	30,721,143	C/T	0.11	1.12 (1.08-1.16)	8.26×10^{-9}	1.12 (1.08-1.16)	8.26×10^{-9}	0.63	100%
6	rs3130665	30,735,979	C/T	0.12	1.12 (1.08-1.16)	4.67×10^{-9}	1.12 (1.08-1.16)	4.67×10^{-9}	0.56	100%
6	rs3095336	30,738,446	G/A	0.12	1.12 (1.08-1.17)	2.87×10^{-9}	1.12 (1.08-1.17)	2.87×10^{-9}	0.77	98%
6	rs3132605	30,739,972	A/C	0.12	1.12 (1.08-1.16)	3.25×10^{-9}	1.12 (1.08-1.16)	3.25×10^{-9}	0.76	98%
6	rs3129978	30,746,331	A/G	0.12	1.12 (1.08-1.17)	3.11×10^{-9}	1.12 (1.08-1.17)	3.11×10^{-9}	0.75	98%
6	rs3130673	30,746,519	G/T	0.12	1.12 (1.08-1.17)	2.56×10^{-9}	1.12 (1.08-1.17)	2.56×10^{-9}	0.75	98%
6	rs3131044	30,758,664	A/C	0.12	1.12 (1.08-1.17)	2.17×10^{-9}	1.12 (1.08-1.17)	2.17×10^{-9}	0.71	98%
6	rs3131050	30,760,025	T/C	0.12	1.12 (1.08-1.17)	3.71×10^{-9}	1.12 (1.08-1.17)	3.71×10^{-9}	0.70	96%
6	rs9262200	30,760,725	G/A	0.12	1.12 (1.08-1.17)	2.62×10^{-9}	1.12 (1.08-1.17)	2.62×10^{-9}	0.73	100%
6	rs3131055	30,761,487	T/C	0.12	1.12 (1.08-1.16)	2.98×10^{-9}	1.12 (1.08-1.16)	2.98×10^{-9}	0.72	100%
6	rs3129985	30,762,542	C/T	0.11	1.12 (1.08-1.16)	3.21×10^{-9}	1.12 (1.08-1.16)	3.21×10^{-9}	0.72	100%
6	rs3131060	30,763,291	G/A	0.11	1.12 (1.08-1.16)	2.96×10^{-9}	1.12 (1.08-1.16)	2.96×10^{-9}	0.72	100%
6	rs3131064	30,763,893	T/C	0.14	1.12 (1.08-1.16)	2.58×10^{-10}	1.12 (1.08-1.16)	2.58×10^{-10}	0.54	100%
6	rs3130641	30,764,081	C/T	0.11	1.12 (1.08-1.17)	6.59×10^{-9}	1.12 (1.08-1.17)	6.59×10^{-9}	0.74	96%
6	rs1264376	30,765,579	C/A	0.12	1.12 (1.08-1.16)	4.62×10^{-9}	1.12 (1.08-1.16)	4.62×10^{-9}	0.69	98%
6	rs3130564	31,101,674	C/T	0.19	1.1 (1.06-1.13)	3.71×10^{-9}	1.1 (1.06-1.13)	3.71×10^{-9}	0.68	98%
6	rs9264740	31,244,331	C/T	0.72	1.09 (1.06-1.12)	9.25×10^{-9}	1.09 (1.06-1.12)	9.25×10^{-9}	0.68	89%
6	rs2596464	31,412,961	T/C	0.48	1.1 (1.06-1.13)	1.33×10^{-9}	1.1 (1.07-1.13)	1.79×10^{-13}	0.14	98%
6	rs2596472	31,428,967	G/A	0.73	1.1 (1.07-1.13)	5.54×10^{-10}	1.1 (1.07-1.13)	5.54×10^{-10}	0.79	95%
6	rs1055388	31,501,737	C/T	0.72	1.09 (1.06-1.12)	4.98×10^{-9}	1.09 (1.06-1.12)	4.98×10^{-9}	0.83	100%
6	rs933208	31,506,648	G/T	0.72	1.09 (1.06-1.12)	4.16×10^{-9}	1.09 (1.06-1.12)	4.16×10^{-9}	0.83	100%
6	rs2239528	31,510,105	A/G	0.72	1.09 (1.06-1.12)	6.14×10^{-9}	1.09 (1.06-1.12)	6.14×10^{-9}	0.84	100%
6	rs2523504	31,510,858	T/C	0.72	1.09 (1.06-1.12)	6.05×10^{-9}	1.09 (1.06-1.12)	6.05×10^{-9}	0.84	100%
6	rs6904608	32,327,727	C/T	0.56	1.08 (1.05-1.1)	4.84×10^{-9}	1.08 (1.05-1.1)	4.84×10^{-9}	0.84	100%
6	rs2073044	32,338,986	C/T	0.24	1.11 (1.08-1.15)	1.24×10^{-10}	1.12 (1.08-1.15)	4.31×10^{-13}	0.30	93%
6	rs9268403	32,341,473	T/C	0.27	1.13 (1.09-1.16)	4.95×10^{-13}	1.13 (1.1-1.16)	5.79×10^{-18}	0.14	98%
6	rs9268429	32,345,052	A/G	0.27	1.12 (1.09-1.16)	1.35×10^{-12}	1.13 (1.09-1.16)	3.03×10^{-17}	0.16	98%
6	rs1980495	32,346,794	A/C	0.26	1.13 (1.09-1.17)	3.55×10^{-11}	1.13 (1.1-1.17)	1.76×10^{-16}	0.11	89%
6	rs8180664	32,347,490	C/T	0.26	1.13 (1.09-1.17)	1.10×10^{-13}	1.13 (1.1-1.16)	4.39×10^{-19}	0.13	100%
6	rs2395157	32,348,145	A/G	0.26	1.13 (1.1-1.17)	9.64×10^{-14}	1.13 (1.1-1.16)	1.92×10^{-19}	0.11	100%
6	rs17423649	32,357,133	C/T	0.16	0.89 (0.86-0.92)	2.68×10^{-10}	0.89 (0.86-0.92)	2.68×10^{-10}	0.49	98%
6	rs9268474	32,357,165	T/C	0.27	1.13 (1.09-1.17)	6.29×10^{-13}	1.13 (1.1-1.16)	8.10×10^{-19}	0.09	100%
6	rs12529049	32,357,715	C/T	0.16	0.89 (0.86-0.92)	1.64×10^{-10}	0.89 (0.86-0.92)	1.64×10^{-10}	0.50	100%
6	rs12525722	32,358,163	A/G	0.16	0.89 (0.86-0.92)	1.79×10^{-10}	0.89 (0.86-0.92)	1.79×10^{-10}	0.51	100%
6	rs17423691	32,358,345	C/A	0.16	0.89 (0.86-0.92)	1.73×10^{-10}	0.89 (0.86-0.92)	1.73×10^{-10}	0.51	100%
6	rs17423698	32,358,368	T/C	0.16	0.89 (0.86-0.92)	1.68×10^{-10}	0.89 (0.86-0.92)	1.68×10^{-10}	0.51	100%
6	rs17495592	32,358,533	A/G	0.16	0.89 (0.86-0.92)	1.51×10^{-10}	0.89 (0.86-0.92)	1.51×10^{-10}	0.51	100%
6	rs9268477	32,359,121	G/A	0.27	1.12 (1.09-1.16)	5.65×10^{-11}	1.13 (1.09-1.16)	3.11×10^{-16}	0.10	91%
6	rs17495612	32,359,431	T/C	0.16	0.89 (0.86-0.92)	1.11×10^{-10}	0.89 (0.86-0.92)	1.11×10^{-10}	0.56	100%
6	rs16870123	32,359,460	G/A	0.16	0.89 (0.86-0.92)	1.27×10^{-10}	0.89 (0.86-0.92)	1.27×10^{-10}	0.54	100%
6	rs17423753	32,360,341	C/A	0.16	0.89 (0.86-0.93)	3.41×10^{-10}	0.89 (0.86-0.93)	3.41×10^{-10}	0.53	100%
6	rs3817969	32,361,388	C/T	0.16	0.89 (0.86-0.92)	2.16×10^{-10}	0.89 (0.86-0.92)	2.16×10^{-10}	0.48	96%
6	rs9268480	32,363,844	C/T	0.27	1.13 (1.09-1.17)	5.88×10^{-13}	1.13 (1.1-1.16)	7.24×10^{-19}	0.09	100%
6	rs4248166	32,366,421	T/C	0.20	0.9 (0.87-0.93)	2.65×10^{-10}	0.9 (0.87-0.93)	2.65×10^{-10}	0.50	100%
6	rs2294881	32,367,604	T/C	0.20	0.91 (0.88-0.93)	8.49×10^{-10}	0.91 (0.88-0.93)	8.49×10^{-10}	0.59	100%
6	rs2294880	32,367,722	A/G	0.26	1.13 (1.09-1.17)	4.81×10^{-10}	1.13 (1.1-1.17)	1.24×10^{-15}	0.09	86%
6	rs3817966	32,367,847	T/C	0.27	1.13 (1.08-1.17)	4.80×10^{-10}	1.13 (1.1-1.16)	6.29×10^{-16}	0.06	89%
6	rs3817963	32,368,087	T/C	0.27	1.13 (1.09-1.17)	7.76×10^{-13}	1.13 (1.1-1.16)	8.10×10^{-19}	0.08	100%
6	rs3817962	32,368,314	C/A	0.26	1.13 (1.08-1.17)	6.80×10^{-10}	1.13 (1.1-1.17)	1.71×10^{-15}	0.08	86%
6	rs2076525	32,370,616	T/C	0.27	1.12 (1.09-1.16)	1.08×10^{-11}	1.13 (1.1-1.16)	2.91×10^{-17}	0.09	96%
6	rs2076524	32,370,684	A/G	0.26	1.13 (1.09-1.17)	1.33×10^{-13}	1.13 (1.1-1.16)	2.80×10^{-19}	0.11	100%
6	rs3793126	32,371,619	A/G	0.28	1.13 (1.09-1.16)	5.78×10^{-13}	1.13 (1.1-1.16)	2.31×10^{-18}	0.09	100%
6	rs3793127	32,371,915	C/T	0.21	1.13 (1.09-1.17)	1.74×10^{-11}	1.14 (1.11-1.17)	4.88×10^{-18}	0.09	100%
6	rs9268493	32,375,330	G/A	0.28	1.13 (1.09-1.16)	2.12×10^{-11}	1.13 (1.09-1.16)	7.47×10^{-17}	0.07	95%
6	rs9268494	32,375,352	A/C	0.27	1.13 (1.09-1.16)	5.70×10^{-12}	1.13 (1.1-1.16)	4.96×10^{-17}	0.11	96%
6	rs9268497	32,375,424	G/A	0.27	1.13 (1.09-1.17)	7.77×10^{-11}	1.13 (1.1-1.17)	1.54×10^{-16}	0.09	89%
6	rs9268499	32,375,695	G/A	0.28	1.13 (1.09-1.17)	1.41×10^{-11}	1.12 (1.09-1.16)	9.06×10^{-17}	0.07	95%
6	rs3763309	32,375,973	C/A	0.21	1.13 (1.09-1.18)	3.31×10^{-12}	1.14 (1.11-1.18)	1.31×10^{-18}	0.11	100%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
6	rs3763311	32,376,176	C/T	0.27	1.13 (1.09-1.17)	1.17×10^{-10}	1.13 (1.1-1.17)	5.25×10^{-16}	0.09	89%
6	rs3763316	32,376,746	C/T	0.27	1.13 (1.09-1.17)	1.97×10^{-13}	1.13 (1.1-1.16)	2.95×10^{-18}	0.16	96%
6	rs9268516	32,379,489	C/T	0.27	1.13 (1.1-1.17)	4.57×10^{-14}	1.14 (1.1-1.17)	4.48×10^{-20}	0.10	100%
6	rs2395163	32,387,809	T/C	0.20	1.12 (1.08-1.17)	8.02×10^{-9}	1.14 (1.1-1.17)	1.55×10^{-16}	0.03	96%
6	rs6926374	32,409,305	A/G	0.43	1.09 (1.06-1.12)	1.20×10^{-9}	1.09 (1.06-1.12)	9.26×10^{-12}	0.33	96%
6	rs2239804	32,411,523	T/C	0.42	1.09 (1.06-1.12)	1.05×10^{-9}	1.1 (1.07-1.12)	2.62×10^{-13}	0.21	100%
6	rs2239803	32,411,833	C/T	0.43	1.09 (1.06-1.12)	2.26×10^{-9}	1.09 (1.07-1.12)	4.96×10^{-12}	0.29	96%
6	rs9268853	32,429,643	T/C	0.31	1.12 (1.08-1.15)	4.04×10^{-12}	1.12 (1.09-1.15)	1.72×10^{-16}	0.17	98%
6	rs9268858	32,429,758	T/C	0.31	1.12 (1.08-1.15)	3.92×10^{-12}	1.12 (1.09-1.15)	1.58×10^{-16}	0.17	98%
6	rs9268877	32,431,147	A/G	0.57	1.09 (1.07-1.12)	1.94×10^{-11}	1.09 (1.07-1.12)	1.94×10^{-11}	0.87	98%
6	rs9268923	32,432,835	C/T	0.36	1.14 (1.11-1.18)	2.79×10^{-19}	1.14 (1.11-1.18)	5.37×10^{-22}	0.36	93%
6	rs2395185	32,433,167	G/T	0.30	1.12 (1.08-1.15)	3.60×10^{-12}	1.12 (1.09-1.15)	1.56×10^{-16}	0.17	98%
6	rs9268969	32,434,349	C/T	0.36	1.14 (1.11-1.18)	2.65×10^{-19}	1.14 (1.11-1.18)	5.29×10^{-22}	0.36	93%
6	rs9268979	32,435,044	T/C	0.55	1.09 (1.06-1.12)	4.07×10^{-10}	1.09 (1.06-1.12)	4.07×10^{-10}	0.80	95%
6	rs9405040	32,439,393	A/C	0.30	1.12 (1.08-1.15)	4.05×10^{-12}	1.12 (1.09-1.15)	2.29×10^{-16}	0.17	98%
6	rs9286790	32,439,828	G/A	0.30	1.12 (1.08-1.15)	1.55×10^{-12}	1.12 (1.09-1.15)	3.96×10^{-16}	0.23	95%
6	rs9269065	32,440,172	T/G	0.48	1.1 (1.07-1.13)	1.01×10^{-9}	1.1 (1.07-1.13)	1.01×10^{-9}	0.51	84%
6	rs9269069	32,440,362	C/T	0.57	1.1 (1.07-1.13)	1.11×10^{-11}	1.1 (1.07-1.13)	1.11×10^{-11}	0.85	98%
6	rs9269070	32,440,451	G/A	0.58	1.09 (1.06-1.12)	4.08×10^{-9}	1.09 (1.06-1.12)	4.08×10^{-9}	0.65	86%
6	rs9269071	32,440,467	T/C	0.57	1.09 (1.06-1.12)	6.42×10^{-11}	1.09 (1.06-1.12)	6.42×10^{-11}	0.84	95%
6	rs9269080	32,440,969	G/A	0.57	1.08 (1.06-1.11)	1.51×10^{-9}	1.08 (1.06-1.11)	1.51×10^{-9}	0.69	95%
6	rs7755212	32,441,408	C/T	0.57	1.09 (1.06-1.12)	3.22×10^{-10}	1.09 (1.06-1.12)	3.22×10^{-10}	0.71	93%
6	rs7739203	32,441,555	A/G	0.57	1.09 (1.06-1.12)	6.44×10^{-11}	1.09 (1.06-1.12)	6.44×10^{-11}	0.84	95%
6	rs7739357	32,441,641	A/G	0.57	1.1 (1.07-1.13)	4.30×10^{-11}	1.1 (1.07-1.13)	4.30×10^{-11}	0.82	91%
6	rs9405112	32,445,600	G/A	0.30	1.12 (1.08-1.15)	9.54×10^{-12}	1.12 (1.09-1.15)	1.71×10^{-16}	0.14	98%
6	rs6916742	32,453,191	T/C	0.55	1.11 (1.08-1.15)	2.25×10^{-10}	1.12 (1.09-1.15)	1.23×10^{-14}	0.14	93%
6	rs2516049	32,570,400	T/C	0.30	1.12 (1.08-1.16)	5.30×10^{-10}	1.12 (1.09-1.15)	3.17×10^{-16}	0.03	98%
6	rs4530903	32,581,889	C/T	0.12	0.87 (0.83-0.91)	1.85×10^{-9}	0.87 (0.83-0.91)	1.85×10^{-9}	0.48	93%
6	rs9272346	32,604,372	G/A	0.56	1.16 (1.13-1.19)	4.80×10^{-28}	1.16 (1.13-1.19)	2.35×10^{-28}	0.46	96%
6	rs9272723	32,609,427	T/C	0.60	1.14 (1.11-1.17)	1.43×10^{-22}	1.14 (1.11-1.17)	1.43×10^{-22}	0.68	96%
6	rs6928482	32,626,249	T/C	0.45	1.11 (1.08-1.15)	7.28×10^{-11}	1.11 (1.08-1.14)	3.85×10^{-16}	0.06	98%
6	rs9273363	32,626,272	C/A	0.26	1.11 (1.07-1.14)	2.74×10^{-11}	1.11 (1.07-1.14)	2.74×10^{-11}	0.96	96%
6	rs6906021	32,626,311	T/C	0.43	1.1 (1.07-1.13)	1.22×10^{-12}	1.1 (1.07-1.13)	1.08×10^{-13}	0.39	96%
6	rs9275141	32,651,117	T/G	0.47	1.11 (1.07-1.14)	9.66×10^{-10}	1.11 (1.08-1.14)	5.29×10^{-16}	0.01	100%
6	rs2858330	32,658,715	T/C	0.46	1.11 (1.07-1.14)	3.51×10^{-10}	1.11 (1.08-1.14)	2.35×10^{-16}	0.03	100%
6	rs17427445	32,663,764	G/A	0.13	0.89 (0.85-0.92)	6.33×10^{-9}	0.89 (0.85-0.92)	4.19×10^{-9}	0.43	93%
6	rs10484561	32,665,420	T/G	0.13	0.89 (0.86-0.93)	2.81×10^{-9}	0.89 (0.86-0.93)	2.42×10^{-9}	0.46	100%
6	rs17427564	32,667,067	T/C	0.13	0.89 (0.85-0.93)	9.52×10^{-9}	0.89 (0.86-0.93)	5.26×10^{-9}	0.41	95%
6	rs10947332	32,677,440	G/A	0.13	0.89 (0.85-0.92)	2.38×10^{-9}	0.89 (0.85-0.92)	1.94×10^{-9}	0.45	98%
6	rs3104405	32,682,308	C/A	0.65	1.11 (1.08-1.14)	1.61×10^{-12}	1.11 (1.08-1.14)	1.61×10^{-12}	0.50	93%
6	rs9275602	32,682,812	C/A	0.15	1.13 (1.09-1.17)	3.57×10^{-10}	1.13 (1.09-1.17)	3.57×10^{-10}	0.47	91%
6	rs241425	32,804,909	A/G	0.55	1.08 (1.05-1.11)	2.58×10^{-9}	1.08 (1.05-1.11)	2.58×10^{-9}	0.73	98%
6	rs2239701	32,805,049	T/C	0.42	1.09 (1.06-1.12)	1.13×10^{-10}	1.09 (1.06-1.12)	1.13×10^{-10}	0.95	95%
6	rs6454802	90,814,199	C/T	0.37	0.93 (0.9-0.95)	9.05×10^{-9}	0.93 (0.9-0.95)	9.05×10^{-9}	0.69	96%
6	rs11753332	90,819,153	G/A	0.37	0.92 (0.9-0.95)	8.49×10^{-10}	0.92 (0.9-0.95)	8.49×10^{-10}	0.74	100%
6	rs12194007	90,823,159	G/T	0.37	0.92 (0.9-0.95)	2.88×10^{-9}	0.92 (0.9-0.95)	2.88×10^{-9}	0.66	95%
6	rs12199079	90,852,258	T/G	0.34	0.92 (0.89-0.94)	1.20×10^{-10}	0.92 (0.89-0.94)	1.20×10^{-10}	0.76	100%
6	rs1010473	90,856,878	G/T	0.32	0.92 (0.89-0.94)	2.02×10^{-9}	0.92 (0.89-0.94)	2.02×10^{-9}	0.84	93%
6	rs1010474	90,857,028	T/C	0.34	0.92 (0.89-0.94)	1.13×10^{-10}	0.92 (0.89-0.94)	1.13×10^{-10}	0.71	100%
6	rs17711850	90,864,870	T/C	0.34	0.92 (0.89-0.94)	9.03×10^{-11}	0.92 (0.89-0.94)	9.03×10^{-11}	0.76	100%
6	rs10455168	90,883,525	T/C	0.34	0.92 (0.89-0.94)	2.58×10^{-11}	0.92 (0.89-0.94)	2.58×10^{-11}	0.78	100%
6	rs10806423	90,886,824	C/T	0.34	0.92 (0.89-0.94)	2.61×10^{-11}	0.92 (0.89-0.94)	2.61×10^{-11}	0.78	100%
6	rs11757155	90,941,240	C/T	0.33	0.91 (0.89-0.94)	3.07×10^{-12}	0.91 (0.89-0.94)	3.07×10^{-12}	0.59	100%
6	rs2021716	90,941,289	C/T	0.33	0.91 (0.89-0.94)	5.95×10^{-12}	0.91 (0.89-0.94)	5.95×10^{-12}	0.58	100%
6	rs17585295	90,944,831	C/T	0.34	0.92 (0.89-0.94)	1.84×10^{-11}	0.92 (0.89-0.94)	1.84×10^{-11}	0.67	100%
6	rs4707609	90,946,479	T/C	0.34	0.92 (0.89-0.94)	1.85×10^{-11}	0.92 (0.89-0.94)	1.85×10^{-11}	0.67	100%
6	rs2875584	90,950,628	C/T	0.33	0.91 (0.89-0.94)	2.69×10^{-12}	0.91 (0.89-0.94)	2.69×10^{-12}	0.60	100%
6	rs17513531	90,951,239	C/T	0.33	0.91 (0.89-0.94)	2.54×10^{-12}	0.91 (0.89-0.94)	2.54×10^{-12}	0.61	100%
6	rs905670	90,958,502	G/A	0.33	0.91 (0.89-0.93)	1.48×10^{-12}	0.91 (0.89-0.93)	1.48×10^{-12}	0.68	100%
6	rs1847472	90,973,159	C/A	0.33	0.91 (0.89-0.94)	6.95×10^{-12}	0.91 (0.89-0.94)	6.95×10^{-12}	0.68	98%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
6	rs943689	90,984,035	C/T	0.33	0.91 (0.89-0.93)	1.23×10^{-12}	0.91 (0.89-0.93)	1.23×10^{-12}	0.75	100%
6	rs2325291	90,986,686	G/A	0.33	0.91 (0.89-0.93)	8.58×10^{-13}	0.91 (0.89-0.93)	8.58×10^{-13}	0.78	100%
6	rs2325292	90,986,749	T/C	0.33	0.91 (0.89-0.93)	9.00×10^{-13}	0.91 (0.89-0.93)	9.00×10^{-13}	0.78	100%
6	rs2174281	90,987,872	T/C	0.45	0.92 (0.9-0.94)	7.78×10^{-11}	0.92 (0.9-0.94)	7.78×10^{-11}	0.51	100%
6	rs4142967	90,996,349	C/T	0.45	0.92 (0.9-0.95)	1.54×10^{-10}	0.92 (0.9-0.95)	1.54×10^{-10}	0.49	100%
6	rs12212193	90,996,769	A/G	0.45	0.92 (0.9-0.94)	8.42×10^{-11}	0.92 (0.9-0.94)	8.42×10^{-11}	0.50	100%
6	rs1504215	91,006,227	G/A	0.33	0.91 (0.89-0.93)	1.77×10^{-12}	0.91 (0.89-0.93)	1.77×10^{-12}	0.81	100%
6	rs6925032	91,008,027	C/A	0.33	0.91 (0.89-0.93)	2.04×10^{-12}	0.91 (0.89-0.93)	2.04×10^{-12}	0.81	100%
6	rs1321859	91,011,673	C/T	0.33	0.91 (0.89-0.93)	2.58×10^{-12}	0.91 (0.89-0.93)	2.58×10^{-12}	0.81	100%
9	rs10975413	6,049,843	A/G	0.19	0.87 (0.83-0.91)	7.69×10^{-9}	0.9 (0.87-0.93)	1.26×10^{-10}	0.01	96%
9	rs380568	6,055,531	T/C	0.19	0.88 (0.84-0.92)	9.43×10^{-9}	0.9 (0.87-0.93)	1.85×10^{-10}	0.00	100%
9	rs343490	6,064,575	A/G	0.19	0.88 (0.84-0.92)	6.75×10^{-9}	0.9 (0.87-0.93)	1.10×10^{-10}	0.00	100%
9	rs343476	6,072,597	T/C	0.82	1.16 (1.1-1.22)	9.15×10^{-9}	1.12 (1.08-1.16)	1.01×10^{-10}	0.00	98%
9	rs378952	6,078,146	C/T	0.81	1.14 (1.09-1.19)	5.55×10^{-9}	1.11 (1.08-1.15)	4.91×10^{-11}	0.01	100%
9	rs371454	6,078,614	C/T	0.81	1.14 (1.09-1.19)	6.45×10^{-9}	1.11 (1.08-1.15)	5.63×10^{-11}	0.01	100%
9	rs413382	6,142,948	C/A	0.81	1.14 (1.09-1.19)	3.47×10^{-9}	1.12 (1.08-1.16)	9.31×10^{-12}	0.01	98%
9	rs369756	6,146,441	G/T	0.23	1.12 (1.09-1.16)	5.36×10^{-12}	1.12 (1.09-1.16)	2.75×10^{-13}	0.34	95%
9	rs450108	6,153,485	T/C	0.42	1.1 (1.07-1.14)	6.46×10^{-9}	1.1 (1.07-1.13)	2.29×10^{-11}	0.14	89%
9	rs1116795	6,155,226	G/T	0.41	1.1 (1.07-1.13)	9.99×10^{-10}	1.09 (1.07-1.12)	4.06×10^{-12}	0.16	98%
9	rs2225537	6,160,578	C/T	0.41	1.1 (1.07-1.13)	8.94×10^{-10}	1.09 (1.07-1.12)	2.69×10^{-12}	0.14	98%
9	rs10124250	6,161,686	C/T	0.41	1.1 (1.07-1.13)	9.61×10^{-10}	1.09 (1.07-1.12)	2.40×10^{-12}	0.14	98%
9	rs10119713	6,163,823	G/A	0.41	1.1 (1.07-1.13)	7.97×10^{-10}	1.09 (1.07-1.12)	2.42×10^{-12}	0.14	98%
9	rs7032572	6,172,380	A/G	0.16	1.18 (1.13-1.23)	1.24×10^{-14}	1.18 (1.14-1.22)	3.85×10^{-23}	0.03	100%
9	rs1412426	6,188,652	A/C	0.68	0.9 (0.86-0.93)	3.20×10^{-9}	0.9 (0.87-0.92)	9.42×10^{-17}	0.00	100%
9	rs1412425	6,188,740	A/C	0.68	0.9 (0.86-0.93)	1.51×10^{-9}	0.89 (0.87-0.92)	3.48×10^{-17}	0.00	100%
9	rs1342326	6,190,076	A/C	0.16	1.18 (1.13-1.23)	4.68×10^{-15}	1.18 (1.15-1.22)	2.11×10^{-24}	0.03	100%
9	rs2095044	6,192,796	T/C	0.73	0.86 (0.83-0.89)	4.09×10^{-16}	0.86 (0.84-0.89)	3.12×10^{-26}	0.01	100%
9	rs2381416	6,193,455	C/A	0.73	0.85 (0.82-0.89)	1.23×10^{-16}	0.86 (0.84-0.88)	4.54×10^{-27}	0.01	100%
9	rs10815370	6,194,831	C/A	0.66	0.89 (0.86-0.93)	3.06×10^{-9}	0.89 (0.87-0.92)	9.99×10^{-17}	0.00	98%
9	rs1888909	6,197,392	T/C	0.73	0.86 (0.82-0.89)	3.26×10^{-16}	0.86 (0.84-0.88)	9.52×10^{-27}	0.01	100%
9	rs992969	6,209,697	A/G	0.75	0.85 (0.82-0.88)	1.08×10^{-17}	0.85 (0.83-0.88)	4.27×10^{-29}	0.01	100%
9	rs3939286	6,210,099	T/C	0.75	0.85 (0.82-0.88)	2.24×10^{-17}	0.86 (0.83-0.88)	2.29×10^{-28}	0.01	100%
9	rs928413	6,213,387	G/A	0.74	0.85 (0.82-0.88)	5.44×10^{-16}	0.86 (0.83-0.88)	1.79×10^{-27}	0.00	98%
9	rs7848215	6,213,468	C/T	0.26	1.18 (1.13-1.23)	3.33×10^{-17}	1.17 (1.14-1.2)	3.08×10^{-28}	0.01	98%
9	rs2066362	6,219,176	G/T	0.16	1.18 (1.13-1.24)	1.07×10^{-14}	1.18 (1.14-1.22)	1.54×10^{-22}	0.05	98%
9	rs12551256	6,231,239	A/G	0.47	0.92 (0.89-0.94)	1.69×10^{-9}	0.92 (0.89-0.94)	2.15×10^{-11}	0.26	96%
9	rs17582919	6,233,376	T/C	0.22	1.13 (1.09-1.17)	1.22×10^{-10}	1.13 (1.1-1.16)	6.73×10^{-16}	0.04	100%
9	rs17498196	6,237,547	A/C	0.22	1.13 (1.09-1.17)	8.84×10^{-11}	1.13 (1.09-1.16)	1.45×10^{-15}	0.06	100%
9	rs10815393	6,240,324	T/C	0.22	1.12 (1.08-1.17)	4.42×10^{-9}	1.12 (1.09-1.16)	7.06×10^{-14}	0.04	95%
11	rs2155219	76,299,194	G/T	0.46	1.11 (1.08-1.15)	2.43×10^{-10}	1.11 (1.08-1.14)	2.90×10^{-15}	0.04	95%
11	rs7927894	76,301,316	C/T	0.37	1.1 (1.07-1.13)	3.52×10^{-11}	1.1 (1.07-1.13)	3.23×10^{-12}	0.38	95%
11	rs7927997	76,301,375	C/T	0.37	1.1 (1.07-1.13)	3.91×10^{-11}	1.1 (1.07-1.13)	8.40×10^{-12}	0.41	91%
15	rs10519067	61,068,347	G/A	0.14	0.89 (0.85-0.92)	8.28×10^{-9}	0.89 (0.85-0.92)	1.49×10^{-10}	0.30	100%
15	rs11071558	61,069,421	A/G	0.14	0.89 (0.85-0.92)	1.85×10^{-10}	0.89 (0.85-0.92)	8.32×10^{-11}	0.44	100%
15	rs11071559	61,069,988	C/T	0.14	0.89 (0.86-0.92)	1.93×10^{-10}	0.89 (0.86-0.92)	1.93×10^{-10}	0.52	100%
15	rs1866316	67,441,997	T/C	0.29	1.12 (1.08-1.15)	3.03×10^{-14}	1.12 (1.08-1.15)	3.03×10^{-14}	0.80	93%
15	rs17293632	67,442,596	C/T	0.26	1.12 (1.09-1.16)	5.10×10^{-14}	1.13 (1.09-1.16)	8.81×10^{-16}	0.36	98%
15	rs10152544	67,444,747	C/T	0.50	0.91 (0.89-0.94)	1.73×10^{-12}	0.91 (0.89-0.94)	1.73×10^{-12}	0.97	96%
15	rs744910	67,446,785	G/A	0.50	0.92 (0.89-0.94)	9.76×10^{-13}	0.92 (0.89-0.94)	9.76×10^{-13}	0.98	100%
15	rs11634793	67,447,452	C/T	0.50	0.92 (0.89-0.94)	1.56×10^{-12}	0.92 (0.89-0.94)	1.56×10^{-12}	0.98	100%
15	rs8032739	67,448,899	A/G	0.30	1.11 (1.08-1.14)	5.58×10^{-14}	1.11 (1.08-1.14)	5.58×10^{-14}	0.77	96%
15	rs2033784	67,449,660	A/G	0.30	1.11 (1.08-1.14)	2.47×10^{-14}	1.11 (1.08-1.14)	2.47×10^{-14}	0.75	100%
15	rs17228058	67,450,305	A/G	0.26	1.12 (1.09-1.16)	1.32×10^{-12}	1.12 (1.09-1.16)	2.85×10^{-15}	0.27	96%
15	rs7173698	67,450,893	A/G	0.30	1.11 (1.08-1.14)	5.83×10^{-14}	1.11 (1.08-1.14)	5.83×10^{-14}	0.76	96%
15	rs4562997	67,458,152	G/A	0.29	1.11 (1.08-1.14)	2.04×10^{-13}	1.11 (1.08-1.14)	2.04×10^{-13}	0.71	100%
15	rs16950687	67,464,013	A/G	0.28	1.1 (1.07-1.13)	5.28×10^{-12}	1.1 (1.07-1.13)	5.28×10^{-12}	0.79	100%
15	rs12708492	67,467,541	T/C	0.51	0.92 (0.9-0.94)	1.88×10^{-11}	0.92 (0.9-0.94)	1.88×10^{-11}	0.85	100%
15	rs17294280	67,468,285	A/G	0.27	1.12 (1.08-1.17)	4.07×10^{-10}	1.13 (1.09-1.16)	3.76×10^{-14}	0.15	96%
16	rs3743976	11,038,824	C/T	0.22	0.91 (0.88-0.94)	4.57×10^{-9}	0.9 (0.88-0.93)	1.78×10^{-10}	0.36	100%
16	rs8062923	11,160,966	A/C	0.76	1.1 (1.07-1.14)	1.45×10^{-9}	1.11 (1.08-1.14)	7.84×10^{-12}	0.28	100%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
16	rs4781035	11,161,178	A/G	0.79	1.1 (1.07-1.14)	8.98×10^{-10}	1.1 (1.07-1.14)	2.81×10^{-10}	0.43	100%
16	rs7192790	11,167,914	C/A	0.20	0.91 (0.88-0.94)	3.65×10^{-9}	0.91 (0.88-0.94)	3.65×10^{-9}	0.52	100%
16	rs12444495	11,170,455	T/C	0.79	1.1 (1.07-1.14)	1.12×10^{-9}	1.1 (1.07-1.14)	6.93×10^{-10}	0.46	95%
16	rs7184491	11,170,761	C/T	0.78	1.1 (1.07-1.14)	6.74×10^{-9}	1.1 (1.07-1.14)	2.03×10^{-9}	0.43	89%
16	rs17806299	11,199,980	G/A	0.20	0.9 (0.88-0.93)	2.09×10^{-10}	0.9 (0.88-0.93)	2.09×10^{-10}	0.51	100%
16	rs12935657	11,219,041	G/A	0.25	0.91 (0.88-0.94)	3.71×10^{-9}	0.9 (0.88-0.93)	2.06×10^{-12}	0.22	98%
16	rs7203459	11,230,703	T/C	0.26	0.91 (0.88-0.94)	8.79×10^{-9}	0.9 (0.88-0.93)	5.59×10^{-12}	0.22	95%
17	rs12950186	37,393,395	A/C	0.85	0.9 (0.87-0.93)	2.03×10^{-9}	0.9 (0.87-0.93)	2.03×10^{-9}	0.84	98%
17	rs2879258	37,399,379	G/T	0.85	0.9 (0.87-0.93)	1.93×10^{-9}	0.9 (0.87-0.93)	1.93×10^{-9}	0.88	100%
17	rs11078895	37,401,051	A/G	0.85	0.9 (0.87-0.93)	1.96×10^{-9}	0.9 (0.87-0.93)	1.96×10^{-9}	0.89	98%
17	rs11655972	37,407,072	C/T	0.85	0.9 (0.87-0.93)	8.02×10^{-10}	0.9 (0.87-0.93)	8.02×10^{-10}	0.90	100%
17	rs3744349	37,414,842	C/T	0.85	0.9 (0.87-0.93)	7.20×10^{-10}	0.9 (0.87-0.93)	7.20×10^{-10}	0.91	100%
17	rs8073907	37,424,149	C/T	0.85	0.9 (0.87-0.93)	1.60×10^{-9}	0.9 (0.87-0.93)	1.60×10^{-9}	0.93	95%
17	rs667239	37,442,241	A/G	0.15	1.11 (1.07-1.15)	6.49×10^{-10}	1.11 (1.07-1.15)	6.49×10^{-10}	0.93	100%
17	rs590051	37,446,571	T/C	0.15	1.11 (1.07-1.15)	6.53×10^{-10}	1.11 (1.07-1.15)	6.53×10^{-10}	0.93	100%
17	rs2302073	37,457,342	A/G	0.15	1.11 (1.08-1.15)	5.94×10^{-10}	1.11 (1.08-1.15)	5.94×10^{-10}	0.93	100%
17	rs584377	37,460,128	G/A	0.15	1.11 (1.07-1.15)	6.04×10^{-10}	1.11 (1.07-1.15)	6.04×10^{-10}	0.93	100%
17	rs649180	37,464,959	A/C	0.15	1.11 (1.07-1.15)	6.49×10^{-10}	1.11 (1.07-1.15)	6.49×10^{-10}	0.93	100%
17	rs2338799	37,513,941	G/A	0.15	1.11 (1.07-1.15)	8.15×10^{-10}	1.11 (1.07-1.15)	8.15×10^{-10}	0.94	100%
17	rs6503504	37,514,412	A/G	0.15	1.11 (1.07-1.15)	1.29×10^{-9}	1.11 (1.07-1.15)	1.29×10^{-9}	0.92	96%
17	rs9908131	37,520,449	T/C	0.15	1.11 (1.07-1.15)	8.73×10^{-10}	1.11 (1.07-1.15)	8.73×10^{-10}	0.94	100%
17	rs7208487	37,543,449	T/G	0.15	1.11 (1.07-1.15)	8.79×10^{-10}	1.11 (1.07-1.15)	8.79×10^{-10}	0.94	100%
17	rs4795358	37,573,065	A/C	0.85	0.9 (0.87-0.94)	6.62×10^{-9}	0.9 (0.87-0.94)	6.62×10^{-9}	0.96	96%
17	rs9646419	37,597,185	A/G	0.85	0.9 (0.87-0.94)	6.48×10^{-9}	0.9 (0.87-0.94)	6.48×10^{-9}	0.96	96%
17	rs12938099	37,612,910	T/G	0.85	0.9 (0.87-0.94)	5.14×10^{-9}	0.9 (0.87-0.94)	5.14×10^{-9}	0.96	96%
17	rs12937013	37,665,571	G/A	0.85	0.9 (0.87-0.93)	2.35×10^{-10}	0.9 (0.87-0.93)	2.35×10^{-10}	0.95	100%
17	rs8069074	37,685,401	A/G	0.85	0.9 (0.87-0.93)	1.54×10^{-9}	0.9 (0.87-0.93)	1.54×10^{-9}	0.93	98%
17	rs11657058	37,699,378	T/G	0.85	0.9 (0.87-0.93)	3.18×10^{-10}	0.9 (0.87-0.93)	3.18×10^{-10}	0.95	100%
17	rs11657153	37,699,729	A/G	0.85	0.9 (0.87-0.93)	5.95×10^{-10}	0.9 (0.87-0.93)	5.95×10^{-10}	0.94	95%
17	rs12947506	37,707,592	T/C	0.85	0.9 (0.87-0.93)	3.83×10^{-10}	0.9 (0.87-0.93)	3.83×10^{-10}	0.95	100%
17	rs7503377	37,708,841	T/C	0.85	0.9 (0.87-0.93)	3.71×10^{-10}	0.9 (0.87-0.93)	3.71×10^{-10}	0.95	100%
17	rs6503521	37,715,551	G/T	0.85	0.89 (0.86-0.93)	1.54×10^{-10}	0.89 (0.86-0.93)	1.54×10^{-10}	0.95	98%
17	rs903507	37,726,423	C/T	0.15	1.12 (1.08-1.16)	3.90×10^{-11}	1.12 (1.08-1.16)	3.90×10^{-11}	0.94	98%
17	rs8182252	37,727,950	T/C	0.17	1.11 (1.07-1.15)	4.28×10^{-9}	1.11 (1.07-1.15)	4.28×10^{-9}	0.79	93%
17	rs1874226	37,729,031	C/T	0.15	1.12 (1.09-1.16)	2.64×10^{-11}	1.12 (1.09-1.16)	2.64×10^{-11}	0.94	98%
17	rs4795385	37,733,148	A/G	0.17	1.13 (1.09-1.17)	1.16×10^{-12}	1.13 (1.09-1.17)	1.16×10^{-12}	0.92	96%
17	rs1877030	37,740,161	T/C	0.84	0.89 (0.86-0.92)	1.80×10^{-12}	0.89 (0.86-0.92)	1.80×10^{-12}	0.97	98%
17	rs12453198	37,741,879	T/C	0.84	0.88 (0.85-0.91)	3.48×10^{-14}	0.88 (0.85-0.91)	3.48×10^{-14}	0.97	98%
17	rs11654954	37,745,979	A/G	0.83	0.88 (0.85-0.91)	1.57×10^{-14}	0.88 (0.85-0.91)	1.57×10^{-14}	0.95	98%
17	rs12453682	37,770,005	C/T	0.70	0.9 (0.88-0.93)	7.00×10^{-12}	0.9 (0.88-0.93)	9.56×10^{-14}	0.29	98%
17	rs1874228	37,775,274	A/G	0.73	0.91 (0.88-0.93)	5.81×10^{-12}	0.91 (0.88-0.93)	5.81×10^{-12}	0.56	96%
17	rs879606	37,781,849	A/G	0.83	0.88 (0.85-0.91)	1.61×10^{-13}	0.88 (0.85-0.91)	1.61×10^{-13}	0.97	95%
17	rs2271309	37,784,990	G/A	0.80	0.89 (0.86-0.92)	4.27×10^{-14}	0.89 (0.86-0.92)	4.27×10^{-14}	0.92	98%
17	rs907094	37,790,371	G/A	0.80	0.89 (0.87-0.92)	1.28×10^{-12}	0.89 (0.87-0.92)	1.28×10^{-12}	0.89	98%
17	rs3764352	37,790,939	C/T	0.80	0.9 (0.87-0.93)	4.64×10^{-10}	0.9 (0.87-0.93)	4.64×10^{-10}	0.88	88%
17	rs9972882	37,807,698	A/C	0.75	0.88 (0.85-0.9)	1.85×10^{-20}	0.88 (0.85-0.9)	1.85×10^{-20}	0.66	98%
17	rs1877031	37,814,080	G/A	0.67	0.89 (0.87-0.91)	1.32×10^{-18}	0.89 (0.87-0.91)	1.32×10^{-18}	0.58	98%
17	rs2271308	37,817,482	T/C	0.73	0.89 (0.86-0.91)	1.93×10^{-17}	0.89 (0.86-0.91)	1.93×10^{-17}	0.69	98%
17	rs931992	37,821,435	G/T	0.67	0.89 (0.87-0.91)	2.55×10^{-18}	0.89 (0.87-0.91)	2.55×10^{-18}	0.56	98%
17	rs1053651	37,822,311	A/C	0.73	0.89 (0.86-0.92)	1.22×10^{-15}	0.89 (0.86-0.92)	1.22×10^{-15}	0.59	93%
17	rs876493	37,824,545	G/A	0.60	0.88 (0.85-0.91)	1.17×10^{-11}	0.88 (0.85-0.91)	1.92×10^{-16}	0.13	82%
17	rs14050	37,828,072	C/T	0.70	0.86 (0.84-0.89)	8.89×10^{-23}	0.86 (0.84-0.89)	8.89×10^{-23}	0.49	88%
17	rs2952151	37,828,496	T/C	0.70	0.86 (0.84-0.89)	2.32×10^{-27}	0.86 (0.84-0.89)	2.32×10^{-27}	0.66	98%
17	rs2941503	37,828,745	A/G	0.70	0.87 (0.84-0.89)	6.42×10^{-23}	0.87 (0.84-0.89)	6.42×10^{-23}	0.53	89%
17	rs907087	37,828,787	G/A	0.70	0.86 (0.84-0.89)	6.67×10^{-23}	0.86 (0.84-0.89)	6.67×10^{-23}	0.49	88%
17	rs903502	37,829,604	C/T	0.68	0.87 (0.85-0.9)	1.43×10^{-24}	0.87 (0.85-0.9)	1.43×10^{-24}	0.62	100%
17	rs2941504	37,830,900	A/G	0.70	0.86 (0.84-0.89)	1.28×10^{-27}	0.86 (0.84-0.89)	1.28×10^{-27}	0.65	98%
17	rs1565922	37,831,035	A/G	0.70	0.86 (0.84-0.89)	3.85×10^{-27}	0.86 (0.84-0.89)	3.85×10^{-27}	0.65	98%
17	rs2934952	37,832,366	G/A	0.71	0.87 (0.84-0.89)	4.33×10^{-24}	0.87 (0.84-0.89)	4.33×10^{-24}	0.49	89%
17	rs2941505	37,832,704	A/G	0.68	0.87 (0.85-0.9)	2.83×10^{-24}	0.87 (0.85-0.9)	2.83×10^{-24}	0.51	100%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
17	rs2941506	37,833,035	A/G	0.68	0.87 (0.85-0.9)	2.21×10^{-22}	0.87 (0.85-0.9)	2.17×10^{-23}	0.43	96%
17	rs907089	37,833,600	G/A	0.68	0.88 (0.85-0.9)	1.42×10^{-22}	0.88 (0.85-0.9)	1.42×10^{-22}	0.51	98%
17	rs2313171	37,833,842	T/C	0.68	0.87 (0.85-0.9)	3.82×10^{-22}	0.87 (0.85-0.9)	2.50×10^{-23}	0.42	96%
17	rs12150298	37,834,541	T/C	0.68	0.88 (0.86-0.9)	9.04×10^{-23}	0.88 (0.86-0.9)	4.46×10^{-23}	0.46	100%
17	rs8078228	37,834,998	C/T	0.68	0.87 (0.85-0.9)	5.04×10^{-22}	0.87 (0.85-0.9)	2.05×10^{-23}	0.41	96%
17	rs11078919	37,835,755	T/C	0.68	0.88 (0.85-0.9)	9.43×10^{-20}	0.88 (0.86-0.9)	2.59×10^{-21}	0.39	95%
17	rs1476278	37,836,243	C/T	0.68	0.88 (0.85-0.9)	7.34×10^{-23}	0.88 (0.85-0.9)	2.15×10^{-23}	0.45	100%
17	rs9303274	37,836,353	T/C	0.68	0.88 (0.85-0.9)	7.40×10^{-21}	0.88 (0.85-0.9)	1.44×10^{-22}	0.39	96%
17	rs2517957	37,838,716	G/A	0.68	0.87 (0.85-0.9)	4.64×10^{-24}	0.87 (0.85-0.9)	3.13×10^{-24}	0.47	100%
17	rs2517958	37,838,751	G/A	0.68	0.87 (0.85-0.9)	5.66×10^{-24}	0.87 (0.85-0.9)	3.07×10^{-24}	0.46	100%
17	rs903501	37,839,493	T/C	0.70	0.87 (0.84-0.9)	1.55×10^{-19}	0.87 (0.84-0.9)	2.68×10^{-21}	0.40	88%
17	rs2517954	37,843,550	T/C	0.69	0.86 (0.84-0.88)	4.84×10^{-28}	0.86 (0.84-0.88)	4.84×10^{-28}	0.63	98%
17	rs2517955	37,843,681	C/T	0.67	0.87 (0.85-0.9)	2.22×10^{-23}	0.87 (0.85-0.9)	2.22×10^{-23}	0.53	98%
17	rs2517956	37,843,859	G/A	0.69	0.86 (0.84-0.89)	1.05×10^{-26}	0.86 (0.84-0.89)	1.05×10^{-26}	0.63	98%
17	rs1565923	37,858,678	A/G	0.70	0.86 (0.84-0.89)	2.09×10^{-25}	0.86 (0.84-0.89)	2.09×10^{-25}	0.50	93%
17	rs2952155	37,861,718	T/C	0.76	0.86 (0.83-0.88)	2.80×10^{-24}	0.86 (0.83-0.88)	2.80×10^{-24}	0.76	98%
17	rs1810132	37,866,005	C/T	0.70	0.86 (0.84-0.88)	7.92×10^{-29}	0.86 (0.84-0.88)	7.92×10^{-29}	0.54	98%
17	rs2952156	37,876,835	A/G	0.70	0.86 (0.84-0.88)	7.55×10^{-29}	0.86 (0.84-0.88)	7.55×10^{-29}	0.55	98%
17	rs907091	37,921,742	C/T	0.48	1.18 (1.14-1.22)	2.00×10^{-20}	1.19 (1.15-1.22)	1.12×10^{-36}	0.01	95%
17	rs907092	37,922,259	G/A	0.48	0.86 (0.83-0.89)	1.55×10^{-18}	0.85 (0.83-0.88)	2.16×10^{-32}	0.01	96%
17	rs10445308	37,938,047	C/T	0.48	0.85 (0.83-0.88)	6.58×10^{-19}	0.85 (0.83-0.87)	3.99×10^{-34}	0.01	98%
17	rs9909593	37,970,149	A/G	0.48	0.86 (0.83-0.89)	1.14×10^{-18}	0.85 (0.83-0.88)	4.16×10^{-34}	0.01	98%
17	rs9303277	37,976,469	C/T	0.52	0.84 (0.82-0.87)	5.43×10^{-22}	0.84 (0.82-0.86)	1.18×10^{-40}	0.01	98%
17	rs3816470	37,985,801	A/G	0.53	0.85 (0.82-0.88)	1.23×10^{-21}	0.84 (0.82-0.86)	2.79×10^{-38}	0.02	96%
17	rs9635726	38,020,141	C/T	0.20	1.17 (1.14-1.21)	1.50×10^{-22}	1.17 (1.14-1.21)	1.50×10^{-22}	0.54	96%
17	rs4795397	38,023,745	A/G	0.48	0.86 (0.83-0.9)	6.09×10^{-15}	0.86 (0.84-0.88)	2.15×10^{-27}	0.01	89%
17	rs11557466	38,024,626	C/T	0.47	0.86 (0.83-0.89)	2.37×10^{-18}	0.85 (0.83-0.88)	6.18×10^{-32}	0.02	95%
17	rs11078925	38,025,208	T/C	0.47	0.86 (0.83-0.88)	2.29×10^{-20}	0.85 (0.83-0.88)	1.01×10^{-33}	0.03	98%
17	rs12150079	38,025,417	G/A	0.32	0.88 (0.85-0.91)	9.80×10^{-13}	0.88 (0.85-0.9)	1.12×10^{-19}	0.05	96%
17	rs11557467	38,028,634	G/T	0.52	0.85 (0.82-0.88)	9.94×10^{-19}	0.85 (0.83-0.87)	1.39×10^{-29}	0.04	88%
17	rs10852936	38,031,714	C/T	0.47	0.86 (0.83-0.89)	1.84×10^{-15}	0.86 (0.83-0.88)	2.00×10^{-26}	0.02	88%
17	rs1054609	38,033,277	A/C	0.47	0.85 (0.83-0.88)	5.07×10^{-20}	0.85 (0.83-0.87)	8.20×10^{-34}	0.02	96%
17	rs9907088	38,035,116	G/A	0.47	0.86 (0.83-0.88)	2.32×10^{-20}	0.85 (0.83-0.88)	6.85×10^{-34}	0.02	98%
17	rs12232497	38,040,119	T/C	0.47	0.86 (0.83-0.88)	2.39×10^{-20}	0.85 (0.83-0.88)	5.47×10^{-34}	0.02	98%
17	rs2872507	38,040,763	G/A	0.47	0.85 (0.83-0.88)	2.76×10^{-20}	0.85 (0.83-0.88)	5.24×10^{-34}	0.02	98%
17	rs9901146	38,043,343	G/A	0.52	0.84 (0.82-0.87)	3.29×10^{-25}	0.84 (0.82-0.86)	1.87×10^{-40}	0.04	98%
17	rs12950743	38,049,233	T/C	0.52	0.84 (0.82-0.87)	2.66×10^{-25}	0.84 (0.82-0.86)	1.75×10^{-40}	0.04	98%
17	rs7359623	38,049,589	C/T	0.51	0.84 (0.82-0.87)	1.16×10^{-23}	0.84 (0.82-0.86)	2.16×10^{-37}	0.05	95%
17	rs8067378	38,051,348	A/G	0.52	0.84 (0.82-0.87)	2.57×10^{-25}	0.84 (0.82-0.86)	2.78×10^{-40}	0.04	98%
17	rs8069176	38,057,197	G/A	0.47	0.85 (0.82-0.88)	1.67×10^{-19}	0.85 (0.83-0.87)	2.92×10^{-36}	0.01	98%
17	rs2305480	38,062,196	G/A	0.46	0.85 (0.82-0.88)	5.62×10^{-19}	0.85 (0.83-0.87)	3.18×10^{-36}	0.00	98%
17	rs2305479	38,062,217	C/T	0.51	0.84 (0.81-0.87)	9.31×10^{-24}	0.84 (0.82-0.86)	1.00×10^{-42}	0.01	98%
17	rs11078926	38,062,976	G/A	0.46	0.85 (0.82-0.89)	6.81×10^{-15}	0.85 (0.83-0.88)	7.13×10^{-29}	0.00	88%
17	rs11078927	38,064,405	C/T	0.46	0.85 (0.82-0.88)	2.31×10^{-19}	0.85 (0.83-0.87)	4.21×10^{-36}	0.01	98%
17	rs2290400	38,066,240	T/C	0.51	0.84 (0.81-0.87)	8.25×10^{-24}	0.84 (0.82-0.86)	1.03×10^{-42}	0.01	98%
17	rs1008723	38,066,267	G/T	0.51	0.84 (0.81-0.87)	3.29×10^{-23}	0.84 (0.82-0.86)	6.29×10^{-42}	0.01	98%
17	rs4795400	38,067,020	C/T	0.47	0.85 (0.82-0.88)	9.86×10^{-19}	0.85 (0.83-0.87)	1.25×10^{-35}	0.00	98%
17	rs869402	38,068,043	T/C	0.49	1.19 (1.15-1.23)	1.35×10^{-21}	1.19 (1.16-1.22)	8.01×10^{-41}	0.01	96%
17	rs7216389	38,069,949	C/T	0.49	1.19 (1.15-1.23)	3.16×10^{-21}	1.2 (1.16-1.23)	2.51×10^{-42}	0.00	98%
17	rs9303280	38,074,031	T/C	0.50	1.18 (1.14-1.23)	6.44×10^{-19}	1.19 (1.16-1.22)	1.38×10^{-38}	0.00	96%
17	rs9303281	38,074,046	G/A	0.48	1.19 (1.15-1.23)	2.49×10^{-21}	1.2 (1.16-1.23)	2.91×10^{-42}	0.00	98%
17	rs7219923	38,074,518	C/T	0.48	1.19 (1.15-1.23)	2.23×10^{-21}	1.2 (1.16-1.23)	2.81×10^{-42}	0.00	98%
17	rs7224129	38,075,426	G/A	0.48	1.19 (1.15-1.23)	1.90×10^{-21}	1.2 (1.17-1.23)	2.45×10^{-42}	0.00	98%
17	rs4378650	38,080,865	A/G	0.51	1.19 (1.14-1.24)	8.37×10^{-17}	1.21 (1.18-1.25)	2.09×10^{-40}	0.00	84%
17	rs8076131	38,080,912	G/A	0.54	1.17 (1.13-1.22)	1.85×10^{-16}	1.18 (1.15-1.21)	2.44×10^{-34}	0.00	96%
17	rs12603332	38,082,807	T/C	0.51	1.18 (1.14-1.22)	3.06×10^{-18}	1.19 (1.16-1.22)	1.01×10^{-37}	0.00	96%
17	rs4795405	38,088,417	T/C	0.55	1.17 (1.13-1.21)	1.66×10^{-16}	1.18 (1.15-1.21)	1.39×10^{-39}	0.00	98%
17	rs4794820	38,089,344	A/G	0.56	1.17 (1.12-1.21)	1.52×10^{-15}	1.18 (1.14-1.21)	8.05×10^{-32}	0.00	95%
17	rs7207600	38,091,660	G/A	0.63	1.15 (1.11-1.19)	1.17×10^{-17}	1.16 (1.13-1.19)	4.72×10^{-29}	0.07	100%
17	rs8079416	38,092,713	T/C	0.44	1.17 (1.13-1.2)	1.45×10^{-22}	1.17 (1.14-1.2)	1.43×10^{-35}	0.08	98%

Chrom	SNP	Position	Allele (R/E)	EAF[a]	OR_{random} (95% CI)[b]	P_{random}[c]	OR_{fixed} (95% CI)[b]	P_{fixed}[d]	P_{het}[e]	% of studies contributing to meta-analysis (per SNP)
17	rs8065126	38,099,035	T/C	0.63	1.15 (1.11-1.18)	9.91×10^{-18}	1.16 (1.13-1.19)	1.79×10^{-27}	0.11	98%
17	rs4795408	38,107,627	G/A	0.44	1.17 (1.13-1.2)	2.00×10^{-21}	1.17 (1.15-1.2)	2.12×10^{-36}	0.05	98%
17	rs9895948	38,108,363	T/C	0.64	1.14 (1.1-1.18)	3.69×10^{-14}	1.15 (1.12-1.18)	1.38×10^{-24}	0.07	91%
17	rs17609240	38,110,689	T/G	0.64	1.14 (1.1-1.18)	6.19×10^{-13}	1.15 (1.12-1.19)	2.86×10^{-24}	0.03	91%
17	rs1007654	38,111,354	A/G	0.64	1.14 (1.11-1.18)	9.11×10^{-18}	1.15 (1.12-1.18)	3.77×10^{-26}	0.15	98%
17	rs1007655	38,111,419	G/A	0.63	1.14 (1.1-1.18)	8.70×10^{-14}	1.15 (1.12-1.19)	1.80×10^{-23}	0.10	88%
17	rs2313640	38,111,845	C/T	0.64	1.14 (1.11-1.18)	8.19×10^{-18}	1.15 (1.12-1.18)	2.96×10^{-26}	0.15	98%
17	rs7218742	38,114,361	A/G	0.64	1.14 (1.11-1.18)	4.27×10^{-18}	1.15 (1.12-1.18)	1.94×10^{-26}	0.16	98%
17	rs7218321	38,114,469	C/T	0.64	1.14 (1.11-1.18)	5.22×10^{-16}	1.15 (1.12-1.18)	3.33×10^{-25}	0.11	95%
17	rs7219080	38,114,516	A/C	0.64	1.14 (1.11-1.18)	4.14×10^{-17}	1.15 (1.12-1.18)	4.90×10^{-26}	0.13	98%
17	rs6503526	38,114,598	C/T	0.44	1.16 (1.13-1.2)	5.82×10^{-21}	1.17 (1.14-1.2)	2.27×10^{-35}	0.05	98%
17	rs6503527	38,114,719	G/A	0.64	1.14 (1.1-1.18)	1.35×10^{-13}	1.15 (1.12-1.18)	4.70×10^{-23}	0.09	89%
17	rs3902025	38,119,254	G/T	0.56	1.15 (1.11-1.19)	3.36×10^{-16}	1.16 (1.13-1.19)	8.34×10^{-31}	0.02	98%
17	rs3894194	38,121,993	G/A	0.44	1.16 (1.12-1.2)	8.43×10^{-20}	1.17 (1.14-1.2)	1.06×10^{-34}	0.03	98%
17	rs7212938	38,122,680	G/T	0.55	0.86 (0.83-0.88)	2.65×10^{-20}	0.85 (0.83-0.88)	7.78×10^{-33}	0.05	96%
17	rs3859192	38,128,648	C/T	0.47	1.15 (1.11-1.18)	1.09×10^{-18}	1.15 (1.12-1.18)	5.38×10^{-28}	0.11	96%
17	rs8075668	38,137,623	C/T	0.46	0.89 (0.87-0.91)	1.07×10^{-20}	0.89 (0.87-0.91)	1.07×10^{-20}	0.66	96%
17	rs2305481	38,138,624	G/A	0.37	0.89 (0.87-0.91)	9.27×10^{-20}	0.89 (0.87-0.91)	9.27×10^{-20}	0.56	100%
17	rs2305482	38,140,927	A/C	0.54	0.92 (0.9-0.94)	7.12×10^{-11}	0.92 (0.9-0.94)	7.12×10^{-11}	0.60	100%
17	rs11078930	38,141,955	C/T	0.35	0.88 (0.85-0.9)	1.49×10^{-20}	0.88 (0.85-0.9)	1.49×10^{-20}	0.65	93%
17	rs4065321	38,143,548	C/T	0.54	0.92 (0.9-0.94)	2.17×10^{-11}	0.92 (0.9-0.94)	2.17×10^{-11}	0.60	96%
17	rs8066582	38,146,929	T/C	0.54	0.92 (0.9-0.94)	8.53×10^{-11}	0.92 (0.9-0.94)	8.53×10^{-11}	0.55	100%
17	rs11658328	38,149,236	T/C	0.54	0.92 (0.9-0.94)	7.43×10^{-11}	0.92 (0.9-0.94)	7.43×10^{-11}	0.62	100%
17	rs2241245	38,151,014	C/T	0.54	0.92 (0.9-0.94)	4.72×10^{-11}	0.92 (0.9-0.94)	4.72×10^{-11}	0.57	100%
17	rs12453334	38,153,473	C/T	0.37	0.89 (0.87-0.91)	2.56×10^{-19}	0.89 (0.87-0.91)	2.56×10^{-19}	0.54	100%
17	rs4794822	38,156,712	C/T	0.38	1.11 (1.08-1.14)	5.96×10^{-12}	1.11 (1.08-1.14)	9.99×10^{-17}	0.13	100%
17	rs8070454	38,160,754	C/T	0.38	1.11 (1.08-1.14)	8.97×10^{-12}	1.11 (1.08-1.14)	1.04×10^{-16}	0.12	100%
17	rs8078723	38,166,879	T/C	0.38	1.11 (1.08-1.14)	1.29×10^{-11}	1.11 (1.08-1.14)	1.03×10^{-16}	0.11	100%
17	rs2227319	38,170,845	G/A	0.37	0.89 (0.87-0.91)	6.20×10^{-20}	0.89 (0.87-0.91)	6.20×10^{-20}	0.58	100%
17	rs25645	38,173,143	G/A	0.36	0.89 (0.86-0.91)	5.18×10^{-20}	0.89 (0.86-0.91)	5.18×10^{-20}	0.50	100%
17	rs1042658	38,173,902	C/T	0.38	1.11 (1.08-1.14)	3.45×10^{-12}	1.11 (1.09-1.14)	6.28×10^{-17}	0.14	100%
17	rs1045929	38,175,426	C/T	0.38	1.11 (1.07-1.15)	8.53×10^{-10}	1.11 (1.08-1.14)	2.76×10^{-14}	0.12	89%
17	rs12309	38,175,462	C/T	0.37	0.88 (0.86-0.91)	1.43×10^{-17}	0.88 (0.86-0.91)	4.83×10^{-18}	0.46	89%
17	rs709592	38,175,553	C/T	0.38	1.11 (1.08-1.14)	3.75×10^{-12}	1.11 (1.09-1.14)	7.06×10^{-17}	0.14	100%
17	rs2302776	38,178,149	A/G	0.45	0.91 (0.88-0.93)	4.38×10^{-13}	0.91 (0.88-0.93)	4.38×10^{-13}	0.83	96%
17	rs3213762	38,178,627	A/G	0.38	1.11 (1.08-1.15)	4.78×10^{-12}	1.12 (1.09-1.15)	3.11×10^{-17}	0.12	96%
17	rs12451897	38,179,275	G/T	0.37	0.89 (0.87-0.91)	1.36×10^{-17}	0.89 (0.87-0.91)	1.36×10^{-17}	0.49	91%
17	rs2302777	38,179,492	A/G	0.37	0.89 (0.86-0.91)	1.69×10^{-20}	0.89 (0.86-0.91)	1.69×10^{-20}	0.64	100%
17	rs9916158	38,182,229	G/T	0.37	0.89 (0.87-0.91)	7.10×10^{-18}	0.89 (0.87-0.91)	7.10×10^{-18}	0.50	93%
17	rs2302774	38,183,090	G/T	0.38	0.89 (0.86-0.91)	3.59×10^{-20}	0.89 (0.86-0.91)	3.59×10^{-20}	0.56	98%
17	rs7502514	38,188,844	A/G	0.62	0.9 (0.87-0.93)	8.15×10^{-12}	0.89 (0.87-0.92)	7.68×10^{-17}	0.13	96%
17	rs3935280	38,189,055	A/G	0.62	0.9 (0.87-0.93)	2.00×10^{-9}	0.9 (0.87-0.92)	4.94×10^{-14}	0.11	86%
17	rs11078936	38,197,914	T/C	0.37	0.89 (0.87-0.92)	7.28×10^{-18}	0.89 (0.87-0.92)	7.28×10^{-18}	0.67	98%
17	rs8065443	38,208,940	A/G	0.59	0.9 (0.88-0.93)	1.07×10^{-11}	0.9 (0.88-0.93)	3.27×10^{-15}	0.19	98%
17	rs868150	38,213,359	A/G	0.59	0.9 (0.88-0.93)	6.71×10^{-12}	0.9 (0.88-0.93)	2.73×10^{-15}	0.20	98%
17	rs17637472	47,461,433	G/A	0.39	1.08 (1.05-1.11)	3.28×10^{-9}	1.08 (1.05-1.11)	3.28×10^{-9}	0.56	98%
17	rs2671659	47,474,529	G/A	0.37	0.92 (0.9-0.95)	7.59×10^{-9}	0.92 (0.9-0.95)	3.70×10^{-9}	0.45	96%

[a]EAF = Effect allele frequency

[b]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele (random & fixed-effects models)

[c]P_{random} is P-value for test of association between SNP and asthma under a random-effects model

[d]P_{fixed} is P-value for test of association between SNP and asthma under a fixed-effects model

[e]P_{het} is the P-value for test of heterogeneity across studies with the use of Cochran's test

Supplementary Table 5. Genetic loci associated with asthma in African ancestry meta-analysis

Results are shown for the lead SNP at each locus reaching $P_{fixed} < 10^{-5}$

Region[a]	Lead SNP	Position	Nearby genes[b]	Allele (R/E)[c]	EAF[d]	OR (95%CI)[e]	P_{fixed}[f]	P_{het}[g]
1p3.1	rs10157802	74,110,649	NEGR1,LRRIQ3	G/A	0.82	0.78 (0.69-0.87)	7.32×10^{-6}	0.66
1q23.3	rs1348135	163,776,298	NUF2,PBX1	C/T	0.05	0.57 (0.44-0.73)	8.76×10^{-6}	0.28
1q42.3	rs10924970	235,362,960	ARID4B,RBM34,GGPS1	T/C	0.61	1.25 (1.14-1.37)	2.87×10^{-6}	0.58
2p23.3	rs4268898	24,490,413	ITSN2,C2orf84,NCOA1	C/T	0.56	0.79 (0.73-0.87)	1.93×10^{-7}	0.48
3p24.2	rs12634582	24,282,432	THRB,NR1D2,RARB	T/C	0.38	1.26 (1.14-1.40)	9.02×10^{-6}	0.88
3p22.3	rs9870718	36,239,406	ARPP21,STAC	C/T	0.36	0.81 (0.74-0.89)	8.71×10^{-6}	0.75
7p14.1	rs10233459	42,040,986	GLI3,INHBA,C7orf25	A/G	0.05	1.57 (1.30-1.91)	4.16×10^{-6}	0.51
11q23.2	rs4938096	114,235,730	NNMT,C11orf71	C/T	0.21	1.30 (1.17-1.44)	1.13×10^{-6}	0.31
12q24.33	rs10773588	129,511,610	GLT1D1,TMEM132D	G/T	0.06	0.59 (0.47-0.74)	4.47×10^{-6}	0.29
14q12	rs10141207	32,691,785	ARHGAP5,AKAP6	G/A	0.35	1.24 (1.13-1.36)	3.93×10^{-6}	0.40
20q13.12	rs16989837	43,859,099	SLP1,SEMG2	C/T	0.10	1.39 (1.21-1.60)	3.11×10^{-6}	0.13

[a]Cytogenetic position of the chromosomal region harboring the lead SNP

[b]Genes coding for proteins; the gene where eventually the lead SNP lies is first indicated followed by the previous gene and next gene

[c]R=reference allele /E=effect allele.

[d]EAF = Effect allele frequency

[e]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele under a fixed-effects model

[f]P_{fixed} is the *P*-value for test of association between SNP and asthma under a fixed-effects model

[g]P_{het} is the *P*-value for test of heterogeneity across studies with the use of Cochran's test

Supplementary Table 6. Genetic loci associated with asthma in Japanese meta-analysis

Results are shown for the lead SNP at each locus reaching $P_{fixed} < 10^{-5}$

Region[a]	Lead SNP	Position	Nearby genes[b]	Allele (R/E)[c]	EAF[d]	OR (95%CI)[e]	P_{fixed}[f]	P_{het}[g]
1q32.1	rs1122396	201,138,428	TMEM9,IGFN1	G/A	0.51	0.76 (0.68-0.85)	1.46×10^{-6}	0.83
7p14.3	rs10951405	34,043,348	BMPER,BBS9,NPSR1	C/T	0.89	1.44 (1.24-1.68)	2.8×10^{-6}	0.28
11q22.1	rs3758697	100,709,894	ARHGAP42,CNTN5,TMEM133	G/A	0.30	1.33 (1.18-1.50)	2.4×10^{-6}	0.20
20p13	rs6084352	3,348,407	C20orf194, SLC4A11, ATRN	A/G	0.30	1.31 (1.16-1.47)	6.61×10^{-6}	0.77

[a]Cytogenetic position of the chromosomal region harboring the lead SNP
[b]Genes coding for proteins; the gene where eventually the lead SNP lies is first indicated followed by the previous gene and next gene
[c]R=reference allele /E=effect allele. [d]EAF = Effect allele frequency
[e]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele under a fixed-effects model
[f]P_{fixed} is the P-value for test of association between SNP and asthma under a fixed-effects model
[g]P_{het} is the P-value for test of heterogeneity across studies using the Cochran's test

Supplementary Table 7. Genetic loci associated with asthma in Latinos

Results are shown for the lead SNP at each locus reaching $P < 10^{-5}$

Region[a]	Lead SNP	Position	Nearby genes[b]	Allele (R/E)[c]	EAF[d]	OR (95%CI)[e]	P[f]
1p31.1	rs2352521	79,256,105	IFI44,ELTD1	C/T	0.72	1.66(1.33-2.06)	4.95×10^{-6}
1q31.3	rs6694672	196,945,789	CFHR2,CFHR5	T/G	0.05	2.13(1.52-2.97)	9.41×10^{-6}
5p13.2	rs12521260	37,881,414	GDNF,EGFLAM	G/T	0.28	1.52(1.27-1.81)	3.04×10^{-6}
8q23.3	rs12542922	117,333,797	TRPS1,EIF3H	A/G	0.28	0.61(0.49-0.74)	1.67×10^{-6}
8q24.12	rs2073617	119,964,283	TNFRSF11B,SAMD12,COLEC10	G/A	0.37	1.46(1.24-1.71)	4.69×10^{-6}
19q13.31	rs4802207	44,600,377	ZNF224,ZNF284,ZNF225	C/T	0.59	0.68(0.57-0.81)	9.51×10^{-6}
21q21.1	rs2825968	21,415,693	TMPRSS15,NCAM2	T/C	0.51	0.69(0.59-0.81)	5.8×10^{-6}

[a]Cytogenetic position of the chromosomal region harboring the lead SNP
[b]Genes coding for proteins; the gene where eventually the lead SNP lies is first indicated followed by the previous gene and next gene
[c]R=reference allele /E=effect allele. [d]EAF = Effect allele frequency
[e]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele
[f]P for test of association between SNP and asthma

Supplementary Table 8. SNPs with $P_{random} \leq 10^{-8}$ in the multi-ancestry meta-analysis

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
2	rs1465325	102,734,551	A/G	0.88 (0.85-0.91)	5.6×10^{-12}	0.88 (0.85-0.91)	3.5×10^{-15}	0.20	100%
2	rs1465324	102,735,612	G/A	0.89 (0.86-0.93)	2.6×10^{-10}	0.89 (0.87-0.92)	2.1×10^{-13}	0.19	100%
2	rs12328681	102,736,867	G/T	0.90 (0.87-0.93)	2.0×10^{-10}	0.89 (0.87-0.92)	4.3×10^{-13}	0.22	100%
2	rs10172039	102,738,785	C/A	0.90 (0.87-0.93)	8.1×10^{-11}	0.89 (0.87-0.92)	1.9×10^{-13}	0.24	100%
2	rs12619383	102,741,718	A/G	0.88 (0.85-0.92)	3.0×10^{-11}	0.88 (0.86-0.91)	6.6×10^{-15}	0.15	100%
2	rs12620132	102,742,115	A/G	0.88 (0.85-0.92)	2.0×10^{-11}	0.88 (0.86-0.91)	4.3×10^{-15}	0.15	100%
2	rs13392285	102,744,338	C/A	0.89 (0.86-0.92)	5.9×10^{-12}	0.89 (0.86-0.92)	3.3×10^{-14}	0.29	100%
2	rs13387400	102,750,020	G/A	0.88 (0.85-0.91)	1.2×10^{-11}	0.88 (0.85-0.91)	2.2×10^{-15}	0.16	100%
2	rs1558641	102,765,865	G/A	0.89 (0.85-0.92)	2.4×10^{-09}	0.88 (0.86-0.91)	2.9×10^{-14}	0.06	100%
2	rs1558640	102,765,878	G/A	0.88 (0.85-0.92)	3.0×10^{-11}	0.88 (0.85-0.91)	1.4×10^{-15}	0.10	100%
2	rs949963	102,769,786	C/T	0.89 (0.86-0.92)	2.3×10^{-10}	0.89 (0.86-0.91)	2.7×10^{-15}	0.05	100%
2	rs871657	102,771,341	C/T	0.89 (0.86-0.92)	5.4×10^{-11}	0.89 (0.86-0.91)	7.9×10^{-16}	0.08	100%
2	rs2287048	102,773,999	C/T	0.89 (0.85-0.92)	5.5×10^{-10}	0.88 (0.86-0.91)	1.5×10^{-14}	0.08	100%
2	rs951192	102,785,854	A/C	0.92 (0.90-0.95)	2.4×10^{-09}	0.92 (0.90-0.95)	1.3×10^{-09}	0.44	100%
2	rs1030021	102,801,478	A/C	0.93 (0.90-0.95)	5.3×10^{-09}	0.93 (0.90-0.95)	3.9×10^{-09}	0.46	100%
2	rs10189629	102,879,464	C/A	0.85 (0.82-0.89)	7.1×10^{-13}	0.86 (0.83-0.89)	3.2×10^{-17}	0.06	98%
2	rs11692065	102,883,975	C/T	0.85 (0.82-0.89)	4.3×10^{-13}	0.86 (0.83-0.89)	2.6×10^{-17}	0.07	98%
2	rs11674302	102,887,128	T/C	0.85 (0.82-0.89)	3.2×10^{-12}	0.86 (0.83-0.89)	2.4×10^{-17}	0.03	98%
2	rs11690644	102,914,214	A/G	0.84 (0.80-0.88)	2.9×10^{-13}	0.84 (0.81-0.87)	4.9×10^{-20}	0.05	88%
2	rs950880	102,932,562	C/A	1.11 (1.08-1.14)	2.6×10^{-17}	1.11 (1.09-1.14)	8.3×10^{-19}	0.41	100%
2	rs13001325	102,939,036	C/T	1.11 (1.08-1.14)	3.6×10^{-17}	1.11 (1.09-1.14)	7.0×10^{-19}	0.40	100%
2	rs12479210	102,949,161	C/T	1.11 (1.09-1.14)	1.3×10^{-17}	1.11 (1.09-1.14)	5.1×10^{-19}	0.41	100%
2	rs13019081	102,950,822	A/C	1.11 (1.09-1.14)	1.3×10^{-17}	1.11 (1.09-1.14)	4.9×10^{-19}	0.41	100%
2	rs17026974	102,952,360	G/A	1.10 (1.07-1.13)	3.5×10^{-13}	1.10 (1.07-1.13)	3.5×10^{-13}	0.59	100%
2	rs3771180	102,953,617	G/T	0.83 (0.80-0.87)	1.7×10^{-18}	0.84 (0.81-0.86)	7.6×10^{-26}	0.05	100%
2	rs13431828	102,954,653	C/T	0.84 (0.81-0.87)	1.2×10^{-18}	0.84 (0.81-0.87)	2.0×10^{-24}	0.10	100%
2	rs13408661	102,955,082	G/A	0.83 (0.80-0.87)	2.1×10^{-18}	0.84 (0.81-0.87)	2.9×10^{-25}	0.06	100%
2	rs873022	102,955,683	G/T	1.10 (1.07-1.13)	2.6×10^{-13}	1.10 (1.07-1.13)	2.6×10^{-13}	0.57	100%
2	rs3771177	102,955,860	G/T	1.10 (1.07-1.13)	2.5×10^{-13}	1.10 (1.07-1.13)	2.5×10^{-13}	0.57	100%
2	rs10173081	102,957,348	C/T	0.83 (0.80-0.87)	1.9×10^{-18}	0.84 (0.81-0.87)	2.6×10^{-25}	0.06	100%
2	rs3732129	102,957,532	T/C	1.10 (1.07-1.13)	3.2×10^{-13}	1.10 (1.07-1.13)	3.2×10^{-13}	0.56	100%
2	rs1420101	102,957,716	C/T	1.12 (1.09-1.15)	3.9×10^{-21}	1.12 (1.09-1.15)	3.9×10^{-21}	0.61	100%
2	rs12905	102,960,007	G/A	1.10 (1.07-1.13)	4.0×10^{-13}	1.10 (1.07-1.13)	4.0×10^{-13}	0.55	100%
2	rs12712142	102,960,584	C/A	1.12 (1.09-1.14)	1.5×10^{-18}	1.12 (1.09-1.14)	1.9×10^{-20}	0.38	98%
2	rs2160203	102,960,824	A/G	0.88 (0.85-0.91)	1.4×10^{-16}	0.88 (0.85-0.91)	1.4×10^{-16}	0.58	85%
2	rs13017455	102,964,742	C/T	1.12 (1.09-1.14)	1.0×10^{-19}	1.12 (1.09-1.14)	2.7×10^{-20}	0.45	100%
2	rs12469506	102,965,871	C/T	1.11 (1.08-1.14)	2.0×10^{-14}	1.11 (1.08-1.14)	9.4×10^{-15}	0.45	97%
2	rs1921622	102,966,067	G/A	1.09 (1.06-1.11)	2.4×10^{-12}	1.09 (1.06-1.11)	1.1×10^{-12}	0.45	100%
2	rs10208293	102,966,310	G/A	0.88 (0.85-0.92)	3.6×10^{-12}	0.88 (0.86-0.91)	9.8×10^{-21}	0.00	100%
2	rs10197862	102,966,549	A/G	0.84 (0.80-0.87)	4.0×10^{-17}	0.84 (0.81-0.87)	1.7×10^{-24}	0.04	100%
2	rs1861245	102,966,906	C/T	0.90 (0.87-0.92)	1.1×10^{-14}	0.90 (0.88-0.92)	3.5×10^{-18}	0.17	100%
2	rs13424006	102,967,236	T/C	0.89 (0.87-0.91)	1.2×10^{-16}	0.89 (0.87-0.91)	1.7×10^{-21}	0.16	100%
2	rs6751967	102,967,413	T/C	0.89 (0.87-0.91)	1.2×10^{-16}	0.89 (0.87-0.91)	1.6×10^{-21}	0.16	100%
2	rs6749114	102,967,587	A/C	0.89 (0.87-0.92)	1.1×10^{-16}	0.89 (0.87-0.91)	2.0×10^{-21}	0.16	100%
2	rs11123923	102,967,844	C/A	1.11 (1.08-1.14)	6.8×10^{-15}	1.11 (1.09-1.14)	9.0×10^{-19}	0.25	100%
2	rs4988955	102,967,928	A/G	0.89 (0.87-0.92)	7.7×10^{-17}	0.89 (0.87-0.91)	2.6×10^{-21}	0.18	100%
2	rs4988956	102,968,007	G/A	0.89 (0.87-0.91)	4.4×10^{-17}	0.89 (0.87-0.91)	1.5×10^{-21}	0.19	100%
2	rs4988957	102,968,075	T/C	0.89 (0.87-0.92)	7.6×10^{-17}	0.89 (0.87-0.91)	2.0×10^{-21}	0.18	100%
2	rs10204137	102,968,212	A/G	0.89 (0.86-0.92)	9.6×10^{-13}	0.89 (0.87-0.92)	1.8×10^{-17}	0.11	85%
2	rs4988958	102,968,285	T/C	0.89 (0.87-0.92)	7.5×10^{-17}	0.89 (0.87-0.91)	1.9×10^{-21}	0.18	100%
2	rs10192157	102,968,356	C/T	0.89 (0.87-0.92)	6.6×10^{-17}	0.89 (0.87-0.91)	2.3×10^{-21}	0.18	100%
2	rs10206753	102,968,362	T/C	0.89 (0.87-0.92)	1.8×10^{-12}	0.89 (0.87-0.92)	9.7×10^{-17}	0.14	83%
2	rs7603730	102,974,371	A/C	0.89 (0.87-0.91)	3.9×10^{-17}	0.89 (0.87-0.91)	7.4×10^{-22}	0.17	100%
2	rs12998521	102,974,417	G/T	1.11 (1.08-1.14)	7.2×10^{-13}	1.11 (1.08-1.14)	3.1×10^{-17}	0.18	98%
2	rs10170583	102,974,764	G/A	0.89 (0.86-0.91)	1.8×10^{-16}	0.89 (0.87-0.91)	1.0×10^{-21}	0.14	100%
2	rs10176664	102,976,172	G/A	0.89 (0.86-0.91)	2.8×10^{-17}	0.89 (0.87-0.91)	2.0×10^{-22}	0.15	100%
2	rs3755276	102,978,459	C/T	0.89 (0.86-0.91)	3.0×10^{-17}	0.89 (0.87-0.91)	2.1×10^{-22}	0.15	100%
2	rs2287037	102,979,028	C/T	1.12 (1.09-1.14)	7.9×10^{-20}	1.12 (1.09-1.14)	3.1×10^{-20}	0.46	100%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
2	rs3771172	102,985,812	C/T	1.10 (1.08-1.13)	6.1×10^{-14}	1.10 (1.08-1.13)	2.5×10^{-14}	0.45	100%
2	rs3771171	102,985,950	T/C	1.10 (1.07-1.13)	4.7×10^{-13}	1.10 (1.08-1.13)	4.2×10^{-14}	0.39	97%
2	rs2160202	102,986,154	G/A	1.10 (1.08-1.13)	4.8×10^{-13}	1.10 (1.08-1.13)	4.1×10^{-14}	0.39	97%
2	rs3771166	102,986,222	G/A	0.88 (0.86-0.90)	1.1×10^{-21}	0.88 (0.86-0.90)	1.1×10^{-23}	0.37	95%
2	rs1974675	102,986,375	G/A	0.88 (0.86-0.90)	1.3×10^{-21}	0.88 (0.86-0.90)	1.1×10^{-23}	0.37	95%
2	rs10439410	102,990,788	G/T	0.91 (0.89-0.94)	2.2×10^{-12}	0.92 (0.90-0.94)	1.1×10^{-13}	0.32	100%
2	rs6758936	102,991,369	G/A	0.91 (0.89-0.94)	2.0×10^{-12}	0.92 (0.90-0.94)	1.3×10^{-13}	0.33	100%
2	rs2041739	102,994,333	C/T	0.91 (0.89-0.94)	1.7×10^{-12}	0.92 (0.90-0.94)	1.3×10^{-13}	0.34	100%
2	rs17027037	102,994,884	A/G	1.10 (1.08-1.13)	1.9×10^{-14}	1.10 (1.08-1.13)	1.9×10^{-14}	0.62	100%
2	rs2080289	102,995,020	G/A	1.10 (1.08-1.13)	2.1×10^{-14}	1.10 (1.08-1.13)	2.1×10^{-14}	0.63	100%
2	rs10208196	102,996,345	G/A	0.92 (0.89-0.94)	1.6×10^{-12}	0.92 (0.90-0.94)	1.4×10^{-13}	0.35	100%
2	rs11683700	102,996,805	C/T	1.10 (1.07-1.13)	1.6×10^{-12}	1.10 (1.07-1.13)	1.0×10^{-13}	0.38	97%
2	rs3213733	102,997,884	C/A	0.88 (0.85-0.91)	4.7×10^{-12}	0.88 (0.86-0.91)	1.6×10^{-15}	0.09	100%
2	rs3213732	102,998,279	A/G	0.92 (0.89-0.94)	1.5×10^{-12}	0.92 (0.90-0.94)	1.3×10^{-13}	0.35	100%
2	rs6760621	102,999,952	T/C	0.91 (0.89-0.94)	3.6×10^{-11}	0.91 (0.89-0.94)	4.7×10^{-12}	0.37	80%
2	rs1035130	103,001,402	C/T	1.10 (1.08-1.13)	1.6×10^{-14}	1.10 (1.08-1.13)	1.6×10^{-14}	0.64	100%
2	rs3771161	103,003,961	C/A	0.87 (0.84-0.91)	4.1×10^{-09}	0.88 (0.85-0.91)	8.6×10^{-13}	0.04	82%
2	rs6706002	103,006,104	A/G	0.91 (0.89-0.94)	1.6×10^{-12}	0.92 (0.90-0.94)	1.0×10^{-13}	0.33	100%
2	rs4851570	103,006,387	A/G	1.10 (1.08-1.13)	1.4×10^{-14}	1.10 (1.08-1.13)	1.4×10^{-14}	0.58	100%
2	rs6749014	103,006,448	C/T	0.92 (0.89-0.94)	1.4×10^{-10}	0.92 (0.89-0.94)	7.0×10^{-12}	0.31	83%
2	rs4851004	103,009,537	C/T	0.92 (0.89-0.94)	5.9×10^{-13}	0.92 (0.90-0.94)	8.7×10^{-14}	0.38	100%
2	rs3771158	103,009,894	A/G	0.88 (0.85-0.91)	8.2×10^{-12}	0.88 (0.86-0.91)	2.9×10^{-15}	0.08	100%
2	rs2287034	103,010,588	C/A	1.10 (1.07-1.13)	6.0×10^{-14}	1.10 (1.07-1.13)	6.0×10^{-14}	0.55	100%
2	rs2287033	103,011,237	T/C	0.91 (0.89-0.94)	5.6×10^{-13}	0.92 (0.89-0.94)	8.2×10^{-14}	0.38	100%
2	rs1135354	103,014,302	T/G	1.10 (1.07-1.14)	1.2×10^{-11}	1.10 (1.07-1.13)	1.2×10^{-12}	0.39	80%
2	rs1420094	103,015,687	C/T	0.92 (0.89-0.94)	4.3×10^{-13}	0.92 (0.90-0.94)	1.2×10^{-13}	0.41	100%
2	rs17027087	103,015,918	C/T	1.10 (1.08-1.13)	2.8×10^{-14}	1.10 (1.08-1.13)	2.8×10^{-14}	0.65	100%
2	rs6710528	103,016,142	C/T	0.92 (0.89-0.94)	1.6×10^{-12}	0.92 (0.90-0.94)	1.7×10^{-13}	0.36	100%
2	rs3732124	103,018,052	C/T	0.92 (0.89-0.94)	1.2×10^{-12}	0.92 (0.90-0.94)	1.6×10^{-13}	0.37	100%
2	rs4851571	103,019,000	C/T	0.92 (0.89-0.94)	1.1×10^{-12}	0.92 (0.90-0.94)	1.8×10^{-13}	0.38	100%
2	rs4851572	103,019,031	G/A	0.92 (0.89-0.94)	1.1×10^{-12}	0.92 (0.90-0.94)	1.7×10^{-13}	0.38	100%
2	rs10202813	103,019,740	G/T	0.88 (0.85-0.91)	1.3×10^{-11}	0.89 (0.86-0.91)	4.6×10^{-15}	0.07	100%
2	rs6710034	103,023,678	G/A	0.92 (0.89-0.94)	3.7×10^{-13}	0.92 (0.90-0.94)	1.4×10^{-13}	0.43	100%
2	rs10181785	103,025,274	C/T	0.88 (0.85-0.91)	7.0×10^{-12}	0.88 (0.86-0.91)	3.5×10^{-15}	0.09	100%
2	rs12712148	103,025,547	G/A	0.88 (0.85-0.92)	1.3×10^{-11}	0.89 (0.86-0.91)	1.4×10^{-14}	0.11	100%
2	rs11687768	103,025,738	A/G	0.88 (0.85-0.91)	5.8×10^{-12}	0.88 (0.86-0.91)	3.1×10^{-15}	0.10	100%
2	rs10203558	103,027,640	T/C	0.92 (0.89-0.94)	7.7×10^{-13}	0.92 (0.90-0.94)	1.6×10^{-13}	0.40	100%
2	rs10200952	103,027,651	A/C	0.91 (0.89-0.94)	1.8×10^{-10}	0.92 (0.89-0.94)	2.5×10^{-11}	0.37	77%
2	rs7586983	103,028,066	C/T	0.88 (0.85-0.91)	8.9×10^{-12}	0.88 (0.86-0.91)	2.9×10^{-15}	0.08	100%
2	rs1420105	103,035,119	T/C	0.91 (0.89-0.94)	2.6×10^{-13}	0.92 (0.89-0.94)	8.3×10^{-14}	0.42	100%
2	rs2293223	103,035,468	C/T	0.88 (0.85-0.91)	1.2×10^{-11}	0.88 (0.86-0.91)	3.6×10^{-15}	0.07	97%
2	rs2293224	103,035,779	T/C	0.92 (0.89-0.94)	6.0×10^{-13}	0.92 (0.90-0.94)	1.4×10^{-13}	0.41	100%
2	rs6743516	103,036,335	A/G	0.92 (0.89-0.94)	5.6×10^{-13}	0.92 (0.90-0.94)	1.5×10^{-13}	0.41	100%
2	rs3771156	103,036,677	C/T	1.10 (1.07-1.13)	4.7×10^{-13}	1.10 (1.07-1.13)	6.1×10^{-14}	0.40	100%
2	rs1420100	103,037,002	C/A	0.92 (0.89-0.94)	5.3×10^{-13}	0.92 (0.90-0.94)	1.6×10^{-13}	0.42	100%
2	rs3771155	103,037,826	A/G	0.92 (0.89-0.94)	4.7×10^{-13}	0.92 (0.90-0.94)	1.1×10^{-13}	0.41	100%
2	rs10206291	103,038,863	T/C	0.92 (0.89-0.94)	5.4×10^{-13}	0.92 (0.90-0.94)	1.6×10^{-13}	0.42	100%
2	rs885088	103,039,044	A/G	0.92 (0.89-0.94)	5.1×10^{-13}	0.92 (0.90-0.94)	1.5×10^{-13}	0.42	100%
2	rs3771154	103,039,360	C/T	0.92 (0.89-0.94)	5.7×10^{-13}	0.92 (0.90-0.94)	1.5×10^{-13}	0.41	100%
2	rs6759479	103,040,047	A/C	0.92 (0.89-0.94)	7.3×10^{-13}	0.92 (0.90-0.94)	2.2×10^{-13}	0.42	100%
2	rs887972	103,040,945	G/A	1.10 (1.07-1.14)	2.7×10^{-11}	1.10 (1.07-1.14)	2.7×10^{-11}	0.49	82%
2	rs887971	103,041,167	T/C	1.10 (1.07-1.13)	2.8×10^{-14}	1.10 (1.07-1.13)	2.8×10^{-14}	0.64	100%
2	rs3755266	103,042,712	G/A	0.92 (0.90-0.94)	4.6×10^{-13}	0.92 (0.90-0.94)	4.6×10^{-13}	0.50	100%
2	rs7559845	103,046,214	T/G	0.92 (0.90-0.94)	4.1×10^{-13}	0.92 (0.90-0.94)	4.1×10^{-13}	0.48	100%
2	rs2310300	103,049,074	A/G	0.92 (0.90-0.94)	2.8×10^{-13}	0.92 (0.90-0.94)	2.8×10^{-13}	0.53	100%
2	rs10166330	103,050,390	C/T	0.88 (0.85-0.91)	9.5×10^{-12}	0.88 (0.86-0.91)	2.4×10^{-15}	0.07	100%
2	rs11681718	103,051,144	A/G	1.10 (1.07-1.13)	3.6×10^{-11}	1.10 (1.07-1.12)	1.2×10^{-12}	0.33	100%
2	rs4851582	103,051,558	T/C	1.10 (1.07-1.13)	3.8×10^{-13}	1.10 (1.07-1.13)	3.8×10^{-13}	0.49	100%
2	rs3755265	103,052,816	C/A	0.92 (0.90-0.94)	7.1×10^{-14}	0.92 (0.90-0.94)	7.1×10^{-14}	0.49	100%
2	rs10176820	103,054,420	T/C	0.89 (0.86-0.92)	1.4×10^{-11}	0.89 (0.86-0.92)	5.0×10^{-14}	0.17	100%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
2	rs2058659	103,054,556	G/A	0.92 (0.90-0.94)	7.5×10^{-14}	0.92 (0.90-0.94)	7.5×10^{-14}	0.56	100%
2	rs17027166	103,055,420	G/A	1.10 (1.07-1.13)	7.6×10^{-13}	1.10 (1.07-1.13)	5.8×10^{-14}	0.37	100%
2	rs13021177	103,056,493	A/G	0.91 (0.89-0.93)	1.1×10^{-13}	0.91 (0.89-0.93)	1.1×10^{-14}	0.36	100%
2	rs10490204	103,056,534	A/C	1.10 (1.07-1.13)	9.7×10^{-12}	1.10 (1.07-1.13)	5.9×10^{-13}	0.36	100%
2	rs17027179	103,057,159	C/T	1.10 (1.07-1.13)	5.5×10^{-13}	1.10 (1.07-1.13)	4.1×10^{-14}	0.37	100%
2	rs2075186	103,057,251	G/T	0.88 (0.85-0.91)	1.6×10^{-11}	0.89 (0.86-0.91)	4.4×10^{-15}	0.07	100%
2	rs10490203	103,059,237	T/G	1.10 (1.07-1.13)	5.2×10^{-13}	1.10 (1.07-1.13)	3.8×10^{-14}	0.37	100%
2	rs3771150	103,060,851	G/A	1.10 (1.07-1.13)	2.1×10^{-11}	1.10 (1.07-1.12)	1.0×10^{-12}	0.35	100%
2	rs11123928	103,061,286	G/A	1.08 (1.05-1.11)	7.0×10^{-09}	1.08 (1.05-1.11)	4.8×10^{-09}	0.46	97%
2	rs17027230	103,079,330	C/T	1.10 (1.07-1.13)	3.1×10^{-11}	1.10 (1.07-1.13)	5.5×10^{-13}	0.29	98%
2	rs10210176	103,079,516	C/A	0.88 (0.85-0.91)	8.6×10^{-12}	0.88 (0.86-0.91)	6.0×10^{-15}	0.10	97%
2	rs10172116	103,087,573	C/T	0.88 (0.85-0.91)	2.2×10^{-11}	0.88 (0.86-0.91)	6.2×10^{-15}	0.07	98%
2	rs4851011	103,089,678	C/T	1.09 (1.06-1.13)	5.6×10^{-10}	1.09 (1.07-1.12)	4.0×10^{-12}	0.24	98%
2	rs17027255	103,090,127	C/T	1.10 (1.07-1.13)	8.9×10^{-11}	1.10 (1.07-1.12)	1.0×10^{-12}	0.26	98%
2	rs17027258	103,091,540	A/G	1.10 (1.07-1.13)	3.3×10^{-11}	1.10 (1.07-1.12)	7.5×10^{-13}	0.30	98%
2	rs13030642	103,091,585	C/A	0.89 (0.85-0.92)	5.7×10^{-11}	0.89 (0.86-0.92)	4.5×10^{-14}	0.09	98%
2	rs13018263	103,092,270	T/C	0.90 (0.88-0.93)	5.0×10^{-10}	0.91 (0.88-0.93)	2.9×10^{-11}	0.25	98%
5	rs12187994	109,950,981	A/C	1.12 (1.08-1.16)	8.8×10^{-09}	1.12 (1.08-1.16)	8.8×10^{-09}	0.73	100%
5	rs12186893	109,952,983	G/A	1.12 (1.08-1.16)	7.9×10^{-09}	1.12 (1.08-1.16)	7.9×10^{-09}	0.75	100%
5	rs3985087	110,072,656	C/A	1.12 (1.08-1.17)	8.5×10^{-09}	1.12 (1.08-1.17)	8.5×10^{-09}	0.90	98%
5	rs17132319	110,074,677	T/G	1.12 (1.08-1.17)	4.5×10^{-09}	1.12 (1.08-1.17)	4.5×10^{-09}	0.86	100%
5	rs665063	110,075,414	C/A	0.90 (0.86-0.93)	4.4×10^{-09}	0.90 (0.86-0.93)	4.4×10^{-09}	0.73	100%
5	rs12187004	110,076,352	A/G	1.13 (1.08-1.17)	4.5×10^{-09}	1.13 (1.08-1.17)	4.5×10^{-09}	0.85	100%
5	rs244411	110,078,480	C/T	0.89 (0.86-0.92)	1.3×10^{-09}	0.89 (0.86-0.92)	1.3×10^{-09}	0.70	98%
5	rs17446534	110,079,450	T/C	1.13 (1.09-1.18)	1.8×10^{-09}	1.13 (1.09-1.18)	1.8×10^{-09}	0.85	100%
5	rs244923	110,080,363	T/C	0.89 (0.85-0.92)	7.5×10^{-10}	0.89 (0.85-0.92)	7.5×10^{-10}	0.68	98%
5	rs381661	110,085,098	C/T	0.86 (0.82-0.89)	8.1×10^{-12}	0.86 (0.82-0.89)	8.1×10^{-12}	0.96	97%
5	rs11548494	110,100,318	G/A	1.14 (1.09-1.19)	9.7×10^{-09}	1.14 (1.09-1.19)	9.7×10^{-09}	0.56	95%
5	rs6893213	110,198,114	C/T	1.15 (1.10-1.20)	3.9×10^{-11}	1.15 (1.10-1.20)	3.9×10^{-11}	0.48	95%
5	rs1837253	110,401,872	T/C	1.16 (1.12-1.20)	1.6×10^{-18}	1.16 (1.13-1.19)	2.0×10^{-25}	0.06	97%
5	rs10455025	110,404,999	A/C	1.15 (1.12-1.18)	9.4×10^{-26}	1.15 (1.12-1.18)	9.4×10^{-26}	0.57	98%
5	rs1898671	110,408,002	C/T	1.14 (1.11-1.17)	4.0×10^{-25}	1.14 (1.11-1.17)	4.0×10^{-25}	0.52	100%
5	rs17624673	110,457,158	C/T	1.14 (1.10-1.17)	3.6×10^{-19}	1.14 (1.11-1.17)	9.5×10^{-23}	0.31	98%
5	rs1043828	110,464,008	T/C	1.13 (1.10-1.16)	2.0×10^{-19}	1.13 (1.10-1.16)	2.7×10^{-22}	0.34	100%
5	rs1438673	110,467,499	C/T	0.90 (0.88-0.93)	4.2×10^{-13}	0.90 (0.88-0.92)	6.1×10^{-19}	0.10	100%
5	rs6594499	110,470,137	C/A	0.91 (0.89-0.93)	3.5×10^{-12}	0.91 (0.88-0.93)	1.2×10^{-16}	0.17	97%
5	rs2162893	110,558,064	A/G	0.91 (0.88-0.93)	2.8×10^{-13}	0.91 (0.88-0.93)	2.8×10^{-13}	0.69	80%
5	rs1457115	110,567,598	C/T	1.08 (1.05-1.10)	2.5×10^{-10}	1.08 (1.05-1.10)	2.5×10^{-10}	0.89	98%
5	rs11950562	131,652,529	A/C	0.92 (0.90-0.95)	9.0×10^{-11}	0.92 (0.90-0.95)	9.0×10^{-11}	0.70	97%
5	rs10058074	131,686,146	G/A	0.93 (0.91-0.95)	2.2×10^{-09}	0.93 (0.91-0.95)	2.2×10^{-09}	0.69	97%
5	rs4705938	131,694,077	T/C	0.93 (0.90-0.95)	1.4×10^{-09}	0.93 (0.90-0.95)	4.3×10^{-10}	0.40	97%
5	rs17622208	131,717,050	G/A	0.92 (0.90-0.95)	2.6×10^{-10}	0.92 (0.90-0.95)	1.5×10^{-10}	0.45	97%
5	rs4540166	131,779,857	T/C	0.92 (0.90-0.95)	9.3×10^{-09}	0.92 (0.90-0.95)	9.3×10^{-09}	0.54	100%
5	rs4371745	131,779,955	T/C	0.92 (0.90-0.95)	9.6×10^{-09}	0.92 (0.90-0.95)	9.6×10^{-09}	0.55	100%
5	rs1023518	131,793,772	G/T	1.08 (1.05-1.11)	7.1×10^{-09}	1.08 (1.05-1.11)	1.6×10^{-09}	0.41	100%
5	rs3857440	131,794,069	G/A	1.08 (1.05-1.11)	2.1×10^{-09}	1.08 (1.06-1.11)	1.0×10^{-09}	0.45	100%
5	rs11745587	131,796,922	G/A	1.08 (1.05-1.10)	1.2×10^{-09}	1.08 (1.05-1.10)	1.2×10^{-09}	0.49	98%
5	rs6894249	131,797,547	A/G	1.09 (1.06-1.11)	3.5×10^{-11}	1.09 (1.06-1.11)	1.4×10^{-11}	0.44	97%
5	rs17622656	131,820,997	G/A	0.91 (0.89-0.94)	2.3×10^{-10}	0.91 (0.89-0.94)	1.2×10^{-11}	0.33	94%
5	rs736801	131,833,599	C/T	0.91 (0.89-0.94)	2.0×10^{-11}	0.91 (0.89-0.94)	6.7×10^{-12}	0.43	94%
5	rs17622991	131,932,753	G/A	1.11 (1.07-1.15)	3.4×10^{-09}	1.11 (1.07-1.14)	3.6×10^{-12}	0.04	100%
5	rs12187537	131,939,904	T/G	1.10 (1.07-1.14)	8.7×10^{-09}	1.10 (1.07-1.13)	1.1×10^{-10}	0.17	100%
5	rs3798135	131,965,109	C/T	1.10 (1.07-1.14)	1.1×10^{-09}	1.10 (1.07-1.13)	4.3×10^{-12}	0.12	100%
5	rs3798134	131,965,179	G/A	1.10 (1.07-1.14)	1.7×10^{-09}	1.10 (1.07-1.13)	5.0×10^{-12}	0.10	100%
5	rs6596087	131,968,609	G/A	1.10 (1.07-1.14)	1.5×10^{-09}	1.10 (1.07-1.13)	6.8×10^{-12}	0.12	100%
5	rs12653750	131,971,902	C/T	1.10 (1.07-1.14)	8.7×10^{-10}	1.10 (1.07-1.13)	2.0×10^{-11}	0.22	100%
5	rs2040704	131,973,177	A/G	1.11 (1.07-1.15)	5.5×10^{-09}	1.10 (1.07-1.14)	3.5×10^{-12}	0.04	100%
5	rs2074369	131,973,663	T/C	1.11 (1.07-1.15)	6.0×10^{-09}	1.11 (1.08-1.14)	6.3×10^{-12}	0.06	91%
5	rs2240032	131,977,127	C/T	1.10 (1.07-1.14)	2.9×10^{-10}	1.10 (1.07-1.13)	1.5×10^{-11}	0.28	100%
5	rs2158177	131,984,058	A/G	1.13 (1.09-1.17)	7.8×10^{-13}	1.13 (1.09-1.17)	7.8×10^{-13}	0.52	97%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
5	rs3091307	131,989,136	A/G	1.13 (1.09-1.17)	2.0×10^{-10}	1.12 (1.09-1.15)	3.8×10^{-14}	0.03	97%
5	rs1295686	131,995,843	T/C	0.89 (0.87-0.92)	2.8×10^{-15}	0.89 (0.87-0.92)	2.8×10^{-15}	0.67	100%
5	rs20541	131,995,964	A/G	0.89 (0.87-0.92)	5.0×10^{-16}	0.89 (0.87-0.92)	5.0×10^{-16}	0.77	98%
5	rs1295685	131,996,445	A/G	0.89 (0.86-0.91)	9.4×10^{-16}	0.89 (0.86-0.91)	9.4×10^{-16}	0.62	98%
5	rs848	131,996,500	A/C	0.89 (0.87-0.92)	9.0×10^{-15}	0.89 (0.87-0.92)	9.0×10^{-15}	0.51	97%
5	rs847	131,996,669	T/C	0.89 (0.87-0.92)	5.5×10^{-13}	0.89 (0.87-0.92)	6.9×10^{-14}	0.37	98%
5	rs4912622	141,490,587	G/A	1.09 (1.06-1.12)	8.5×10^{-09}	1.09 (1.06-1.11)	7.1×10^{-12}	0.12	100%
5	rs7705042	141,492,419	C/A	1.09 (1.06-1.12)	7.9×10^{-09}	1.09 (1.06-1.12)	3.1×10^{-12}	0.11	100%
6	rs3132616	30,416,456	A/G	1.12 (1.08-1.17)	6.3×10^{-09}	1.12 (1.08-1.17)	6.3×10^{-09}	0.68	89%
6	rs3094024	30,495,860	A/G	1.12 (1.08-1.17)	7.1×10^{-09}	1.12 (1.08-1.17)	7.1×10^{-09}	0.67	95%
6	rs3130117	30,508,956	G/A	1.12 (1.08-1.17)	3.4×10^{-09}	1.12 (1.08-1.17)	3.4×10^{-09}	0.56	97%
6	rs3130247	30,515,043	T/C	1.12 (1.08-1.17)	6.2×10^{-09}	1.12 (1.08-1.17)	6.2×10^{-09}	0.58	97%
6	rs3132610	30,544,401	A/G	1.13 (1.08-1.17)	1.2×10^{-09}	1.13 (1.08-1.17)	1.2×10^{-09}	0.64	97%
6	rs9262130	30,603,519	G/A	1.12 (1.08-1.17)	2.3×10^{-09}	1.12 (1.08-1.17)	2.3×10^{-09}	0.69	97%
6	rs9262135	30,618,906	A/G	1.12 (1.08-1.17)	5.2×10^{-09}	1.12 (1.08-1.17)	5.2×10^{-09}	0.74	95%
6	rs9262143	30,652,781	C/T	1.12 (1.08-1.17)	3.0×10^{-09}	1.12 (1.08-1.17)	3.0×10^{-09}	0.75	95%
6	rs3095330	30,693,633	A/G	1.11 (1.07-1.15)	4.1×10^{-09}	1.11 (1.07-1.15)	3.1×10^{-09}	0.46	79%
6	rs1059612	30,708,955	C/T	1.13 (1.09-1.17)	3.4×10^{-10}	1.13 (1.09-1.17)	3.4×10^{-10}	0.61	97%
6	rs2284174	30,713,580	T/C	1.10 (1.07-1.14)	1.4×10^{-09}	1.10 (1.07-1.14)	1.4×10^{-09}	0.60	100%
6	rs3129973	30,721,143	C/T	1.12 (1.08-1.16)	3.5×10^{-09}	1.12 (1.08-1.16)	3.5×10^{-09}	0.74	97%
6	rs3095326	30,725,841	C/T	1.12 (1.08-1.16)	5.7×10^{-09}	1.12 (1.08-1.16)	5.7×10^{-09}	0.76	97%
6	rs3130665	30,735,979	C/T	1.12 (1.08-1.16)	2.1×10^{-09}	1.12 (1.08-1.16)	2.1×10^{-09}	0.58	97%
6	rs3095336	30,738,446	G/A	1.12 (1.08-1.16)	1.2×10^{-09}	1.12 (1.08-1.16)	1.2×10^{-09}	0.79	95%
6	rs3132605	30,739,972	A/C	1.12 (1.08-1.16)	1.2×10^{-09}	1.12 (1.08-1.16)	1.2×10^{-09}	0.77	95%
6	rs3129978	30,746,331	A/G	1.12 (1.08-1.17)	1.3×10^{-09}	1.12 (1.08-1.17)	1.3×10^{-09}	0.75	95%
6	rs3132600	30,746,367	C/T	1.12 (1.08-1.17)	4.3×10^{-09}	1.12 (1.08-1.17)	4.3×10^{-09}	0.61	92%
6	rs3130673	30,746,519	G/T	1.12 (1.08-1.17)	1.1×10^{-09}	1.12 (1.08-1.17)	1.1×10^{-09}	0.75	95%
6	rs3131044	30,758,664	A/C	1.12 (1.08-1.17)	9.5×10^{-10}	1.12 (1.08-1.17)	9.5×10^{-10}	0.61	95%
6	rs3131050	30,760,025	T/C	1.12 (1.08-1.17)	1.7×10^{-09}	1.12 (1.08-1.17)	1.7×10^{-09}	0.60	94%
6	rs9262200	30,760,725	G/A	1.12 (1.08-1.16)	1.2×10^{-09}	1.12 (1.08-1.16)	1.2×10^{-09}	0.61	97%
6	rs3131055	30,761,487	T/C	1.12 (1.08-1.16)	1.4×10^{-09}	1.12 (1.08-1.16)	1.4×10^{-09}	0.59	97%
6	rs3129984	30,761,572	C/T	1.12 (1.08-1.16)	4.6×10^{-09}	1.12 (1.08-1.16)	4.0×10^{-09}	0.47	97%
6	rs3129985	30,762,542	C/T	1.12 (1.08-1.16)	1.6×10^{-09}	1.12 (1.08-1.16)	1.6×10^{-09}	0.58	97%
6	rs3131060	30,763,291	G/A	1.12 (1.08-1.16)	1.9×10^{-09}	1.12 (1.08-1.16)	1.9×10^{-09}	0.60	97%
6	rs3130641	30,764,081	C/T	1.12 (1.08-1.16)	4.1×10^{-09}	1.12 (1.08-1.16)	4.1×10^{-09}	0.73	94%
6	rs1264376	30,765,579	C/A	1.12 (1.08-1.17)	1.4×10^{-09}	1.12 (1.08-1.17)	1.4×10^{-09}	0.78	89%
6	rs3130955	31,054,511	C/A	1.08 (1.05-1.11)	6.6×10^{-09}	1.08 (1.05-1.10)	3.0×10^{-09}	0.35	98%
6	rs3130564	31,101,674	C/T	1.10 (1.07-1.14)	1.6×10^{-10}	1.10 (1.07-1.14)	1.6×10^{-10}	0.54	95%
6	rs2596464	31,412,961	T/C	1.09 (1.06-1.12)	3.1×10^{-10}	1.09 (1.07-1.12)	4.2×10^{-14}	0.15	98%
6	rs2596472	31,428,967	G/A	1.10 (1.06-1.13)	3.4×10^{-10}	1.10 (1.06-1.13)	3.4×10^{-10}	0.74	95%
6	rs3099844	31,448,976	C/A	1.12 (1.08-1.16)	1.4×10^{-09}	1.12 (1.08-1.16)	1.4×10^{-09}	0.56	97%
6	rs2855812	31,472,720	G/T	1.10 (1.07-1.13)	8.9×10^{-12}	1.10 (1.07-1.13)	1.9×10^{-12}	0.39	100%
6	rs3134950	32,127,477	C/A	1.07 (1.05-1.10)	5.0×10^{-09}	1.07 (1.05-1.10)	5.0×10^{-09}	0.55	100%
6	rs1061808	32,136,547	T/G	1.07 (1.05-1.10)	4.9×10^{-09}	1.07 (1.05-1.10)	4.9×10^{-09}	0.56	98%
6	rs9368716	32,306,090	G/A	1.08 (1.05-1.10)	1.7×10^{-10}	1.08 (1.05-1.10)	1.7×10^{-10}	0.71	100%
6	rs9268301	32,319,637	G/A	1.10 (1.07-1.12)	2.9×10^{-11}	1.10 (1.07-1.13)	1.6×10^{-13}	0.34	98%
6	rs1265762	32,321,115	C/A	1.07 (1.05-1.10)	1.8×10^{-09}	1.07 (1.05-1.10)	1.8×10^{-09}	0.89	100%
6	rs1265760	32,321,872	T/C	1.07 (1.05-1.10)	2.0×10^{-09}	1.07 (1.05-1.10)	2.0×10^{-09}	0.89	100%
6	rs1265758	32,323,529	A/G	1.08 (1.05-1.10)	6.1×10^{-10}	1.08 (1.05-1.10)	6.1×10^{-10}	0.81	100%
6	rs3129909	32,325,710	G/A	1.07 (1.05-1.10)	9.3×10^{-10}	1.07 (1.05-1.10)	9.3×10^{-10}	0.81	100%
6	rs2395150	32,326,045	G/A	1.08 (1.05-1.10)	4.5×10^{-10}	1.08 (1.05-1.10)	4.5×10^{-10}	0.82	98%
6	rs6904608	32,327,727	C/T	1.08 (1.05-1.10)	3.9×10^{-10}	1.08 (1.05-1.10)	3.9×10^{-10}	0.85	100%
6	rs6904636	32,327,781	C/T	1.07 (1.05-1.10)	4.2×10^{-09}	1.07 (1.05-1.10)	4.2×10^{-09}	0.90	100%
6	rs2073044	32,338,986	C/T	1.11 (1.08-1.14)	1.3×10^{-12}	1.11 (1.08-1.14)	1.4×10^{-13}	0.42	94%
6	rs9268403	32,341,473	T/C	1.13 (1.09-1.16)	1.9×10^{-14}	1.13 (1.10-1.16)	1.7×10^{-19}	0.14	98%
6	rs9268429	32,345,052	A/G	1.12 (1.09-1.15)	4.7×10^{-13}	1.12 (1.09-1.15)	3.5×10^{-18}	0.12	98%
6	rs1980495	32,346,794	A/C	1.14 (1.10-1.18)	1.9×10^{-12}	1.14 (1.11-1.17)	2.5×10^{-18}	0.09	82%
6	rs8180664	32,347,490	C/T	1.13 (1.09-1.16)	2.2×10^{-14}	1.13 (1.10-1.16)	4.0×10^{-20}	0.10	100%
6	rs2395157	32,348,145	A/G	1.13 (1.09-1.16)	1.6×10^{-14}	1.13 (1.10-1.16)	1.5×10^{-20}	0.10	100%
6	rs17423649	32,357,133	C/T	0.90 (0.87-0.93)	3.4×10^{-09}	0.90 (0.87-0.93)	1.3×10^{-09}	0.40	98%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
6	rs9268474	32,357,165	T/C	1.13 (1.09-1.16)	6.0×10^{-14}	1.13 (1.10-1.16)	6.1×10^{-20}	0.09	100%
6	rs12529049	32,357,715	C/T	0.90 (0.87-0.93)	3.1×10^{-09}	0.90 (0.87-0.93)	1.2×10^{-09}	0.40	100%
6	rs12525722	32,358,163	A/G	0.90 (0.87-0.93)	3.4×10^{-09}	0.90 (0.88-0.93)	1.4×10^{-09}	0.40	100%
6	rs17423691	32,358,345	C/A	0.90 (0.87-0.94)	8.6×10^{-09}	0.90 (0.88-0.93)	2.0×10^{-09}	0.35	100%
6	rs17423698	32,358,368	T/C	0.90 (0.87-0.94)	9.3×10^{-09}	0.91 (0.88-0.94)	2.1×10^{-09}	0.35	100%
6	rs9268477	32,359,121	G/A	1.13 (1.09-1.17)	2.7×10^{-12}	1.13 (1.10-1.16)	1.4×10^{-17}	0.11	83%
6	rs9268480	32,363,844	C/T	1.12 (1.09-1.16)	6.2×10^{-14}	1.13 (1.10-1.15)	1.6×10^{-19}	0.11	100%
6	rs4248166	32,366,421	T/C	0.91 (0.88-0.94)	4.7×10^{-10}	0.91 (0.88-0.94)	2.7×10^{-10}	0.45	100%
6	rs2294881	32,367,604	T/C	0.91 (0.89-0.94)	1.7×10^{-09}	0.91 (0.89-0.94)	1.7×10^{-09}	0.57	100%
6	rs2294880	32,367,722	A/G	1.13 (1.09-1.17)	1.1×10^{-11}	1.14 (1.10-1.17)	6.4×10^{-17}	0.12	79%
6	rs3817966	32,367,847	T/C	1.13 (1.09-1.17)	1.3×10^{-11}	1.13 (1.10-1.16)	1.2×10^{-17}	0.07	85%
6	rs3817963	32,368,087	T/C	1.12 (1.09-1.16)	6.4×10^{-13}	1.12 (1.09-1.15)	2.7×10^{-19}	0.06	100%
6	rs3817962	32,368,314	C/A	1.13 (1.09-1.17)	3.0×10^{-11}	1.13 (1.10-1.17)	7.3×10^{-17}	0.10	79%
6	rs2076525	32,370,616	T/C	1.12 (1.08-1.15)	1.0×10^{-12}	1.12 (1.09-1.15)	8.2×10^{-18}	0.12	97%
6	rs2076524	32,370,684	A/G	1.13 (1.09-1.16)	1.4×10^{-14}	1.13 (1.10-1.16)	6.1×10^{-20}	0.13	100%
6	rs3793126	32,371,619	A/G	1.12 (1.09-1.16)	1.4×10^{-13}	1.12 (1.09-1.15)	5.8×10^{-19}	0.09	100%
6	rs3793127	32,371,915	C/T	1.13 (1.09-1.16)	1.2×10^{-13}	1.13 (1.10-1.16)	3.8×10^{-18}	0.22	100%
6	rs9268493	32,375,330	G/A	1.13 (1.09-1.16)	2.1×10^{-11}	1.13 (1.09-1.16)	7.5×10^{-17}	0.07	80%
6	rs9268494	32,375,352	A/C	1.12 (1.09-1.16)	1.3×10^{-12}	1.12 (1.09-1.16)	2.6×10^{-17}	0.14	88%
6	rs9268497	32,375,424	G/A	1.13 (1.09-1.17)	1.9×10^{-11}	1.13 (1.10-1.16)	8.6×10^{-17}	0.11	82%
6	rs3763309	32,375,973	C/A	1.13 (1.10-1.17)	1.7×10^{-14}	1.13 (1.10-1.17)	1.1×10^{-18}	0.25	100%
6	rs3763311	32,376,176	C/T	1.13 (1.09-1.17)	6.6×10^{-12}	1.13 (1.10-1.16)	1.4×10^{-16}	0.14	82%
6	rs3763312	32,376,348	G/A	1.13 (1.08-1.17)	3.2×10^{-09}	1.14 (1.10-1.18)	1.2×10^{-14}	0.14	80%
6	rs3763316	32,376,746	C/T	1.12 (1.09-1.16)	5.1×10^{-14}	1.12 (1.10-1.15)	9.6×10^{-19}	0.16	97%
6	rs9268516	32,379,489	C/T	1.13 (1.10-1.16)	3.5×10^{-15}	1.13 (1.10-1.16)	8.0×10^{-21}	0.12	100%
6	rs9268542	32,384,721	A/G	1.08 (1.05-1.11)	8.9×10^{-09}	1.09 (1.07-1.12)	7.0×10^{-13}	0.14	100%
6	rs2395163	32,387,809	T/C	1.12 (1.08-1.16)	1.5×10^{-10}	1.13 (1.10-1.16)	5.8×10^{-17}	0.09	97%
6	rs4321864	32,399,187	C/A	1.09 (1.06-1.13)	2.0×10^{-09}	1.11 (1.08-1.13)	1.9×10^{-15}	0.08	100%
6	rs9268614	32,402,778	T/G	1.12 (1.08-1.15)	2.1×10^{-10}	1.13 (1.10-1.16)	1.4×10^{-16}	0.10	100%
6	rs6926374	32,409,305	A/G	1.08 (1.05-1.11)	1.4×10^{-09}	1.09 (1.06-1.11)	5.0×10^{-12}	0.29	97%
6	rs2239804	32,411,523	T/C	1.08 (1.06-1.11)	1.1×10^{-09}	1.09 (1.07-1.12)	1.6×10^{-13}	0.19	100%
6	rs2239803	32,411,833	C/T	1.08 (1.05-1.11)	1.4×10^{-09}	1.09 (1.06-1.11)	2.5×10^{-12}	0.28	97%
6	rs9268831	32,427,748	C/T	1.09 (1.06-1.12)	8.5×10^{-09}	1.09 (1.07-1.12)	8.4×10^{-14}	0.04	100%
6	rs9268853	32,429,643	T/C	1.12 (1.09-1.15)	6.1×10^{-17}	1.12 (1.09-1.15)	1.8×10^{-18}	0.39	98%
6	rs9268858	32,429,758	T/C	1.12 (1.09-1.15)	5.5×10^{-17}	1.12 (1.09-1.15)	1.5×10^{-18}	0.39	98%
6	rs9268877	32,431,147	A/G	1.09 (1.07-1.12)	4.0×10^{-13}	1.09 (1.07-1.12)	4.0×10^{-13}	0.78	98%
6	rs9268923	32,432,835	C/T	1.14 (1.11-1.17)	1.3×10^{-24}	1.14 (1.11-1.17)	1.3×10^{-24}	0.62	94%
6	rs2395185	32,433,167	G/T	1.12 (1.09-1.15)	3.6×10^{-17}	1.12 (1.09-1.15)	1.1×10^{-18}	0.40	98%
6	rs9268969	32,434,349	C/T	1.15 (1.12-1.18)	1.6×10^{-25}	1.15 (1.12-1.18)	1.6×10^{-25}	0.65	94%
6	rs9268979	32,435,044	T/C	1.09 (1.06-1.12)	2.4×10^{-11}	1.09 (1.06-1.12)	2.4×10^{-11}	0.81	95%
6	rs9405040	32,439,393	A/C	1.12 (1.09-1.15)	3.8×10^{-17}	1.12 (1.09-1.15)	1.5×10^{-18}	0.40	98%
6	rs9286790	32,439,828	G/A	1.12 (1.09-1.15)	4.8×10^{-18}	1.12 (1.09-1.15)	4.8×10^{-18}	0.48	95%
6	rs9269065	32,440,172	T/G	1.10 (1.07-1.13)	8.4×10^{-11}	1.10 (1.07-1.13)	8.4×10^{-11}	0.50	74%
6	rs9269069	32,440,362	C/T	1.10 (1.07-1.12)	2.8×10^{-13}	1.10 (1.07-1.12)	2.8×10^{-13}	0.83	98%
6	rs9269070	32,440,451	G/A	1.09 (1.06-1.12)	3.5×10^{-10}	1.09 (1.06-1.12)	3.5×10^{-10}	0.61	76%
6	rs9269071	32,440,467	T/C	1.09 (1.07-1.12)	1.6×10^{-12}	1.09 (1.07-1.12)	1.6×10^{-12}	0.82	95%
6	rs9269080	32,440,969	G/A	1.09 (1.06-1.11)	3.9×10^{-11}	1.09 (1.06-1.11)	3.9×10^{-11}	0.69	95%
6	rs7755212	32,441,408	C/T	1.09 (1.06-1.12)	8.7×10^{-12}	1.09 (1.06-1.12)	8.7×10^{-12}	0.70	94%
6	rs7739203	32,441,555	A/G	1.09 (1.07-1.12)	1.8×10^{-12}	1.09 (1.07-1.12)	1.8×10^{-12}	0.83	95%
6	rs7739357	32,441,641	A/G	1.10 (1.07-1.12)	1.8×10^{-12}	1.10 (1.07-1.12)	1.8×10^{-12}	0.80	92%
6	rs9405112	32,445,600	G/A	1.12 (1.09-1.15)	1.8×10^{-16}	1.12 (1.09-1.15)	1.3×10^{-18}	0.35	98%
6	rs6916742	32,453,191	T/C	1.11 (1.08-1.14)	2.3×10^{-11}	1.11 (1.08-1.14)	9.9×10^{-16}	0.14	94%
6	rs2516049	32,570,400	T/C	1.11 (1.07-1.14)	2.0×10^{-10}	1.11 (1.08-1.14)	3.2×10^{-16}	0.04	98%
6	rs9272346	32,604,372	G/A	1.16 (1.12-1.19)	5.7×10^{-24}	1.16 (1.13-1.18)	8.2×10^{-32}	0.14	97%
6	rs9272723	32,609,427	T/C	1.14 (1.11-1.18)	2.9×10^{-20}	1.14 (1.11-1.17)	6.9×10^{-26}	0.15	97%
6	rs6928482	32,626,249	T/C	1.11 (1.08-1.15)	1.8×10^{-12}	1.11 (1.09-1.14)	4.8×10^{-19}	0.03	98%
6	rs9273363	32,626,272	C/A	1.10 (1.07-1.14)	2.7×10^{-12}	1.10 (1.07-1.14)	2.7×10^{-12}	0.99	97%
6	rs6906021	32,626,311	T/C	1.10 (1.06-1.13)	8.4×10^{-10}	1.10 (1.07-1.12)	3.9×10^{-14}	0.05	97%
6	rs9275141	32,651,117	T/G	1.11 (1.07-1.14)	1.8×10^{-10}	1.11 (1.08-1.13)	1.2×10^{-17}	0.01	100%
6	rs2858330	32,658,715	T/C	1.10 (1.07-1.14)	1.1×10^{-10}	1.11 (1.08-1.13)	7.3×10^{-18}	0.01	100%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
6	rs16898264	32,677,152	G/A	1.09 (1.06-1.11)	1.3×10^{-09}	1.09 (1.06-1.11)	1.3×10^{-09}	0.48	83%
6	rs10947332	32,677,440	G/A	0.89 (0.85-0.92)	4.5×10^{-09}	0.89 (0.86-0.93)	6.6×10^{-10}	0.24	98%
6	rs3104405	32,682,308	C/A	1.10 (1.07-1.13)	1.3×10^{-12}	1.10 (1.07-1.13)	2.4×10^{-13}	0.41	94%
6	rs2239701	32,805,049	T/C	1.08 (1.06-1.11)	2.3×10^{-10}	1.08 (1.06-1.11)	2.3×10^{-10}	0.88	95%
6	rs6454802	90,814,199	C/T	0.93 (0.90-0.95)	7.4×10^{-09}	0.93 (0.90-0.95)	7.4×10^{-09}	0.72	88%
6	rs11753332	90,819,153	G/A	0.92 (0.90-0.95)	7.2×10^{-10}	0.92 (0.90-0.95)	7.2×10^{-10}	0.81	95%
6	rs12194007	90,823,159	G/T	0.92 (0.90-0.95)	2.8×10^{-09}	0.92 (0.90-0.95)	2.8×10^{-09}	0.72	91%
6	rs12199079	90,852,258	T/G	0.92 (0.90-0.94)	1.3×10^{-10}	0.92 (0.90-0.94)	1.3×10^{-10}	0.83	97%
6	rs1010473	90,856,878	G/T	0.92 (0.89-0.94)	1.1×10^{-09}	0.92 (0.89-0.94)	1.1×10^{-09}	0.89	85%
6	rs1010474	90,857,028	T/C	0.92 (0.90-0.94)	1.1×10^{-10}	0.92 (0.90-0.94)	1.1×10^{-10}	0.82	97%
6	rs17711850	90,864,870	T/C	0.92 (0.90-0.94)	1.1×10^{-10}	0.92 (0.90-0.94)	1.1×10^{-10}	0.79	97%
6	rs10455168	90,883,525	T/C	0.92 (0.89-0.94)	1.6×10^{-11}	0.92 (0.89-0.94)	1.6×10^{-11}	0.88	97%
6	rs10806423	90,886,824	C/T	0.92 (0.89-0.94)	1.5×10^{-11}	0.92 (0.89-0.94)	1.5×10^{-11}	0.88	97%
6	rs11757155	90,941,240	C/T	0.91 (0.89-0.94)	4.0×10^{-12}	0.91 (0.89-0.94)	4.0×10^{-12}	0.63	100%
6	rs2021716	90,941,289	C/T	0.91 (0.89-0.94)	8.6×10^{-12}	0.91 (0.89-0.94)	8.6×10^{-12}	0.59	97%
6	rs17585295	90,944,831	C/T	0.92 (0.90-0.94)	1.1×10^{-10}	0.92 (0.90-0.94)	1.1×10^{-10}	0.67	100%
6	rs4707609	90,946,479	T/C	0.92 (0.90-0.94)	1.1×10^{-10}	0.92 (0.90-0.94)	1.1×10^{-10}	0.68	100%
6	rs2875584	90,950,628	C/T	0.92 (0.89-0.94)	8.7×10^{-12}	0.92 (0.89-0.94)	8.7×10^{-12}	0.62	100%
6	rs17513531	90,951,239	C/T	0.92 (0.89-0.94)	7.9×10^{-12}	0.92 (0.89-0.94)	7.9×10^{-12}	0.61	100%
6	rs905670	90,958,502	G/A	0.91 (0.89-0.94)	3.2×10^{-12}	0.91 (0.89-0.94)	3.2×10^{-12}	0.71	100%
6	rs1847472	90,973,159	C/A	0.92 (0.89-0.94)	1.4×10^{-11}	0.92 (0.89-0.94)	1.4×10^{-11}	0.74	98%
6	rs943689	90,984,035	C/T	0.91 (0.89-0.94)	2.2×10^{-12}	0.91 (0.89-0.94)	2.2×10^{-12}	0.76	100%
6	rs2325291	90,986,686	G/A	0.91 (0.89-0.94)	2.2×10^{-12}	0.91 (0.89-0.94)	2.2×10^{-12}	0.80	100%
6	rs2325292	90,986,749	T/C	0.91 (0.89-0.94)	1.5×10^{-12}	0.91 (0.89-0.94)	1.5×10^{-12}	0.81	100%
6	rs2174281	90,987,872	T/C	0.92 (0.90-0.95)	9.1×10^{-11}	0.92 (0.90-0.95)	9.1×10^{-11}	0.62	100%
6	rs4142967	90,996,349	C/T	0.92 (0.90-0.95)	7.0×10^{-11}	0.92 (0.90-0.95)	7.0×10^{-11}	0.56	100%
6	rs12212193	90,996,769	A/G	0.92 (0.90-0.95)	6.7×10^{-11}	0.92 (0.90-0.95)	6.7×10^{-11}	0.58	100%
6	rs1504215	91,006,227	G/A	0.91 (0.89-0.94)	1.5×10^{-12}	0.91 (0.89-0.94)	1.5×10^{-12}	0.89	97%
6	rs6925032	91,008,027	C/A	0.91 (0.89-0.94)	1.6×10^{-12}	0.91 (0.89-0.94)	1.6×10^{-12}	0.89	97%
6	rs1321859	91,011,673	C/T	0.91 (0.89-0.94)	2.2×10^{-12}	0.91 (0.89-0.94)	2.2×10^{-12}	0.87	97%
8	rs13275219	81,259,826	T/C	0.93 (0.91-0.95)	1.2×10^{-09}	0.93 (0.91-0.95)	1.2×10^{-09}	0.58	100%
8	rs4739735	81,259,877	C/T	0.93 (0.91-0.95)	1.2×10^{-09}	0.93 (0.91-0.95)	7.5×10^{-10}	0.45	100%
8	rs3913969	81,261,064	C/T	0.93 (0.91-0.95)	1.6×10^{-09}	0.93 (0.91-0.95)	1.6×10^{-09}	0.49	100%
8	rs7462675	81,263,962	C/A	0.93 (0.91-0.95)	1.0×10^{-09}	0.93 (0.91-0.95)	1.0×10^{-09}	0.51	100%
8	rs1911713	81,266,044	G/A	0.92 (0.90-0.95)	2.3×10^{-10}	0.92 (0.90-0.95)	1.4×10^{-10}	0.45	98%
8	rs6992476	81,267,706	A/G	0.93 (0.91-0.95)	9.9×10^{-10}	0.93 (0.91-0.95)	9.9×10^{-10}	0.51	100%
8	rs7012968	81,267,808	T/C	0.93 (0.90-0.95)	8.9×10^{-10}	0.93 (0.90-0.95)	1.5×10^{-10}	0.37	100%
8	rs6473222	81,267,937	A/G	0.93 (0.90-0.95)	7.7×10^{-10}	0.93 (0.90-0.95)	1.3×10^{-10}	0.37	100%
8	rs6473223	81,268,155	T/C	0.92 (0.90-0.95)	1.3×10^{-10}	0.92 (0.90-0.95)	1.3×10^{-10}	0.49	100%
8	rs6987042	81,273,883	A/G	0.93 (0.90-0.95)	5.5×10^{-10}	0.93 (0.90-0.95)	1.2×10^{-10}	0.39	100%
8	rs11786704	81,275,860	A/C	0.93 (0.90-0.95)	9.1×10^{-10}	0.93 (0.90-0.95)	2.1×10^{-10}	0.38	100%
8	rs13275449	81,276,113	G/A	0.93 (0.90-0.95)	6.8×10^{-10}	0.93 (0.90-0.95)	6.8×10^{-10}	0.60	97%
8	rs12543811	81,278,885	G/A	0.92 (0.90-0.95)	1.1×10^{-10}	0.92 (0.90-0.95)	1.1×10^{-10}	0.54	100%
8	rs13270496	81,280,666	A/C	0.93 (0.91-0.95)	1.3×10^{-09}	0.93 (0.91-0.95)	1.3×10^{-09}	0.50	97%
8	rs6473225	81,281,007	G/A	0.93 (0.90-0.95)	2.8×10^{-10}	0.93 (0.90-0.95)	2.8×10^{-10}	0.49	100%
8	rs7837153	81,283,376	A/C	0.93 (0.90-0.95)	5.1×10^{-10}	0.93 (0.90-0.95)	5.1×10^{-10}	0.64	97%
9	rs380568	6,055,531	T/C	0.88 (0.85-0.92)	4.3×10^{-09}	0.90 (0.88-0.93)	1.4×10^{-10}	0.01	100%
9	rs343490	6,064,575	A/G	0.88 (0.85-0.92)	2.4×10^{-09}	0.90 (0.87-0.93)	6.9×10^{-11}	0.01	100%
9	rs343476	6,072,597	T/C	1.14 (1.09-1.20)	1.8×10^{-09}	1.12 (1.08-1.15)	3.7×10^{-11}	0.01	98%
9	rs189348	6,073,194	T/C	1.14 (1.09-1.20)	3.3×10^{-09}	1.12 (1.08-1.15)	8.8×10^{-11}	0.01	98%
9	rs378952	6,078,146	C/T	1.13 (1.09-1.18)	8.7×10^{-10}	1.11 (1.08-1.15)	1.6×10^{-11}	0.03	98%
9	rs371454	6,078,614	C/T	1.13 (1.09-1.18)	9.8×10^{-10}	1.11 (1.08-1.15)	1.7×10^{-11}	0.02	98%
9	rs340921	6,090,160	G/T	1.12 (1.08-1.17)	3.0×10^{-09}	1.11 (1.08-1.14)	4.2×10^{-11}	0.03	98%
9	rs531759	6,091,996	C/T	1.13 (1.08-1.17)	2.0×10^{-09}	1.11 (1.08-1.15)	1.9×10^{-11}	0.02	98%
9	rs639247	6,092,089	T/G	1.13 (1.08-1.17)	2.0×10^{-09}	1.11 (1.08-1.15)	2.0×10^{-11}	0.02	98%
9	rs9408638	6,096,931	A/G	1.13 (1.08-1.17)	2.0×10^{-09}	1.11 (1.08-1.14)	3.3×10^{-11}	0.03	98%
9	rs437389	6,099,531	T/C	1.13 (1.09-1.18)	8.5×10^{-10}	1.11 (1.08-1.15)	8.9×10^{-12}	0.03	98%
9	rs340906	6,106,086	T/C	1.13 (1.09-1.17)	1.7×10^{-09}	1.11 (1.08-1.15)	2.2×10^{-11}	0.02	98%
9	rs340905	6,106,169	A/C	1.13 (1.09-1.17)	1.4×10^{-09}	1.11 (1.08-1.15)	1.5×10^{-11}	0.02	98%
9	rs340904	6,106,779	C/A	1.13 (1.09-1.18)	1.7×10^{-09}	1.11 (1.08-1.15)	1.6×10^{-11}	0.02	98%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
9	rs974936	6,111,703	A/C	1.13 (1.09-1.17)	1.1×10^{-09}	1.11 (1.08-1.15)	1.2×10^{-11}	0.03	98%
9	rs441616	6,113,940	T/C	1.13 (1.09-1.18)	1.4×10^{-09}	1.11 (1.08-1.15)	1.0×10^{-11}	0.02	98%
9	rs1556470	6,115,538	C/T	1.13 (1.09-1.18)	1.4×10^{-09}	1.11 (1.08-1.15)	8.6×10^{-12}	0.02	98%
9	rs374672	6,119,038	C/T	1.13 (1.09-1.18)	1.2×10^{-09}	1.11 (1.08-1.15)	7.0×10^{-12}	0.02	98%
9	rs443175	6,123,556	T/C	1.13 (1.09-1.18)	8.0×10^{-10}	1.11 (1.08-1.15)	3.8×10^{-12}	0.02	98%
9	rs1755531	6,124,250	T/G	1.13 (1.09-1.18)	1.2×10^{-09}	1.11 (1.08-1.15)	6.8×10^{-12}	0.02	98%
9	rs1970089	6,124,359	T/C	1.13 (1.09-1.18)	7.8×10^{-10}	1.12 (1.08-1.15)	3.5×10^{-12}	0.02	98%
9	rs1537285	6,124,584	T/G	1.13 (1.09-1.18)	1.2×10^{-09}	1.11 (1.08-1.15)	6.2×10^{-12}	0.02	98%
9	rs1332292	6,124,862	T/C	1.13 (1.09-1.18)	1.2×10^{-09}	1.11 (1.08-1.15)	6.7×10^{-12}	0.02	98%
9	rs7039066	6,125,539	T/C	1.13 (1.09-1.18)	1.2×10^{-09}	1.11 (1.08-1.15)	6.9×10^{-12}	0.02	98%
9	rs340915	6,126,588	A/G	1.13 (1.09-1.18)	1.2×10^{-09}	1.11 (1.08-1.15)	6.7×10^{-12}	0.02	98%
9	rs340914	6,126,799	A/G	1.13 (1.09-1.18)	1.1×10^{-09}	1.11 (1.08-1.15)	6.5×10^{-12}	0.02	98%
9	rs340913	6,127,330	T/C	1.13 (1.09-1.18)	1.6×10^{-09}	1.11 (1.08-1.15)	8.3×10^{-12}	0.02	98%
9	rs340912	6,127,851	A/G	1.13 (1.09-1.18)	8.8×10^{-10}	1.11 (1.08-1.15)	4.1×10^{-12}	0.02	98%
9	rs340908	6,128,897	T/C	1.13 (1.09-1.18)	8.8×10^{-10}	1.11 (1.08-1.15)	5.2×10^{-12}	0.02	98%
9	rs340907	6,129,637	A/C	1.13 (1.09-1.18)	7.5×10^{-10}	1.11 (1.08-1.15)	5.4×10^{-12}	0.03	98%
9	rs1888906	6,131,460	G/A	1.13 (1.09-1.18)	6.8×10^{-10}	1.12 (1.08-1.15)	3.7×10^{-12}	0.02	98%
9	rs376690	6,134,926	C/T	1.13 (1.08-1.17)	1.8×10^{-09}	1.11 (1.08-1.15)	1.5×10^{-11}	0.03	98%
9	rs413382	6,142,948	C/A	1.13 (1.09-1.18)	3.8×10^{-10}	1.12 (1.08-1.15)	2.3×10^{-12}	0.05	95%
9	rs386880	6,144,333	C/T	1.09 (1.06-1.12)	3.5×10^{-09}	1.09 (1.06-1.11)	2.2×10^{-10}	0.23	98%
9	rs369756	6,146,441	G/T	1.11 (1.08-1.15)	1.1×10^{-09}	1.11 (1.08-1.14)	2.3×10^{-12}	0.15	95%
9	rs450108	6,153,485	T/C	1.10 (1.06-1.14)	8.4×10^{-09}	1.10 (1.07-1.12)	1.5×10^{-11}	0.11	82%
9	rs1116795	6,155,226	G/T	1.09 (1.06-1.12)	8.1×10^{-09}	1.09 (1.06-1.11)	1.0×10^{-11}	0.08	98%
9	rs10124250	6,161,686	C/T	1.09 (1.06-1.12)	6.1×10^{-09}	1.09 (1.06-1.11)	2.6×10^{-12}	0.05	98%
9	rs10119713	6,163,823	G/A	1.09 (1.06-1.12)	3.8×10^{-09}	1.09 (1.06-1.11)	3.2×10^{-12}	0.07	98%
9	rs7032572	6,172,380	A/G	1.18 (1.13-1.23)	1.4×10^{-16}	1.18 (1.14-1.22)	1.3×10^{-24}	0.06	97%
9	rs1412426	6,188,652	A/C	0.90 (0.87-0.93)	4.2×10^{-10}	0.90 (0.88-0.92)	5.9×10^{-18}	0.00	100%
9	rs1412425	6,188,740	A/C	0.90 (0.87-0.93)	2.0×10^{-10}	0.90 (0.87-0.92)	2.2×10^{-18}	0.00	100%
9	rs1342326	6,190,076	A/C	1.17 (1.12-1.21)	8.6×10^{-14}	1.17 (1.14-1.21)	2.9×10^{-24}	0.01	97%
9	rs2095044	6,192,796	T/C	0.86 (0.83-0.89)	1.3×10^{-17}	0.87 (0.84-0.89)	2.1×10^{-27}	0.01	100%
9	rs2381416	6,193,455	C/A	0.86 (0.83-0.89)	1.3×10^{-17}	0.86 (0.84-0.89)	4.8×10^{-28}	0.01	100%
9	rs10815370	6,194,831	C/A	0.90 (0.86-0.93)	4.6×10^{-10}	0.90 (0.87-0.92)	4.7×10^{-18}	0.00	98%
9	rs1888909	6,197,392	T/C	0.86 (0.83-0.89)	2.4×10^{-18}	0.86 (0.84-0.89)	1.3×10^{-28}	0.02	100%
9	rs992969	6,209,697	A/G	0.86 (0.83-0.88)	7.2×10^{-20}	0.86 (0.84-0.88)	3.3×10^{-30}	0.02	100%
9	rs3939286	6,210,099	T/C	0.86 (0.83-0.89)	1.9×10^{-17}	0.86 (0.84-0.89)	2.4×10^{-28}	0.01	100%
9	rs928413	6,213,387	G/A	0.86 (0.83-0.89)	3.5×10^{-16}	0.86 (0.84-0.89)	2.1×10^{-27}	0.00	98%
9	rs7848215	6,213,468	C/T	1.16 (1.12-1.20)	2.0×10^{-16}	1.16 (1.13-1.19)	2.3×10^{-27}	0.01	98%
9	rs2066362	6,219,176	G/T	1.16 (1.11-1.21)	6.0×10^{-13}	1.16 (1.13-1.20)	9.7×10^{-21}	0.02	95%
9	rs17582919	6,233,376	T/C	1.13 (1.09-1.17)	1.7×10^{-11}	1.13 (1.10-1.16)	7.1×10^{-17}	0.05	91%
9	rs17498196	6,237,547	A/C	1.13 (1.09-1.17)	5.0×10^{-12}	1.13 (1.10-1.16)	7.7×10^{-17}	0.08	97%
9	rs10815393	6,240,324	T/C	1.12 (1.08-1.17)	4.4×10^{-09}	1.12 (1.09-1.16)	7.1×10^{-14}	0.04	80%
9	rs10491836	6,331,421	C/A	1.11 (1.07-1.15)	2.9×10^{-09}	1.11 (1.08-1.14)	9.5×10^{-15}	0.01	97%
9	rs16924356	6,331,610	G/A	1.11 (1.07-1.15)	2.8×10^{-09}	1.11 (1.08-1.14)	1.3×10^{-14}	0.01	97%
10	rs2589561	9,046,645	A/G	0.91 (0.88-0.94)	3.5×10^{-09}	0.91 (0.88-0.94)	3.5×10^{-09}	0.82	95%
11	rs7130588	76,270,683	A/G	1.09 (1.06-1.12)	3.4×10^{-11}	1.09 (1.06-1.12)	2.5×10^{-11}	0.46	98%
11	rs2155219	76,299,194	G/T	1.11 (1.08-1.15)	5.1×10^{-13}	1.11 (1.08-1.14)	1.1×10^{-17}	0.08	95%
11	rs7927894	76,301,316	C/T	1.10 (1.08-1.13)	2.2×10^{-14}	1.10 (1.08-1.13)	2.2×10^{-14}	0.56	95%
11	rs7927997	76,301,375	C/T	1.10 (1.07-1.13)	3.2×10^{-13}	1.10 (1.07-1.13)	3.2×10^{-13}	0.53	92%
12	rs167769	57,503,775	C/T	1.08 (1.05-1.11)	3.9×10^{-09}	1.08 (1.05-1.11)	4.6×10^{-10}	0.31	98%
15	rs1351544	61,042,867	G/T	0.90 (0.87-0.93)	9.8×10^{-09}	0.90 (0.87-0.93)	4.9×10^{-10}	0.31	97%
15	rs8025324	61,043,378	G/A	0.90 (0.87-0.93)	2.6×10^{-09}	0.90 (0.87-0.93)	2.6×10^{-09}	0.53	94%
15	rs12900122	61,055,411	C/T	0.90 (0.87-0.93)	2.1×10^{-09}	0.90 (0.87-0.93)	7.4×10^{-10}	0.42	100%
15	rs16943087	61,056,035	A/G	0.90 (0.87-0.93)	4.5×10^{-09}	0.90 (0.87-0.93)	1.6×10^{-10}	0.29	100%
15	rs2279292	61,057,770	T/C	0.90 (0.87-0.93)	2.1×10^{-09}	0.90 (0.87-0.93)	2.9×10^{-10}	0.37	100%
15	rs11633029	61,065,553	T/C	0.90 (0.87-0.93)	5.7×10^{-09}	0.90 (0.87-0.93)	3.7×10^{-11}	0.21	100%
15	rs11637671	61,065,607	A/G	0.90 (0.87-0.93)	6.3×10^{-09}	0.90 (0.87-0.93)	4.0×10^{-11}	0.21	100%
15	rs10519067	61,068,347	G/A	0.89 (0.86-0.92)	7.8×10^{-10}	0.89 (0.86-0.92)	1.4×10^{-12}	0.19	100%
15	rs11071558	61,069,421	A/G	0.89 (0.86-0.92)	1.3×10^{-09}	0.89 (0.86-0.92)	3.1×10^{-12}	0.19	100%
15	rs11071559	61,069,988	C/T	0.90 (0.86-0.93)	2.2×10^{-09}	0.89 (0.87-0.92)	2.6×10^{-11}	0.24	100%
15	rs1866316	67,441,997	T/C	1.11 (1.08-1.14)	1.7×10^{-14}	1.11 (1.08-1.14)	1.7×10^{-14}	0.81	94%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
15	rs17293632	67,442,596	C/T	1.12 (1.08-1.15)	1.5×10^{-11}	1.12 (1.09-1.15)	1.9×10^{-15}	0.18	97%
15	rs10152544	67,444,747	C/T	0.92 (0.90-0.94)	1.9×10^{-13}	0.92 (0.90-0.94)	1.9×10^{-13}	0.96	97%
15	rs744910	67,446,785	G/A	0.92 (0.90-0.94)	9.9×10^{-14}	0.92 (0.90-0.94)	9.9×10^{-14}	0.98	100%
15	rs11634793	67,447,452	C/T	0.92 (0.90-0.94)	1.7×10^{-13}	0.92 (0.90-0.94)	1.7×10^{-13}	0.98	100%
15	rs8032739	67,448,899	A/G	1.10 (1.08-1.13)	1.1×10^{-14}	1.10 (1.08-1.13)	1.1×10^{-14}	0.77	97%
15	rs2033784	67,449,660	A/G	1.10 (1.08-1.13)	7.4×10^{-15}	1.10 (1.08-1.13)	7.4×10^{-15}	0.76	100%
15	rs17228058	67,450,305	A/G	1.12 (1.08-1.15)	9.4×10^{-11}	1.12 (1.09-1.15)	5.4×10^{-15}	0.14	95%
15	rs7173698	67,450,893	A/G	1.10 (1.08-1.13)	1.1×10^{-14}	1.10 (1.08-1.13)	1.1×10^{-14}	0.76	97%
15	rs4562997	67,458,152	G/A	1.10 (1.07-1.13)	5.2×10^{-14}	1.10 (1.07-1.13)	5.2×10^{-14}	0.75	100%
15	rs16950687	67,464,013	A/G	1.09 (1.07-1.12)	1.3×10^{-12}	1.09 (1.07-1.12)	1.3×10^{-12}	0.81	100%
15	rs12708492	67,467,541	T/C	0.92 (0.90-0.94)	6.5×10^{-13}	0.92 (0.90-0.94)	6.5×10^{-13}	0.90	100%
15	rs17294280	67,468,285	A/G	1.12 (1.08-1.16)	2.3×10^{-10}	1.13 (1.09-1.16)	1.6×10^{-14}	0.15	92%
16	rs17802927	11,037,738	A/G	0.91 (0.88-0.94)	3.6×10^{-10}	0.91 (0.88-0.94)	3.6×10^{-10}	0.55	98%
16	rs3743976	11,038,824	C/T	0.91 (0.88-0.93)	3.1×10^{-10}	0.90 (0.88-0.93)	8.6×10^{-11}	0.44	94%
16	rs17229044	11,062,936	C/T	0.91 (0.88-0.94)	3.9×10^{-09}	0.91 (0.88-0.94)	2.1×10^{-10}	0.36	100%
16	rs12921922	11,064,321	T/C	0.91 (0.88-0.94)	5.9×10^{-09}	0.91 (0.88-0.93)	8.9×10^{-11}	0.30	94%
16	rs8062923	11,160,966	A/C	1.10 (1.06-1.13)	2.0×10^{-09}	1.10 (1.07-1.13)	2.8×10^{-11}	0.31	100%
16	rs4781035	11,161,178	A/G	1.10 (1.07-1.13)	2.5×10^{-09}	1.10 (1.07-1.13)	2.5×10^{-10}	0.38	100%
16	rs12444495	11,170,455	T/C	1.10 (1.07-1.14)	4.8×10^{-10}	1.10 (1.07-1.14)	4.8×10^{-10}	0.53	83%
16	rs17806299	11,199,980	G/A	0.91 (0.88-0.94)	2.7×10^{-10}	0.91 (0.88-0.94)	2.7×10^{-10}	0.49	100%
16	rs12935657	11,219,041	G/A	0.91 (0.88-0.94)	3.0×10^{-09}	0.90 (0.88-0.93)	1.8×10^{-12}	0.23	98%
17	rs12950186	37,393,395	A/C	0.90 (0.87-0.93)	3.7×10^{-11}	0.90 (0.87-0.93)	3.7×10^{-11}	0.94	98%
17	rs2879258	37,399,379	G/T	0.90 (0.88-0.93)	8.3×10^{-10}	0.90 (0.88-0.93)	8.3×10^{-10}	0.96	100%
17	rs11078895	37,401,051	A/G	0.90 (0.88-0.93)	7.1×10^{-11}	0.90 (0.88-0.93)	7.1×10^{-11}	0.96	98%
17	rs11655972	37,407,072	C/T	0.90 (0.87-0.93)	2.6×10^{-11}	0.90 (0.87-0.93)	2.6×10^{-11}	0.96	100%
17	rs3744349	37,414,842	C/T	0.90 (0.87-0.93)	2.3×10^{-11}	0.90 (0.87-0.93)	2.3×10^{-11}	0.97	100%
17	rs8073907	37,424,149	C/T	0.90 (0.87-0.93)	6.7×10^{-10}	0.90 (0.87-0.93)	6.7×10^{-10}	0.95	83%
17	rs667239	37,442,241	A/G	1.11 (1.07-1.14)	3.6×10^{-11}	1.11 (1.07-1.14)	3.6×10^{-11}	0.97	100%
17	rs590051	37,446,571	T/C	1.11 (1.07-1.14)	4.1×10^{-11}	1.11 (1.07-1.14)	4.1×10^{-11}	0.97	100%
17	rs2302073	37,457,342	A/G	1.11 (1.07-1.14)	3.7×10^{-11}	1.11 (1.07-1.14)	3.7×10^{-11}	0.97	100%
17	rs584377	37,460,128	G/A	1.11 (1.07-1.14)	3.9×10^{-11}	1.11 (1.07-1.14)	3.9×10^{-11}	0.97	100%
17	rs649180	37,464,959	A/C	1.11 (1.07-1.14)	8.3×10^{-11}	1.11 (1.07-1.14)	8.3×10^{-11}	0.98	100%
17	rs2338799	37,513,941	G/A	1.11 (1.07-1.14)	4.0×10^{-11}	1.11 (1.07-1.14)	4.0×10^{-11}	0.97	100%
17	rs6503504	37,514,412	A/G	1.11 (1.07-1.14)	6.5×10^{-11}	1.11 (1.07-1.14)	6.5×10^{-11}	0.97	97%
17	rs9908131	37,520,449	T/C	1.11 (1.07-1.14)	4.4×10^{-11}	1.11 (1.07-1.14)	4.4×10^{-11}	0.97	100%
17	rs11078898	37,536,480	A/G	1.09 (1.06-1.12)	8.6×10^{-09}	1.09 (1.06-1.11)	4.9×10^{-10}	0.27	100%
17	rs7208487	37,543,449	T/G	1.11 (1.07-1.14)	6.4×10^{-11}	1.11 (1.07-1.14)	6.4×10^{-11}	0.97	100%
17	rs9906612	37,547,631	A/C	1.10 (1.07-1.14)	6.9×10^{-10}	1.10 (1.07-1.14)	6.9×10^{-10}	0.99	97%
17	rs6503513	37,561,613	A/G	1.09 (1.06-1.12)	5.9×10^{-09}	1.09 (1.06-1.12)	5.9×10^{-09}	0.92	97%
17	rs4795358	37,573,065	A/C	0.91 (0.88-0.93)	2.3×10^{-10}	0.91 (0.88-0.93)	2.3×10^{-10}	0.98	97%
17	rs9646419	37,597,185	A/G	0.91 (0.88-0.93)	2.0×10^{-10}	0.91 (0.88-0.93)	2.0×10^{-10}	0.99	97%
17	rs12938099	37,612,910	T/G	0.90 (0.88-0.93)	1.2×10^{-10}	0.90 (0.88-0.93)	1.2×10^{-10}	0.98	97%
17	rs12449852	37,632,088	A/G	0.90 (0.87-0.93)	5.2×10^{-09}	0.90 (0.87-0.93)	5.2×10^{-09}	0.97	94%
17	rs12936996	37,665,554	G/A	0.92 (0.89-0.95)	8.9×10^{-09}	0.92 (0.90-0.94)	4.0×10^{-10}	0.25	98%
17	rs12937013	37,665,571	G/A	0.90 (0.87-0.93)	6.9×10^{-12}	0.90 (0.87-0.93)	6.9×10^{-12}	0.98	100%
17	rs7503705	37,669,704	A/G	0.92 (0.89-0.94)	2.1×10^{-09}	0.92 (0.89-0.94)	1.2×10^{-10}	0.28	100%
17	rs11078913	37,671,714	G/T	0.92 (0.89-0.94)	8.9×10^{-09}	0.92 (0.89-0.94)	2.8×10^{-10}	0.23	98%
17	rs8065963	37,681,332	C/T	0.92 (0.89-0.94)	3.1×10^{-09}	0.92 (0.89-0.94)	1.4×10^{-10}	0.25	100%
17	rs8069074	37,685,401	A/G	0.90 (0.87-0.93)	4.5×10^{-11}	0.90 (0.87-0.93)	4.5×10^{-11}	0.97	98%
17	rs12450559	37,694,709	G/A	0.92 (0.89-0.94)	2.6×10^{-09}	0.92 (0.89-0.94)	1.4×10^{-10}	0.27	100%
17	rs4239222	37,696,235	G/T	0.92 (0.89-0.95)	3.3×10^{-09}	0.92 (0.90-0.94)	2.0×10^{-10}	0.28	100%
17	rs11657058	37,699,378	T/G	0.90 (0.87-0.93)	8.6×10^{-12}	0.90 (0.87-0.93)	8.6×10^{-12}	0.98	100%
17	rs11657153	37,699,729	A/G	0.90 (0.87-0.93)	2.3×10^{-10}	0.90 (0.87-0.93)	2.3×10^{-10}	0.95	86%
17	rs11654018	37,703,740	T/C	0.92 (0.89-0.94)	2.7×10^{-09}	0.92 (0.90-0.94)	2.0×10^{-10}	0.29	100%
17	rs2303316	37,704,217	A/G	0.92 (0.89-0.95)	9.0×10^{-09}	0.92 (0.90-0.94)	4.0×10^{-10}	0.24	100%
17	rs12947506	37,707,592	T/C	0.90 (0.87-0.93)	1.0×10^{-11}	0.90 (0.87-0.93)	1.0×10^{-11}	0.98	100%
17	rs7503377	37,708,841	T/C	0.90 (0.87-0.93)	2.3×10^{-11}	0.90 (0.87-0.93)	2.3×10^{-11}	0.99	100%
17	rs7216086	37,709,422	G/A	0.92 (0.89-0.95)	6.7×10^{-09}	0.92 (0.90-0.94)	3.0×10^{-10}	0.25	100%
17	rs11078915	37,715,426	T/C	0.92 (0.89-0.94)	8.7×10^{-10}	0.92 (0.89-0.94)	7.6×10^{-11}	0.31	100%
17	rs6503521	37,715,551	G/T	0.89 (0.87-0.92)	1.4×10^{-11}	0.89 (0.87-0.92)	1.4×10^{-11}	0.98	98%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
17	rs903507	37,726,423	C/T	1.12 (1.08-1.15)	1.1×10^{-12}	1.12 (1.08-1.15)	1.1×10^{-12}	0.97	98%
17	rs8182252	37,727,950	T/C	1.11 (1.07-1.14)	1.4×10^{-09}	1.11 (1.07-1.14)	1.4×10^{-09}	0.84	82%
17	rs1874226	37,729,031	C/T	1.12 (1.08-1.15)	1.5×10^{-12}	1.12 (1.08-1.15)	1.5×10^{-12}	0.96	98%
17	rs4795385	37,733,148	A/G	1.13 (1.09-1.16)	3.0×10^{-14}	1.13 (1.09-1.16)	3.0×10^{-14}	0.97	97%
17	rs1619021	37,739,274	G/A	0.91 (0.89-0.94)	7.6×10^{-11}	0.91 (0.89-0.94)	1.1×10^{-11}	0.35	98%
17	rs1877030	37,740,161	T/C	0.89 (0.86-0.92)	2.6×10^{-13}	0.89 (0.86-0.92)	2.6×10^{-13}	0.99	98%
17	rs12453198	37,741,879	T/C	0.89 (0.86-0.92)	1.9×10^{-14}	0.89 (0.86-0.92)	1.9×10^{-14}	0.95	98%
17	rs11654954	37,745,979	A/G	0.89 (0.86-0.91)	8.9×10^{-15}	0.89 (0.86-0.91)	8.9×10^{-15}	0.93	98%
17	rs12453682	37,770,005	C/T	0.90 (0.88-0.92)	6.9×10^{-14}	0.90 (0.88-0.92)	3.7×10^{-16}	0.27	98%
17	rs1874228	37,775,274	A/G	0.90 (0.88-0.93)	4.2×10^{-14}	0.90 (0.88-0.93)	4.2×10^{-14}	0.58	97%
17	rs879606	37,781,849	A/G	0.89 (0.86-0.92)	1.4×10^{-12}	0.89 (0.86-0.92)	1.4×10^{-12}	0.96	88%
17	rs2271309	37,784,990	G/A	0.89 (0.86-0.91)	1.9×10^{-16}	0.89 (0.86-0.91)	1.9×10^{-16}	0.93	98%
17	rs907094	37,790,371	G/A	0.89 (0.87-0.92)	6.4×10^{-15}	0.89 (0.87-0.92)	6.4×10^{-15}	0.91	98%
17	rs3764352	37,790,939	C/T	0.90 (0.87-0.93)	5.5×10^{-11}	0.90 (0.87-0.93)	5.5×10^{-11}	0.91	80%
17	rs9972882	37,807,698	A/C	0.88 (0.86-0.91)	2.2×10^{-21}	0.88 (0.86-0.91)	2.2×10^{-21}	0.78	98%
17	rs1877031	37,814,080	G/A	0.89 (0.87-0.91)	1.0×10^{-21}	0.89 (0.87-0.91)	1.0×10^{-21}	0.61	98%
17	rs2271308	37,817,482	T/C	0.89 (0.87-0.92)	3.4×10^{-18}	0.89 (0.87-0.92)	3.4×10^{-18}	0.81	98%
17	rs931992	37,821,435	G/T	0.89 (0.87-0.91)	2.3×10^{-21}	0.89 (0.87-0.91)	2.3×10^{-21}	0.62	98%
17	rs1053651	37,822,311	A/C	0.89 (0.87-0.92)	1.6×10^{-15}	0.89 (0.87-0.92)	1.6×10^{-15}	0.66	85%
17	rs876493	37,824,545	G/A	0.88 (0.85-0.91)	5.9×10^{-13}	0.88 (0.85-0.90)	2.4×10^{-17}	0.17	76%
17	rs14050	37,828,072	C/T	0.87 (0.84-0.89)	6.3×10^{-23}	0.87 (0.84-0.89)	6.3×10^{-23}	0.58	80%
17	rs2952151	37,828,496	T/C	0.87 (0.85-0.89)	3.8×10^{-28}	0.87 (0.85-0.89)	3.8×10^{-28}	0.67	98%
17	rs2941503	37,828,745	A/G	0.87 (0.85-0.89)	6.8×10^{-23}	0.87 (0.85-0.89)	6.8×10^{-23}	0.48	82%
17	rs907087	37,828,787	G/A	0.87 (0.84-0.89)	6.0×10^{-23}	0.87 (0.84-0.89)	6.0×10^{-23}	0.51	80%
17	rs903502	37,829,604	C/T	0.88 (0.86-0.90)	1.0×10^{-26}	0.88 (0.86-0.90)	1.0×10^{-26}	0.79	100%
17	rs2941504	37,830,900	A/G	0.87 (0.85-0.89)	1.3×10^{-27}	0.87 (0.85-0.89)	1.3×10^{-27}	0.57	98%
17	rs1565922	37,831,035	A/G	0.87 (0.85-0.89)	7.0×10^{-28}	0.87 (0.85-0.89)	7.0×10^{-28}	0.72	98%
17	rs2934952	37,832,366	G/A	0.87 (0.85-0.89)	1.2×10^{-23}	0.87 (0.85-0.89)	1.2×10^{-23}	0.48	82%
17	rs2941505	37,832,704	A/G	0.88 (0.86-0.90)	2.0×10^{-25}	0.88 (0.86-0.90)	2.0×10^{-25}	0.62	100%
17	rs2941506	37,833,035	A/G	0.88 (0.86-0.90)	1.4×10^{-24}	0.88 (0.86-0.90)	1.4×10^{-24}	0.54	97%
17	rs907089	37,833,600	G/A	0.88 (0.86-0.90)	8.8×10^{-24}	0.88 (0.86-0.90)	8.8×10^{-24}	0.62	98%
17	rs2313171	37,833,842	T/C	0.88 (0.86-0.90)	1.6×10^{-24}	0.88 (0.86-0.90)	1.6×10^{-24}	0.54	97%
17	rs12150298	37,834,541	T/C	0.88 (0.86-0.90)	2.3×10^{-24}	0.88 (0.86-0.90)	2.3×10^{-24}	0.58	100%
17	rs8078228	37,834,998	C/T	0.88 (0.86-0.90)	1.4×10^{-24}	0.88 (0.86-0.90)	1.4×10^{-24}	0.52	97%
17	rs11078919	37,835,755	T/C	0.88 (0.86-0.91)	1.4×10^{-22}	0.88 (0.86-0.91)	1.4×10^{-22}	0.52	95%
17	rs1476278	37,836,243	C/T	0.88 (0.86-0.90)	2.8×10^{-26}	0.88 (0.86-0.90)	2.8×10^{-26}	0.62	100%
17	rs9303274	37,836,353	T/C	0.88 (0.86-0.90)	1.9×10^{-25}	0.88 (0.86-0.90)	1.9×10^{-25}	0.56	97%
17	rs2517957	37,838,716	G/A	0.87 (0.85-0.90)	2.3×10^{-27}	0.87 (0.85-0.90)	2.3×10^{-27}	0.59	100%
17	rs2517958	37,838,751	G/A	0.87 (0.85-0.90)	2.2×10^{-27}	0.87 (0.85-0.90)	2.2×10^{-27}	0.58	100%
17	rs903501	37,839,493	T/C	0.88 (0.85-0.90)	2.0×10^{-17}	0.87 (0.85-0.90)	1.1×10^{-20}	0.31	80%
17	rs2517954	37,843,550	T/C	0.87 (0.85-0.89)	2.1×10^{-28}	0.87 (0.85-0.89)	2.1×10^{-28}	0.60	98%
17	rs2517955	37,843,681	C/T	0.87 (0.85-0.90)	1.3×10^{-26}	0.87 (0.85-0.90)	1.3×10^{-26}	0.64	98%
17	rs2517956	37,843,859	G/A	0.87 (0.85-0.90)	3.3×10^{-27}	0.87 (0.85-0.90)	3.3×10^{-27}	0.62	98%
17	rs1565923	37,858,678	A/G	0.86 (0.84-0.89)	2.1×10^{-25}	0.86 (0.84-0.89)	2.1×10^{-25}	0.50	79%
17	rs2952155	37,861,718	T/C	0.87 (0.84-0.89)	2.9×10^{-26}	0.87 (0.84-0.89)	2.9×10^{-26}	0.84	98%
17	rs1810132	37,866,005	C/T	0.87 (0.84-0.89)	2.9×10^{-30}	0.87 (0.84-0.89)	2.9×10^{-30}	0.59	98%
17	rs2952156	37,876,835	A/G	0.87 (0.84-0.89)	2.2×10^{-30}	0.87 (0.84-0.89)	2.2×10^{-30}	0.52	98%
17	rs907091	37,921,742	C/T	1.18 (1.14-1.22)	2.8×10^{-20}	1.18 (1.15-1.21)	3.1×10^{-36}	0.01	86%
17	rs907092	37,922,259	G/A	0.85 (0.83-0.88)	2.5×10^{-23}	0.85 (0.83-0.87)	3.0×10^{-37}	0.02	97%
17	rs10445308	37,938,047	C/T	0.85 (0.83-0.88)	1.8×10^{-24}	0.85 (0.83-0.87)	7.3×10^{-39}	0.03	98%
17	rs9909593	37,970,149	A/G	0.85 (0.83-0.88)	5.1×10^{-24}	0.85 (0.83-0.87)	7.2×10^{-39}	0.02	98%
17	rs9303277	37,976,469	C/T	0.85 (0.83-0.88)	9.6×10^{-26}	0.85 (0.83-0.87)	4.9×10^{-43}	0.02	98%
17	rs3816470	37,985,801	A/G	0.85 (0.83-0.88)	1.2×10^{-26}	0.85 (0.83-0.87)	6.5×10^{-41}	0.05	97%
17	rs9635726	38,020,141	C/T	1.16 (1.13-1.20)	1.5×10^{-23}	1.16 (1.13-1.20)	1.5×10^{-23}	0.52	95%
17	rs4795397	38,023,745	A/G	0.86 (0.83-0.89)	2.5×10^{-16}	0.86 (0.84-0.88)	8.0×10^{-29}	0.01	82%
17	rs11557466	38,024,626	C/T	0.85 (0.83-0.88)	8.1×10^{-22}	0.85 (0.83-0.87)	4.5×10^{-36}	0.02	95%
17	rs11078925	38,025,208	T/C	0.85 (0.83-0.88)	2.1×10^{-24}	0.85 (0.83-0.87)	2.8×10^{-38}	0.03	98%
17	rs12150079	38,025,417	G/A	0.88 (0.85-0.90)	2.4×10^{-15}	0.88 (0.85-0.90)	1.1×10^{-21}	0.08	97%
17	rs11557467	38,028,634	G/T	0.85 (0.82-0.88)	3.3×10^{-21}	0.85 (0.83-0.87)	3.5×10^{-31}	0.07	80%
17	rs10852936	38,031,714	C/T	0.86 (0.83-0.89)	3.1×10^{-17}	0.86 (0.83-0.88)	2.1×10^{-27}	0.03	80%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
17	rs1054609	38,033,277	A/C	0.86 (0.83-0.88)	1.1×10^{-24}	0.85 (0.83-0.88)	3.3×10^{-37}	0.05	97%
17	rs9907088	38,035,116	G/A	0.86 (0.83-0.88)	1.6×10^{-24}	0.85 (0.83-0.87)	6.5×10^{-38}	0.04	98%
17	rs12232497	38,040,119	T/C	0.85 (0.82-0.88)	1.6×10^{-24}	0.85 (0.83-0.87)	9.7×10^{-39}	0.03	98%
17	rs2872507	38,040,763	G/A	0.86 (0.83-0.88)	2.0×10^{-24}	0.85 (0.83-0.87)	8.1×10^{-38}	0.04	98%
17	rs9901146	38,043,343	G/A	0.85 (0.82-0.87)	9.0×10^{-30}	0.84 (0.83-0.87)	6.1×10^{-44}	0.06	98%
17	rs12950743	38,049,233	T/C	0.85 (0.82-0.87)	6.8×10^{-30}	0.84 (0.82-0.87)	5.6×10^{-44}	0.06	98%
17	rs7359623	38,049,589	C/T	0.85 (0.82-0.87)	1.9×10^{-27}	0.84 (0.82-0.87)	2.0×10^{-41}	0.05	95%
17	rs8067378	38,051,348	A/G	0.85 (0.83-0.88)	1.5×10^{-28}	0.85 (0.83-0.87)	4.8×10^{-42}	0.07	98%
17	rs8069176	38,057,197	G/A	0.85 (0.82-0.88)	2.0×10^{-23}	0.85 (0.83-0.87)	4.6×10^{-41}	0.01	98%
17	rs2305480	38,062,196	G/A	0.85 (0.82-0.87)	3.5×10^{-23}	0.85 (0.83-0.87)	2.7×10^{-41}	0.00	98%
17	rs2305479	38,062,217	C/T	0.84 (0.81-0.87)	2.0×10^{-28}	0.84 (0.82-0.86)	1.0×10^{-46}	0.02	98%
17	rs11078926	38,062,976	G/A	0.85 (0.81-0.88)	2.6×10^{-16}	0.85 (0.82-0.87)	5.3×10^{-31}	0.00	80%
17	rs11078927	38,064,405	C/T	0.85 (0.82-0.87)	1.4×10^{-23}	0.85 (0.82-0.87)	2.1×10^{-41}	0.01	98%
17	rs2290400	38,066,240	T/C	0.85 (0.82-0.88)	1.5×10^{-25}	0.85 (0.83-0.87)	1.5×10^{-43}	0.01	98%
17	rs1008723	38,066,267	G/T	0.84 (0.82-0.87)	6.1×10^{-29}	0.84 (0.82-0.86)	9.0×10^{-46}	0.03	98%
17	rs4795400	38,067,020	C/T	0.85 (0.82-0.88)	7.5×10^{-23}	0.85 (0.83-0.87)	5.5×10^{-41}	0.00	98%
17	rs869402	38,068,043	T/C	1.19 (1.15-1.23)	1.3×10^{-25}	1.20 (1.17-1.22)	2.5×10^{-46}	0.00	97%
17	rs7216389	38,069,949	C/T	1.19 (1.15-1.23)	6.7×10^{-26}	1.19 (1.17-1.22)	8.3×10^{-47}	0.01	98%
17	rs9303280	38,074,031	T/C	1.18 (1.15-1.22)	9.3×10^{-25}	1.19 (1.16-1.22)	3.0×10^{-43}	0.01	97%
17	rs9303281	38,074,046	G/A	1.18 (1.14-1.22)	2.4×10^{-24}	1.19 (1.16-1.22)	6.2×10^{-45}	0.00	98%
17	rs7219923	38,074,518	C/T	1.18 (1.14-1.22)	2.2×10^{-24}	1.19 (1.16-1.21)	2.5×10^{-44}	0.01	98%
17	rs7224129	38,075,426	G/A	1.18 (1.14-1.22)	8.9×10^{-25}	1.19 (1.16-1.22)	6.4×10^{-45}	0.01	98%
17	rs4378650	38,080,865	A/G	1.19 (1.14-1.24)	6.0×10^{-18}	1.21 (1.18-1.24)	3.8×10^{-41}	0.00	74%
17	rs8076131	38,080,912	G/A	1.18 (1.14-1.22)	9.8×10^{-21}	1.18 (1.15-1.21)	1.5×10^{-39}	0.00	97%
17	rs12603332	38,082,807	T/C	1.17 (1.14-1.21)	8.9×10^{-23}	1.18 (1.15-1.21)	3.9×10^{-41}	0.01	97%
17	rs4795402	38,085,385	A/C	1.11 (1.07-1.14)	2.5×10^{-10}	1.11 (1.08-1.14)	3.0×10^{-15}	0.06	100%
17	rs4795405	38,088,417	T/C	1.17 (1.13-1.21)	4.0×10^{-21}	1.18 (1.15-1.21)	5.7×10^{-44}	0.00	98%
17	rs4794820	38,089,344	A/G	1.16 (1.12-1.20)	3.1×10^{-18}	1.17 (1.14-1.20)	3.9×10^{-34}	0.01	95%
17	rs7207600	38,091,660	G/A	1.14 (1.11-1.17)	5.6×10^{-18}	1.15 (1.12-1.18)	3.3×10^{-28}	0.09	98%
17	rs8079416	38,092,713	T/C	1.14 (1.11-1.18)	1.3×10^{-19}	1.15 (1.13-1.18)	1.3×10^{-33}	0.03	98%
17	rs8065126	38,099,035	T/C	1.14 (1.11-1.17)	1.2×10^{-18}	1.14 (1.12-1.17)	1.2×10^{-26}	0.17	98%
17	rs4795408	38,107,627	G/A	1.15 (1.12-1.19)	1.6×10^{-20}	1.16 (1.13-1.19)	1.5×10^{-35}	0.03	98%
17	rs9895948	38,108,363	T/C	1.13 (1.10-1.17)	3.8×10^{-13}	1.15 (1.12-1.18)	9.0×10^{-24}	0.05	83%
17	rs17609240	38,110,689	T/G	1.13 (1.09-1.18)	5.8×10^{-12}	1.15 (1.12-1.18)	2.3×10^{-23}	0.03	83%
17	rs1007654	38,111,354	A/G	1.13 (1.09-1.16)	1.3×10^{-15}	1.14 (1.11-1.16)	4.4×10^{-24}	0.11	98%
17	rs1007655	38,111,419	G/A	1.14 (1.10-1.17)	3.9×10^{-13}	1.15 (1.12-1.18)	1.3×10^{-22}	0.10	80%
17	rs2313640	38,111,845	C/T	1.13 (1.09-1.16)	1.2×10^{-15}	1.14 (1.11-1.16)	3.5×10^{-24}	0.11	98%
17	rs7218742	38,114,361	A/G	1.13 (1.10-1.16)	1.2×10^{-16}	1.14 (1.11-1.17)	1.2×10^{-24}	0.15	98%
17	rs7218321	38,114,469	C/T	1.12 (1.08-1.15)	4.4×10^{-12}	1.13 (1.10-1.16)	4.8×10^{-22}	0.04	95%
17	rs7219080	38,114,516	A/C	1.12 (1.09-1.15)	3.6×10^{-13}	1.13 (1.10-1.16)	6.2×10^{-23}	0.05	98%
17	rs6503526	38,114,598	C/T	1.15 (1.12-1.18)	2.2×10^{-20}	1.16 (1.13-1.19)	6.0×10^{-35}	0.03	98%
17	rs6503527	38,114,719	G/A	1.13 (1.09-1.17)	1.6×10^{-12}	1.14 (1.11-1.17)	4.4×10^{-22}	0.06	79%
17	rs3902025	38,119,254	G/T	1.13 (1.09-1.16)	8.4×10^{-15}	1.14 (1.12-1.17)	8.8×10^{-29}	0.01	98%
17	rs3894194	38,121,993	G/A	1.15 (1.12-1.18)	2.4×10^{-20}	1.16 (1.13-1.18)	1.4×10^{-34}	0.03	98%
17	rs7212938	38,122,680	G/T	0.87 (0.84-0.89)	2.6×10^{-19}	0.86 (0.84-0.88)	5.0×10^{-32}	0.04	95%
17	rs3859192	38,128,648	C/T	1.13 (1.09-1.16)	3.5×10^{-14}	1.13 (1.11-1.16)	9.4×10^{-26}	0.01	97%
17	rs8075668	38,137,623	C/T	0.90 (0.88-0.92)	5.8×10^{-15}	0.90 (0.88-0.92)	1.6×10^{-19}	0.21	97%
17	rs2305481	38,138,624	G/A	0.90 (0.87-0.92)	1.8×10^{-15}	0.89 (0.87-0.92)	1.0×10^{-19}	0.24	100%
17	rs2305482	38,140,927	A/C	0.93 (0.90-0.95)	4.1×10^{-10}	0.93 (0.90-0.95)	5.2×10^{-11}	0.38	100%
17	rs11078930	38,141,955	C/T	0.88 (0.86-0.90)	6.6×10^{-21}	0.88 (0.86-0.90)	6.6×10^{-21}	0.65	94%
17	rs4065321	38,143,548	C/T	0.92 (0.90-0.95)	1.5×10^{-10}	0.92 (0.90-0.94)	1.8×10^{-11}	0.38	97%
17	rs8066582	38,146,929	T/C	0.93 (0.90-0.95)	1.0×10^{-09}	0.93 (0.91-0.95)	6.7×10^{-11}	0.34	100%
17	rs11658328	38,149,236	T/C	0.93 (0.90-0.95)	3.6×10^{-10}	0.93 (0.91-0.95)	7.3×10^{-11}	0.40	100%
17	rs2241245	38,151,014	C/T	0.93 (0.90-0.95)	5.4×10^{-10}	0.93 (0.90-0.95)	4.2×10^{-11}	0.35	100%
17	rs12453334	38,153,473	C/T	0.89 (0.87-0.92)	2.4×10^{-19}	0.89 (0.87-0.92)	2.4×10^{-19}	0.57	100%
17	rs4794822	38,156,712	C/T	1.10 (1.07-1.13)	1.9×10^{-11}	1.10 (1.08-1.13)	2.0×10^{-16}	0.09	100%
17	rs8070454	38,160,754	C/T	1.10 (1.07-1.13)	1.2×10^{-11}	1.10 (1.08-1.13)	9.3×10^{-17}	0.09	100%
17	rs8078723	38,166,879	T/C	1.10 (1.07-1.13)	1.6×10^{-11}	1.10 (1.08-1.13)	9.1×10^{-17}	0.08	100%
17	rs2227319	38,170,845	G/A	0.89 (0.87-0.92)	9.7×10^{-20}	0.89 (0.87-0.92)	9.7×10^{-20}	0.53	100%
17	rs25645	38,173,143	G/A	0.89 (0.87-0.91)	2.1×10^{-20}	0.89 (0.87-0.91)	2.1×10^{-20}	0.56	100%

Chrom	SNP	Position	Allele (R/E)	OR_{random} (95% CI)[a]	P_{random}[b]	OR_{fixed} (95% CI)[a]	P_{fixed}[c]	P_{het}[d]	% of studies contributing to meta-analysis (per SNP)
17	rs1042658	38,173,902	C/T	1.10 (1.07-1.13)	3.8×10^{-11}	1.10 (1.08-1.13)	1.3×10^{-16}	0.07	100%
17	rs1045929	38,175,426	C/T	1.10 (1.07-1.14)	3.2×10^{-09}	1.11 (1.08-1.14)	1.4×10^{-13}	0.12	82%
17	rs12309	38,175,462	C/T	0.88 (0.86-0.91)	2.0×10^{-18}	0.88 (0.86-0.91)	2.0×10^{-18}	0.54	82%
17	rs709592	38,175,553	C/T	1.10 (1.07-1.13)	4.4×10^{-11}	1.10 (1.08-1.13)	1.4×10^{-16}	0.07	100%
17	rs2302776	38,178,149	A/G	0.91 (0.89-0.94)	4.5×10^{-13}	0.91 (0.89-0.94)	4.5×10^{-13}	0.71	97%
17	rs3213762	38,178,627	A/G	1.10 (1.07-1.14)	2.2×10^{-11}	1.11 (1.08-1.13)	4.8×10^{-17}	0.07	97%
17	rs12451897	38,179,275	G/T	0.89 (0.87-0.91)	7.9×10^{-18}	0.89 (0.87-0.91)	7.9×10^{-18}	0.57	83%
17	rs2302777	38,179,492	A/G	0.89 (0.87-0.91)	1.1×10^{-20}	0.89 (0.87-0.91)	1.1×10^{-20}	0.63	100%
17	rs9916158	38,182,229	G/T	0.90 (0.87-0.92)	1.1×10^{-14}	0.89 (0.87-0.92)	2.1×10^{-17}	0.34	86%
17	rs2302774	38,183,090	G/T	0.89 (0.87-0.91)	2.8×10^{-20}	0.89 (0.87-0.91)	2.8×10^{-20}	0.57	98%
17	rs7502514	38,188,844	A/G	0.91 (0.88-0.93)	1.5×10^{-10}	0.90 (0.88-0.92)	1.9×10^{-16}	0.05	97%
17	rs11078936	38,197,914	T/C	0.90 (0.87-0.92)	3.5×10^{-18}	0.90 (0.87-0.92)	3.5×10^{-18}	0.75	98%
17	rs8065443	38,208,940	A/G	0.91 (0.89-0.94)	1.7×10^{-10}	0.91 (0.89-0.93)	5.5×10^{-15}	0.08	98%
17	rs868150	38,213,359	A/G	0.91 (0.89-0.94)	9.4×10^{-11}	0.91 (0.89-0.93)	4.2×10^{-15}	0.10	98%
17	rs17637472	47,461,433	G/A	1.08 (1.05-1.11)	6.6×10^{-09}	1.08 (1.05-1.11)	1.1×10^{-09}	0.35	98%

[a]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele (random & fixed-effects models)

[b]P_{random} is P-value for test of association between SNP and asthma under a random-effects model

[c]P_{fixed} is P-value for test of association between SNP and asthma under a fixed-effects model

[d]P_{het} is the P-value for test of heterogeneity across studies with the use of Cochran's test

Supplementary Table 9. Genetic loci associated with pediatric asthma

Results are shown for the lead SNP at each locus reaching $P_{random} < 5 \times 10^{-8}$

Region[a]	Lead SNP	Position	Nearby Genes[b]	Alleles (R/E)[c]	OR (95%CI)[d]	P_{random}[e]	P_{fixed}[f]	P_{het}[g]
2q12.1	rs4988958	102,968,285	IL1RL1,IL1RL2, IL18R1	T/C	0.85 (0.82-0.89)	5.36×10^{-13}	5.36×10^{-13}	0.78
5q31.1	rs1295685	131,996,445	IL13,RAD50,IL4	A/G	0.86 (0.82-0.9)	1.67×10^{-9}	1.67×10^{-9}	0.89
6p21.33	rs2596464	31,412,961	MICA,MICB	T/C	1.12 (1.08-1.17)	1.35×10^{-8}	1.35×10^{-8}	0.47
9p24.1	rs12551256	6,231,239	IL33, RANBP6, TPD52L3	A/G	0.89 (0.86-0.93)	2.77×10^{-8}	2.77×10^{-8}	0.51
17q12-q21	rs8069176	38,057,197	ZPBP2,GSDMB	G/A	0.8 (0.77-0.83)	4.42×10^{-26}	4.42×10^{-26}	0.77

[a]Cytogenetic position of the chromosomal region harboring the lead SNP
[b]Genes coding for proteins; the gene where eventually the lead SNP lies is first indicated followed by the previous gene and next gene
[c]R=reference allele /E=effect allele.
[d]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele under a random-effects model
[e]P_{random} is the P-value for test of association between SNP and asthma under a random-effects model
[f]P_{fixed} is the P-value for test of association between SNP and asthma under a fixed-effects model
[g]P_{het} is the P-value for test of heterogeneity across studies with the use of Cochran’s test

Supplementary Table 10. Association of 17q12-21 SNPs with asthma in multi-ancestry and pediatric meta-analyses

			Multi-ancestry meta-analysis				Pediatric subgroup meta-analysis			
SNP	Position	Allele (R/E)[a]	OR (95% CI)[b]	P_{random}[c]	P_{fixed}[d]	P_{het}[e]	OR (95% CI)[b]	P_{random}[c]	P_{fixed}[d]	P_{het}[e]
rs12950186	37,393,395	A/C	0.9 (0.87-0.93)	3.67E-11	3.67E-11	0.94	0.9 (0.85-0.95)	1.93E-04	1.93E-04	0.72
rs11078893	37,396,679	T/C	0.92 (0.89-0.95)	8.69E-08	1.29E-09	0.20	0.9 (0.86-0.95)	5.65E-05	5.65E-05	0.53
rs2879258	37,399,379	G/T	0.9 (0.88-0.93)	8.33E-10	8.34E-10	0.96	0.91 (0.86-0.95)	2.55E-04	2.55E-04	0.78
rs11078895	37,401,051	A/G	0.9 (0.88-0.93)	7.11E-11	7.11E-11	0.96	0.9 (0.85-0.95)	1.42E-04	1.42E-04	0.79
rs3964723	37,403,979	C/T	0.92 (0.9-0.95)	1.94E-08	7.61E-10	0.24	0.9 (0.86-0.95)	1.76E-05	1.77E-05	0.58
rs2061342	37,405,657	T/G	0.92 (0.89-0.95)	7.12E-08	1.34E-09	0.17	0.9 (0.86-0.95)	1.39E-05	1.39E-05	0.60
rs11655972	37,407,072	C/T	0.9 (0.87-0.93)	2.65E-11	2.65E-11	0.96	0.9 (0.86-0.95)	1.91E-04	1.91E-04	0.80
rs2168785	37,407,135	C/T	0.92 (0.89-0.95)	9.45E-08	1.04E-09	0.14	0.9 (0.86-0.95)	1.73E-05	1.73E-05	0.59
rs755500	37,409,865	G/A	0.92 (0.9-0.95)	1.55E-08	4.91E-10	0.23	0.9 (0.86-0.95)	1.38E-05	1.38E-05	0.60
rs752314	37,410,700	C/T	0.92 (0.89-0.95)	1.42E-08	3.59E-10	0.21	0.9 (0.86-0.95)	1.42E-05	1.42E-05	0.59
rs3744349	37,414,842	C/T	0.9 (0.88-0.93)	2.29E-11	2.29E-11	0.97	0.9 (0.85-0.95)	9.87E-05	9.87E-05	0.82
rs11078897	37,415,870	C/T	0.92 (0.89-0.95)	1.59E-08	4.02E-10	0.21	0.9 (0.86-0.95)	1.48E-05	1.48E-05	0.59
rs2338755	37,419,317	T/C	0.92 (0.89-0.95)	1.68E-08	4.11E-10	0.21	0.9 (0.86-0.95)	1.51E-05	1.51E-05	0.59
rs8073907	37,424,149	C/T	0.9 (0.87-0.93)	6.73E-10	6.73E-10	0.95	0.9 (0.85-0.95)	4.08E-04	4.08E-04	0.82
rs8079590	37,426,201	T/C	0.91 (0.88-0.95)	6.72E-07	4.85E-09	0.12	0.9 (0.85-0.95)	1.04E-04	4.64E-05	0.39
rs4795355	37,427,382	C/T	0.92 (0.89-0.95)	4.51E-08	8.17E-10	0.18	0.9 (0.86-0.95)	1.45E-05	1.45E-05	0.60
rs600010	37,433,517	T/C	0.92 (0.89-0.95)	5.11E-08	8.45E-10	0.17	0.9 (0.86-0.95)	1.48E-05	1.48E-05	0.60
rs602688	37,439,496	T/C	1.09 (1.05-1.12)	5.02E-08	8.09E-10	0.17	1.11 (1.06-1.16)	1.57E-05	1.57E-05	0.60
rs588193	37,440,439	A/C	1.09 (1.06-1.12)	2.07E-08	4.65E-10	0.20	1.11 (1.06-1.16)	1.70E-05	1.70E-05	0.59
rs801426	37,441,109	G/A	1.09 (1.06-1.12)	2.67E-08	4.42E-10	0.18	1.11 (1.06-1.16)	1.69E-05	1.69E-05	0.60
rs667239	37,442,241	A/G	1.11 (1.08-1.14)	3.57E-11	3.57E-11	0.97	1.11 (1.05-1.17)	1.94E-04	1.94E-04	0.80
rs590051	37,446,571	T/C	1.11 (1.07-1.14)	4.06E-11	4.06E-11	0.97	1.11 (1.05-1.17)	1.73E-04	1.73E-04	0.83
rs632202	37,453,294	C/A	1.09 (1.06-1.12)	7.42E-08	1.19E-09	0.16	1.11 (1.06-1.16)	1.27E-05	1.27E-05	0.61
rs620686	37,453,617	A/G	1.09 (1.06-1.12)	2.08E-08	4.86E-10	0.20	1.11 (1.06-1.16)	1.61E-05	1.61E-05	0.60
rs2302073	37,457,342	A/G	1.11 (1.08-1.14)	3.74E-11	3.74E-11	0.97	1.11 (1.05-1.17)	1.79E-04	1.79E-04	0.83
rs584377	37,460,128	G/A	1.11 (1.08-1.14)	3.87E-11	3.87E-11	0.97	1.11 (1.05-1.17)	1.79E-04	1.79E-04	0.84
rs10491129	37,461,643	T/G	1.09 (1.05-1.12)	6.00E-08	9.20E-10	0.16	1.11 (1.06-1.16)	1.48E-05	1.48E-05	0.61
rs649180	37,464,959	A/C	1.11 (1.07-1.14)	8.28E-11	8.28E-11	0.98	1.11 (1.05-1.17)	1.86E-04	1.86E-04	0.83
rs9904334	37,468,336	G/A	1.09 (1.06-1.12)	2.07E-08	5.25E-10	0.21	1.11 (1.06-1.16)	1.64E-05	1.64E-05	0.60
rs8066704	37,477,218	C/T	1.09 (1.06-1.12)	1.83E-08	4.19E-10	0.20	1.11 (1.06-1.16)	1.68E-05	1.68E-05	0.60
rs8070695	37,478,062	G/A	1.09 (1.05-1.12)	5.45E-08	9.86E-10	0.17	1.11 (1.06-1.16)	1.53E-05	1.53E-05	0.60
rs9944411	37,483,599	T/C	1.09 (1.05-1.12)	2.78E-08	7.32E-10	0.21	1.11 (1.06-1.16)	1.57E-05	1.58E-05	0.60
rs7220650	37,487,168	T/C	1.09 (1.06-1.12)	1.41E-08	3.45E-10	0.21	1.11 (1.06-1.16)	1.62E-05	1.62E-05	0.60
rs9916302	37,499,949	T/C	1.09 (1.05-1.12)	2.83E-08	8.44E-10	0.22	1.11 (1.06-1.16)	1.64E-05	1.64E-05	0.60
rs8069451	37,504,933	T/C	1.09 (1.06-1.12)	1.97E-08	6.38E-10	0.23	1.11 (1.06-1.17)	5.45E-06	5.45E-06	0.57
rs9894586	37,505,421	C/T	1.09 (1.06-1.12)	3.79E-08	5.24E-10	0.19	1.11 (1.06-1.16)	2.04E-05	2.04E-05	0.55
rs9892055	37,510,402	C/T	1.09 (1.06-1.12)	2.63E-08	7.66E-10	0.21	1.11 (1.06-1.16)	1.52E-05	1.52E-05	0.61
rs2338799	37,513,941	G/A	1.11 (1.07-1.14)	4.03E-11	4.03E-11	0.97	1.11 (1.05-1.17)	1.96E-04	1.96E-04	0.84
rs6503503	37,514,373	G/A	1.09 (1.05-1.12)	2.13E-08	8.52E-10	0.24	1.11 (1.06-1.16)	1.66E-05	1.66E-05	0.60
rs6503504	37,514,412	A/G	1.11 (1.07-1.14)	6.48E-11	6.48E-11	0.97	1.11 (1.05-1.17)	2.02E-04	2.02E-04	0.84
rs8076494	37,516,722	T/C	1.09 (1.05-1.12)	1.99E-08	7.94E-10	0.24	1.11 (1.06-1.16)	1.59E-05	1.59E-05	0.60
rs9908131	37,520,449	T/C	1.11 (1.07-1.14)	4.41E-11	4.41E-11	0.97	1.11 (1.05-1.17)	1.96E-04	1.96E-04	0.84
rs7223438	37,521,355	T/C	1.09 (1.05-1.12)	6.32E-08	1.46E-09	0.19	1.11 (1.06-1.16)	1.65E-05	1.65E-05	0.60
rs6503507	37,525,274	C/T	1.09 (1.06-1.12)	2.55E-08	8.31E-10	0.22	1.11 (1.06-1.16)	1.61E-05	1.61E-05	0.60
rs11078898	37,536,480	A/G	1.09 (1.06-1.12)	8.58E-09	4.88E-10	0.27	1.11 (1.06-1.16)	1.59E-05	1.59E-05	0.61
rs7221875	37,543,328	G/A	1.09 (1.05-1.12)	6.63E-08	2.11E-09	0.20	1.11 (1.06-1.16)	1.18E-05	1.18E-05	0.61
rs7208487	37,543,449	T/G	1.11 (1.07-1.14)	6.42E-11	6.42E-11	0.97	1.1 (1.05-1.16)	2.92E-04	2.92E-04	0.82
rs9906612	37,547,631	A/C	1.1 (1.07-1.14)	6.92E-10	6.92E-10	0.99	1.11 (1.05-1.17)	1.98E-04	1.98E-04	0.84
rs10491128	37,551,988	G/A	1.08 (1.05-1.11)	5.94E-08	3.06E-09	0.25	1.11 (1.06-1.16)	1.42E-05	1.42E-05	0.60
rs6503513	37,561,613	A/G	1.09 (1.06-1.12)	5.85E-09	5.85E-09	0.92	1.11 (1.05-1.17)	7.08E-05	7.08E-05	0.95
rs4795357	37,569,551	T/C	0.92 (0.9-0.95)	5.98E-08	2.74E-09	0.24	0.9 (0.86-0.94)	1.08E-05	1.08E-05	0.61
rs4795358	37,573,065	A/C	0.91 (0.88-0.93)	2.28E-10	2.28E-10	0.98	0.9 (0.86-0.95)	1.17E-04	1.17E-04	0.85
rs7501488	37,576,417	T/G	0.92 (0.9-0.95)	2.87E-08	1.44E-09	0.25	0.9 (0.86-0.94)	1.02E-05	1.02E-05	0.60
rs10445306	37,591,422	A/G	0.92 (0.89-0.95)	1.06E-08	3.77E-10	0.25	0.9 (0.86-0.94)	7.67E-06	7.67E-06	0.60
rs9646419	37,597,185	A/G	0.91 (0.88-0.93)	1.99E-10	1.99E-10	0.99	0.9 (0.85-0.95)	9.57E-05	9.57E-05	0.84
rs4795369	37,609,120	G/A	0.93 (0.9-0.95)	2.76E-07	2.62E-08	0.24	0.9 (0.86-0.94)	8.53E-06	8.53E-06	0.61

SNP	Position	Allele (R/E)[a]	Multi-ancestry meta-analysis OR (95% CI)[b]	P_{random}[c]	P_{fixed}[d]	P_{het}[e]	Pediatric subgroup meta-analysis OR (95% CI)[b]	P_{random}[c]	P_{fixed}[d]	P_{het}[e]
rs12938099	37,612,910	T/G	0.9 (0.88-0.93)	1.18E-10	1.18E-10	0.98	0.9 (0.85-0.95)	7.40E-05	7.40E-05	0.85
rs4390625	37,620,347	A/G	0.92 (0.89-0.95)	6.00E-08	1.50E-09	0.19	0.9 (0.86-0.94)	7.13E-06	7.13E-06	0.57
rs11078901	37,625,912	C/T	0.92 (0.89-0.95)	5.55E-08	9.90E-10	0.21	0.9 (0.86-0.94)	9.62E-06	9.62E-06	0.51
rs12449852	37,632,088	A/G	0.9 (0.87-0.93)	5.19E-09	5.19E-09	0.97	0.9 (0.85-0.95)	3.64E-04	3.64E-04	0.71
rs12948906	37,644,854	C/T	0.91 (0.88-0.95)	8.71E-07	1.23E-08	0.15	0.89 (0.85-0.94)	5.91E-05	2.39E-05	0.39
rs11870631	37,645,129	C/T	0.92 (0.89-0.95)	5.01E-08	1.63E-09	0.21	0.9 (0.86-0.94)	6.95E-06	6.95E-06	0.58
rs2018026	37,659,606	G/A	0.92 (0.89-0.95)	5.56E-08	8.89E-10	0.20	0.9 (0.86-0.94)	9.16E-06	9.16E-06	0.53
rs6503518	37,660,469	A/G	0.91 (0.88-0.95)	8.09E-07	1.13E-08	0.15	0.89 (0.85-0.94)	5.41E-05	2.36E-05	0.40
rs11078907	37,662,954	C/T	0.92 (0.89-0.95)	3.22E-08	1.11E-09	0.23	0.9 (0.86-0.94)	6.95E-06	6.95E-06	0.59
rs7225096	37,664,443	T/C	0.92 (0.89-0.95)	3.76E-08	1.29E-09	0.23	0.9 (0.86-0.94)	7.27E-06	7.27E-06	0.59
rs12936996	37,665,554	G/A	0.92 (0.89-0.95)	8.90E-09	4.02E-10	0.25	0.9 (0.86-0.94)	7.23E-06	7.23E-06	0.59
rs12937013	37,665,571	G/A	0.9 (0.87-0.93)	6.86E-12	6.86E-12	0.98	0.9 (0.85-0.95)	6.69E-05	6.70E-05	0.83
rs7503705	37,669,704	A/G	0.92 (0.89-0.94)	2.15E-09	1.16E-10	0.28	0.9 (0.86-0.94)	5.36E-06	5.36E-06	0.62
rs11078913	37,671,714	G/T	0.92 (0.89-0.94)	8.88E-09	2.83E-10	0.23	0.9 (0.86-0.94)	3.73E-06	3.73E-06	0.62
rs11658678	37,680,096	C/T	0.91 (0.89-0.94)	1.05E-08	1.74E-10	0.22	0.9 (0.86-0.94)	4.51E-06	4.51E-06	0.57
rs8065963	37,681,332	C/T	0.92 (0.89-0.94)	3.08E-09	1.39E-10	0.25	0.9 (0.86-0.94)	4.76E-06	4.76E-06	0.62
rs8069074	37,685,401	A/G	0.9 (0.87-0.93)	4.53E-11	4.53E-11	0.97	0.9 (0.85-0.95)	5.47E-05	5.47E-05	0.82
rs12450559	37,694,709	G/A	0.92 (0.89-0.94)	2.58E-09	1.41E-10	0.27	0.9 (0.86-0.94)	4.57E-06	4.57E-06	0.60
rs4239222	37,696,235	G/T	0.92 (0.89-0.95)	3.29E-09	2.05E-10	0.28	0.9 (0.86-0.94)	4.16E-06	4.16E-06	0.61
rs11657058	37,699,378	T/G	0.9 (0.87-0.93)	8.60E-12	8.60E-12	0.98	0.9 (0.85-0.95)	6.66E-05	6.66E-05	0.80
rs11657153	37,699,729	A/G	0.9 (0.87-0.93)	2.28E-10	2.28E-10	0.95	0.89 (0.84-0.95)	6.16E-04	6.16E-04	0.66
rs11654018	37,703,740	T/C	0.92 (0.89-0.94)	2.67E-09	2.04E-10	0.29	0.9 (0.86-0.94)	5.63E-06	5.63E-06	0.58
rs2303316	37,704,217	A/G	0.92 (0.89-0.95)	9.04E-09	3.97E-10	0.24	0.9 (0.86-0.94)	4.59E-06	4.59E-06	0.61
rs12947506	37,707,592	T/C	0.9 (0.87-0.93)	1.03E-11	1.03E-11	0.98	0.9 (0.85-0.95)	8.79E-05	8.79E-05	0.80
rs7503377	37,708,841	T/C	0.9 (0.87-0.93)	2.27E-11	2.27E-11	0.99	0.9 (0.85-0.95)	8.57E-05	8.58E-05	0.79
rs7216086	37,709,422	G/A	0.92 (0.89-0.95)	6.74E-09	3.01E-10	0.25	0.9 (0.86-0.94)	5.42E-06	5.42E-06	0.60
rs11078915	37,715,426	T/C	0.92 (0.89-0.94)	8.69E-10	7.62E-11	0.31	0.9 (0.86-0.94)	2.90E-06	2.90E-06	0.60
rs6503521	37,715,551	G/T	0.89 (0.87-0.92)	1.37E-11	1.37E-11	0.98	0.89 (0.85-0.94)	5.72E-05	5.72E-05	0.76
rs7503195	37,722,515	G/A	0.93 (0.91-0.96)	2.53E-07	2.53E-07	0.52	0.93 (0.89-0.97)	1.41E-03	1.41E-03	0.52
rs903507	37,726,423	C/T	1.12 (1.09-1.15)	1.13E-12	1.13E-12	0.97	1.13 (1.07-1.19)	2.70E-05	2.70E-05	0.80
rs8182252	37,727,950	T/C	1.11 (1.07-1.15)	1.43E-09	1.43E-09	0.84	1.13 (1.07-1.2)	4.10E-05	4.10E-05	0.92
rs1874226	37,729,031	C/T	1.12 (1.08-1.15)	1.51E-12	1.51E-12	0.96	1.13 (1.07-1.19)	2.05E-05	2.05E-05	0.80
rs4795385	37,733,148	A/G	1.13 (1.09-1.16)	2.95E-14	2.95E-14	0.97	1.15 (1.09-1.21)	5.91E-07	5.91E-07	0.80
rs1619021	37,739,274	G/A	0.91 (0.89-0.94)	7.61E-11	1.09E-11	0.35	0.89 (0.85-0.93)	1.02E-06	1.02E-06	0.65
rs1877030	37,740,161	T/C	0.89 (0.86-0.92)	2.55E-13	2.56E-13	0.99	0.88 (0.84-0.93)	1.11E-05	1.11E-05	0.80
rs12453198	37,741,879	T/C	0.89 (0.86-0.92)	1.93E-14	1.93E-14	0.95	0.89 (0.84-0.93)	7.84E-06	7.84E-06	0.51
rs11654954	37,745,979	A/G	0.89 (0.86-0.91)	8.91E-15	8.91E-15	0.93	0.88 (0.84-0.93)	5.31E-06	5.31E-06	0.53
rs12453682	37,770,005	C/T	0.9 (0.88-0.92)	6.89E-14	3.75E-16	0.27	0.87 (0.83-0.91)	7.29E-10	9.40E-11	0.37
rs1874228	37,775,274	A/G	0.9 (0.88-0.93)	4.22E-14	4.23E-14	0.58	0.87 (0.83-0.91)	4.28E-09	4.28E-09	0.67
rs879606	37,781,849	A/G	0.89 (0.86-0.92)	1.36E-12	1.36E-12	0.96	0.88 (0.83-0.93)	4.29E-06	4.29E-06	0.78
rs2271309	37,784,990	G/A	0.89 (0.86-0.91)	1.95E-16	1.95E-16	0.93	0.87 (0.83-0.91)	7.98E-09	7.98E-09	0.88
rs907094	37,790,371	G/A	0.89 (0.87-0.92)	6.37E-15	6.37E-15	0.91	0.87 (0.83-0.91)	8.33E-09	8.33E-09	0.85
rs3764352	37,790,939	C/T	0.9 (0.87-0.93)	5.45E-11	5.45E-11	0.91	0.86 (0.82-0.91)	4.31E-07	4.31E-07	0.96
rs9972882	37,807,698	A/C	0.88 (0.86-0.91)	2.19E-21	2.19E-21	0.78	0.86 (0.82-0.9)	7.40E-12	7.40E-12	0.54
rs1877031	37,814,080	G/A	0.89 (0.87-0.91)	1.05E-21	1.05E-21	0.61	0.85 (0.82-0.89)	6.25E-14	6.26E-14	0.82
rs2271308	37,817,482	T/C	0.89 (0.87-0.92)	3.42E-18	3.42E-18	0.81	0.86 (0.83-0.9)	1.28E-11	1.28E-11	0.79
rs931992	37,821,435	G/T	0.89 (0.87-0.91)	2.26E-21	2.26E-21	0.62	0.85 (0.82-0.89)	7.28E-14	7.28E-14	0.84
rs1053651	37,822,311	A/C	0.89 (0.87-0.92)	1.62E-15	1.62E-15	0.66	0.85 (0.8-0.89)	1.01E-09	1.01E-09	0.78
rs876493	37,824,545	G/A	0.88 (0.85-0.91)	5.89E-13	2.44E-17	0.17	0.83 (0.79-0.88)	1.05E-10	3.58E-11	0.42
rs14050	37,828,072	C/T	0.87 (0.84-0.89)	6.28E-23	6.29E-23	0.58	0.83 (0.79-0.88)	6.42E-12	2.14E-13	0.35
rs2952151	37,828,496	T/C	0.87 (0.85-0.89)	3.78E-28	3.78E-28	0.67	0.84 (0.81-0.88)	3.89E-15	6.94E-16	0.41
rs2941503	37,828,745	A/G	0.87 (0.85-0.89)	6.79E-23	6.79E-23	0.48	0.83 (0.79-0.88)	3.22E-12	1.77E-13	0.37
rs907087	37,828,787	G/A	0.87 (0.84-0.89)	6.00E-23	6.00E-23	0.51	0.83 (0.79-0.88)	4.82E-12	1.65E-13	0.35
rs903502	37,829,604	C/T	0.88 (0.86-0.9)	1.00E-26	1.00E-26	0.79	0.84 (0.81-0.88)	1.03E-15	1.03E-15	0.68
rs2941504	37,830,900	A/G	0.87 (0.85-0.89)	1.28E-27	1.28E-27	0.57	0.84 (0.81-0.88)	1.53E-14	1.50E-15	0.39
rs1565922	37,831,035	A/G	0.87 (0.85-0.89)	6.99E-28	6.99E-28	0.72	0.84 (0.81-0.88)	1.82E-14	1.18E-15	0.38
rs2934952	37,832,366	G/A	0.87 (0.85-0.89)	1.19E-23	1.19E-23	0.48	0.83 (0.79-0.88)	5.56E-10	8.84E-13	0.24
rs2941505	37,832,704	A/G	0.88 (0.86-0.9)	1.98E-25	1.98E-25	0.62	0.84 (0.81-0.88)	1.06E-15	1.06E-15	0.60
rs2941506	37,833,035	A/G	0.88 (0.86-0.9)	1.42E-24	1.42E-24	0.54	0.84 (0.81-0.88)	1.11E-15	1.11E-15	0.59

SNP	Position	Allele (R/E)[a]	Multi-ancestry meta-analysis OR (95% CI)[b]	P_{random}[c]	P_{fixed}[d]	P_{het}[e]	Pediatric subgroup meta-analysis OR (95% CI)[b]	P_{random}[c]	P_{fixed}[d]	P_{het}[e]
rs907089	37,833,600	G/A	0.88 (0.86-0.9)	8.78E-24	8.78E-24	0.62	0.84 (0.81-0.88)	1.31E-15	1.31E-15	0.62
rs2313171	37,833,842	T/C	0.88 (0.86-0.9)	1.57E-24	1.57E-24	0.54	0.84 (0.81-0.88)	1.33E-15	1.33E-15	0.59
rs12150298	37,834,541	T/C	0.88 (0.86-0.9)	2.33E-24	2.33E-24	0.58	0.85 (0.81-0.88)	2.23E-15	2.23E-15	0.58
rs8078228	37,834,998	C/T	0.88 (0.86-0.9)	1.38E-24	1.38E-24	0.52	0.84 (0.81-0.88)	1.11E-15	1.11E-15	0.57
rs11078919	37,835,755	T/C	0.88 (0.86-0.91)	1.43E-22	1.43E-22	0.52	0.84 (0.81-0.88)	1.23E-15	1.23E-15	0.57
rs1476278	37,836,243	C/T	0.88 (0.86-0.9)	2.82E-26	2.82E-26	0.62	0.84 (0.81-0.88)	1.28E-15	1.28E-15	0.57
rs9303274	37,836,353	T/C	0.88 (0.86-0.9)	1.87E-25	1.87E-25	0.56	0.84 (0.81-0.88)	1.26E-15	1.27E-15	0.56
rs2517957	37,838,716	G/A	0.87 (0.85-0.9)	2.31E-27	2.31E-27	0.59	0.84 (0.81-0.88)	9.79E-16	9.79E-16	0.57
rs2517958	37,838,751	G/A	0.87 (0.85-0.9)	2.18E-27	2.18E-27	0.58	0.84 (0.81-0.88)	9.28E-16	9.28E-16	0.57
rs903501	37,839,493	T/C	0.88 (0.85-0.9)	1.96E-17	1.07E-20	0.31	0.83 (0.78-0.88)	1.55E-09	5.29E-12	0.26
rs2517954	37,843,550	T/C	0.87 (0.85-0.89)	2.09E-28	2.09E-28	0.60	0.84 (0.81-0.88)	3.76E-15	3.76E-15	0.51
rs2517955	37,843,681	C/T	0.87 (0.85-0.9)	1.26E-26	1.26E-26	0.64	0.85 (0.81-0.88)	7.27E-15	7.27E-15	0.70
rs2517956	37,843,859	G/A	0.87 (0.85-0.9)	3.31E-27	3.31E-27	0.62	0.84 (0.81-0.88)	5.77E-15	5.77E-15	0.49
rs1565923	37,858,678	A/G	0.86 (0.84-0.89)	2.09E-25	2.09E-25	0.50	0.84 (0.79-0.89)	5.15E-10	1.28E-11	0.32
rs2952155	37,861,718	T/C	0.87 (0.84-0.89)	2.92E-26	2.92E-26	0.84	0.85 (0.81-0.89)	1.93E-12	1.93E-12	0.74
rs1810132	37,866,005	C/T	0.87 (0.84-0.89)	2.94E-30	2.94E-30	0.59	0.84 (0.81-0.88)	2.42E-15	2.42E-15	0.50
rs2952156	37,876,835	A/G	0.87 (0.84-0.89)	2.24E-30	2.24E-30	0.52	0.84 (0.81-0.88)	2.42E-15	2.42E-15	0.51
rs907091	37,921,742	C/T	1.18 (1.14-1.22)	2.82E-20	3.14E-36	0.01	1.26 (1.2-1.32)	5.59E-20	1.03E-21	0.38
rs907092	37,922,259	G/A	0.85 (0.83-0.88)	2.52E-23	2.96E-37	0.02	0.81 (0.78-0.84)	3.73E-24	3.73E-24	0.69
rs10445308	37,938,047	C/T	0.85 (0.83-0.88)	1.76E-24	7.29E-39	0.03	0.81 (0.77-0.84)	1.55E-24	1.55E-24	0.80
rs9909593	37,970,149	A/G	0.85 (0.83-0.88)	5.13E-24	7.22E-39	0.02	0.81 (0.77-0.84)	8.23E-25	8.23E-25	0.85
rs9303277	37,976,469	C/T	0.85 (0.83-0.88)	9.57E-26	4.88E-43	0.02	0.8 (0.77-0.84)	1.24E-25	1.24E-25	0.62
rs3816470	37,985,801	A/G	0.85 (0.83-0.88)	1.23E-26	6.46E-41	0.05	0.81 (0.78-0.85)	8.83E-22	8.83E-22	0.60
rs9635726	38,020,141	C/T	1.16 (1.13-1.2)	1.50E-23	1.50E-23	0.52	1.17 (1.12-1.23)	4.53E-11	4.53E-11	0.57
rs4795397	38,023,745	A/G	0.86 (0.83-0.89)	2.55E-16	7.99E-29	0.01	0.8 (0.76-0.84)	1.64E-19	1.64E-19	0.79
rs11557466	38,024,626	C/T	0.85 (0.83-0.88)	8.06E-22	4.55E-36	0.02	0.81 (0.77-0.84)	6.37E-24	6.37E-24	0.83
rs11078925	38,025,208	T/C	0.85 (0.83-0.88)	2.15E-24	2.82E-38	0.03	0.81 (0.77-0.84)	2.36E-24	2.36E-24	0.87
rs12150079	38,025,417	G/A	0.88 (0.85-0.9)	2.45E-15	1.14E-21	0.08	0.82 (0.79-0.86)	7.87E-17	7.87E-17	0.65
rs11557467	38,028,634	G/T	0.85 (0.82-0.88)	3.27E-21	3.50E-31	0.07	0.8 (0.76-0.84)	4.02E-21	4.02E-21	0.51
rs10852936	38,031,714	C/T	0.86 (0.83-0.89)	3.10E-17	2.13E-27	0.03	0.8 (0.76-0.84)	6.80E-21	6.80E-21	0.81
rs1054609	38,033,277	A/C	0.86 (0.83-0.88)	1.14E-24	3.27E-37	0.05	0.8 (0.77-0.84)	7.56E-25	7.56E-25	0.88
rs9907088	38,035,116	G/A	0.86 (0.83-0.88)	1.58E-24	6.50E-38	0.04	0.81 (0.77-0.84)	9.80E-25	9.80E-25	0.86
rs12232497	38,040,119	T/C	0.85 (0.83-0.88)	1.57E-24	9.74E-39	0.03	0.8 (0.77-0.84)	9.16E-25	9.16E-25	0.86
rs2872507	38,040,763	G/A	0.86 (0.83-0.88)	2.02E-24	8.06E-38	0.04	0.81 (0.77-0.84)	1.65E-24	1.65E-24	0.86
rs9901146	38,043,343	G/A	0.85 (0.82-0.87)	9.03E-30	6.09E-44	0.06	0.81 (0.77-0.84)	3.37E-25	3.37E-25	0.63
rs12950743	38,049,233	T/C	0.85 (0.82-0.87)	6.78E-30	5.58E-44	0.06	0.81 (0.77-0.84)	3.00E-25	3.00E-25	0.62
rs7359623	38,049,589	C/T	0.85 (0.82-0.87)	1.93E-27	2.03E-41	0.05	0.8 (0.77-0.84)	1.46E-24	1.46E-24	0.67
rs8067378	38,051,348	A/G	0.85 (0.83-0.88)	1.46E-28	4.78E-42	0.07	0.81 (0.77-0.84)	6.58E-25	6.58E-25	0.62
rs8069176	38,057,197	G/A	0.85 (0.82-0.88)	1.97E-23	4.55E-41	0.01	0.8 (0.77-0.83)	4.42E-26	4.42E-26	0.77
rs2305480	38,062,196	G/A	0.85 (0.82-0.88)	3.47E-23	2.72E-41	4.6×10^{-3}	0.8 (0.77-0.83)	5.37E-26	5.37E-26	0.74
rs2305479	38,062,217	C/T	0.84 (0.81-0.87)	2.00E-28	1.03E-46	0.02	0.8 (0.77-0.84)	6.20E-26	6.21E-26	0.51
rs11078926	38,062,976	G/A	0.85 (0.81-0.88)	2.57E-16	5.28E-31	1.8×10^{-3}	0.79 (0.75-0.83)	7.56E-22	7.56E-22	0.75
rs11078927	38,064,405	C/T	0.85 (0.82-0.87)	1.45E-23	2.14E-41	0.01	0.8 (0.77-0.84)	1.78E-25	1.78E-25	0.79
rs2290400	38,066,240	T/C	0.85 (0.82-0.88)	1.51E-25	1.46E-43	0.01	0.8 (0.77-0.84)	7.81E-25	7.81E-25	0.51
rs1008723	38,066,267	G/T	0.84 (0.82-0.87)	6.13E-29	8.99E-46	0.03	0.8 (0.77-0.84)	4.96E-26	4.96E-26	0.48
rs4795400	38,067,020	C/T	0.85 (0.82-0.88)	7.48E-23	5.51E-41	3.6×10^{-3}	0.8 (0.77-0.84)	1.51E-25	1.51E-25	0.76
rs869402	38,068,043	T/C	1.19 (1.15-1.23)	1.27E-25	2.52E-46	4.4×10^{-3}	1.24 (1.19-1.3)	3.97E-24	6.38E-25	0.43
rs7216389	38,069,949	C/T	1.19 (1.15-1.23)	6.73E-26	8.27E-47	0.01	1.25 (1.19-1.3)	7.97E-23	7.17E-26	0.32
rs9303280	38,074,031	T/C	1.18 (1.15-1.22)	9.30E-25	2.96E-43	0.01	1.24 (1.19-1.3)	3.43E-21	6.91E-25	0.28
rs9303281	38,074,046	G/A	1.18 (1.14-1.22)	2.41E-24	6.20E-45	4.4×10^{-3}	1.25 (1.19-1.3)	3.60E-23	5.35E-26	0.33
rs7219923	38,074,518	C/T	1.18 (1.14-1.22)	2.20E-24	2.47E-44	0.01	1.25 (1.19-1.3)	3.46E-23	5.52E-26	0.33
rs7224129	38,075,426	G/A	1.18 (1.14-1.22)	8.94E-25	6.40E-45	0.01	1.25 (1.2-1.31)	1.29E-24	1.30E-26	0.38
rs4378650	38,080,865	A/G	1.19 (1.14-1.24)	5.99E-18	3.78E-41	2.9×10^{-3}	1.23 (1.17-1.3)	5.39E-15	1.01E-19	0.18
rs8076131	38,080,912	G/A	1.18 (1.14-1.22)	9.81E-21	1.48E-39	1.7×10^{-3}	1.25 (1.2-1.3)	6.18E-25	6.18E-25	0.72
rs12603332	38,082,807	T/C	1.17 (1.14-1.21)	8.90E-23	3.87E-41	0.01	1.23 (1.18-1.29)	2.41E-20	1.54E-23	0.30
rs17608925	38,082,831	T/C	0.9 (0.87-0.94)	3.26E-07	3.26E-07	0.48	0.87 (0.81-0.94)	2.35E-04	2.35E-04	0.85
rs3744246	38,084,350	T/C	1.11 (1.07-1.15)	5.08E-08	1.06E-13	0.01	1.16 (1.1-1.22)	8.22E-09	8.22E-09	0.70
rs4795402	38,085,385	A/C	1.11 (1.07-1.14)	2.50E-10	2.98E-15	0.06	1.14 (1.09-1.2)	3.38E-08	2.56E-08	0.45
rs4795403	38,085,722	T/C	1.11 (1.07-1.16)	1.50E-07	2.20E-13	2.7×10^{-3}	1.16 (1.1-1.22)	1.31E-08	1.31E-08	0.62

			Multi-ancestry meta-analysis				Pediatric subgroup meta-analysis			
SNP	**Position**	**Allele (R/E)[a]**	**OR (95% CI)[b]**	**P_{random}[c]**	**P_{fixed}[d]**	**P_{het}[e]**	**OR (95% CI)[b]**	**P_{random}[c]**	**P_{fixed}[d]**	**P_{het}[e]**
rs4795404	38,085,791	A/C	1.11 (1.07-1.15)	6.14E-08	1.40E-13	0.01	1.16 (1.1-1.22)	9.06E-09	9.06E-09	0.68
rs4795405	38,088,417	T/C	1.17 (1.13-1.21)	4.05E-21	5.74E-44	1.4 x10^{-3}	1.23 (1.18-1.28)	2.33E-22	2.33E-22	0.63
rs4794820	38,089,344	A/G	1.16 (1.12-1.2)	3.12E-18	3.89E-34	0.01	1.24 (1.19-1.3)	7.18E-23	7.18E-23	0.79
rs7207600	38,091,660	G/A	1.14 (1.11-1.17)	5.63E-18	3.34E-28	0.09	1.19 (1.14-1.25)	2.54E-15	2.54E-15	0.53
rs8079416	38,092,713	T/C	1.15 (1.11-1.18)	1.28E-19	1.28E-33	0.03	1.2 (1.15-1.25)	4.84E-17	6.83E-18	0.40
rs8065126	38,099,035	T/C	1.14 (1.11-1.17)	1.19E-18	1.25E-26	0.17	1.19 (1.14-1.24)	8.54E-15	8.54E-15	0.56
rs4795408	38,107,627	G/A	1.15 (1.12-1.19)	1.59E-20	1.54E-35	0.03	1.19 (1.14-1.25)	8.71E-16	2.57E-17	0.34
rs9895948	38,108,363	T/C	1.14 (1.1-1.17)	3.76E-13	9.00E-24	0.05	1.22 (1.16-1.28)	5.46E-14	5.46E-14	0.75
rs17609240	38,110,689	T/G	1.13 (1.09-1.18)	5.76E-12	2.30E-23	0.03	1.22 (1.16-1.29)	2.92E-14	2.93E-14	0.75
rs1007654	38,111,354	A/G	1.13 (1.09-1.16)	1.29E-15	4.36E-24	0.11	1.17 (1.12-1.22)	1.94E-13	1.94E-13	0.47
rs1007655	38,111,419	G/A	1.14 (1.1-1.18)	3.89E-13	1.28E-22	0.10	1.22 (1.15-1.28)	7.76E-14	7.76E-14	0.79
rs2313640	38,111,845	C/T	1.13 (1.09-1.16)	1.20E-15	3.51E-24	0.11	1.17 (1.12-1.22)	2.27E-13	2.27E-13	0.47
rs7218742	38,114,361	A/G	1.13 (1.1-1.16)	1.18E-16	1.23E-24	0.15	1.18 (1.13-1.23)	1.61E-13	1.61E-13	0.50
rs7218321	38,114,469	C/T	1.12 (1.08-1.15)	4.44E-12	4.81E-22	0.04	1.17 (1.13-1.23)	1.82E-13	1.82E-13	0.47
rs7219080	38,114,516	A/C	1.12 (1.09-1.15)	3.59E-13	6.21E-23	0.05	1.17 (1.12-1.23)	4.12E-13	2.08E-13	0.43
rs6503526	38,114,598	C/T	1.15 (1.12-1.18)	2.17E-20	5.96E-35	0.03	1.19 (1.14-1.24)	3.90E-16	5.36E-17	0.40
rs6503527	38,114,719	G/A	1.13 (1.09-1.17)	1.59E-12	4.41E-22	0.06	1.18 (1.12-1.24)	5.45E-11	4.74E-12	0.34
rs3902025	38,119,254	G/T	1.13 (1.1-1.16)	8.44E-15	8.79E-29	0.01	1.18 (1.13-1.23)	1.71E-15	1.71E-15	0.80
rs3894194	38,121,993	G/A	1.15 (1.12-1.18)	2.43E-20	1.45E-34	0.03	1.2 (1.15-1.25)	8.21E-18	2.62E-18	0.43
rs7212938	38,122,680	G/T	0.87 (0.84-0.89)	2.56E-19	4.95E-32	0.04	0.82 (0.78-0.86)	1.70E-15	1.89E-18	0.24
rs3859192	38,128,648	C/T	1.13 (1.09-1.16)	3.50E-14	9.38E-26	0.01	1.17 (1.12-1.23)	1.94E-10	3.70E-14	0.09
rs8075668	38,137,623	C/T	0.9 (0.88-0.92)	5.83E-15	1.58E-19	0.21	0.88 (0.84-0.92)	4.01E-08	6.42E-10	0.20
rs2305481	38,138,624	G/A	0.9 (0.87-0.92)	1.84E-15	1.01E-19	0.24	0.89 (0.85-0.93)	2.62E-07	3.20E-08	0.29
rs2305482	38,140,927	A/C	0.93 (0.9-0.95)	4.09E-10	5.23E-11	0.38	0.91 (0.88-0.95)	1.77E-05	1.77E-05	0.64
rs11078930	38,141,955	C/T	0.88 (0.86-0.9)	6.64E-21	6.64E-21	0.65	0.87 (0.83-0.91)	1.00E-09	1.00E-09	0.47
rs4065321	38,143,548	C/T	0.92 (0.9-0.95)	1.51E-10	1.75E-11	0.38	0.91 (0.88-0.95)	1.52E-05	1.52E-05	0.61
rs8066582	38,146,929	T/C	0.93 (0.9-0.95)	1.02E-09	6.68E-11	0.34	0.91 (0.88-0.95)	1.56E-05	1.56E-05	0.60
rs11658328	38,149,236	T/C	0.93 (0.91-0.95)	3.60E-10	7.31E-11	0.40	0.92 (0.88-0.95)	1.89E-05	1.89E-05	0.65
rs2241245	38,151,014	C/T	0.93 (0.9-0.95)	5.38E-10	4.20E-11	0.36	0.91 (0.88-0.95)	1.53E-05	1.53E-05	0.65
rs12453334	38,153,473	C/T	0.89 (0.87-0.92)	2.43E-19	2.43E-19	0.57	0.88 (0.85-0.92)	3.54E-09	3.19E-09	0.46
rs4794822	38,156,712	C/T	1.1 (1.07-1.13)	1.89E-11	1.96E-16	0.09	1.13 (1.08-1.17)	1.02E-08	1.02E-08	0.57
rs8070454	38,160,754	C/T	1.1 (1.07-1.13)	1.24E-11	9.29E-17	0.09	1.13 (1.08-1.17)	9.77E-09	9.77E-09	0.58
rs8078723	38,166,879	T/C	1.1 (1.07-1.13)	1.56E-11	9.13E-17	0.08	1.13 (1.08-1.18)	9.46E-09	9.46E-09	0.59
rs2227319	38,170,845	G/A	0.89 (0.87-0.92)	9.69E-20	9.69E-20	0.53	0.88 (0.85-0.92)	9.38E-09	4.97E-09	0.42
rs25645	38,173,143	G/A	0.89 (0.87-0.91)	2.05E-20	2.05E-20	0.56	0.88 (0.84-0.92)	3.98E-09	3.98E-09	0.55
rs1042658	38,173,902	C/T	1.1 (1.07-1.13)	3.83E-11	1.26E-16	0.07	1.13 (1.08-1.17)	1.49E-08	1.49E-08	0.57
rs1045929	38,175,426	C/T	1.1 (1.07-1.14)	3.25E-09	1.36E-13	0.12	1.16 (1.1-1.22)	3.71E-09	3.71E-09	0.72
rs12309	38,175,462	C/T	0.88 (0.86-0.91)	2.02E-18	2.02E-18	0.54	0.86 (0.82-0.91)	3.16E-09	3.16E-09	0.69
rs709592	38,175,553	C/T	1.1 (1.07-1.13)	4.40E-11	1.45E-16	0.07	1.13 (1.08-1.17)	1.55E-08	1.55E-08	0.57
rs2302776	38,178,149	A/G	0.91 (0.89-0.94)	4.47E-13	4.47E-13	0.71	0.91 (0.87-0.95)	3.48E-06	3.48E-06	0.63
rs3213762	38,178,627	A/G	1.1 (1.07-1.14)	2.20E-11	4.77E-17	0.07	1.13 (1.08-1.17)	1.98E-08	1.98E-08	0.55
rs12451897	38,179,275	G/T	0.89 (0.87-0.91)	7.88E-18	7.88E-18	0.57	0.87 (0.82-0.91)	1.95E-08	1.95E-08	0.62
rs2302777	38,179,492	A/G	0.89 (0.87-0.91)	1.13E-20	1.13E-20	0.63	0.88 (0.85-0.92)	6.24E-09	6.24E-09	0.49
rs9916158	38,182,229	G/T	0.9 (0.87-0.92)	1.07E-14	2.06E-17	0.34	0.88 (0.84-0.93)	1.85E-06	2.98E-07	0.31
rs2302774	38,183,090	G/T	0.89 (0.87-0.91)	2.79E-20	2.79E-20	0.57	0.89 (0.85-0.93)	2.46E-08	2.46E-08	0.47
rs7502514	38,188,844	A/G	0.91 (0.88-0.93)	1.50E-10	1.88E-16	0.05	0.89 (0.85-0.93)	5.31E-08	5.31E-08	0.57
rs3935280	38,189,055	A/G	0.91 (0.87-0.94)	1.05E-07	6.35E-13	0.05	0.86 (0.81-0.9)	4.78E-09	4.78E-09	0.78
rs11078936	38,197,914	T/C	0.9 (0.87-0.92)	3.52E-18	3.52E-18	0.75	0.88 (0.85-0.92)	6.53E-09	6.53E-09	0.51
rs8065443	38,208,940	A/G	0.91 (0.89-0.94)	1.73E-10	5.47E-15	0.08	0.89 (0.85-0.93)	2.45E-08	2.45E-08	0.46
rs868150	38,213,359	A/G	0.91 (0.89-0.94)	9.43E-11	4.23E-15	0.10	0.89 (0.85-0.93)	2.03E-08	2.03E-08	0.50
rs7502966	38,216,522	C/T	1.07 (1.04-1.1)	1.52E-07	1.52E-07	0.85	1.08 (1.03-1.13)	1.04E-03	1.04E-03	0.63

[a]R=reference allele /E=effect allele

[b]Odds-ratios (ORs) and 95% Confidence Intervals (CI) were computed for the effect allele under a random-effects model

[c]P_{random} for test of association between SNP and asthma under a random-effects model

[d]P_{fixed} for test of association between SNP and asthma under a fixed-effects model

[e]P_{het} for test of heterogeneity across studies with the use of Cochran's Q test

Supplementary Table 11. Association between cis-gene transcripts in blood and lung and 17q12-21 SNPs

a. Association between lead asthma SNPs (rs2952156 in multi-ancestry meta-analysis and rs8069176 in pediatric meta-analysis) and cis-gene transcripts

Asthma SNP	Position	Nearby genes[a]	Source database[b]	Tissue[c]	Gene	$P_{transcript}$[d]	Gene	$P_{transcript}$[d]	Gene	$P_{transcript}$[d]	Gene	$P_{transcript}$[d]
rs2952156	37,876,835	ERBB2	Blood_eQTL	Blood	ORMDL3	5.2 x10^{-109}	GSDMB	3.7 x10^{-90}	PPP1R1B	1.8 x10^{-8}		
		PGAP3	GTEx	Blood	GSDMB	1.1 x10^{-9}	ORMDL3	3.7 x10^{-6}				
		C17orf37	MuTHER	LCLs	ORMDL3	3.3 x10^{-16}	ZPBP2	3.3 x10^{-11}	GSDMB	9.9 x10^{-7}		
			MRCA	LCLs	ORMDL3	1.1 x10^{-13}	GSDMB	9.3 x10^{-8}				
			MRCE	LCLs	GSDMB	7.7 x10^{-17}	ORMDL3	5.6 x10^{-15}				
			GTEx	Lung	PGAP3	1.0 x10^{-9}	ORMDL3	1.5 x10^{-7}				
			Hao, 2012	Lung	CDK12	2.0 x10^{-20}	GSDMA	1.3 x10^{-13}	PGAP3	1.1 x10^{-8}	GSDMB	3.9 x10^{-8}
rs8069176	38,057,197	ZPBP2	Blood_eQTL	Blood	ORMDL3	9.8 x10^{-198}	GSDMB	9.8 x10^{-198}				
		GSDMB	GTEx	Blood	ORMDL3	1.2 x10^{-26}	GSDMB	3.1 x10^{-22}				
			MuTHER	LCLs	ORMDL3	2.6 x10^{-29}	ZPBP2	5.5 x10^{-14}	GSDMB	1.9 x10^{-12}		
			MRCA	LCLs	ORMDL3	1.0 x10^{-24}	GSDMB	4.3 x10^{-15}				
			MRCE	LCLs	GSDMB	1.0 x10^{-33}	ORMDL3	2.7 x10^{-29}				
			GTEx	Lung	ORMDL3	3.6 x10^{-9}	GSDMA	1.6 x10^{-8}				
			Hao, 2012	Lung	GSDMA	2.2 x10^{-31}	GSDMB	3.8 x10^{-12}	CDK12	2.9 x10^{-7}	ORMDL3	1.6x 10^{-5}

[a]The gene where eventually the lead SNP lies is first indicated followed by the previous and next genes

[b]eQTL databases are described in Online Methods

[c]Blood is whole blood; LCL = lymphoblastoid cell lines; Lung is whole lung tissue

[d]$P_{transcript}$ is the P-value for test of association of asthma-associated SNP with gene transcript

b. Association analysis of *ORMDL3* and *PGAP3* transcripts with their most significantly associated SNPs (peak SNPs) and the 17q12-21 asthma-associated SNPs

This analysis focused on *ORMDL3* transcript in blood (showing the strongest association with both 17q12-21 asthma SNPs, rs2952156 and rs8069176, in the majority of five blood eQTL databases) and *PGAP3* transcript in lung (associated with rs2952156), as shown above. It used the summary statistics from the GTEx eQTL-database, available in both blood (n=338 samples) and lung (n=278 samples).

We first performed association analysis of these gene transcripts with their respective peak SNPs and then by conditioning on the lead asthma-associated SNPs (using the GCTA software (PMID 23756893) and the large pan-European ECRHS study as the reference to estimate LD between SNPs, similarly to the approximate conditional analysis conducted for asthma and explained in detail in the Online Methods).

As can be seen in the following table, rs8069176 accounts for a large part of the association of the peak SNP (rs9303281) with *ORMDL3* transcript in blood while rs2952156 accounts for a large part of the association of the peak SNP (rs2941505) with *PGAP3* transcript in lung.

		Association of lead asthma SNP with gene transcript			Association of peak SNP with gene transcript				
Tissue	Gene_transcript	Asthma SNP	Position	$P_{transcript}$[a]	Peak SNP[b]	Position	r^2[c]	$P_{transcript}$[d]	$P^{e}_{adj\ for\ asthma\ SNP}$
Blood	ORMDL3	rs2952156	37,876,835	3.7 x10^{-6}	rs9303281	38,074,046	0.39	6.3 x10^{-30}	7.6 x10^{-23}
		rs8069176	38,057,197	1.2 x10^{-26}	rs9303281	38,074,046	0.79	6.3 x10^{-30}	2.2 x10^{-4}
Lung	PGAP3	rs2952156	37,876,835	1.0 x10^{-9}	rs2941505	37,832,704	0.84	5.6 x10^{-12}	1.5 x10^{-3}
		rs8069176	38,057,197	1.4 x10^{-3}	rs2941505	37,832,704	0.35	5.6 x10^{-12}	2.6 x10^{-9}

[a]P-value for association of the asthma SNP with gene transcript

[b]Most significant SNP (Peak SNP) associated with the gene transcript

[c]Correlation (r^2) between the asthma SNP and the peak SNP

[d]P-value for association of the peak SNP with gene transcript

[e]P-value for association of the peak SNP with gene transcript while conditioning on the asthma SNP

Supplementary Table 12. Asthma loci reported in the GWAS catalog wih P < $5x10^{-8}$ and not replicated in TAGC meta-analyses

Information from TAGC meta-analysis										Information from GWAS Catalog													
REGION	Position build 37	TAGC SNP	Multi-ancestry (23,948 ca) P_{random}	European ancestry (19,954 ca) P_{random}	African ancestry (2,149 ca) P_{fixed}	Japanese (1,239 ca) P_{fixed}	Latino (606 ca) P	Pediatric (8,976 ca) P_{random}	r^2 (TAGC SNP, catalog SNP)	Catalog SNP	P-value	Pubmed.id	Mapped Genes	Ancestry of published studies	Total # cases in published study	#cases in study discovery samples	#cases in study replication samples	# cases from published study in TAGC	% of study cases in TAGC Multi-ancestry	% of study cases in TAGC EU	% of study cases in TAGC AF	% of study cases in TAGC JAP	% of study cases in TAGC LAT
7q22.3	105,658,450	rs6967330	$9.1x10^{-4}$	$3.2x10^{-3}$	0.37	0.21	NA	$1.7x10^{-3}$	1	rs6967330	$P_{fix}=3x10^{-14}$*** $P_{ran}=3x10^{-7}$	24241537	CDHR3	EU (D); EU (R)	8,414	1,173	7,241	6,876	0.29	0.34	NA	NA	NA
10q24.2	100,739,769	rs17111026*	0.16	0.02	0.47	0.87	0.91	0.72	0.76	rs12570188	$5.0 x10^{-8}$	23829686	HPSE2	EU, AF, LAT	527	one ethnic group	other ethnic groups	0	0	0	0	NA	0
4q12	59,213,845	rs17218161*	NA	NA	NA	NA	NA	NA	NA	rs17218161	$2.0 x10^{-8}$	23829686	SRIP1 - MIR548AG1	EU, AF, LAT	527	one ethnic group	other ethnic groups	0	0	0	0	NA	0
9p23	12,521,825	rs16929097*	0.81	0.62	0.31	NA	0.85	0.13	1	rs16929097	$8.0 x10^{-9}$	23829686	JKAMPP1 - TYRP1	EU, AF, LAT	527	one ethnic group	other ethnic groups	0	0	0	0	NA	0
1q21.3	154,426,263	rs4129267	$8.5 x10^{-7}$	$4.5x10^{-6}$	0.92	$1.5x10^{-3}$	0.68	0.08	1	rs4129267	$2.0 x10^{-8}$	21907864	IL6R	EU	15,797	12,475	3,322	12,687	0.53	0.64	NA	NA	NA
5q12.1	59,369,793	rs1588265	0.55	0.65	0.79	0.95	0.42	0.59	1	rs1588265	$3.0 x10^{-8}$	19426955	PDE4D	EU (D); EU, AF, LAT (R)	7,346	359	6,987	3,011	0.13	0.15	0.21	NA	0.58
12q13.2	56,412,486	rs1701704	$1.5x10^{-3}$	$5.2x10^{-3}$	0.67	$4.5 x10^{-4}$	0.22	0.21	1	rs1701704	$2.0 x10^{-13}$	21804548	IKZF4	JAP	7,171	1,532	5,639	301	0.01	NA	NA	0.24	NA
4q31.21	144,003,158	rs7686660	0.88	0.99	0.86	0.69	0.53	0.19	1	rs7686660	$2.0 x10^{-12}$	21804548	LOC729675	JAP	7,171	1,532	5,639	301	0.01	NA	NA	0.24	NA
22q12.3	37,534,033	rs2284033	$7.9 x10^{-5}$	$5.3 x10^{-5}$	0.58	0.49	0.52	$1.6 x10^{-3}$	1	rs2284033	$1.0 x10^{-8}$	20860503	IL2RB	EU	10,365	10,365	NA	8,082	0.34	0.41	NA	NA	NA
8q24.11	118,025,644	rs3019885	0.99	0.81	0.11	0.47	0.09	0.86	1	rs3019885	$5.0 x10^{-13}$	21814517	SLC30A8	JAP (D); JAP,KOR (R)	2,591	938	1,653	938	0.04	NA	NA	0.76	NA
1q31.3	197,325,907	rs2786098	0.87	0.49	0.96	0.15	0.23	0.83	1	rs2786098	$2.0 x10^{-13}$	20032318	CRB1, DENND1B	EU, AF	3,377	793	2,584	1,088	0.05	0.03	0.21	NA	NA
1q23.1	158,932,554	rs1101999**	NA	NA	$1.1x10^{-4}$	NA	NA	NA	1	rs1101999	$4.0 x10^{-9}$	21804549	PYHIN1	AF (D); AF (R)	3,759	1,612	2,147	1,257	0.05	NA	0.58	NA	NA

The number of cases included in each TAGC meta-analysis is shown in parentheses

EU=European-ancestry, AF= African-ancestry, JAP=Japanese, LAT= Latino, KOR=Korean; D = discovery; R =replication

*The frequency of effect allele at 10p24.2, 4q12 and 9p23 loci (Pubmed.id=23829686) is <2% in European-ancestry populations (81% of the 527 study trios are from European-ancestry); no SNP found in LD with rs17218161 in TAGC

**The frequency of effect allele at 1q23.1 locus (Pubmed.id=21804549) is 0.30 in African ancestry populations in whom it was discovered but is very low in other populations

*** Only $P_{fixed}=3x10^{-14}$ is reported in the catalog while in the publication (PMID 24241537), there is significant evidence for heterogeneity (P=0.02) and $P_{random}= 3x10^{-7}$ is not genome-wide significant

Supplementary Table 13. Approximate conditional analysis of asthma-associated loci

Approximate conditional analysis, using the GCTA software (PMID 21167468), is based on summary meta-analysis statistics under a fixed-effects model. This analysis was only conducted in European-ancestry populations that are assumed to share a similar LD pattern Note that this analysis could not be done at the 9p24.1 locus which shows heterogeneity in SNP effect size across studies. At the 17q12-21, this analysis was restricted to the pediatric subgroup in which this locus does not show heterogeneity (see Online Methods for details).

							Meta-analysis results[e]			Conditional analysis results[f]		
Cytogenetic Region	**Conditional SNP[a]**	**SNP**	**Position**	**Nearby genes[b]**	**Effect allele[c]**	**EAF[d]**	**Beta**	**SE**	**P_{fixed}**	**Beta**	**SE**	**P_{fixed}**
New asthma susceptibility loci												
5q31.3	TOP	rs7705042	141,492,419	NDFIP1, GNPDA1, SPRY4	A	0.63	0.08	0.01	8.5×10^{-10}			
	rs7705042	rs13359221	141,035,880	ARAP3,FCHSD1,PCDH1	A	0.05	0.09	0.03	1.6×10^{-3}	0.09	0.03	1.6×10^{-3}
6p22.1	TOP	rs1233578	28,712,247	GPX5, TRIM27	G	0.13	0.10	0.02	5.3×10^{-9}			
	rs1233578	rs7509	27,418,847	ZNF184,ZNF319,HIST1H2BL	G	0.54	-0.04	0.01	6.1×10^{-4}	-0.03	0.01	5.9×10^{-3}
6q15	TOP	rs2325291	90,986,686	BACH2, GJA10,MAP3K7	A	0.33	-0.10	0.01	8.6×10^{-13}			
	rs2325291	rs1144157	91,184,183	BACH2, MAP3K7	G	0.67	-0.05	0.01	7.7×10^{-5}	-0.05	0.01	1.2×10^{-4}
12q13.3	TOP	rs167769	57,503,775	STAT6,NAB2,LRP1	T	0.40	0.08	0.01	5.5×10^{-9}			
	rs167769	rs10876932	57,217,358	HSD17B6, SDR9C7	G	0.58	-0.04	0.01	5.7×10^{-4}	-0.05	0.01	1.2×10^{-4}
17q21.33	TOP	rs17637472	47,461,433	ZNF652,PHB	A	0.39	0.08	0.01	3.3×10^{-9}			
	rs17637472	rs7214992	47,196,053	IGF2BP1,B4GALNT2	T	0.24	-0.04	0.02	3.2×10^{-3}	-0.05	0.02	1.6×10^{-3}
New asthma signals at loci previously reported for asthma in ancestry-specifc populations												
6p21.33	TOP*	rs2596464	31,412,961	MICA, MICB	C	0.48	0.09	0.01	1.8×10^{-13}			
	rs2596464	rs2855812	31,472,720	MICB,MICA,MCCD1	T	0.23	0.09	0.01	2.8×10^{-10}	0.07	0.01	4.3×10^{-7}
	rs2596464 + rs2855812	rs2844510	31,410,408	MICA,MICB	T	0.11	0.08	0.02	3.5×10^{-5}	0.09	0.02	1.5×10^{-6}
	rs2596464 + rs2855812 +rs2844510	rs9263879	31,171,581	POU5F1, HLA-C	A	0.12	-0.07	0.02	4.4×10^{-4}	-0.07	0.02	1.1×10^{-3}
10p14	TOP*	rs1663687	9,054,787	GATA3,CELF2	A	0.39	-0.08	0.01	1.5×10^{-10}			
	rs1663687	rs2646437	8,566,311	GATA3,CELF2	A	0.47	-0.06	0.01	9.4×10^{-6}	-0.05	0.01	4.8×10^{-5}
Asthma signals previoulsy reported for asthma plus hay fever												
8q21.13	TOP*	rs10957979	81,289,787	TPD52, ZBTB10	G	0.65	-0.07	0.01	2.3×10^{-8}			
	rs10957979	rs12675564	80,864,649	MRPS28,HEY1,TPD52	G	0.72	0.03	0.01	0.01	0.04	0.01	7.8×10^{-3}
16p13.13	TOP	rs17806299	11,199,980	CLEC16A,DEXI, SOCS1	A	0.20	-0.10	0.02	2.1×10^{-10}			
	rs17806299	rs193772	11,299,077	CLEC16A,SOCS1	C	0.87	-0.09	0.02	2.6×10^{-6}	-0.07	0.02	1.5×10^{-4}
Known asthma loci												
2q12	TOP	rs3771180	102,953,617	IL1RL1,IL1RL2,IL18R1	T	0.14	-0.17	0.02	1.5×10^{-20}			
	rs3771180	rs1420101	102,957,716	IL1RL1,IL1RL2,IL18R1	T	0.37	0.12	0.01	9.1×10^{-20}	0.08	0.01	2.2×10^{-11}
5q22.1	TOP	rs10455025	110,404,999	SLC25A46,TSLP	C	0.34	0.14	0.01	2.0×10^{-25}			
	rs10455025	rs6893213	110,198,114	SLC25A46,TSLP	T	0.08	0.15	0.02	7.9×10^{-11}	0.13	0.02	2.5×10^{-9}
	rs10455025 + rs6893213	rs10043185	109,976,588	TMEM232,MAN2A1,SLC25A46	A	0.05	0.07	0.03	0.02	0.12	0.03	1.1×10^{-4}
5q31	TOP	rs20541	131,995,964	IL13,RAD50,IL4	G	0.79	-0.12	0.02	1.4×10^{-14}			
	rs20541	rs6894249	131,797,547	SLC22A5,IRF1	G	0.39	0.09	0.01	2.2×10^{-11}	0.08	0.01	1.3×10^{-9}
6p21.32	TOP	rs9272346	32,604,372	HLADRB1,HLA-DQA1	A	0.56	0.15	0.01	2.4×10^{-28}			
	rs9272346	rs3763309	32,375,973	BTNL2,HLA-DRA	A	0.21	0.13	0.02	1.3×10^{-18}	0.09	0.01	1.2×10^{-9}
	rs9272346 + rs3763309	rs241429	32,803,840	TAP2,HLA-DOB,PSMB8	G	0.58	-0.07	0.01	2.9×10^{-8}	-0.05	0.01	4.8×10^{-5}
11q13.5	TOP	rs2155219	76,299,194	C11orf30, LRRC32	T	0.46	0.11	0.01	2.9×10^{-15}			
	rs2155219	rs4944120	76,436,948	LRRC32,TSKU	G	0.24	-0.02	0.01	0.12	-0.03	0.01	2.5×10^{-2}
15q22.2	TOP	rs11071558	61,069,421	RORA,NARG2,VPS13C	G	0.14	-0.12	0.02	8.3×10^{-11}			
	rs11071558	rs339992	60,913,505	RORA,NARG2,VPS13C	G	0.12	-0.06	0.02	4.2×10^{-3}	-0.06	0.02	3.8×10^{-3}
15q22.33	TOP	rs17293632	67,442,596	SMAD3,SMAD6,AAGAB	T	0.26	0.12	0.01	8.8×10^{-16}			
	rs17293632	rs2053295	67,391,739	SMAD3,SMAD6,AAGAB	A	0.88	0.01	0.02	0.5	0.06	0.02	7.3×10^{-4}
17q12-q21	TOP	rs2305479	38,062,217	GSDMB, ZBP2,ORMDL3	T	0.51	-0.23	0.02	2.8×10^{-24}			
	rs2305479	rs3859192	38,119,254	GSDMA,LRRC3C,PSMD3	T	0.47	0.19	0.02	1.9×10^{-16}	0.09	0.02	3.4×10^{-5}

[a]In the conditional SNP field, 'TOP' indicates we present the unadjusted results for the top SNP at each locus; otherwise the rsIDs of the top (and subsequent SNPs) used to adjust other SNPs are listed

[b]The gene where eventually the lead SNP lies is first indicated followed by the previous and next genes

[c]The effect allele is the allele for which the regression coefficients (betas) are computed; [d]EAF= Effect allele frequency in European-ancestry populations.

[e]Under the heading meta-analysis results, beta, SE and P are the regression coefficient, standard error and P-values in fixed-effects meta-analysis of European ancestry populations

[f]Under the heading conditional analysis results, beta, SE and P are the regression coefficient, standard error and P-values following adjustment by the SNP(s) listed in the 'Conditional SNP' field.

Note that the TOP SNP in European-ancestry meta-analysis under a fixed-effects may differ from the TOP SNP under a random-effects model (Table 1); these TOP SNPs are indicated by a star.

Supplementary Table 14. Associations between SNPs at the nine novel asthma loci and cis-gene expression in blood and lung

The eQTL databases for blood and lung were interrogated for the lead SNPs (shown in Table 1) and all SNPs having r^2 between 0.50 and 1 with the lead SNPs.
This table shows the most significant associations between asthma SNPs and transcripts among all associations having $P_{transcript} < 10^{-5}$

Region	Asthma SNP	Position	LD (r^2/D') with lead SNP	Alleles (R/E)[a]	Source database[b]	Tissue[c]	Gene (expression)	$P_{transcript}$[d]	Gene (expression)	$P_{transcript}$[d]	Gene (expression)	$P_{transcript}$[d]	Gene (expression)	$P_{transcript}$[d]	Gene (expression)	$P_{transcript}$[d]	Reference PMID
New asthma susceptibility loci																	
5q31.3	rs7705042	141,492,419		C/A	Blood_eQTL	Blood	NDFIP1	2.73×10^{-9}	GNPDA1	5.98×10^{-6}							24013639
					MRCA	LCLs	NDFIP1	6.85×10^{-9}									23345460
					MRCE	LCLs	NDFIP1	1.60×10^{-7}									23345460
					GTEx	Blood	NDFIP1	3.78×10^{-6}									25954001
6q15	rs10455168	90,883,525	0.94/1 with rs2325291	T/C	Blood_eQTL	Blood	BACH2	2.98×10^{-10}									24013639
12q13.3	rs167769	57,503,775		C/T	Blood_eQTL	Blood	STAT6	9.81×10^{-198}	NEMP1	1.64×10^{-11}							24013639
					MuTHER	LCLs	STAT6	1.63×10^{-22}									22941192
					MRCE	LCLs	STAT6	2.26×10^{-19}									23345460
					Hao et al, 2012	Lung	STAT6	3.7×10^{-37}									23209423
	rs12368672	55,798,737	0.87/0.98 with rs167769		GHS_Express	Monocytes	STAT6	3.38×10^{-77}									20502693
	rs324011	55,788,449	0.95/1 with rs167769		Blood_eQTL	Blood	STAT6	9.81×10^{-198}	TMEM194A	7.1×10^{-12}							24013639
					MuTHER	LCLs	STAT6	6.53×10^{-26}									22941192
					MRCE	LCLs	STAT6	1.99×10^{-19}									23345460
					Hao *et al*, 2012	Lung	STAT6	1.09×10^{-38}									23209423
17q21.33	rs17637472	47,461,433		G/A	Blood_eQTL	Blood	GNGT2	2.13×10^{-52}	PHOSPHO1	3.17×10^{-12}							24013639
					MuTHER	LCLs	GNGT2	2.38×10^{-11}									22941192
					MRCE	LCLs	GNGT2	5.25×10^{-13}									23345460
					GHS_Express	Monocytes	GNGT2	2.98×10^{-8}									20502693
New asthma signals at loci previoulsy reported for asthma in ancestry-specific populations																	
6p21.33	rs3131064	30,763,893		T/C	Blood_eQTL	Blood	IER3	8.58×10^{-47}	FLOT1	9.07×10^{-33}	VARS2	3.67×10^{-30}					24013639
					MuTHER	LCLs	HCG22	4.55×10^{-7}	ZNRD1	9.7×10^{-6}							22941192
					MRCA	LCLs	HLA-C	1.15×10^{-13}									23345460
					GTEx	Lung	HLA-J	6.26×10^{-7}									25954001
					Hao *et al*, 2012	Lung	TUBB	2.3×10^{-16}	HLA-A	1.9×10^{-13}	HLA-C	5.6×10^{-12}	CDSN	8.2×10^{-10}	APOM	1.7×10^{-8}	23209423
	rs2596464 lead SNP in conditional analysis (fixed-effects model)	31,412,961		T/C	Blood_eQTL	Blood	MICB	6.87×10^{-21}									24013639
					GTEx	Blood	MICA	7.45×10^{-12}									25954001
					MuTHER	LCLs	HCG22	9.45×10^{-10}	MICB	2.02×10^{-9}	LST1	1.37×10^{-6}					
					MRCE	LCLs	MICA	4.41×10^{-11}									22941192
					GHS_Express	Monocytes	HLA-C	4.14×10^{-18}	HCG27	5.00×10^{-11}	MICB	1.17×10^{-6}					20502693
					GTEx	Lung	MICA	2.49×10^{-9}									25954001
					Hao et al, 2012	Lung	CDSN	4.75×10^{-19}	AGPAT1	2.44×10^{-12}	MICB	1.56×10^{-6}					23209423
Asthma signals previously reported for asthma plus hay fever																	
16p13.13	rs17806299	11,199,980		G/A	Blood_eQTL	Blood	DEXI	2.23×10^{-43}									24013639
					MRCE	LCLs	SOCS1	1.04×10^{-7}									23345460
					GHS_Express	Monocytes	DEXI	3.62×10^{-20}									20502693

[a]R=reference allele /E=effect allele

[b]eQTL databases are described in Online Methods

[c]Blood is whole blood; LCL = lymphoblastoid cell lines; Lung is whole lung tissue

[d]$P_{transcript}$ is the *P*-value for test of association of SNP with gene transcript

Supplementary Table 15. Overlap between TAGC asthma association signals ($P_{random} < 10^{-4}$) and GWAS signals with diseases/traits in the GWAS catalog.

This Table has three parts: (i) autoimmune diseases are in the first part of the table; (ii) three allergic phenotypes in the second part; and (iii) the rest of the top 10 traits (in the number of hits in the catalog) are last. Asthma association signals are those having $P_{random} < 10^{-4}$ in the multi-ancestry meta-analysis. For each disease and trait, we selected one GWAS SNP per chromosomal band as reported in the variable "Region" in the GWAS catalog; SNPs associated with multiple diseases in the GWAS catalog could appear in counts in multiple rows.

Rank[a]	Disease/Trait	Number of GWAS catalog entries	Number of SNPs associated with asthma at $P_{random} < 10^{-4}$ in TAGC multi-ancestry meta-analysis	Enrichment *P*-value[b]
Auto-immune diseases				
2	Inflammatory bowel disease	97	6	9.8×10^{-16}
4	Crohn's disease	89	9	6.3×10^{-25}
8	Rheumatoid arthritis	59	4	4.5×10^{-11}
11	Ulcerative colitis	54	4	3.1×10^{-11}
14	Multiple sclerosis	49	3	1.8×10^{-8}
23	Systemic lupus erythematosus	35	2	5.9×10^{-6}
25	Type 1 diabetes	34	5	2.7×10^{-15}
30	Celiac disease	29	3	3.6×10^{-9}
38	Vitiligo	23	4	8.8×10^{-18}
Allergy-related phenotypes				
65	Self-reported allergy	16	12	Highly significant
67	Atopic dermatitis	14	5	Highly significant
99	Allergic sensitization	9	7	Highly significant
Top 10 traits in the number of hits in the GWAS catalog				
1	Height	162	3	6.8×10^{-7}
3	Blood metabolite levels	96	2	4.5×10^{-5}
5	Cholesterol, total	66	2	2.1×10^{-5}
6	HDL cholesterol	64	2	2.0×10^{-5}
7	Type 2 diabetes	61	0	1
9	Breast cancer	56	0	1
10	Prostate cancer	56	0	1

[a]Rank of the disease or trait in the number of unique signals in the GWAS catalog (PMID: 24316577)

[b]The enrichment *P*-value is the binomial tail probability for observing the shown number of TAGC SNPs with $P_{random}<10^{-4}$ among the SNPs reported in the GWAS catalog for a given disease or trait.

We investigated overlap with nine auto-immune diseases, three allergic phenotypes and seven other traits with large number of associations, and a conservative Bonferroni correction implies an adjusted significance threshold for enrichment of 0.05/19 =0.003.

Supplementary Table 16. Overlap between TAGC asthma signals ($P_{random}<10^{-3}$ in multi-ancestry meta-analysis) and GWAS signals with diseases/traits in the GWAS catalog

Information from the NHGRI GWAS catalog[a]							Information from TAGC asthma meta-analysis		
Disease.Trait	Region	Chr_position (build 38)	Reported Genes	Mapped Gene	Strongest SNP -Risk Allele	P_Value	P_{fixed}[b]	P_{random}[b]	P_{het}[c]
Common traits (Other)	1q21.3	152,520,678	LCE3E	CRCT1 - LCE3E	rs499697-G	1×10^{-10}	4.3×10^{-4}	9.6×10^{-4}	0.13
Fibrinogen	1q21.3	154,453,788	IL6R	IL6R	rs4129267-T	6×10^{-27}	8.1×10^{-8}	8.5×10^{-7}	0.19
C-reactive protein	1q21.3	154,453,788	IL6R	IL6R	rs4129267-C	2×10^{-48}	8.1×10^{-8}	8.5×10^{-7}	0.19
Protein quantitative trait loci	1q21.3	154,453,788	IL6R	IL6R	rs4129267-?	2×10^{-57}	8.1×10^{-8}	8.5×10^{-7}	0.19
Celiac disease and Rheumatoid arthritis	1q24.2	167,442,147	CD247	CD247	rs864537-?	2×10^{-11}	1.4×10^{-4}	4.6×10^{-4}	0.30
Ulcerative colitis	2q11.2	102,047,167	IL1R2	IL1R2 - IL1R1	rs2310173-T	3×10^{-12}	2.5×10^{-5}	2.5×10^{-5}	1.00
Self-reported allergy	2q12.1	102,263,004	IL1RL2, IL1RL1	IL1RL2 - IL1RL1	rs10189629-A	2×10^{-16}	3.2×10^{-17}	7.1×10^{-13}	0.06
Serum protein levels (sST2)	2q12.1	102,316,102	IL1RL1	IL1RL1	rs950880-A	7×10^{-94}	8.3×10^{-19}	2.6×10^{-17}	0.41
Eosinophil counts	2q12.1	102,341,256	IL1RL1	IL1RL1	rs1420101-A	5×10^{-14}	3.9×10^{-21}	3.9×10^{-21}	0.61
Crohn's disease	2q33.1	198,032,171	PLCL1	PLCL1	rs6738825-A	4×10^{-9}	5.0×10^{-4}	5.0×10^{-4}	0.53
Self-reported allergy	2q33.1	198,049,348	PLCL1	PLCL1	rs10497813-G	6×10^{-10}	3.7×10^{-4}	3.7×10^{-4}	0.65
Menarche (age at onset)	3q22.1	132,891,908	TMEM108, NPHP3	NPHP3-AS1 - TMEM108	rs6439371-G	1×10^{-8}	7.5×10^{-4}	7.5×10^{-4}	0.65
Allergic sensitization	3q28	188,354,725	LPP, BCL6	LPP	rs9865818-G	3×10^{-10}	5.2×10^{-5}	1.6×10^{-4}	0.01
Vitiligo	3q28	188,394,766	LPP	LPP	rs1464510-T	1×10^{-11}	1.0×10^{-6}	2.2×10^{-5}	4.4×10^{-3}
Celiac disease	3q28	188,394,766	LPP	LPP	rs1464510-A	3×10^{-40}	1.0×10^{-6}	2.2×10^{-5}	4.4×10^{-3}
Self-reported allergy	3q28	188,411,191	LPP, BCL6	LPP	rs9860547-A	1×10^{-9}	7.4×10^{-5}	3.2×10^{-4}	4.4×10^{-3}
Self-reported allergy	4p14	38,809,930	TLR1,TLR6,TLR10	TLR1 - TLR6	rs2101521-A	5×10^{-21}	8.1×10^{-4}	8.1×10^{-4}	0.74
Allergic sensitization	4p14	38,811,255	TLR1,TLR6, TLR10, MIR574, FAM114A1	TLR1 - TLR6	rs17616434-T	5×10^{-11}	1.0×10^{-5}	5.2×10^{-5}	0.22
Type 1 diabetes	4q27	122,211,337	IL2	KIAA1109	rs4505848-?	5×10^{-13}	2.7×10^{-6}	5.4×10^{-5}	0.21
Self-reported allergy	4q27	122,408,207	ADAD1	ADAD1	rs17388568-A	4×10^{-8}	4.1×10^{-5}	6.2×10^{-4}	0.11
Allergic sensitization	5q22.1	110,854,353	SLC25A46, TSLP, WDR36, CAMK4	SLC25A46 - TSLP	rs10056340-G	5×10^{-14}	3.2×10^{-8}	3.2×10^{-8}	0.67
Eosinophilic esophagitis (pediatric)	5q22.1	111,069,977	WDR36	TSLP	rs3806932-?	3×10^{-9}	3.6×10^{-9}	4.5×10^{-8}	0.36
Self-reported allergy	5q22.1	111,131,801	WDR36, CAMK4, TSLP	WDR36 - RPS3AP21	rs1438673-C	2×10^{-20}	6.1×10^{-19}	4.2×10^{-13}	0.10
Inflammatory bowel disease	5q23.3	130,681,594	Intergenic	ARL2BPP4 - RPL11P2	rs4836519-T	4×10^{-10}	7.6×10^{-4}	7.6×10^{-4}	0.73
Crohn's disease	5q31.1	132,067,045	IL3, ACSL6, P4HA2, PDLIM4, SLC22A4	IL3 - CSF2	rs3091338-T	4×10^{-8}	1.8×10^{-4}	3.0×10^{-4}	0.39
Blood metabolite levels	5q31.1	132,316,836	SLC22A4	SLC22A4;LOC553103	rs11950562-A	2×10^{-41}	9.0×10^{-11}	9.0×10^{-11}	0.70
Blood metabolite ratios	5q31.1	132,329,685	SLC22A4	SLC22A4;LOC553103	rs272889-A	3×10^{-51}	1.9×10^{-5}	1.9×10^{-5}	0.55
Metabolic traits	5q31.1	132,329,685	SLC22A4	SLC22A4;LOC553103	rs272889-A	7×10^{-16}	1.9×10^{-5}	1.9×10^{-5}	0.55
Height	5q31.1	132,350,453	FLJ44796	LOC553103	rs10058074-A	4×10^{-12}	2.2×10^{-9}	2.2×10^{-9}	0.69
Inflammatory bowel disease	5q31.1	132,435,113	IRF1, IL13, CSF2, SLC22A4, IL4, IL3, IL5, PDLIM4, SLC22A5, ACSL6	C5orf56	rs2188962-T	1×10^{-52}	7.3×10^{-10}	7.1×10^{-8}	0.15
Platelet counts	5q31.1	132,484,229	IRF1	IRF1	rs2070729-A	1×10^{-10}	2.3×10^{-9}	4.5×10^{-8}	0.30
Atopic dermatitis	5q31.1	132,660,151	IL13, RAD50	IL13	rs1295686-A	2×10^{-17}	2.8×10^{-15}	2.8×10^{-15}	0.67
IgE levels	5q31.1	132,660,272	IL13	IL13	rs20541-A	3×10^{-18}	5.0×10^{-16}	5.0×10^{-16}	0.77
Psoriasis	5q31.1	132,660,272	IL13	IL13	rs20541-G	5×10^{-15}	5.0×10^{-16}	5.0×10^{-16}	0.77
Hodgkin's lymphoma	5q31.1	132,662,721	IL13	IL13 - IL4	rs2069757-A	2×10^{-11}	3.3×10^{-7}	3.3×10^{-7}	0.82
Crohn's disease	5q31.3	142,099,500	NDFIP1	MRPL11P2 - NDFIP1	rs11167764-C	2×10^{-9}	1.5×10^{-8}	1.5×10^{-6}	0.12
Schizophrenia or bipolar disorder	6p22.1	27,742,386	MHC	TRNAI25	rs17693963-?	3×10^{-11}	6.0×10^{-7}	6.0×10^{-7}	0.74
Schizophrenia, schizoaffective disorder or bipolar disorder	6p22.1	27,742,386	MHC	TRNAI25	rs17693963-?	2×10^{-9}	6.0×10^{-7}	6.0×10^{-7}	0.74
Pulmonary function	6p22.1	28,354,519	ZKSCAN3, ZNF323	ZKSCAN3	rs6903823-G	2×10^{-10}	8.6×10^{-8}	8.6×10^{-8}	0.62
Barrett's esophagus	6p22.1	29,388,554	MHC, OR2D12, OR2D13	TRNAI25	rs9257809-A	4×10^{-9}	3.8×10^{-6}	3.8×10^{-6}	0.77
Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined)	6p22.1	30,064,745	MHC region	PPP1R11;ZNRD1	rs8321-?	8×10^{-9}	4.6×10^{-7}	4.6×10^{-7}	0.93
Schizophrenia	6p22.1	30,197,496	MHC, TRIM26	TRIM26	rs2523722-G	1×10^{-16}	5.7×10^{-8}	5.7×10^{-8}	0.79
Myasthenia gravis	6p21.33	31,090,563	NR	TRNAI25	rs3130544-A	2×10^{-90}	1.8×10^{-8}	1.8×10^{-8}	0.48
Chronic hepatitis B infection	6p21.33	31,162,816	TCF19	TCF19	rs1419881-?	1×10^{-18}	6.9×10^{-5}	1.2×10^{-4}	0.30
HIV-1 control	6p21.33	31,175,805	PSORS1C3	PSORS1C3	rs3131018-C	4×10^{-16}	1.4×10^{-4}	2.3×10^{-4}	0.35
Psoriasis	6p21.33	31,344,549	HLA-C	TRNAI25	rs3134792-?	1×10^{-9}	3.1×10^{-6}	5.0×10^{-6}	0.44

		Information from the NHGRI GWAS catalog[a]					Information from TAGC asthma meta-analysis		
Disease.Trait	Region	Chr_position (build 38)	Reported Genes	Mapped Gene	Strongest SNP -Risk Allele	P_Value	P_{fixed}[b]	P_{random}[b]	P_{het}[c]
Self-reported allergy	6p21.33	31,384,336	HLA-C, MICA	TRNAI25	rs9266772-C	3×10^{-12}	8.5×10^{-6}	2.3×10^{-5}	0.36
Rheumatoid arthritis (ACPA-negative)	6p21.33	31,385,552	HLA-B,MICA	TRNAI25	rs2596565-?	9×10^{-9}	1.0×10^{-7}	1.0×10^{-6}	0.27
Allergic sensitization	6p21.33	31,386,405	HLA-B, MICA, HLA-C, MICB	TRNAI25	rs6932730-T	4×10^{-8}	5.2×10^{-5}	2.0×10^{-4}	0.31
Height	6p21.33	31,386,783	HLA-B	TRNAI25	rs13437082-?	5×10^{-8}	5.8×10^{-5}	2.9×10^{-4}	0.11
Beta-2 microglubulin plasma levels	6p21.33	31,394,533	HLA-B	LOC101929072	rs16899524-C	1×10^{-8}	7.5×10^{-6}	1.0×10^{-5}	0.44
Metabolic syndrome	6p21.33	31,481,199	HCG26, MICB	TRNAI25	rs3099844-A	2×10^{-8}	1.4×10^{-9}	1.4×10^{-9}	0.56
Neonatal lupus	6p21.33	31,481,199	TNF,NFKBIL1,LTA,LTB,AIF1	TRNAI25	rs3099844-?	5×10^{-10}	1.4×10^{-9}	1.4×10^{-9}	0.56
Dengue shock syndrome	6p21.33	31,507,709	MICB	MICB	rs3132468-?	4×10^{-11}	1.4×10^{-7}	1.2×10^{-5}	0.16
Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN)	6p21.33	31,537,703	BAT1, HCP5, MICC, PPIAP9, PSORS1C1, POLR2LP, CCHCR1, TCF19, POU5F1, HLA-C, HCP5, PSORS1C3, HLA-B*5801	DDX39B;SNORD117;ATP6V1G2-DDX39B	rs2734583-?	2×10^{-8}	3.8×10^{-8}	3.8×10^{-8}	0.65
Lung adenocarcinoma	6p21.33	31,652,743	BAT3, APOM	BAG6;APOM	rs3117582-C	5×10^{-12}	7.1×10^{-7}	7.1×10^{-7}	0.51
Lung cancer	6p21.33	31,652,743	BAT3	BAG6;APOM	rs3117582-?	4×10^{-10}	7.1×10^{-7}	7.1×10^{-7}	0.51
Systemic lupus erythematosus	6p21.33	31,902,549	C2	C2;ZBTB12	rs558702-A	8×10^{-21}	1.8×10^{-6}	1.8×10^{-6}	0.51
Hematology traits	6p21.33	31,973,120	ZBTB12, CFB, STK19	DXO;STK19	rs389884-C	2×10^{-8}	1.4×10^{-6}	1.4×10^{-6}	0.56
Serum total protein level	6p21.32	32,142,202	Intergenic	TRNAI25	rs204999-A	3×10^{-9}	2.3×10^{-4}	5.6×10^{-4}	0.01
Phospholipid levels (plasma)	6p21.32	32,168,770	AGPAT1	AGPAT1;EGFL8;PPT2-EGFL8	rs1061808-?	8×10^{-10}	4.9×10^{-9}	4.9×10^{-9}	0.56
Atopic dermatitis	6p21.32	32,190,542	GPSM3	PBX2;GPSM3	rs176095-T	8×10^{-20}	4.8×10^{-5}	2.2×10^{-4}	9.0×10^{-3}
Complement C3 and C4 levels	6p21.32	32,197,667	HLA-DRA	NOTCH4	rs2071278-G	4×10^{-72}	4.6×10^{-5}	3.5×10^{-4}	0.10
Systemic sclerosis	6p21.32	32,222,629	NOTCH4	NOTCH4	rs443198-?	9×10^{-21}	3.2×10^{-6}	1.7×10^{-5}	0.26
Nephropathy	6p21.32	32,251,066	Intergenic	C6orf10	rs3115573-?	1×10^{-9}	5.8×10^{-5}	5.8×10^{-5}	0.55
Chronic lymphocytic leukemia	6p21.32	32,289,789	HLA	C6orf10	rs926070-A	4×10^{-8}	1.2×10^{-6}	1.2×10^{-6}	0.51
Lumiracoxib-related liver injury	6p21.32	32,338,202	HLA-DRB1	C6orf10	rs3129900-?	7×10^{-25}	1.4×10^{-5}	5.6×10^{-5}	0.32
Multiple sclerosis	6p21.32	32,368,410	C6orf10	C6orf10	rs3129934-T	7×10^{-16}	1.2×10^{-5}	5.9×10^{-5}	0.30
Graves' disease	6p21.32	32,369,853	MHC	C6orf10	rs2273017-A	2×10^{-22}	1.0×10^{-5}	1.0×10^{-5}	0.68
Hepatitis C induced liver cirrhosis	6p21.32	32,400,310	BTNL2	BTNL2	rs3817963-A	1×10^{-8}	2.7×10^{-19}	6.4×10^{-13}	0.06
Lung adenocarcinoma	6p21.32	32,400,310	BTNL2	BTNL2	rs3817963-G	3×10^{-10}	2.7×10^{-19}	6.4×10^{-13}	0.06
Multiple sclerosis (OCB status)	6p21.32	32,400,310	BTNL2	BTNL2	rs3817963-?	6×10^{-10}	2.7×10^{-19}	6.4×10^{-13}	0.06
Vitiligo	6p21.32	32,405,921	BTNL2, HLA-DRA, HLA-DQA1	BTNL2;LOC101929163	rs3806156-T	7×10^{-19}	6.3×10^{-11}	1.1×10^{-6}	1.5×10^{-3}
Parkinson's disease	6p21.32	32,420,032	LOC642072	TRNAI25	rs2395163-?	3×10^{-11}	5.8×10^{-17}	1.5×10^{-10}	0.09
Cholesterol, total	6p21.32	32,444,658	HLA	HLA-DRA	rs3177928-A	1×10^{-21}	1.3×10^{-6}	2.0×10^{-5}	0.16
LDL cholesterol	6p21.32	32,444,658	HLA	HLA-DRA	rs3177928-A	3×10^{-17}	1.3×10^{-6}	2.0×10^{-5}	0.16
Hodgkin's lymphoma	6p21.32	32,460,508	HLA class II, HLA class I	TRNAI25	rs6903608-C	7×10^{-31}	5.4×10^{-5}	3.8×10^{-4}	0.20
Rheumatoid arthritis	6p21.32	32,461,866	HLA-DRA	TRNAI25	rs9268853-C	5×10^{-10}9	1.8×10^{-18}	6.1×10^{-17}	0.39
Ulcerative colitis	6p21.32	32,461,866	HLA-DRB5, HLA-DQA1, HLA-DRB1, HLA-DRA, BTNL2	TRNAI25	rs9268853-T	1×10^{-55}	1.8×10^{-18}	6.1×10^{-17}	0.39
IgA nephropathy	6p21.32	32,609,603	HLA-DRB1	TRNAI25	rs660895-G	4×10^{-20}	3.2×10^{-16}	1.1×10^{-6}	8.0×10^{-4}
Lymphoma	6p21.32	32,614,112	HLA-DRB5, HLA-DQA1	TRNAI25	rs4530903-T	2×10^{-8}	1.1×10^{-8}	2.0×10^{-7}	0.13
Schizophrenia	6p21.32	32,634,492	HLA-DQA1	TRNAI25	rs9272219-G	7×10^{-8}	2.0×10^{-5}	2.9×10^{-5}	0.42
Type 1 diabetes	6p21.32	32,636,595	HLA	HLA-DQA1	rs9272346-G	6×10^{-12}9	8.2×10^{-32}	5.7×10^{-24}	0.14
Immunoglobulin A	6p21.32	32,638,107	HLA-DRB1	HLA-DQA1	rs2187668-A	2×10^{-33}	1.0×10^{-5}	5.3×10^{-5}	0.31
Celiac disease	6p21.32	32,638,107	HLA-DQA1, HLA-DQB1	HLA-DQA1	rs2187668-A	1×10^{-50}	1.0×10^{-5}	5.3×10^{-5}	0.31
Autoimmune hepatitis type-1	6p21.32	32,638,107	HLA-DQA1	HLA-DQA1	rs2187668-?	2×10^{-78}	1.0×10^{-5}	5.3×10^{-5}	0.31
Nephropathy (idiopathic membranous)	6p21.32	32,638,107	HLA-DQA1	HLA-DQA1	rs2187668-?	8×10^{-93}	1.0×10^{-5}	5.3×10^{-5}	0.31
Allergic sensitization	6p21.32	32,658,534	HLA-DQB1, HLA-DQA1,	TRNAI25	rs6906021-C	2×10^{-12}	3.9×10^{-14}	8.4×10^{-10}	0.05
Self-reported allergy	6p21.32	32,658,534	HLA-DQA1, HLA-DQB1	TRNAI25	rs6906021-C	7×10^{-15}	3.9×10^{-14}	8.4×10^{-10}	0.05
Follicular lymphoma	6p21.32	32,696,681	HLA-DQB1	TRNAI25	rs2647012-G	2×10^{-21}	1.0×10^{-6}	6.7×10^{-4}	0.02
HPV seropositivity	6p21.32	32,697,183	HLA-DQB1	TRNAI25	rs9357152-G	1×10^{-14}	1.6×10^{-7}	4.5×10^{-7}	0.41
Hepatocellular carcinoma (hepatitis B virus related)	6p21.32	32,698,518	HLA-DQ	TRNAI25	rs9275319-A	3×10^{-17}	7.6×10^{-5}	6.0×10^{-4}	0.31
Hepatitis B	6p21.32	32,702,478	HLA-DQB1	TRNAI25	rs2856718-A	4×10^{-37}	2.0×10^{-8}	1.9×10^{-7}	0.27
Chronic hepatitis B infection	6p21.32	32,702,478	HLA-DQ	TRNAI25	rs2856718-?	2×10^{-24}	2.0×10^{-8}	1.9×10^{-7}	0.27
Systemic lupus erythematosus	6p21.32	32,711,222	HLA-DQA2	TRNAI25	rs9275572-A	5×10^{-16}	4.8×10^{-7}	4.1×10^{-4}	0.04
Chronic hepatitis C infection	6p21.32	32,711,222	HLA-DQB1, HLA-DQA1	TRNAI25	rs9275572-T	4×10^{-16}	4.8×10^{-7}	4.1×10^{-4}	0.04
Hepatocellular carcinoma	6p21.32	32,711,222	HLA-DQ, HLA-DR	TRNAI25	rs9275572-A	6×10^{-9}	4.8×10^{-7}	4.1×10^{-4}	0.04
Alopecia areata	6p21.32	32,711,222	HLA-DQA2	TRNAI25	rs9275572-G	1×10^{-35}	4.8×10^{-7}	4.1×10^{-4}	0.04

			Information from the NHGRI GWAS catalog[a]				Information from TAGC asthma meta-analysis		
Disease.Trait	Region	Chr_position (build 38)	Reported Genes	Mapped Gene	Strongest SNP -Risk Allele	P_Value	P_{fixed}[b]	P_{random}[b]	P_{het}[c]
Pulmonary function (interaction)	6p21.32	32,712,799	HLA-DQB1, HLA-DQA2	TRNAI25	rs7764819-T	4×10^{-9}	1.2×10^{-5}	1.2×10^{-5}	0.50
Crohn's disease	6p21.32	32,713,151	HLA-DQA2, HLA-DRB1, HLA-DQA1, HLA-DQB1, HLA-DOB, PSMB9	TRNAI25	rs7765379-G	9×10^{-59}	8.2×10^{-6}	8.2×10^{-6}	0.55
Thyroid peroxidase antibody positivity	6q15	90,170,674	BACH2	BACH2	rs10944479-A	4×10^{-8}	2.2×10^{-6}	2.2×10^{-6}	0.93
Celiac disease	6q15	90,216,893	BACH2, MAP3K7	BACH2	rs10806425-A	4×10^{-10}	3.6×10^{-6}	3.6×10^{-6}	0.85
Vitiligo	6q15	90,247,744	BACH2	BACH2	rs3757247-A	3×10^{-8}	4.2×10^{-6}	4.2×10^{-6}	0.79
Inflammatory bowel disease	6q15	90,263,440	Intergenic	BACH2	rs1847472-C	2×10^{-10}	1.4×10^{-11}	1.4×10^{-11}	0.74
Crohn's disease	6q15	90,263,440	BACH2	BACH2	rs1847472-G	5×10^{-9}	1.4×10^{-11}	1.4×10^{-11}	0.74
Multiple sclerosis	6q15	90,287,050	BACH2	BACH2	rs12212193-G	4×10^{-8}	6.7×10^{-11}	6.7×10^{-11}	0.58
Rheumatoid arthritis	6q21	106,219,660	ATG5	ATG5	rs9372120-G	8×10^{-10}	1.1×10^{-5}	1.1×10^{-5}	0.48
Pulmonary function	6q21	108,946,847	ARMC2	ARMC2	rs2798641-T	8×10^{-9}	9.6×10^{-4}	9.6×10^{-4}	0.74
Multiple sclerosis	6q23.3	137,646,077	OLIG3	BTF3L4P3 - TNFAIP3	rs13192841-A	1×10^{-8}	9.5×10^{-5}	3.5×10^{-4}	0.02
Mean corpuscular hemoglobin	6q24.1	139,514,552	CITED2	CITED2 - ATP5F1P6	rs668459-T	9×10^{-9}	2.3×10^{-5}	8.5×10^{-4}	0.01
Mean corpuscular volume	6q24.1	139,514,552	CITED2	CITED2 - ATP5F1P6	rs668459-T	4×10^{-8}	2.3×10^{-5}	8.5×10^{-4}	0.01
Atopic dermatitis	7p22.2	3,089,155	CARD11	CARD11 - SDK1	rs4722404-G	8×10^{-9}	1.5×10^{-5}	1.5×10^{-5}	0.48
QRS duration	7p12.3	46,580,547	IGFBP3	TTC4P1 - HMGN1P19	rs7784776-G	1×10^{-9}	5.6×10^{-4}	5.6×10^{-4}	0.58
Self-reported allergy	8q21.13	80,355,920	TPD52, ZBTB10	RPS5P5 - ZBTB10	rs6473223-T	8×10^{-8}	1.3×10^{-10}	1.3×10^{-10}	0.49
Self-reported allergy	9p24.1	6,172,380	RANBP6, IL33	RANBP6 - GTF3AP1	rs7032572-G	2×10^{-9}	1.3×10^{-24}	1.4×10^{-16}	0.06
Coronary heart disease	9p21.3	22,103,814	CDKN2A/2B	CDKN2B-AS1	rs1333042-?	1×10^{-9}	5.1×10^{-4}	5.1×10^{-4}	0.82
Breast cancer	9q31.2	108,126,198	Intergenic	CHCHD4P2 - RPL36P14	rs865686-T	1×10^{-34}	2.8×10^{-4}	7.1×10^{-4}	0.39
Blood metabolite levels	9q34.2	133,278,431	ABO	ABO - SURF6	rs651007-T	6×10^{-20}	4.4×10^{-4}	4.4×10^{-4}	0.99
Serum alkaline phosphatase levels	9q34.2	133,278,431	SURF6, ABO	ABO - SURF6	rs651007-A	1×10^{-56}	4.4×10^{-4}	4.4×10^{-4}	0.99
End-stage coagulation	9q34.2	133,278,431	ABO	ABO - SURF6	rs651007-C	2×10^{-25}	4.4×10^{-4}	4.4×10^{-4}	0.99
Metabolite levels	9q34.2	133,278,431	ABO	ABO - SURF6	rs651007-A	6×10^{-9}	4.4×10^{-4}	4.4×10^{-4}	0.99
E-selectin levels	9q34.2	133,278,431	ABO	ABO - SURF6	rs651007-T	2×10^{-82}	4.4×10^{-4}	4.4×10^{-4}	0.99
Urinary metabolites (H-NMR features)	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-T	1×10^{-28}	3.1×10^{-4}	3.1×10^{-4}	1.00
Red blood cell traits	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-T	9×10^{-18}	3.1×10^{-4}	3.1×10^{-4}	1.00
Liver enzyme levels (alkaline phosphatase)	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-T	$3 \times 10^{-12}3$	3.1×10^{-4}	3.1×10^{-4}	1.00
Coronary heart disease	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-C	4×10^{-14}	3.1×10^{-4}	3.1×10^{-4}	1.00
Soluble levels of adhesion molecules	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-T	2×10^{-41}	3.1×10^{-4}	3.1×10^{-4}	1.00
Soluble E-selectin levels	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-C	1×10^{-29}	3.1×10^{-4}	3.1×10^{-4}	1.00
Coronary artery disease or ischemic stroke	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-?	2×10^{-9}	3.1×10^{-4}	3.1×10^{-4}	1.00
Coronary artery disease or large artery stroke	9q34.2	133,278,724	ABO	ABO - SURF6	rs579459-?	3×10^{-8}	3.1×10^{-4}	3.1×10^{-4}	1.00
Blood metabolite ratios	9q34.2	133,278,860	ABO	ABO - SURF6	rs649129-T	9×10^{-37}	2.9×10^{-4}	2.9×10^{-4}	1.00
Venous thromboembolism	9q34.2	133,279,294	ABO	ABO - SURF6	rs495828-T	3×10^{-16}	2.6×10^{-4}	2.6×10^{-4}	1.00
Hematological and biochemical traits	9q34.2	133,279,294	ABO	ABO - SURF6	rs495828-T	4×10^{-59}	2.6×10^{-4}	2.6×10^{-4}	1.00
Red blood cell count	9q34.2	133,279,294	ABO	ABO - SURF6	rs495828-T	3×10^{-12}	2.6×10^{-4}	2.6×10^{-4}	1.00
Angiotensin-converting enzyme activity	9q34.2	133,279,294	ABO	ABO - SURF6	rs495828-A	3×10^{-8}	2.6×10^{-4}	2.6×10^{-4}	1.00
Self-reported allergy	10p14	9,011,169	GATA3	RNA5SP299 - LINC00709	rs962993-T	2×10^{-8}	6.7×10^{-9}	3.3×10^{-6}	0.13
Breast cancer	10p12.31	21,744,013	MLLT10, DNAJC1	MLLT10	rs7072776-A	4×10^{-14}	1.2×10^{-4}	1.2×10^{-4}	0.77
Crohn's disease	10q21.2	62,710,915	Intergenic	ZNF365 - ALDH7A1P4	rs224136-?	1×10^{-10}	6.9×10^{-5}	2.5×10^{-4}	0.28
Mean platelet volume	10q21.3	63,290,899	JMJD1C, NRBF2, REEP3	JMJD1C	rs7075195-A	3×10^{-18}	2.3×10^{-4}	2.9×10^{-4}	0.45
Forced vital capacity	11p11.2	45,229,181	PRDM11	PRDM11	rs2863171-C	9×10^{-10}	3.8×10^{-4}	3.8×10^{-4}	0.51
Blood metabolite levels	11q12.2	61,783,884	FADS1	MYRF	rs174535-T	2×10^{-94}	2.9×10^{-5}	2.9×10^{-5}	1.00
Phospholipid levels (plasma)	11q12.2	61,784,455	C11orf9	MYRF	rs174536-A	1×10^{-63}	1.8×10^{-5}	1.8×10^{-5}	1.00
Oleic acid (18:1n-9) plasma levels	11q12.2	61,790,331	C11orf10, C11orf9, FADS1, FADS2, FADS3, FEN1, RAB3IL1	TMEM258	rs102275-C	2×10^{-32}	3.8×10^{-5}	3.8×10^{-5}	1.00
Palmitoleic acid (16:1n-7) plasma levels	11q12.2	61,790,331	C11orf0, C11orf9, FADS1, FADS2, FEN1	TMEM258	rs102275-T	7×10^{-13}	3.8×10^{-5}	3.8×10^{-5}	1.00
Stearic acid (18:0) plasma levels	11q12.2	61,790,331	C11orf10, FADS1, FADS2, FEN1, FADS3	TMEM258	rs102275-C	1×10^{-20}	3.8×10^{-5}	3.8×10^{-5}	1.00
Crohn's disease	11q12.2	61,790,331	FADS1	TMEM258	rs102275-C	2×10^{-11}	3.8×10^{-5}	3.8×10^{-5}	1.00
Inflammatory bowel disease	11q12.2	61,796,827	C11orf9,FADS1,FADS2	FEN1	rs4246215-T	2×10^{-15}	4.0×10^{-6}	4.0×10^{-6}	1.00
Platelet counts	11q12.2	61,796,827	FEN1	FEN1	rs4246215-T	3×10^{-10}	4.0×10^{-6}	4.0×10^{-6}	1.00
Cholesterol, total	11q12.2	61,802,358	FADS1, FADS2, FADS3	FADS1	rs174546-T	3×10^{-37}	1.8×10^{-5}	1.8×10^{-5}	1.00
HDL cholesterol	11q12.2	61,802,358	FADS1, FADS2, FADS3	FADS1	rs174546-T	8×10^{-28}	1.8×10^{-5}	1.8×10^{-5}	1.00
LDL cholesterol	11q12.2	61,802,358	FADS1, FADS2, FADS3	FADS1	rs174546-T	2×10^{-39}	1.8×10^{-5}	1.8×10^{-5}	1.00
Triglycerides	11q12.2	61,802,358	FADS1, FADS2, FADS3	FADS1	rs174546-T	7×10^{-38}	1.8×10^{-5}	1.8×10^{-5}	1.00

Information from the NHGRI GWAS catalog[a]							Information from TAGC asthma meta-analysis		
Disease.Trait	Region	Chr_position (build 38)	Reported Genes	Mapped Gene	Strongest SNP -Risk Allele	P_Value	P_{fixed}[b]	P_{random}[b]	P_{het}[c]
Plasma omega-6 polyunsaturated fatty acid levels (arachidonic acid)	11q12.2	61,803,311	FADS2, C11orf9, FEN1, FADS1, FADS3, RAB3IL1, BEST1, DAGLA, FTH1, INCENP, SYT7, SCGB2A1, SCGB1D1, AHNAK, SCGB2A2	FADS1	rs174547-C	0E+00	2.1×10^{-5}	2.1×10^{-5}	1.00
Plasma omega-6 polyunsaturated fatty acid levels (gamma-linolenic acid)	11q12.2	61,803,311	FADS1, DAGLA, C11orf9, C11orf10, FEN1, FADS2, FADS3, RAB3IL1, FTH1, DAGLA, BEST1	FADS1	rs174547-T	2×10^{-72}	2.1×10^{-5}	2.1×10^{-5}	1.00
Metabolic traits	11q12.2	61,803,311	FADS1	FADS1	rs174547-C	9×10^{-11}6	2.1×10^{-5}	2.1×10^{-5}	1.00
Resting heart rate	11q12.2	61,803,311	FADS1	FADS1	rs174547-C	2×10^{-9}	2.1×10^{-5}	2.1×10^{-5}	1.00
Lipid metabolism phenotypes	11q12.2	61,803,311	FADS1, FADS2, FADS3	FADS1	rs174547-?	8×10^{-26}2	2.1×10^{-5}	2.1×10^{-5}	1.00
Heart rate	11q12.2	61,803,910	FADS1	FADS1	rs174549-A	1×10^{-22}	3.7×10^{-5}	3.7×10^{-5}	1.00
Metabolite levels	11q12.2	61,803,910	FADS1	FADS1	rs174549-G	2×10^{-30}	3.7×10^{-5}	3.7×10^{-5}	1.00
Fasting glucose-related traits	11q12.2	61,804,006	FADS1	FADS1	rs174550-T	2×10^{-15}	2.1×10^{-5}	2.1×10^{-5}	1.00
Fasting glucose-related traits (interaction with BMI)	11q12.2	61,804,006	FADS1	FADS1	rs174550-?	2×10^{-9}	2.1×10^{-5}	2.1×10^{-5}	1.00
Rheumatoid arthritis	11q12.2	61,828,092	FADS1, FADS2, FADS3	FADS2	rs968567-C	2×10^{-8}	4.2×10^{-4}	4.2×10^{-4}	0.95
P wave duration	11q12.2	61,837,342	FADS2, C11orf9	FADS2	rs174577-A	3×10^{-8}	2.7×10^{-4}	2.7×10^{-4}	0.91
Liver enzyme levels (alkaline phosphatase)	11q12.2	61,855,668	C11orf10, FADS1, FADS2	FADS2	rs174601-T	3×10^{-9}	2.6×10^{-4}	2.6×10^{-4}	0.95
Atopic dermatitis	11q13.1	65,784,486	OVOL1	AP5B1 - OVOL1	rs479844-G	1×10^{-13}	3.0×10^{-5}	3.0×10^{-5}	0.48
Atopic dermatitis	11q13.5	76,559,639	C11orf30,LRRC32	C11orf30 - LRRC32	rs7130588-G	4×10^{-13}	2.5×10^{-11}	3.4×10^{-11}	0.46
Allergic sensitization	11q13.5	76,588,150	C11orf30, LRRC32	C11orf30 - LRRC32	rs2155219-T	1×10^{-18}	1.1×10^{-17}	5.1×10^{-13}	0.08
Self-reported allergy	11q13.5	76,588,150	C11orf30, LRRC32	C11orf30 - LRRC32	rs2155219-T	2×10^{-19}	1.1×10^{-17}	5.1×10^{-13}	0.08
Inflammatory bowel disease	11q13.5	76,588,150	Intergenic	C11orf30 - LRRC32	rs2155219-T	4×10^{-36}	1.1×10^{-17}	5.1×10^{-13}	0.08
Allergic rhinitis	11q13.5	76,588,150	C11orf30, LRRC32	C11orf30 - LRRC32	rs2155219-T	4×10^{-8}	1.1×10^{-17}	5.1×10^{-13}	0.08
IgE grass sensitization	11q13.5	76,588,150	C11orf30, LRRC32	C11orf30 - LRRC32	rs2155219-T	1×10^{-8}	1.1×10^{-17}	5.1×10^{-13}	0.08
Ulcerative colitis	11q13.5	76,588,150	Intergenic	C11orf30 - LRRC32	rs2155219-T	5×10^{-16}	1.1×10^{-17}	5.1×10^{-13}	0.08
Crohn's disease	11q13.5	76,590,331	C11orf30	C11orf30 - LRRC32	rs7927997-T	6×10^{-13}	3.2×10^{-13}	3.2×10^{-13}	0.53
Inflammatory bowel disease	12q13.11	47,814,585	VDR	HDAC7	rs11168249-C	8×10^{-9}	4.4×10^{-5}	5.3×10^{-4}	0.19
Vitiligo	12q13.2	56,007,301	PMEL, DGKA, CDK2, RAB5B, SUOX, ZNFN1A4, RPS26, ERBB3, PA2G4	IKZF4	rs10876864-G	8×10^{-12}	8.9×10^{-8}	3.2×10^{-4}	3.0×10^{-3}
Allergic sensitization	12q13.3	57,095,926	STAT6	NAB2;STAT6	rs1059513-T	1×10^{-14}	3.9×10^{-7}	3.9×10^{-7}	0.65
IgE levels	12q13.3	57,095,926	STAT6, NAB2	NAB2;STAT6	rs1059513-C	2×10^{-12}	3.9×10^{-7}	3.9×10^{-7}	0.65
C-reactive protein levels	12q24.31	120,986,153	HNF1A, C12orf43, OASL	HNF1A	rs2393791-G	3×10^{-10}	8.6×10^{-5}	8.7×10^{-4}	0.21
C-reactive protein and white blood cell count	12q24.31	120,986,153	HNF1A	HNF1A	rs2393791-C	3×10^{-9}	8.6×10^{-5}	8.7×10^{-4}	0.21
Gamma glutamyl transpeptidase	12q24.31	120,986,153	HNF1A	HNF1A	rs2393791-G	7×10^{-30}	8.6×10^{-5}	8.7×10^{-4}	0.21
Liver enzyme levels (gamma-glutamyl transferase)	12q24.31	120,987,058	HNF1A, C12orf27	HNF1A	rs7310409-G	7×10^{-45}	8.4×10^{-5}	8.5×10^{-4}	0.21
C-reactive protein	12q24.31	120,987,058	HNF1A	HNF1A	rs7310409-G	3×10^{-8}	8.4×10^{-5}	8.5×10^{-4}	0.21
Head circumference (infant)	12q24.31	123,338,164	SBNO1	SBNO1	rs7980687-A	8×10^{-9}	3.2×10^{-5}	8.6×10^{-4}	0.06
Primary biliary cirrhosis	14q24.1	68,286,876	RAD51L1	RAD51B	rs911263-T	2×10^{-11}	1.1×10^{-5}	1.1×10^{-5}	0.97
Age-related macular degeneration	14q24.1	68,318,360	RAD51B	RAD51B	rs8017304-A	9×10^{-11}	3.9×10^{-5}	3.9×10^{-5}	0.78
Primary tooth development (number of teeth)	14q24.1	68,322,207	RAD51L1	RAD51B	rs1956529-T	3×10^{-8}	7.3×10^{-5}	7.3×10^{-5}	0.84
Height	14q24.1	68,346,398	RAD51L1	RAD51B	rs1570106-T	8×10^{-9}	2.0×10^{-4}	2.7×10^{-4}	0.42
Inflammatory bowel disease	15q22.33	67,150,258	SMAD3	SMAD3	rs17293632-T	6×10^{-16}	1.9×10^{-15}	1.5×10^{-11}	0.18
Crohn's disease	15q22.33	67,150,258	SMAD3	SMAD3	rs17293632-T	3×10^{-19}	1.9×10^{-15}	1.5×10^{-11}	0.18
Self-reported allergy	15q22.33	67,157,967	SMAD3	SMAD3	rs17228058-G	1×10^{-8}	5.4×10^{-15}	9.4×10^{-11}	0.14
Corneal structure	15q22.33	67,175,169	SMAD3	SMAD3	rs12913547-T	5×10^{-10}	9.1×10^{-6}	3.5×10^{-5}	0.27
Height	15q25.2	83,911,404	ADAMTSL3	ADAMTSL3	rs11259933-A	1×10^{-19}	7.3×10^{-5}	7.3×10^{-5}	0.83
Type 1 diabetes autoantibodies	16p13.13	11,086,016	CLEC16A	CLEC16A	rs12708716-G	5×10^{-14}	1.1×10^{-7}	4.5×10^{-5}	0.07
Primary biliary cirrhosis	16p13.13	11,093,926	CLEC16A	CLEC16A	rs12924729-G	3×10^{-12}	4.2×10^{-6}	4.0×10^{-4}	0.07
Type 1 diabetes	16p13.13	11,144,926	KIAA0350	CLEC16A	rs2903692-G	7×10^{-11}	2.4×10^{-7}	1.8×10^{-4}	0.04
Rheumatoid arthritis	17q12	39,583,908	MED1	CDK12 - NEUROD2	rs1877030-C	2×10^{-8}	2.6×10^{-13}	2.6×10^{-13}	0.99
Primary biliary cirrhosis	17q12	39,820,216	IKZF3, ZPBP2, GSDMB, ORMDL3	IKZF3	rs9303277-T	4×10^{-9}	4.9×10^{-43}	9.6×10^{-26}	0.02
Ulcerative colitis	17q12	39,884,510	IKZF3, ORMDL3, IKZF3, PNMT, ZPBP2, GSDML	ZPBP2 - GSDMB	rs2872507-A	5×10^{-11}	8.1×10^{-38}	2.0×10^{-24}	0.04
Crohn's disease	17q12	39,884,510	GSMDL,ZPBP2,ORMDL3,IKZF3	ZPBP2 - GSDMB	rs2872507-A	2×10^{-9}	8.1×10^{-38}	2.0×10^{-24}	0.04
Cervical cancer	17q12	39,895,095	GSDMB	ZPBP2 - GSDMB	rs8067378-G	9×10^{-10}	4.8×10^{-42}	1.5×10^{-28}	0.07
Fractional exhaled nitric oxide (childhood)	17q12	39,900,944	ZPBP2, GSDMB	ZPBP2 - GSDMB	rs8069176-A	2×10^{-8}	4.6×10^{-41}	2.0×10^{-23}	6.1×10^{-3}
Type 1 diabetes	17q12	39,909,987	ORMDL3	GSDMB	rs2290400-?	6×10^{-13}	1.5×10^{-43}	1.5×10^{-25}	0.01

Information from the NHGRI GWAS catalog[a]							Information from TAGC asthma meta-analysis		
Disease.Trait	Region	Chr_position (build 38)	Reported Genes	Mapped Gene	Strongest SNP -Risk Allele	P_Value	P_{fixed}[b]	P_{random}[b]	P_{het}[c]
Self-reported allergy	17q12	39,917,778	GSDMB, IKZF3	GSDMB	rs9303280-T	9×10^{-9}	3.0×10^{-43}	9.3×10^{-25}	0.01
Hematological parameters	17q21.1	39,954,436	GSDMA, ORMDL3	LRRC3C - GSDMA	rs17609240-G	9×10^{-9}	2.3×10^{-23}	5.8×10^{-12}	0.03
White blood cell types	17q21.1	40,000,459	PSMD3, CSF3	PSMD3 - CSF3	rs4794822-T	4×10^{-16}	2.0×10^{-16}	1.9×10^{-11}	0.09
Neutrophil count	17q21.1	40,000,459	PSMD3, CSF3	PSMD3 - CSF3	rs4794822-C	6×10^{-10}	2.0×10^{-16}	1.9×10^{-11}	0.09
C-reactive protein and white blood cell count	17q21.1	40,010,626	Intergenic	PSMD3 - CSF3	rs8078723-C	3×10^{-9}	9.1×10^{-17}	1.6×10^{-11}	0.08
White blood cell count	17q21.1	40,010,626	GSDMB, ORMDL3, GSDMA, PSMD3, CSF3, MED24, SNORD124, THRA, NR1D1	PSMD3 - CSF3	rs8078723-T	2×10^{-31}	9.1×10^{-17}	1.6×10^{-11}	0.08
Diastolic blood pressure	17q21.33	49,363,104	ZNF652, PHB	ZNF652;LOC102724596	rs16948048-G	5×10^{-9}	7.2×10^{-9}	1.9×10^{-8}	0.39
Sex hormone-binding globulin levels	17q21.33	49,368,389	ZNF652	LOC102724596	rs2411984-A	4×10^{-14}	5.6×10^{-5}	8.4×10^{-4}	0.10

[a]Variables extracted from the GWAS catalog (highlighted in blue) are defined in the catalog web site: https://www.ebi.ac.uk/gwas/

[b]TAGC Variables are highlighted in orange: P_{fixed} and P_{random} are the P-values for association with asthma in multi-ancestry meta-analysis under fixed-effects and random-effects models, respectively

[c]P_{het} is the P-value for heterogeneity in SNP effect size across TAGC studies using the Cochran's Q test

Supplementary Table 17. Enrichment of asthma risk SNPs in promoter and enhancer marks by cell type

The results presented in this table are for 16 out of the 18 asthma loci shown in Table 1

The 6p21.33 and 6p21.32 loci spanning the HLA complex were excluded because of high variability and LD in the region

The method used to assess enrichment is described in detail in the Online Methods

The enhancer and promoter histone marks were defined using a 15 state model applied to ROADMAP and ENCODE data (PMID:25693563; http://egg2.wustl.edu/roadmap/data)

					Active promoters		Active and inactive promoters		Active enhancers		Active and inactive enhancers	
EID[a]	Group[a]	Standardized Epigenome name[a]	Anatomy[a]	Type[a]	AST loci[b]	FDR[c]	AST loci[b]	FDR[c]	AST loci[b]	FDR[c]	AST loci[b]	FDR[c]
E001	ESC	ES-I3 Cells	ESC	PrimaryCulture	7	0.075	7	0.130	8	0.133	8	0.166
E002	ESC	ES-WA7 Cells	ESC	PrimaryCulture	2	0.697	2	0.770	6	0.045	6	0.063
E003	ESC	H1 Cells	ESC	PrimaryCulture	5	0.171	5	0.222	6	0.269	7	0.187
E004	ES-deriv	H1 BMP4 Derived Mesendoderm Cultured Cells	ESC_DERIVED	ESCDerived	3	0.407	3	0.463	5	0.246	5	0.266
E005	ES-deriv	H1 BMP4 Derived Trophoblast Cultured Cells	ESC_DERIVED	ESCDerived	2	0.645	2	0.659	8	0.083	8	0.102
E006	ES-deriv	H1 Derived Mesenchymal Stem Cells	ESC_DERIVED	ESCDerived	3	0.414	3	0.434	7	0.142	7	0.187
E007	ES-deriv	H1 Derived Neuronal Progenitor Cultured Cells	ESC_DERIVED	ESCDerived	2	0.680	2	0.696	6	0.133	6	0.151
E008	ESC	H9 Cells	ESC	PrimaryCulture	4	0.319	4	0.387	6	0.095	6	0.109
E009	ES-deriv	H9 Derived Neuronal Progenitor Cultured Cells	ESC_DERIVED	ESCDerived	5	0.179	5	0.219	5	0.348	5	0.403
E010	ES-deriv	H9 Derived Neuron Cultured Cells	ESC_DERIVED	ESCDerived	6	0.113	6	0.136	6	0.357	6	0.414
E011	ES-deriv	hESC Derived CD184+ Endoderm Cultured Cells	ESC_DERIVED	ESCDerived	6	0.149	6	0.208	7	0.188	7	0.213
E012	ES-deriv	hESC Derived CD56+ Ectoderm Cultured Cells	ESC_DERIVED	ESCDerived	4	0.218	4	0.305	7	0.104	7	0.140
E013	ES-deriv	hESC Derived CD56+ Mesoderm Cultured Cells	ESC_DERIVED	ESCDerived	5	0.173	5	0.219	9	0.029	9	0.035
E014	ESC	HUES48 Cells	ESC	PrimaryCulture	7	0.060	7	0.114	10	0.021	10	0.032
E015	ESC	HUES6 Cells	ESC	PrimaryCulture	7	0.070	7	0.130	9	0.055	9	0.052
E016	ESC	HUES64 Cells	ESC	PrimaryCulture	7	0.060	7	0.114	10	0.016	10	0.025
E017	IMR90	IMR90 fetal lung fibroblasts Cell Line	LUNG	CellLine	5	0.179	5	0.219	8	0.089	8	0.118
E018	iPSC	iPS-15b Cells	IPSC	PrimaryCulture	5	0.198	5	0.261	8	0.109	8	0.144
E019	iPSC	iPS-18 Cells	IPSC	PrimaryCulture	7	0.060	7	0.114	7	0.231	8	0.160
E020	iPSC	iPS-20b Cells	IPSC	PrimaryCulture	6	0.149	6	0.222	9	0.028	9	0.038
E021	iPSC	iPS DF 6.9 Cells	IPSC	PrimaryCulture	3	0.437	3	0.489	6	0.085	6	0.102
E022	iPSC	iPS DF 19.11 Cells	IPSC	PrimaryCulture	2	0.707	3	0.473	10	0.008	10	0.011
E023	Mesench	Mesenchymal Stem Cell Derived Adipocyte Cultured Cells	FAT	PrimaryCulture	5	0.370	5	0.392	9	0.083	9	0.097
E024	ESC	ES-UCSF4 Cells	ESC	PrimaryCulture	3	0.455	3	0.489	8	0.133	8	0.163
E025	Mesench	Adipose Derived Mesenchymal Stem Cell Cultured Cells	FAT	PrimaryCulture	6	0.213	6	0.246	11	0.029	12	0.012
E026	Mesench	Bone Marrow Derived Cultured Mesenchymal Stem Cells	STROMAL_CONNECTIVE	PrimaryCulture	5	0.280	5	0.304	9	0.040	10	0.015
E027	Epithelial	Breast Myoepithelial Primary Cells	BREAST	PrimaryCell	5	0.218	5	0.246	8	0.166	8	0.187
E028	Epithelial	Breast variant Human Mammary Epithelial Cells (vHMEC)	BREAST	PrimaryCulture	5	0.157	5	0.188	10	0.030	10	0.038
E029	HSC & B-cell	Primary monocytes from peripheral blood	BLOOD	PrimaryCell	3	0.414	4	0.250	10	0.008	10	0.012
E030	HSC & B-cell	Primary neutrophils from peripheral blood	BLOOD	PrimaryCell	6	0.112	7	0.074	8	0.023	8	0.031
E031	HSC & B-cell	Primary B cells from cord blood	BLOOD	PrimaryCell	7	0.060	7	0.074	10	0.001	10	0.001
E032	HSC & B-cell	Primary B cells from peripheral blood	BLOOD	PrimaryCell	3	0.414	3	0.426	10	0.003	10	0.008
E033	Blood & T-cell	Primary T cells from cord blood	BLOOD	PrimaryCell	6	0.127	6	0.168	11	0.001	11	0.001
E034	Blood & T-cell	Primary T cells from peripheral blood	BLOOD	PrimaryCell	5	0.166	5	0.189	12	0.001	12	0.001
E035	HSC & B-cell	Primary hematopoietic stem cells	BLOOD	PrimaryCell	6	0.124	6	0.139	9	0.014	9	0.017
E036	HSC & B-cell	Primary hematopoietic stem cells short term culture	BLOOD	PrimaryCell	5	0.205	5	0.223	11	0.003	11	0.004
E037	Blood & T-cell	Primary T helper memory cells from peripheral blood 2	BLOOD	PrimaryCell	5	0.179	5	0.208	12	0.001	12	0.001
E038	Blood & T-cell	Primary T helper naive cells from peripheral blood	BLOOD	PrimaryCell	6	0.112	6	0.130	11	0.001	11	0.001
E039	Blood & T-cell	Primary T helper naive cells from peripheral blood	BLOOD	PrimaryCell	5	0.190	5	0.219	11	0.001	11	0.001

EID[a]	Group[a]	Standardized Epigenome name[a]	Anatomy[a]	Type[a]	Active promoters		Active and inactive promoters		Active enhancers		Active and inactive enhancers	
					AST loci[b]	FDR[c]	AST loci[b]	FDR[c]	AST loci[b]	FDR[c]	AST loci[b]	FDR[c]
E040	Blood & T-cell	Primary T helper memory cells from peripheral blood 1	BLOOD	PrimaryCell	6	0.079	6	0.114	11	0.001	11	0.001
E041	Blood & T-cell	Primary T helper cells PMA-I stimulated	BLOOD	PrimaryCell	7	0.070	7	0.098	10	0.001	10	0.004
E042	Blood & T-cell	Primary T helper 17 cells PMA-I stimulated	BLOOD	PrimaryCell	4	0.224	4	0.260	10	0.001	10	0.002
E043	Blood & T-cell	Primary T helper cells from peripheral blood	BLOOD	PrimaryCell	5	0.191	5	0.219	11	0.001	11	0.002
E044	Blood & T-cell	Primary T regulatory cells from peripheral blood	BLOOD	PrimaryCell	7	0.060	7	0.074	11	0.001	11	0.001
E045	Blood & T-cell	Primary T cells effector/memory enriched from peripheral blood	BLOOD	PrimaryCell	7	0.060	7	0.074	11	0.001	11	0.001
E046	HSC & B-cell	Primary Natural Killer cells from peripheral blood	BLOOD	PrimaryCell	6	0.075	6	0.114	9	0.010	9	0.017
E047	Blood & T-cell	Primary T CD8+ naive cells from peripheral blood	BLOOD	PrimaryCell	5	0.171	5	0.203	10	0.001	10	0.003
E048	Blood & T-cell	Primary T CD8+ memory cells from peripheral blood	BLOOD	PrimaryCell	7	0.060	7	0.074	11	0.001	11	0.001
E049	Mesench	Mesenchymal Stem Cell Derived Chondrocyte Cultured Cells	STROMAL_CONNECTIVE	PrimaryCulture	5	0.289	5	0.310	9	0.069	11	0.013
E050	HSC & B-cell	Primary hematopoietic stem cells G-CSF-mobilized Female	BLOOD	PrimaryCell	6	0.144	6	0.150	9	0.040	9	0.059
E051	HSC & B-cell	Primary hematopoietic stem cells G-CSF-mobilized Male	BLOOD	PrimaryCell	7	0.127	7	0.142	9	0.040	9	0.058
E052	Myosat	Muscle Satellite Cultured Cells	MUSCLE	PrimaryCulture	6	0.171	6	0.208	10	0.021	11	0.007
E053	Neurosph	Cortex derived primary cultured neurospheres	BRAIN	PrimaryCulture	4	0.280	4	0.290	7	0.213	7	0.259
E054	Neurosph	Ganglion Eminence derived primary cultured neurospheres	BRAIN	PrimaryCulture	5	0.218	5	0.251	6	0.222	6	0.246
E055	Epithelial	Foreskin Fibroblast Primary Cells skin01	SKIN	PrimaryCulture	5	0.218	6	0.208	8	0.083	8	0.130
E056	Epithelial	Foreskin Fibroblast Primary Cells skin02	SKIN	PrimaryCulture	4	0.364	5	0.246	10	0.001	10	0.005
E057	Epithelial	Foreskin Keratinocyte Primary Cells skin02	SKIN	PrimaryCulture	4	0.364	5	0.250	11	0.006	11	0.007
E058	Epithelial	Foreskin Keratinocyte Primary Cells skin03	SKIN	PrimaryCulture	5	0.218	5	0.246	11	0.006	11	0.009
E059	Epithelial	Foreskin Melanocyte Primary Cells skin01	SKIN	PrimaryCulture	4	0.280	4	0.305	7	0.049	7	0.077
E061	Epithelial	Foreskin Melanocyte Primary Cells skin03	SKIN	PrimaryCulture	3	0.468	4	0.287	8	0.133	8	0.166
E062	Blood & T-cell	Primary mononuclear cells from peripheral blood	BLOOD	PrimaryCell	3	0.414	3	0.469	8	0.001	8	0.001
E063	Adipose	Adipose Nuclei	FAT	PrimaryTissue	5	0.224	5	0.260	7	0.203	7	0.241
E065	Heart	Aorta	VASCULAR	PrimaryTissue	5	0.179	5	0.208	5	0.072	5	0.077
E066	Other	Liver	LIVER	PrimaryTissue	5	0.218	5	0.246	10	0.015	10	0.016
E067	Brain	Brain Angular Gyrus	BRAIN	PrimaryTissue	5	0.218	5	0.256	6	0.133	6	0.155
E068	Brain	Brain Anterior Caudate	BRAIN	PrimaryTissue	4	0.488	4	0.511	8	0.040	8	0.046
E069	Brain	Brain Cingulate Gyrus	BRAIN	PrimaryTissue	5	0.218	5	0.260	6	0.168	6	0.187
E070	Brain	Brain Germinal Matrix	BRAIN	PrimaryTissue	4	0.284	4	0.370	5	0.269	5	0.313
E071	Brain	Brain Hippocampus Middle	BRAIN	PrimaryTissue	4	0.441	4	0.489	6	0.238	6	0.262
E072	Brain	Brain Inferior Temporal Lobe	BRAIN	PrimaryTissue	4	0.437	4	0.473	5	0.301	5	0.319
E073	Brain	Brain_Dorsolateral_Prefrontal_Cortex	BRAIN	PrimaryTissue	5	0.218	5	0.260	6	0.095	6	0.110
E074	Brain	Brain Substantia Nigra	BRAIN	PrimaryTissue	4	0.395	4	0.420	5	0.354	5	0.379
E075	Digestive	Colonic Mucosa	GI_COLON	PrimaryTissue	5	0.201	5	0.239	6	0.023	6	0.030
E076	Sm. Muscle	Colon Smooth Muscle	GI_COLON	PrimaryTissue	5	0.213	5	0.246	7	0.116	7	0.133
E077	Digestive	Duodenum Mucosa	GI_DUODENUM	PrimaryTissue	7	0.106	7	0.130	5	0.321	6	0.187
E078	Sm. Muscle	Duodenum Smooth Muscle	GI_DUODENUM	PrimaryTissue	5	0.218	5	0.260	6	0.099	6	0.125
E079	Digestive	Esophagus	GI_ESOPHAGUS	PrimaryTissue	5	0.171	5	0.208	6	0.094	6	0.115
E080	Other	Fetal Adrenal Gland	ADRENAL	PrimaryTissue	4	0.218	4	0.261	9	0.058	9	0.107
E081	Brain	Fetal Brain Male	BRAIN	PrimaryTissue	3	0.395	3	0.421	6	0.247	6	0.340
E082	Brain	Fetal Brain Female	BRAIN	PrimaryTissue	4	0.362	4	0.426	4	0.347	4	0.376
E083	Heart	Fetal Heart	HEART	PrimaryTissue	3	0.437	3	0.453	8	0.167	8	0.187
E084	Digestive	Fetal Intestine Large	GI_INTESTINE	PrimaryTissue	3	0.488	4	0.346	7	0.133	7	0.166
E085	Digestive	Fetal Intestine Small	GI_INTESTINE	PrimaryTissue	5	0.179	5	0.222	5	0.495	5	0.544
E086	Other	Fetal Kidney	KIDNEY	PrimaryTissue	5	0.193	5	0.227	7	0.040	7	0.049
E087	Other	Pancreatic Islets	PANCREAS	PrimaryTissue	4	0.426	4	0.453	3	0.496	3	0.501
E088	Other	Fetal Lung	LUNG	PrimaryTissue	6	0.112	6	0.136	8	0.129	8	0.161
E089	Muscle	Fetal Muscle Trunk	MUSCLE	PrimaryTissue	4	0.224	4	0.261	6	0.123	7	0.140

EID[a]	Group[a]	Standardized Epigenome name[a]	Anatomy[a]	Type[a]	Active promoters AST loci[b]	Active promoters FDR[c]	Active and inactive promoters AST loci[b]	Active and inactive promoters FDR[c]	Active enhancers AST loci[b]	Active enhancers FDR[c]	Active and inactive enhancers AST loci[b]	Active and inactive enhancers FDR[c]
E090	Muscle	Fetal Muscle Leg	MUSCLE_LEG	PrimaryTissue	5	0.171	5	0.208	10	0.024	10	0.046
E091	Other	Placenta	PLACENTA	PrimaryTissue	4	0.224	4	0.260	8	0.067	8	0.102
E092	Digestive	Fetal Stomach	GI_STOMACH	PrimaryTissue	4	0.218	4	0.287	8	0.049	8	0.091
E093	Thymus	Fetal Thymus	THYMUS	PrimaryTissue	4	0.218	4	0.260	10	0.003	10	0.006
E094	Digestive	Gastric	GI_STOMACH	PrimaryTissue	2	0.685	2	0.685	5	0.239	5	0.244
E095	Heart	Left Ventricle	HEART	PrimaryTissue	3	0.488	3	0.512	8	0.050	8	0.063
E096	Other	Lung	LUNG	PrimaryTissue	5	0.149	5	0.160	8	0.021	8	0.025
E097	Other	Ovary	OVARY	PrimaryTissue	4	0.341	4	0.342	6	0.163	6	0.172
E098	Other	Pancreas	PANCREAS	PrimaryTissue	3	0.488	3	0.489	7	0.133	7	0.144
E099	Other	Placenta Amnion	PLACENTA	PrimaryTissue	2	0.645	2	0.657	5	0.239	5	0.281
E100	Muscle	Psoas Muscle	MUSCLE	PrimaryTissue	5	0.191	5	0.223	7	0.045	7	0.050
E101	Digestive	Rectal Mucosa Donor 29	GI_RECTUM	PrimaryTissue	6	0.190	6	0.222	7	0.019	7	0.023
E102	Digestive	Rectal Mucosa Donor 31	GI_RECTUM	PrimaryTissue	5	0.218	5	0.248	8	0.030	8	0.035
E103	Sm. Muscle	Rectal Smooth Muscle	GI_RECTUM	PrimaryTissue	6	0.171	6	0.208	5	0.201	5	0.205
E104	Heart	Right Atrium	HEART	PrimaryTissue	5	0.218	5	0.246	9	0.010	9	0.010
E105	Heart	Right Ventricle	HEART	PrimaryTissue	5	0.213	5	0.241	6	0.135	6	0.158
E106	Digestive	Sigmoid Colon	GI_COLON	PrimaryTissue	3	0.384	3	0.413	7	0.046	7	0.063
E107	Muscle	Skeletal Muscle Male	MUSCLE	PrimaryTissue	5	0.218	5	0.260	9	0.021	9	0.035
E108	Muscle	Skeletal Muscle Female	MUSCLE	PrimaryTissue	5	0.220	5	0.260	8	0.062	8	0.087
E109	Digestive	Small Intestine	GI_INTESTINE	PrimaryTissue	4	0.191	4	0.222	6	0.058	6	0.072
E110	Digestive	Stomach Mucosa	GI_STOMACH	PrimaryTissue	4	0.218	4	0.246	7	0.133	7	0.166
E111	Sm. Muscle	Stomach Smooth Muscle	GI_STOMACH	PrimaryTissue	6	0.191	6	0.223	5	0.196	5	0.241
E112	Thymus	Thymus	THYMUS	PrimaryTissue	6	0.079	6	0.130	6	0.047	6	0.058
E113	Other	Spleen	SPLEEN	PrimaryTissue	4	0.198	4	0.222	8	0.040	8	0.049
E114	ENCODE2012	A549 EtOH 0.02pct Lung Carcinoma Cell Line	LUNG	CellLine	6	0.191	6	0.222	6	0.179	6	0.187
E115	ENCODE2012	Dnd41 TCell Leukemia Cell Line	BLOOD	CellLine	6	0.112	6	0.130	7	0.049	7	0.059
E116	ENCODE2012	GM12878 Lymphoblastoid Cells	BLOOD	PrimaryCulture	6	0.205	7	0.144	9	0.015	10	0.005
E117	ENCODE2012	HeLa-S3 Cervical Carcinoma Cell Line	CERVIX	CellLine	7	0.079	7	0.114	7	0.095	7	0.102
E118	ENCODE2012	HepG2 Hepatocellular Carcinoma Cell Line	LIVER	CellLine	4	0.365	5	0.266	8	0.094	9	0.065
E119	ENCODE2012	HMEC Mammary Epithelial Primary Cells	BREAST	PrimaryCulture	5	0.213	5	0.232	9	0.062	9	0.072
E120	ENCODE2012	HSMM Skeletal Muscle Myoblasts Cells	MUSCLE	PrimaryCulture	5	0.213	5	0.246	9	0.023	10	0.008
E121	ENCODE2012	HSMM cell derived Skeletal Muscle Myotubes Cells	MUSCLE	PrimaryCulture	5	0.213	5	0.246	11	0.001	11	0.002
E122	ENCODE2012	HUVEC Umbilical Vein Endothelial Primary Cells	VASCULAR	PrimaryCulture	6	0.127	6	0.147	9	0.026	9	0.032
E123	ENCODE2012	K562 Leukemia Cells	BLOOD	PrimaryCulture	7	0.078	7	0.114	8	0.034	8	0.038
E124	ENCODE2012	Monocytes-CD14+ RO01746 Primary Cells	BLOOD	PrimaryCell	9	0.060	9	0.074	9	0.008	9	0.013
E125	ENCODE2012	NH-A Astrocytes Primary Cells	BRAIN	PrimaryCulture	5	0.218	5	0.248	7	0.133	7	0.157
E126	ENCODE2012	NHDF-Ad Adult Dermal Fibroblast Primary Cells	SKIN	PrimaryCulture	5	0.218	5	0.251	10	0.022	10	0.026
E127	ENCODE2012	NHEK-Epidermal Keratinocyte Primary Cells	SKIN	PrimaryCulture	4	0.414	4	0.451	13	0.001	13	0.001
E128	ENCODE2012	NHLF Lung Fibroblast Primary Cells	LUNG	PrimaryCulture	6	0.127	6	0.150	7	0.087	7	0.100
E129	ENCODE2012	Osteoblast Primary Cells	BONE	PrimaryCulture	6	0.173	6	0.208	11	0.006	11	0.007

The enhancer and promoter histone marks were defined using a 15 state model applied to ROADMAP and ENCODE data (PMID:25693563; http://egg2.wustl.edu/roadmap/data)

[a]EID is the cell type number; the following variables are group, standardized epigenome name, anatomy and type for each cell type (see PMID:25693563 for more details)

[b]AST_loci is the number of asthma loci that co-localize to a promoter or enhancer mark

[c]FDR is the Benjamini-Hochberg false discovery rate

Supplementary Table 18. Enrichment of TAGC asthma-associated loci in DNAse I hypersensitive sites (DHSs) by cell type

The results presented in this table are for 16 out of the 18 asthma loci shown in Table 1

The 6p21.33 and 6p21.32 loci spanning the HLA complex were excluded because of high variability and LD in the region

The method used to assess enrichment is described in detail in the Online Methods

The DHSs were available in 51 cell types using ROADMAP and ENCODE data (PMID:25693563; http://egg2.wustl.edu/roadmap/data)

EID[a]	Group[a]	Standardized Epigenome name[a]	Anatomy[a]	Type[a]	AST_loci[b]	FDR[c]
E005	ES-deriv	H1 BMP4 Derived Trophoblast Cultured Cells	ESC_DERIVED	ESCDerived	4	0.678
E006	ES-deriv	H1 Derived Mesenchymal Stem Cells	ESC_DERIVED	ESCDerived	5	0.678
E007	ES-deriv	H1 Derived Neuronal Progenitor Cultured Cells	ESC_DERIVED	ESCDerived	6	0.429
E008	ESC	H9 Cells	ESC	PrimaryCulture	10	0.024
E017	IMR90	IMR90 fetal lung fibroblasts Cell Line	LUNG	CellLine	3	0.920
E021	iPSC	iPS DF 6.9 Cells	IPSC	PrimaryCulture	8	0.251
E022	iPSC	iPS DF 19.11 Cells	IPSC	PrimaryCulture	5	0.747
E028	Epithelial	Breast variant Human Mammary Epithelial Cells (vHMEC)	BREAST	PrimaryCulture	8	0.168
E029	HSC & B-cell	Primary monocytes from peripheral blood	BLOOD	PrimaryCell	3	0.744
E032	HSC & B-cell	Primary B cells from peripheral blood	BLOOD	PrimaryCell	8	0.057
E033	Blood & T-cell	Primary T cells from cord blood	BLOOD	PrimaryCell	8	0.043
E034	Blood & T-cell	Primary T cells from peripheral blood	BLOOD	PrimaryCell	10	0.005
E046	HSC & B-cell	Primary Natural Killer cells from peripheral blood	BLOOD	PrimaryCell	8	0.048
E050	HSC & B-cell	Primary hematopoietic stem cells G-CSF-mobilized Female	BLOOD	PrimaryCell	7	0.232
E051	HSC & B-cell	Primary hematopoietic stem cells G-CSF-mobilized Male	BLOOD	PrimaryCell	0	1.000
E055	Epithelial	Foreskin Fibroblast Primary Cells skin01	SKIN	PrimaryCulture	0	1.000
E056	Epithelial	Foreskin Fibroblast Primary Cells skin02	SKIN	PrimaryCulture	0	1.000
E057	Epithelial	Foreskin Keratinocyte Primary Cells skin02	SKIN	PrimaryCulture	9	0.013
E059	Epithelial	Foreskin Melanocyte Primary Cells skin01	SKIN	PrimaryCulture	9	0.156
E080	Other	Fetal Adrenal Gland	ADRENAL	PrimaryTissue	6	0.445
E081	Brain	Fetal Brain Male	BRAIN	PrimaryTissue	7	0.393
E082	Brain	Fetal Brain Female	BRAIN	PrimaryTissue	7	0.381
E083	Heart	Fetal Heart	HEART	PrimaryTissue	9	0.156
E084	Digestive	Fetal Intestine Large	GI_INTESTINE	PrimaryTissue	4	0.710
E085	Digestive	Fetal Intestine Small	GI_INTESTINE	PrimaryTissue	4	0.568
E086	Other	Fetal Kidney	KIDNEY	PrimaryTissue	6	0.523
E088	Other	Fetal Lung	LUNG	PrimaryTissue	8	0.381
E089	Muscle	Fetal Muscle Trunk	MUSCLE	PrimaryTissue	8	0.240
E090	Muscle	Fetal Muscle Leg	MUSCLE_LEG	PrimaryTissue	9	0.161
E091	Other	Placenta	PLACENTA	PrimaryTissue	6	0.558
E092	Digestive	Fetal Stomach	GI_STOMACH	PrimaryTissue	6	0.438
E093	Thymus	Fetal Thymus	THYMUS	PrimaryTissue	8	0.130
E094	Digestive	Gastric	GI_STOMACH	PrimaryTissue	3	0.710
E097	Other	Ovary	OVARY	PrimaryTissue	5	0.541
E098	Other	Pancreas	PANCREAS	PrimaryTissue	5	0.541
E100	Muscle	Psoas Muscle	MUSCLE	PrimaryTissue	5	0.592
E109	Digestive	Small Intestine	GI_INTESTINE	PrimaryTissue	6	0.393
E114	ENCODE2012	A549 EtOH 0.02pct Lung Carcinoma Cell Line	LUNG	CellLine	3	0.839
E116	ENCODE2012	GM12878 Lymphoblastoid Cells	BLOOD	PrimaryCulture	9	0.043
E117	ENCODE2012	HeLa-S3 Cervical Carcinoma Cell Line	CERVIX	CellLine	8	0.148
E118	ENCODE2012	HepG2 Hepatocellular Carcinoma Cell Line	LIVER	CellLine	4	0.678
E119	ENCODE2012	HMEC Mammary Epithelial Primary Cells	BREAST	PrimaryCulture	9	0.076
E120	ENCODE2012	HSMM Skeletal Muscle Myoblasts Cells	MUSCLE	PrimaryCulture	6	0.541
E121	ENCODE2012	HSMM cell derived Skeletal Muscle Myotubes Cells	MUSCLE	PrimaryCulture	7	0.449
E122	ENCODE2012	HUVEC Umbilical Vein Endothelial Primary Cells	VASCULAR	PrimaryCulture	7	0.161
E123	ENCODE2012	K562 Leukemia Cells	BLOOD	PrimaryCulture	7	0.240
E124	ENCODE2012	Monocytes-CD14+ RO01746 Primary Cells	BLOOD	PrimaryCell	6	0.322
E125	ENCODE2012	NH-A Astrocytes Primary Cells	BRAIN	PrimaryCulture	8	0.168
E126	ENCODE2012	NHDF-Ad Adult Dermal Fibroblast Primary Cells	SKIN	PrimaryCulture	5	0.710
E127	ENCODE2012	NHEK-Epidermal Keratinocyte Primary Cells	SKIN	PrimaryCulture	7	0.245
E128	ENCODE2012	NHLF Lung Fibroblast Primary Cells	LUNG	PrimaryCulture	6	0.496

[a]EID is the cell type number; the following variables are group, standardized epigenome name, anatomy and type for each cell type (PMID:25693563)

[b]AST_loci is the number of asthma loci that co-localize to a DHSs

[c]FDR is the Benjamini-Hochberg false discovery rate

Supplementary Table 19. Results of GRAIL analysis for genome-wide significant asthma-associated loci

The 18 TAGC asthma-associated loci are ordered according to P_{GRAIL} from lowest to highest, see Online Methods for details on GRAIL method (PMID: 19557189); no gene was found by GRAIL at 10p14 locus

Region	Lead SNP	Start[a]	Stop[a]	P_{GRAIL}[b] for the region
5q22.1	rs10455025	110,429,500	110,519,500	8.65E-08
9p24.1	rs992969	6,134,500	6,207,000	5.39E-07
12q13.3	rs167769	55,606,500	55,835,500	1.63E-06
2q12	rs1420101	102,282,914	102,461,414	1.75E-06
5q31	rs20541	131,904,000	132,034,500	3.84E-06
6p21.32	rs9272346	32,447,500	32,790,500	2.64E-04
16p13.13	rs17806299	10,925,500	11,215,000	5.82E-04
6p21.33	rs3131064	30,332,000	31,536,500	1.07E-03
6p22.1	rs1233578	28,283,500	29,463,500	1.24E-03
17q12-q21	rs2952156	34,634,000	35,343,500	1.28E-02
11q13.5	rs7927894	75,802,500	76,016,000	1.81E-02
6q15	rs2325291	90,867,000	91,080,500	5.01E-02
17q21.33	rs17637472	44,675,500	44,834,000	5.20E-02
8q21.13	rs12543811	81,052,000	81,745,500	8.25E-02
15q22.2	rs11071558	58,803,500	58,922,000	5.80E-01
5q31.3	rs7705042	141,394,500	141,546,000	6.14E-01
15q22.33	rs2033784	65,225,500	65,255,500	6.54E-01
10p14	rs2589561	8,828,500	9,406,000	NA

[a]Start and stop are the start and stop positions of the regions defined by GRAIL

[b]P_{GRAIL} measures the strength of relatedness of each region with the other regions estimated by mining PubMed abstracts; the P-value is corrected for the number of genes assigned to that region by GRAIL.

Supplementary Note

Study descriptions, Funding and acknowledgements, and Contributing groups

Study Descriptions

All studies obtained approval from their local ethical committees. All participants provided written informed consent. The ethical statement will not be provided for each individual study

Australian Asthma Genetics Consortium (AAGC)

Subjects: Participants were drawn from two cohorts described in greater detail elsewhere[1]: the Australian Asthma Genetics Consortium (AAGC) cohort (n=1,810) and the Queensland Institute of Medical Research (QIMR) GWAS cohort (n=4,157). Of the 2110 asthmatic patients, 1,269 (60%) were classified as having childhood asthma (defined by an age-of-onset at or before age 16 years) 515 (24%) patients with later onset asthma (age-of-onset after the age of 16 years) and 326 (16%) with unknown age-of-onset. 1,232 (58%) of asthmatics were atopic, as defined by a positive skin prick test response to at least one common allergen; 1,444 (68%) had at least one first-degree relative with asthma; and 760 (36%) reported lifetime smoking. The 3,857 controls included 2,030 (53%) individuals who were classified as asthma-free based on clinical examination (109 [3%]) or epidemiological questionnaires (2,592 [50%]). The remaining 1,827 (47%) individuals provided no information about their asthma status but were included in the analysis to improve power. Mean age was 34 years (SD 16.2, range 2–92) and 3,267 (55%) were women. All participants were confirmed to be unrelated and of European ancestry based on genetic data.

Genotyping and QC: The Australian GWAS included data for 4,293 (72%) individuals genotyped with Illumina 610K array and 1,674 (28%) with Illumina 370K array[1]. The same single-nucleotide polymorphism (SNP) quality control filters were applied to each dataset individually, including the removal of SNPs with call rate lower than 95%, minor allele frequency (MAF) lower than 0·01, and Hardy-Weinberg equilibrium test $p<10^{-6}$.

Data Imputation and Analysis: Autosomal SNPs passing quality control were used to impute 7·8 million variants available from the combined 1000 genomes (60 individuals from the CEU collection; March 2010 release) and HapMap 3 (955 individuals from 11 populations; February 2009 release) reference panels with IMPUTE2[2]. The 610K and 370K datasets were imputed separately. After imputation, we excluded SNPs with imputation information <0·3, MAF <0·01, or Hardy-Weinberg equilibrium test $p<10^{-6}$. We also excluded from analysis SNPs with significant (p<0·001) allele frequency differences between the two imputation analysis groups (from case–case and control–control comparisons). After quality control, genotype data for 5·7 million SNPs were merged across the 610K and 370K datasets; only results for Hapmap2 SNPS were provided to TAGC. Individual SNPs were then tested for association with lifetime physician-diagnosed asthma with a Cochran-Mantel-Haenszel test as implemented in PLINK [3], with two strata corresponding to the two imputation analysis groups.

ALLERGEN Consortium

Canadian Cohorts (see http://www.genopha.ca/)

Subjects: The Canadian Asthma Primary Prevention Study (CAPPS[4]) was initiated in 1995 to assess the effectiveness of a multifaceted intervention program on the primary prevention of asthma in high-risk infants. Infants at high risk for developing asthma and other allergic disorders were identified and their mothers were recruited during their third trimester of pregnancy. Infants at high risk were defined as those who had a parent with asthma or two first-degree relatives with allergies or atopic disorders. The study had two recruitment centers in Canada, (Vancouver and Winnipeg). In total, there were 545 families recruited into the study (549 infants, 4 sets of twins). Loss to follow-up was minimal, with 86% of the families completing the questionnaire at the 7-year time point. There have been numerous publications on this cohort evaluating the effectiveness of the intervention strategy. For genetic analysis blood samples have been obtained from the children, and both parents.

The Study of Asthma Genes and Environment Study (SAGE[5]) is a population-based sample of 16,320 children, born in the province of Manitoba, Canada in the year of 1995. In 2002, a one-page survey was mailed to families to enquire about their health and home environment exposure. Questions included several chronic conditions in childhood, including hayfever, food allergy and asthma. Parents were asked for permission to be contacted for further study and to link the survey data to their child's health care database records. Children were stratified according to the presence of asthma (n=392), to the presence of hayfever or food allergy (n=192) and neither (n=3,002). Children with neither condition were further grouped by rural and urban location; the latter were further stratified by low and high income neighborhoods. All children in the asthma and allergy strata were invited to participate in the case-control study, as were a random sample (n=200) from the strata of children with neither condition. Following consent from parents to participate in the study, children were assessed for allergic phenotypes.

After QC a total of 766 subjects from CAPPS were retained analyses (360 cases/ 406 controls) and a total of 1022 subjects from SAGE (353 cases / 669 controls).

Genotyping and QC: Genome-wide SNP genotyping was performed using the Illumina Human610 quad array of which 821 subjects from the Canadian Cohorts (CAPPS n=414 and SAGE n=407) were included in the GABRIEL consortium GWAS analyses[6], using the GABRIEL QC protocol. The remaining 967 subjects (CAPPS n=352 and SAGE n=615) were genotyped using the same chip (Illumina Human610 quad array) and the following QC protocols : < 97% call rate for both samples and SNPs, evaluation of Hardy-Weinberg Equilibrium (HWE), heterozygosity (3 s.d.), ethnicity checks using multidimensional scaling, checks for duplicate samples, verification of reported family relationships and Mendelian errors.

Data Imputation and Analysis: Imputation was performed using MACH with HapMap2 CEU as the reference population. Statistical analyses were performed using STATA (childhood/offspring generation) to account for sibling relationships and PLINK (case-control) for adults/parents.

Saguenay Lac Saint Jean Study (SLSJ)

Subjects: The Saguenay-Lac-Saint-Jean (SLSJ) asthma study, consists of French-Canadian families ascertained through asthmatic probands[7]. Probands were included in the study if they fulfill at least two of the following criteria: 1) a minimum of three clinic visits for acute asthma within one year; 2) two or more asthma-related hospital admissions within one year; or 3) steroid dependency, as defined by either six months of oral, or one year of inhaled corticosteroid use. Individuals from 253 independent families were included in the study. Families were included in the study if at least one parent was available for phenotypic assessment, at least one parent was unaffected, and all four grandparents were of French-Canadian origin. Family members were considered asthmatics if both a self-reported history of asthma and a history of physician-diagnosed asthma were available, or by clinical evaluation following a methacholine provocation test. After QC a total of 1,199 subjects were retained in the GWAS analyses.

Genotyping and QC: Genome-wide SNP genotyping was performed using the Illumina Human610 Quad array, as part of the GABRIEL consortium (see GABRIEL paragraph below for details).

Data Imputation and Analysis: Imputation and analysis were done as part of the GABRIEL consortium (see GABRIEL paragraph below).

APCAT Consortium

The APCAT Consortium includes 21,858 European-ancestry subjects (2,055 physician-diagnosed asthmatics and 19,803 asthma-free controls) with available genome-wide data that participated in seven population based-studies, five studies from Finland (the Northern Finland Birth Cohort 1966 [NFBC66]; Helsinki Birth Cohort [HBC]; Health 2000 [H2000]; FINRISK, including FINRISK 1992, 1997, 2002 and 2007; and the Young Finns Study), the European Prospective Investigation of Cancer, Norfolk (EPIC-Norfolk) and Framingham Heart Study from the United States.

Framingham Heart Study:

Subjects: The FHS is a collection of cohorts recruited to investigate cardiovascular disease and its risk factors as described in detail elsewhere[8] . Asthma was classified based on self-report of a physician's diagnosis; 797 asthmatics and 6,463 controls were included in TAGC study.

Genotyping and QC: Genome-wide SNP genotyping was performed using Affymetrix 5.0 BeadChip. Individuals with high heterozygosity or imbreeding and missingness >0.03 were removed and only SNPs with call rate>0.95, HWE $P>10^{-6}$ and MAF>0.01 were used in the imputation.

Data Imputation and Analysis: Imputation was carried out on 413,905 SNPs using MACH 1.0 software and HapMap2 CEU (Release 22, Build 36) as reference panel. After imputation, we used SNPs with an Rsq threshold of >0.3 and MAF threshold of >1%. The association statistic for each SNP was calculated assuming an additive genetic model adjusting for sex, and age using a GEE model to take into account familial dependencies (GWAF R package).

Northern Finland Birth Cohort of 1966:

Subjects: The NFBC1966 study[9] [http://kelo.oulu.fi/NFBC/] includes 12,058 live born individuals, of European descent, with expected dates of birth during 1966 in the provinces of Oulu and Lapland, in Finland. Cohort has been followed up since early pregnancy until adult age. All those living in Northern Finland or in the capital area were invited to a clinical examination and blood sampling at age 31 years. Information on asthma used in this analysis was collected at this time point; 364 asthmatics and 3,502 controls were included in TAGC study.

Genotyping and QC: Genotyping was carried out using Illumina's HumanCNV370-Duo BeadChip. Individuals with high heterozygosity or imbreeding were removed and only SNPs with call rate>0.95, HWE $P>10^{-4}$ and MAF>0.01 were used in the imputation.

Data imputation and analysis: Imputation was performed on 328,007 SNPs using IMPUTE 0.3.1 and HapMap2 CEU (Release 21, Build 35). After imputation, we used SNPs with an information threshold of >0.4 and MAF threshold of >1%. The association statistic for each SNP was calculated assuming an additive genetic model adjusting for sex, and ancestry-informative principal components. Association analysis performed in QUICKTEST v0.94.

EPIC-Norfolk:

Subjects: EPIC-Norfolk is part of the large multi-centre Europe-wide EPIC programme looking at the connection between diet and cancer[10]. There were over 30,000 participants aged 45 – 70 at recruitment who lived in Norwich and the surrounding towns and rural areas. They have been contributing information about their diet, lifestyle and health through questionnaires, and through health checks carried out by EPIC nurses. In 2006, a GWAS for obesity was carried out on 3,867 individuals. A case-cohort design was used in which the subcohort (N=2,566) was a random sample of the cohort at baseline and cases were part of the remaining individuals with a value of BMI being 30 kg/m2 or greater (N=1,301). Unlike controls in the commonly used case-control design, the subcohort was an unselected population sample allowing for a variety of traits to be investigated. The EPIC-Norfolk obese cases and the EPIC-Norfolk population based subcohorts were considered as two different samples in in the present TAGC study. Asthmatics were defined as a positive response to the question *"Has the doctor ever told you that you have asthma?"* which was asked at baseline survey. The remaining individuals served as healthy controls unless they had bronchitis or FEV1 < 70% predicted for age, height and sex.

Genotyping and QC: Genotyping was carried out using Affymetrix 500K BeadChip. Individuals with high heterozygosity or imbreeding and missingness > 0.06 were removed and only SNPs with call rate>0.90, HWE $P>10^{-6}$ and MAF>0.01 were used in the imputation.

Data imputation and analysis: Imputation was performed on 397,438 SNPs using IMPUTE 0.3.1 and HapMap2 CEU (Release 21) as reference panel. After imputation, we used SNPs with an information threshold of >0.4 and MAF threshold of >1%. Data analysis was conducted separately in EPIC-Norforlk Obese and EPIC-Norforlk population-based studies (number of cases and controls are show in Supplementary Table 1). The association statistic for each SNP was calculated assuming an additive genetic model adjusting for sex, ancestry-informative principal components, and age. Association analysis between individual SNP and asthma was performed in each sub-study using SNPTEST 1.1.5.

FINRISK

Subjects: This study is a population survey of risk factors for chronic diseases in Finland[11]. The survey has been executed every five years from 1972 using independent, random and representative population samples from five geographical areas of the country. Participants have completed a health-related questionnaire and undergone a physical examination including measurement of anthropometric traits and blood draw. For the FINRISK 1992 cohort, asthmatics were individuals who have answered “YES” to the question “*Have you had any of the following diseases diagnosed or treated by a doctor during the past year (last 12 months)?:* Asthma of the lungs”. For the FINRISK 1997, 2002 and 2007 cohorts, asthmatics were individuals who have answered “YES to the question: “*Have you ever been diagnosed with asthma?”*. In all FINRISK surveys the rest of the participants served as controls if their age was less than or equal to 70 years and they did not report pulmonary emphysema, or chronic bronchitis during the last 12 months.

Genotyping and QC: Participants were genotyped using Illumina 610K and Affymetrix 6.0 arrays. For QC, Individuals with high heterozygosity or imbreeding and missingness > 0.05 were removed and only SNPs with call rate>0.95, HWE P>10^{-6} and MAF>0.01 were used in the imputation

Data imputation: Imputation was performed on 554,988 (Illumina) and 727,478 (Affymetrics) SNPs using MACH 1.0.16 and HapMap2 CEU (Release 22, Build 36) as reference panel. After imputation, we used SNPs with an Rsq threshold of >0.3 and MAF threshold of >1%.

Health 2000 Study

Subjects: The study was conducted in 2000[12] and included home interview, completion of several questionnaires, laboratory and anthropometrical measurements, spirometry with bronchodilator test and clinical examination by a physician. Further information was obtained by record linkage with the National Hospital Discharge Register and the National Social Insurance Institutions register data on reimbursement of asthma medication. Information about asthma was based on the following question: *"Has a doctor ever diagnosed you with one of the following illnesses?"* One of the listed illnesses was asthma and those who responded "YES" were considered to have asthma. The rest of the participants were taken as controls if their age was less than or equal to 70 years and they never had had chronic bronchitis.

Genotyping and QC: Samples were genotyped with Illumina 610K or 370K arrays. Individuals with high heterozygosity or imbreeding and missingness > 0.05 were removed and only SNPs with call rate>0.95, HWE P>10^{-6} and MAF>0.01 were used in the imputation

Data imputation: Imputation was performed on 555,388 SNPs using MACH 1.0.16 and HapMap2 CEU (Release 22, Build 36) as reference panel. After imputation, we used SNPs with an Rsq threshold of >0.3 and MAF threshold of >1%.

Helsinki Birth Cohort Study (HBCS)

The HBCS[13] includes 8,760 subjects born in Helsinki between 1934 and 1944. Between 2001 and 2004, a representative subset of 928 males and 1,075 females participated in a clinical study focusing upon cardiovascular and metabolic outcomes and cognitive functions. Information on asthma, smoking and alcohol intake is available from questionnaires for 2,003 individuals who participated in the clinical study. Information about asthma was based on the following question: *"Have you ever had any of the following illnesses diagnosed or treated by a doctor?"* One of the listed illnesses was *"Asthma of the lungs"* and those responding "YES" to this item were considered as having asthma. Those participants who responded to the same question as having emphysema or chronic bronchitis were excluded and the others were taken as controls. All participants were less than 70 years of age.

Genotyping and QC: Genotyping was performed with the Illumina 670K array. Individuals with high heterozygosity or imbreeding and missingness > 0.05 were removed and only SNPs with call rate>0.95, HWE P>10^{-6} and MAF>0.01 were used in the imputation

Data imputation: Imputation was performed on 546,814 SNPs using MACH 1.0.16 and HapMap2 CEU (Release 22, Build 36) as reference panel After imputation, we used SNPs with an Rsq threshold of >0.3 and MAF threshold of >1%.

Young Finns Study (YFS)

Subjects: The Young Finns cohort[14] is a longitudinal population study sample on the evolution of cardiovascular risk factors from childhood to adulthood. The first cross-sectional survey was conducted in 1980 in five Finnish university cities and included 3,596 participants who were in the age groups of 3, 6, 9, 12, 15, and 18 years and were randomly chosen from the national population register; equal ratios of males and females were selected in each age group. In 2007, 2,204 subjects now aged 30 to 45 years participated in the latest follow-up study. Information about asthma was based on a following question: *"Do you have at the moment or have you had a long-term illness, handicap or injury diagnosed by a doctor?"* Those responding "YES" and specifying among the given alternatives "Asthma of the lungs" were considered as having asthma. The rest of the participants were taken as controls, except those who reported having chronic bronchitis. All YFS participants were less than 70 years of age.

Genotyping and QC: 1,963 individuals with available physician-diagnosed asthma status were genotyped with the Illumina 670K array. Individuals with high heterozygosity or imbreeding and missingness > 0.05 were removed and only SNPs with call rate>0.95, HWE P>10^{-6} and MAF>0.01 were used in the imputation

Data imputation: Imputation was performed on 546,677 SNPs using MACH 1.0 and HapMap2 CEU (Release 22, Build 36) as reference panel. After imputation, we used SNPs with an Rsq threshold of >0.3 and MAF threshold of >1%.

Statistical analysis of FINRISK, Health 2000, HBCS and YFS: The four studies were analyzed together with an adjustment term for cohort. Association analysis between individual SNP and asthma was performed using Plink v1.07. Lambda for asthma analysis was 1.02.

CARe Consortium

Subjects: The CARe consortium datasets which contributed to TAGC included African-American participants from four population-basoed studies: Atherosclerosis Risk in Communities (ARIC), Coronary Artery Risk Development in young Adults (CARDIA), Jackson Heart Study (JHS), and Multi- Ethnic Study of

Atherosclerosis (MESA). The number of asthma cases and controls from each study are shown in Supplementary Table 1.

CARDIA: The CARDIA study is a prospective, multi-center investigation of the natural history and etiology of cardiovascular disease in 5,115 individuals age 18 to 30 years of age at the time of initial examination (1985–1986) and drawn from four communities: Birmingham, AL; Chicago, IL; Minneapolis, MN; and Oakland, CA. Each participant's age, race, and sex were self-reported during the recruitment phase and verified during the baseline clinic visit. Genotype data were available on 955 African-American individuals. A subset of these subjects contributed to the asthma GWAS.

JHS: The Jackson Heart Study is a prospective population-based study to evaluate common complex diseases among 5,301 African Americans age 34 to 84 years at the time of initial examination (2000 – 2004) and drawn from the Jackson, Mississippi metropolitan area. Genotype data were available on 3,030 African-American individuals (some JHS participants are also enrolled in ARIC, and were analyzed with the ARIC dataset; 2,145 individuals are uniquely associated with JHS). Information on asthma was available for 2,162 African American individuals.

The **ARIC** and **MESA** study contains subject from African ancestry and subject of European ancestry and are described below.

In the CARe Consortium, asthma was defined as a positive response to the question "Has a doctor ever told you that you have asthma?" or "Have you ever had asthma?" on any of the available questionnaires derived from the individual studies. The agreement between these two different questions, where available to analyze, was very good, leading us to think that subject reports of asthma stemmed from of a medical diagnosis (kappa statistic with 95% confidence intervals for individual studies are as follows: ARIC 0.82 CI 0.80-0.85, CARDIA 0.81 CI 0.77-0.83, JHS 0.80 CI 0.78-0.83). The remaining subjects served as healthy controls if they did not report any of the following conditions: wheezing, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, chronic cough, chronic sputum production, or other lung disease. Individuals were excluded from the control group if they had <70 % of the predicted FEV1 based on race- and sex-specific NHANES III prediction equations adjusting for age and height, or FEV1/FVC less than lower limits of normal for age, race and sex [15].

Genotyping and QC: Samples were genotyped at the Broad Institute using the Affymetrix Genome-Wide Human SNP Array 6.0. A subset of 24 markers including a gender confirmation assay were also genotyped using the Sequenom MassArray System. Genotypes were called using Birdseed v1.33. Quality control steps were performed using the software PLINK, EIGENSTRAT and PREST-Plus (http://fisher.utstat.toronto.edu/sun/Software/Prest/). Multiple QC procedures were performed including: confirming genotype concordance between Suquenom iPLEX and Affy6.0; removing samples with a genome-wide genotyping success rate <95%, SNPs with genotyping success rate <90%, monomorphic SNPs, and SNPs that mapped to several genomic locations; removing poor quality DNA (identified by estimating heterozygosity rates); removing sample duplicates, contaminated samples, and cryptic relationships (identified by using genome-wide genotype data to estimate identity-by-descent between all pairwise combinations); outlier samples were removed (identified based on nearest neighbor and "clustering based on missingness" analyses in PLINK); removing SNPs with minor allele frequency (MAF) <1% or with genotyping success rate <95%; in JHS, excluding SNPs with an unusually high number of Mendel errors; and excluding SNPs that showed association with specific chemistry plates. Because several different ethnic groups were represented, with the expectation of differing genotype frequencies and admixture, no filters were applied for Hardy- Weinberg probability values.

Data Imputation and Analysis: To increase coverage and facilitate comparison with other datasets, we imputed genotype data using MACH version 1.0.16[16]. Imputation were done using European and African ancestry reference panels. The resulting set of SNPs was conservatively filtered to remove low imputation quality (RSQ <0.4) or minor allele frequency SNPs (MAF <0.01), for which association results would be less reliable. Analysis of association of asthma with individuals SNPs was carried out using logistic regression statistical framework in PLINK for unrelated cohorts or using R (GWAF package) scripts that model family structure for family data.

MESA: Multi-Ethnic Study of Atherosclerosis

Subjects: The Multi-Ethnic Study of Atherosclerosis (MESA) is a population-based longitudinal study of subclinical cardiovascular disease [17]. Between 2000 and 2002, MESA recruited 6,814 men and women 45–84 years of age from six US sites that were free of clinical cardiovascular disease. The MESA Family Study recruited 1,595 African American and Hispanic family members ages 45–84 years of age specifically for genetic analysis and the MESA Air Pollution Study recruited an additional 257 participants[18]. Endpoints for asthma included self-reported history of asthma ("Have you ever had asthma?") and childhood asthma (Participants were asked at what age they "first developed symptoms." Those who reported symptoms at < 16 years of age were classified as having childhood asthma). For the current effort, genetic analyses in MESA were restricted to self-reported European-ancestry participants (MESA African-ancestry were analyzed separately through CARe). Analyses of asthma included 267 cases and 2,381 controls, while analyses of pediatric asthma included 84 cases and 1361 controls.

Genotyping and QC: All participants were genotyped using the Affymetrix Human SNP array 6.0 (Affymetrix Inc., Santa Clara, CA), with 897,981 single-nucleotide polymorphisms (SNPs) passing study-specific quality control.

Data Imputation and Analysis: IMPUTE2 was used to perform imputation of an additional ~2 million SNPs in each race/ethnic group (using HapMap Phase I and II as reference panel (release #24, NCBI Build 36) for inclusion in GWAS analyses[19,20]. Multivariate additive genetic models were adjusted for age, sex, study site and principal components of ancestry. We examined genomic control values of all GWAS for evidence of residual population stratification, undetected family structure, or other sources of inflation in type I error.

CHARGE Consortium studies included in the TAGC Consortium

ARIC: Atherosclerosis Risk in Communities study

The Atherosclerosis Risk in Communities (ARIC) Study, sponsored by the National Heart, Lung and Blood Institute (NHLBI), is a prospective epidemiologic study conducted in four U.S. communities.[21] The four communities are Forsyth County, NC; Jackson, MS; the northwest suburbs of Minneapolis, MN; and Washington County, MD. Three cohorts represent the ethnic mix of their communities; the Jackson cohort, its African-American population. ARIC was designed to investigate the etiology and natural history of atherosclerosis, the etiology of clinical atherosclerotic diseases, and variation in cardiovascular risk factors, medical care and disease by race, gender, location, and date. ARIC has coordinating, ultrasound, pulmonary, and electrocardiographic centers and three central laboratories.

The Cohort began in 1987: each ARIC field center randomly selected and recruited a cohort sample of approximately 4,000 individuals aged 45-64 from a defined population in their community. A total of 15,792 participants received an extensive examination, including medical, social, and demographic data. These participants were examined with the baseline visit occurring in 1987-89, the second visit in 1990-92, the third visit in 1993-95, the fourth visit in 1996-98, and the fifth visit in 2011-13. Follow-up occurs yearly by telephone to maintain contact with participants and to assess health status of the cohort. Asthma was defined based on self-report of whether the participant had been diagnosed with asthma

Genotyping and QC: Genotyping was done using the AffymetrixGeneChip SNP Array 6.0. Quality control steps for genotyping data included exclusions for call rate <95% (participant level and SNP level), minor allele frequency <1%, HWE P<10-6, no chromosomal location, suspected first-degree relative of an included individual based on genotype data, or more than 8 standard deviations for any of the first ten principal components. There were 9,173 Caucasian subjects with genotyping data, asthma definition, and complete covariate information.

Data Imputation and Analysis: MACH (version 1.0.16) was used to impute all autosomal SNPs with reference to HapMap CEU (release 22, build 35) from the 669,450 SNPs. Imputed SNPs failing additional quality control criteria (monomorphism, HWE $P<10^{-6}$, or genotype frequencies between two genotyping phases differing by $P<10^{-6}$) were excluded, leaving 2,515,866 genotyped or imputed SNPs for analysis. Association analysis between each individual SNP and asthma was done using logistic regression and the ProbABEL v.0.1-3 software.

CHS: Cardiovascular Health Study

Subjects: The Cardiovascular Health Study (CHS) is a population-based cohort study of risk factors for CHD and stroke in adults > 65 years conducted across four field centers. The original predominantly European ancestry cohort of 5,201 persons was recruited in 1989-1990 from random samples of the Medicare eligibility lists and an additional 687 African-Americans were enrolled subsequently for a total sample of 5,888. DNA was extracted from blood samples drawn on all participants at their baseline examination. In 2007-2008, genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai on 3,980 Cardiovascular Health Study participants who were free of CVD at baseline, consented to genetic testing, and had DNA available for genotyping. Participants were excluded from analysis for sex mismatch, discordance with prior genotyping, or call rate < 95%. Non-European ancestry participants were excluded from this study. A total of 1,908 persons were excluded from the GWAS study sample due to the presence at study baseline of coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke or transient ischemic attack or lack of available DNA. Genotyping has been attempted to date in 3,397 self-identified white participants, and was successful in 3,291 persons. Of these, 3,237 subjects had information on asthma status: 179 self-reported a physician diagnosis of asthma (ever asthma), and the remaining 3,058 were used as controls.

Genotyping and QC: Genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai using the Illumina 370CNV BeadChip system. Genotypes were called using the Illumina BeadStudio software as above. A set of 306,655 autosomal genotyped SNPs remained after exclusions for: call rate < 97%, HWE $P < 10^{-5}$, more than two duplicate errors or Mendelian inconsistency (for reference HapMap CEU) or no mapping in dbSNP.

Data Imputation and Analysis: Imputation was performed using BIMBAM (v0.99)[22] with reference to HapMap CEU (release 22, build 36). The analysis dataset included 2,397,023 genotyped or imputed SNPs. Statistical analysis was performed using logistic regression with robust SE estimates in R[23]. Adjustments were made for age at baseline, gender, and clinic site.

deCODE Genetics

Subjects: Icelandic asthma patients over 18 years of age (n=1,675) who attended an asthma clinic or emergency room at the National University Hospital of Iceland or the Icelandic Medical Center (Laeknasetrid) during the years 1977 to 2008 were recruited [24,25]. Asthma diagnosis was based on a combination of physician's diagnosis, a positive reply to the question: „Has a doctor confirmed your asthma diagnosis?", questionnaires pertaining to asthma symptoms and ICD diagnosis when receiving emergency care [24,25]. Atopy status (defined by at least one positive response to allergens) determined by skin prick testing was available for part of the cohort. Icelandic controls (n=33,408) were participants from various deCODE genetics programs without known asthma. The study was funded by deCODE Genetics.

Genotyping and QC: Genome-wide SNP genotyping of 38,446 Icelanders was done using Illumina HumanHap300 or HumanHapCNV370 SNP chips. After excluding SNPs with MAF < 1%, with genotype yield < 96%, or with P value for deviation from HW equilibrium < 10^{-6}, 290,447 SNPs were used for imputation. After excluding samples with < 98% genotype yield, and individuals with asthma related phenotypes from the controls, 1,675 asthma cases and 33,408 controls were included in the association analysis.

Data Imputation and Analysis: Imputation of the HapMap Phase 2 Release 22 SNPs was performed using IMPUTE[26] with the CEU phased haplotypes as a reference. Tests of allelic association were performed for both genotyped and imputed SNPs using logistic regression implemented in the SNPTEST software, using the –method score option to deal imputation uncertainty. To correct for relatedness of study individuals, and for possible population stratification, the resulting chi-square test statistic was divided by the genomic inflation factor λ_g = 1.26.

EAGLE Consortium

COPSAC

Subjects: The COPSAC 2000 birth cohort study is a prospective clinical study of a birth cohort of 411 infants born to mothers with a history of asthma. The newborns were running at the age of 1 month, the recruitment of which was previously described in detail [27-29]. Asthma was diagnosed longitudinally by the research physicians based upon a predefined algorithm as previously described [28,29]. Diagnostic criteria included (1) recurrent episodes of troublesome lung symptoms recorded in the daily diary cards as five episodes within 6 months, each episode lasting at least three consecutive days; (2) symptoms typical of asthma based on doctors interviews of the parents at the clinical research unit; (3) need for intermittent rescue use of inhaled β2-agonist; and (4) response to a 3-month course of inhaled corticosteroids and relapse when stopping treatment. Cases in the current study were defined from having an asthma diagnosis before age 7 years and controls as children with clinical follow-up to age 7 years and no asthma diagnosis.

Genotyping and QC: High throughput genome-wide SNP genotyping were performed using the Illumina Infinium™ II HumanHap550 v1, v3 or quad BeadChip platform (Illumina, San Diego), at the Children's Hospital of Philadelphia's Center for Applied Genomics. All family structures were validated by means of identity-by-descent comparison of all subjects in the data set (proportion identity by descent). Sex was checked by calculating heterozygosity rates of the X chromosome and comparing with reported sex. Low-quality samples were removed based on call rate (<97%), and low-quality markers were removed based on call rate (<98% removed), low minor allele frequency (≤0.1% excluded), or being out of Hardy-Weinberg equilibrium ($P < 10^{-6}$, excluded). Also, principal component analysis-based removal of non-European samples was performed (using HapMap as reference).

Data Imputation and Analysis: Imputation to the CEU panel of HapMap release 22 was performed using MACH 1.0.12[30] using phased haplotypes as reference. The genomic build was hg18/NCBI36. Statistical association tests were performed on 2,434,240 variants using SNPTEST v2.2.0, using a genetic additive model and taking genotype uncertainty into account.

Danish National Birth Cohort (DNBC)

Subjects: The Danish National Birth Cohort (DNBC) is a collection of data on 92,274 pregnant women recruited between 1996 and 2002 [31]. The participating women were interviewed twice during pregnancy and the children are followed through childhood and adolescence. Children were considered to be cases for the "ever asthma" phenotype if a) they had self-reported asthma (by mother) in the DNBC questionnaire at age 7, or b) if they had any ICD-10 diagnosis code in the chapters J45-J46 recorded in the Danish Hospital Discharge Register before age 7.

Genotyping and QC: Genotype data were available from a genome-wide association study on preterm birth nested within the DNBC [32] performed with the Illumina 660 Quad chip (Illumina, Inc., San Diego, CA). The children used in the current study were all born in gestational week 37 or later. The children as well as their parents and grandparents were born in Northwestern Europe. Subjects were filtered based on < 95% call rates, and markers were filtered based on < 98% call rates, Hardy-Weinberg equilibrium p-values < 10^{-3}, and minor allele frequencies < 0.01. Total number of asthma cases and controls passing QC was 113 and 850, respectively, and the total number of markers passing QC was 508,059.

Data Imputation and Analysis: Imputation of the HapMap Phase 2 Release 22 SNPs was performed using MACH version 1.0.16 [30] with the CEU phased haplotypes as a reference. Tests of allelic association were performed by logistic regression using PLINK version 1.07 for genotyped SNPs and MACH2DAT version 1.0.10 for imputed SNPs.

GENERATION R

The Generation R Study[33] is a population-based prospective cohort study from fetal life onwards in Rotterdam, the Netherlands (http://www.generationr.nl). Assessments in pregnant women and children consisted of physical examinations, fetal ultrasounds, biological samples, and questionnaires. All children were born between April 2002 and January 2006. For the current study, physician-diagnosed ever asthma (no; yes) was assessed using questions adapted from the International Study on Asthma and Allergy in Childhood (ISAAC) at age 6 years.

Genotyping and QC: A GWA scan was performed on DNA isolated from cord blood samples using the Illumina 610 Quad array. Quality control comprised exclusion of duplicates, sex mismatches and low sample call rates. Further, SNPs with call rates <98%, low minor allele frequencies (<0.1%), and significant deviations from Hardy-Weinberg equilibrium ($P < 1x10^{-6}$) were excluded.

Data Imputation and analysis: Imputation was performed using MACH with HapMap2 CEU as the reference population. Statistical analyses were performed using GRIMP[34].

GINA Plus/LISA Plus

Subjects: The influence of Life-style factors on the development of the Immune System and Allergies in East and West Germany PLUS the influence of traffic emissions and genetics (LISAplus) Study is a population based birth cohort study. A total of 3,097 healthy, fullterm neonates were recruited between

1997 and 1999 in Munich, Leipzig, Wesel and Bad Honnef. The participants were not pre-selected based on family history of allergic diseases[35,36].

A total of 5,991 mothers and their newborns were recruited into the German Infant study on the influence of Nutrition Intervention PLUS environmental and genetic influences on allergy development (GINIplus) between September 1995 and June 1998 in Munich and Wesel. Infants with at least one allergic parent and/or sibling were allocated to the interventional study arm investigating the effect of different hydrolysed formulas for allergy prevention in the first year of life[37]. All children without a family history of allergic diseases and children whose parents did not give consent for the intervention were allocated to the non-interventional arm. Detailed descriptions of the LISAplus and GINIplus studies have been published elsewhere [35] and [37], respectively. Information on ever having physician-diagnosed asthma and related symptoms was collected using self-administered questionnaires completed by the parents. The questionnaires were completed at 6, 12, 18, 24 months, 4 and 6 years of age in the LISAplus study and 1, 2, 3, 4 and 6 years in the GINIplus study asking for physician diagnosed asthma at each year of age since the previous follow-up and wheeze in the past 12 months. DNA was collected at the age 6 and 10 years.

Genotyping and QC: Genotyping was performed using the Affymetrix Human SNP Array 5.0 and Affymetrix Human SNP Array 6.0. Genotypes were called using BRLMM-P algorithm (5.0), respectively BIRDSEED V2 algorithm (6.0). In each of the two data sets, criteria for exclusion of individuals were: a call rate below 95%, a heterozygosity outside mean +/- 4sd, a failure of the sex check or a failure of the similarity quality control using MDS analysis based on IBS. Criteria for exclusion of variants were: a call rate below 95%, a MAF < 0.01 and a HWE p-value <0.01 (n=396) / < 0.00001 (n=755).

Data Imputation and Analysis: Imputation was carried out in IMPUTE2 using the HapMap release 22, NBCI build 36 of the CEU reference population. Genome-wide association analysis of asthma phenotypes was conducted using SNPTEST V2 regressing expected allelic dosage on case-control status.

Manchester Asthma and Allergy Study (MAAS)

Subjects: The Manchester Asthma and Allergy Study is an unselected (i.e. population-based), birth cohort study[38-42]. The setting is the maternity catchment area of Wythenshawe and Stepping Hill Hospitals, comprising of 50 square miles of South Manchester and Cheshire, UK, a stable mixed urban-rural population. Cases were children with asthma ever by age 6. All pregnant women were screened for eligibility at antenatal visits (8th-10th week of pregnancy). The study was explained to the parents, and informed consent for initial questionnaires and skin prick testing was obtained. Both parents completed a questionnaire about their and their partner's history of asthma and allergic diseases and smoking habits. If the pregnant woman's partner was not present at the antenatal clinic visit, an invitation was sent for him to attend an open-access evening clinic for skin prick testing and questionnaire. Once both parents had completed questionnaires and skin prick testing, a full explanation of the proposed future follow-up for the child was given. Of the 1,499 couples who met the inclusion criteria (<10 weeks of pregnancy, maternal age >18 years, questionnaire and skin test data available for both parents), 288 declined to take part in the study. A total of 1,185 participants had at least some evaluable data. The children have been followed prospectively, and attended review clinics at ages 1, 3, 5, 8 and 11 years.

Genotyping and QC: DNA samples were genotyping on an Illumina 610 quad chip. The Illumina genotypes were called using the Illumina GenCall application following the manufacturer's instructions. Quality control criteria for samples included: 97% call rate, exclusion of samples with an outlier autosomal heterozygosity (scree-plot visualization) gender validation and sequenome genotype concordance. Quality control criteria for SNPs included a 95% call rate, HWE > $5.9x10^{-7}$, minor allele frequency > 0.005.

Data Imputation and Analysis: Genotypes were imputed with IMPUTE[2] version 2.1.2 with 1000 genomes and hapmap phase 3 reference genotypes. Association analysis was carried out using SNPTEST v2.4.0[26] using frequentist with the score method.

RAINE

Subjects: The Western Australian Pregnancy Cohort (Raine) Study is a prospective pregnancy cohort where 2,900 were recruited from King Edward Memorial Hospital between 1989 and 1991[43]. Data were collected throughout pregnancy and the children have been followed-up at ages 1, 2, 3, 5, 8, 10, 14, 17, 18, 20 and 22. Individuals who were ever diagnosed by a doctor with asthma were cases, all other individuals were classified as controls.

Genotyping and QC: Genome-wide SNP genotyping of 1,593 individuals was performed on Illumina's Human660W-Quad BeadChip. Replicates were investigated and the sample with the higher proportion of missing data was excluded. Possible cryptic relatedness between individuals in the cohort was examined, and any pair of individuals who were related with a $\pi > 0.1875$ was investigated and the individual with the higher proportion of missing data was excluded. Subjects were further filtered based on < 97% call rates. SNP QC was carried out in accordance to WTCCC recommendations[44]; in short, markers were filtered based on < 95% call rates, Hardy-Weinberg equilibrium p-values < $5.7x10^{-7}$, and minor allele frequencies < 0.01. The total number of markers passing QC was 535,632.

Data Imputation and Analysis: Imputation was performed using MACH version 1.0.18c and Minimac with the HapMap2 release 22 as a reference. Tests of allelic association were performed for both genotyped and imputed SNPs using logistic regression with SNPTEST v2.2.0.

B58C: British 1958 birth cohort

Subjects: The British 1958 Birth Cohort (also known as the National Child Development Study) is based on all persons born in Britain during one week in 1958. They were followed up at ages 7, 11 and 16 years by parental interviews and examinations by school medical officers, and at ages 23, 33 and 42 years by means of interviews. The presence of diagnosed asthma or a history of wheezy bronchitis were ascertained by parental interviews in childhood[45]. In adulthood, questionnaires were used to define asthma ever, wheezing ever, and wheezing episodes in the previous 12 months[46,47]. During 2002-2004 all cohort members still in contact with the study team were visited for a biomedical examination [48] and invited to contribute blood samples with consent for DNA extraction. The lifetime prevalence of asthma or wheeze in the full cohort was 49·9% and in the subgroup with DNA samples was 48·8%.

For the purposes of this meta-analysis, cases (N=986) were defined as those with a history of "asthma ever" at any age up to 42 years, and controls (N=5,505) were defined as the remainder of the cohort, including those with a history of wheeze or wheezy bronchitis, but no asthma. This followed the convention set by the GABRIEL consortium [6].

Genotyping and QC: Non-overlapping subsets of the British 1958 cohort DNA collection were genotyped as control samples by the Wellcome Trust Case-Control Consortium [49]and the Type 1 Diabetes Genetics Consortium [50], using the Illumina 550K array. From the remainder of the samples, all asthmatic cases and a sample of non-asthmatics were genotyped by the GABRIEL consortium using the Illumina 610K array [6]. These three genome-wide datasets were combined before imputation, selecting 532,203 SNPs which were common to the three deposits.

Each of the three subsets was restricted to subjects of white European ethnicity, but ancestry outliers on principal components analysis were excluded from all analyses. Samples with low average call rate (<98%) and sex mismatches were also removed. SNPs used for imputation excluded those with a call rate <95%, minor allele frequency < 1%, HWE p-value <0.0001 or discordant allele frequencies across the three deposits (p<0.0001 for pairwise comparisons). For chromosome X, the test of HWE was restricted to females, and additionally, SNPs with discordant allele frequencies between males and females (p<0.0001) were excluded. As a result, 494,161 (93%) of the 532,203 genotyped SNPs were used for imputation.

Data Imputation and Analysis: Imputation against the HapMap 2 (release 21) CEU reference panel was carried out using MACH 1.0.16. Statistical analysis used the *palogist* procedure in ProbABEL 0.1-3[51].

EVE Consortium

STAMPEED: SNP Typing for Association with Multiple Phenotypes from Existing Epidemiologic Data

Subjects: The STAMPEED asthma project includes subjects from the Chicago Asthma Genetics Study (C.A.G.) as well as from SARP and CSGA. CAG included both European American and African American subjects collected at The University of Chicago from a) families ascertained through affected sib pairs, b) affected children and their parents, c) adults and children with severe persistent asthma, and d) non-asthmatic control subjects (over the age of 18 years). Samples a-c were recruited in the adult and/or pediatric asthma clinics at University of Chicago Hospital; controls were recruited from the medical center at large. SARP and CSGA included both European American and African American subjects. Control subjects and subjects with mild to severe asthma were recruited at the NHLBI funded Severe Asthma Research Program (SARP) centers and the NHLBI Collaborative Studies on the Genetics of Asthma (CSGA) and characterized according to asthma severity (see[52,53]).

Genotyping and QC: Genotyping was performed on the Illumina 1Mv1 platform, with individual genotypes called using clustering algorithms as implemented in the BeadStudio software by Illumina. The resulting number of markers was 1,033,467 prior to additional QC measures. Markers were filtered based on 95% call rates, Hardy-Weinberg equilibrium p-values > 10^{-5}, consistency in allele frequency from the HapMap ASW (chi-square p-value > 10^{-5}), and <5 heterozygous genotype calls in males for X-linked markers. The total number of markers following QC was 1,025,129. Subjects were filtered based on 95% call rates, matching genetic and reported sex (Fstat on X chromosome between -0.2 and 0.3 for females, and between 0.8 and 1 for males), consistency in self-reported ethnicity based on a principal component analysis in Eigenstrat (no obvious clustering with the HapMap CEU for African Americans, and the HapMap YRI for European Americans), and high or low heterozygosity (Fstat < 0.5 and > -0.2). Samples were flagged for unexpected pairwise relatedness (IBD > 30%) or genetic identity (IBS > 90%), with subsequent filtering performed by selecting a single sample from the pair (or group) having the highest call rate.

Data Imputation and Analysis: Imputation of the phase 2, release 21 HapMap SNPs was performed using MACH, with the consensus CEU haplotypes used as a reference for the European American cases and controls, and the combined consensus CEU and YRI haplotypes for the African American cases and controls. Tests of allelic association were performed on dosages for both genotyped and imputed SNPs using logistic regression in R (http://CRAN.R-project.org/). For the set of African American cases and controls, local ancestry was used as a covariate at the SNP level as estimated using the set of genotyped SNPs in the program LAMP - Local Ancestry in adMixed Populations[54]. Admixture in African Americans was modeled under 7 generations of admixture with a 2-population model of 81% ancestry from Africa and 19% ancestry from Europe (α=[0.81, 0.19]) as estimated based on the first principal component in a PCA analysis using EIGENSTRAT[55]). Windows were offset by a factor of 0.2, the cutoff for linkage was set to 0.1, and a constant recombination rate was set to 10^{-8}. Local ancestry for imputed SNPs was obtained from the next closest genotyped SNP**.**

CHS: The Children's Health Study

Subjects: The Children's Health Study (CHS) is an ongoing cohort study in southern California investigating both genetic and environmental factors related to childhood asthma and lung function growth. The Children's Health Study GWAS was based on a nested case-control sample of 1,249 asthmatics and 1,751 controls selected from within the cohort. All subjects in this GWAS sample were either Hispanic white (HW) (n=1,398) or non-Hispanic white (NHW) (n=1,602). Based on questionnaire responses, children were characterized as having doctor-diagnosed asthma at study entry or during active follow-up (cases), or as never having a diagnosis of asthma (controls).

Genotyping and QC: Study samples were genotyped at the USC Epigenome Center using the Illumina HumanHap550, HumanHap550-Duo or Human610-Quad BeadChip microarrays. Individuals were excluded from analysis with call rates < 90% (n=155). The HumanHap550, HumanHap550-Duo and Human610-Quad contained 366, 366 and 418 SNPs respectively that overlapped with a candidate gene study containing a large number of the subjects in this study (n=2,905). The average concordance rate between matching subjects for these overlapping SNPs was > 99.69% for > 99% of the samples having a call rate > 90%. Subjects with poor concordance with genotypes from the candidate gene study were excluded (n=19). SNPs were excluded prior to imputation if they were not concordant between Illumina genotyped HapMap samples and HapMap2_r21 (< 95% in any population) or not concordant between Illumina genotyped HapMap samples on the HumanHap550 and Human610 (< 95% in any population) (n=8,616). Additionally, SNPs were filtered if they had a call rate < 95% (n=84,381) or departed from Hardy-Weinberg equilibrium ($p < 10^{-5}$) in controls in HW and NHW samples separately (n=762 and 766 respectively).

Data Imputation and Analysis: Imputation was performed with MACH v1.0.16 using the HapMap phase 2 release 21 consensus CEU haplotypes as a reference for the NHW subjects and CEU+ASN haplotypes for the HW subjects. Tests of allelic association were performed on dosages for both genotyped and imputed SNPs using logistic regression using R (www.R-project.org), adjusting for age, community of residence, sex, and ancestry covariates derived from the program STRUCTURE[56] applied to 557 ancestrally informative markers.

GRAAD: Genomic Research on Asthma in the African Diaspora

Subjects: The Genomic Research on Asthma in the African Diaspora study consists of 498 asthma cases and 500 non-asthmatic controls from the Baltimore-Washington, D.C. metropolitan area who self-reported as African American. Because asthma is often characterized by onset during childhood, there was a deliberate decision to favor adults in the control group to minimize including controls with the potential for developing asthma. A standardized questionnaire based on either the American Thoracic Society[57] or International Study of Asthma and Allergy in Childhood (ISAAC)[58] was administered by a clinical coordinator. Asthma was defined as both a reported history of asthma, and a documented history of physician-diagnosed asthma (past or current). All controls (except 50, see below) were likewise administered a standardized questionnaire and were determined to be negative for a history of asthma. Asthma status on 50 controls participating in a study of the genetics of human pigmentation [59] was not explicitly determined, although "known clinical disease" was among the exclusion criteria. The study protocol was approved by the institutional review board at either the Johns Hopkins University or Howard University.

Genotyping and QC: Details of genotyping and quality control (QC) have been previously described[60]. Briefly, genotypes were generated at the Center for Inherited Disease Research (CIDR) for 665,352 SNPs on the Illumina HumanHap650Y Versions 1 and 3 BeadChips and the Illumina Infinium II assay protocol. Genotypes were released for 994 GRAAD samples for SNPs with < 5% missing data, no replicate error among other standard QC protocols. Relationships between individuals within each study were verified using PLINK and RELPAL[61], and marker-level QC parameters (including minor allele frequency, differential missing rates between cases and controls, and Hardy Weinberg Equilibrium) were evaluated in PLINK. The genetic structure of African American cases and controls was evaluated using unrelated individuals from the three HapMap "continental" ancestral populations (CEU, YRI, and ASN; www.hapmap.org) using 416 SNPs identified as ancestry informative markers (AIMs) selected for maximal difference between African and European populations in STRUCTURE.

Data Imputation and Analysis: Genotypes were imputed at all HapMap phase 2, release 21 SNPs using MACH, and using a combined panel of the HapMap CEU, YRI and ASN phased haplotypes. For the case-control sample (GRAAD), a two sample t-test was used to compare the allele dosage between cases and controls.

SAPPHIRE: The Study of Asthma Phenotypes and Pharmacogenomic Interactions by Race-Ethnicity

Subjects: Study participants received their care through a large health system serving southeast Michigan. Cases were part of the Study of Asthma Phenotypes and Pharmacogenomic Interactions by Race-Ethnicity (SAPPHIRE) (n=149), and met the following criteria: age 12-56 years, a prior clinical diagnosis of asthma, no recorded diagnosis of chronic obstructive pulmonary disease (COPD) or congestive heart failure (CHF), a baseline FEV_1 between 40-90% predicted, >12% baseline bronchodilator reversibility, no smoking in the preceding year or <10 pack-year smoking history total, no oral or inhaled corticosteroid use in the 4 weeks preceding screening, and not pregnant at the time of enrollment and not intending to get pregnant during the study period. Controls were obtained from a separate cohort, the Wayne County Health Environment Allergy and Asthma Longitudinal Study. All were women ≥ 21 years of age who also resided in the Detroit metropolitan area and received their care from the same health system. The analytic group for the meta-analysis was restricted to individuals who reported being African American. The Institutional Review Board of Henry Ford Health System approved all of the components of this study.

Genotyping and QC: Genotyping for the cases was performed on the Affymetrix Genome-Wide Human SNP Array 6.0, whereas control individuals were genotyped on either the Mapping 500K Array and the Genome-Wide Human SNP Array 5.0 (Affymetrix, Inc., Santa Clara, California). Genotyping calls and the chip quality control (QC) call rate were assessed using Affymetrix Genotyping Console. Subjects with the following were excluded from the analysis: missing information for one chip (i.e., for those genotyped on the 2 chip Mapping 500K Array), genetic sex inconsistent with reported sex, chips which did not meet the manufacture's recommended QC call rate, and <90% overall call rate. In order to appropriately match cases and controls, genetic ancestry was estimated in all individuals using markers informative for African and European ancestry and the program PSMIX[62]. We restricted the control set to individuals with ≥30% African ancestry (n=132), which was the lower limit of African ancestry among the cases. Single nucleotide polymorphisms (SNPs) common to all genotyping platforms were selected and subjected to the following additional criteria: call rate ≥ 95% and an exact Hardy-Weinberg equilibrium test with p-value $>10^{-5}$ among the controls.

Data Imputation and Analysis: A total of 404,088 SNPs were used to impute the HapMap phase 2, release 21 SNPs using MACH with the phased HapMap CEU and YRI haplotypes as a reference. Case/control association tests for asthma status were performed using logistic regression in R (http://CRAN.R-project.org/) on genotype dosages, and adjusting for the first principal component from EIGENSTRAT.

JAARC: Japanese Adult Asthma Research Consortium

Subjects: We selected subjects with childhood-onset asthma from the case subjects who participated in a genome-wide association study (GWAS) for adult asthma in the Japanese population[63]. A total of 301 subjects with a history of childhood-onset asthma (asthma onset by 15 years of age; age [mean ± sd], 39.4±14.8) years; female [%], 47.8) were recruited by physicians' interviews. All subjects with asthma were diagnosed by physicians according to the American Thoracic Society criteria. A total of 3,304 control subjects for the GWAS (age [mean ± sd], 52.5±15.1) years; female [%], 44.4) were recruited as described[63].

Genotyping and QC: For the GWAS, we genotyped 301 cases using the Illumina HumanHap610-Quad BeadChip and 3,304 controls using the Illumina HumanHap550 BeadChip. We conducted allele sharing analysis and performed principal component analysis for the genotype data of the samples along with European (CEU), African (YRI) and East Asian (Japanese [JPT], and Han Chinese [CHB]) individuals obtained from the Phase II HapMap database by using SMARTPCA. We excluded related samples and outliers who were away from the east Asian cluster. We also excluded SNPs with minor allele frequencies of less than 0.01 in both cases and controls. SNPs having call rates ≥99% in both cases and controls were used for the association study. We conducted exact Hardy-Weinberg equilibrium (HWE) analysis, and SNPs with *P* values less than the cut-off values of the HWE test ($P < 10^{-6}$ in controls) were also excluded from the analysis.

Data Imputation and Analysis: Imputation of HapMap2, Release21 SNPs was performed using MACH with the JPT+CHB haplotypes as a reference. SNPs with *P* values of HWE in the control group $\geq 1\times10^{-6}$ were imputed. In the GWAS, the statistical significance of the association with each SNP was assessed using a logistic regression analysis.

JPAC: Japan Pediatric Asthma Consortium

Subjects: The part of the study population, genotyping and quality control have been previously described[64]. All subjects with asthma were child or child-onset (<15 years old) asthmatics in Japan. Patients were recruited from 3 pediatric hospitals and 1 pediatric clinic, and the diagnosis of the asthma in all patients was confirmed by specialists in pediatric allergology on the basis of the criteria of the National Institutes of Health, USA, with minor modifications. The control for the GWAS were healthy Japanese adult subjects from Tokyo who had no current history of asthma. All subjects were self-reported Japanese origin.

Genotyping and QC: Genome-wide SNP genotyping of 978 pediatric asthmatics and 694 controls was performed on Illumina's HumanHap550v3/610 Genotyping BeadChip (Illumina, Inc., San Diego, CA). We examined the potential genetic relatedness on the basis of pairwise identity by state for all of the successfully genotyped samples using the EIGENSTRAT software , and we excluded samples belonging to Han Chinese or Ryukyu, an island located in southern Japan. Subjects were filtered based on < 95% call rates, and markers were filtered based on < 95% call rates, Hardy-Weinberg equilibrium p-values < 10^{-4}, and minor allele frequencies < 0.01. Total number of pediatric asthmatics and controls passing QC was 938 and 672, respectively, and the total number of markers passing QC was 482,803 for HumanHap 610 and 435,199 for HumanHap550v3.

Data Imputation and Analysis: Imputation of the HapMap Phase 2 Release 21 SNPs was performed using MACH version 1.0.17 with the JPT+CHB phased haplotypes as a reference. Tests of allelic association were performed for both genotyped and imputed SNPs using logistic regression with MACH2DAT software version 1.1.9.

GABRIEL Consortium

The GABRIEL Consortium includes 19 studies that contributed to TAGC. Seven of the 19 studies were split into two datasets according to age of onset of asthma (before or after 16 years of age); the INDUSTRIAL subgroup included four studies and the German MAS and MAGICS studies were combined.

EGEA: Briefly, the EGEA study (N=2,120 subjects) combines a case-control and a family-based study of asthma cases with three surveys over 20 years (EGEA1: 1991-1995, EGEA2: 2003-2007 and EGEA3: 2011-2013). The whole study population included 388 asthmatic probands recruited in chest clinics and their 1,317 family members (probands' parents and/or siblings) plus 415 population-based controls[65]. The probands (asthmatics and controls) were between 7 and 70 years old at time of study. All subjects were of European ancestry and were born in France. Data collected through face-to-face interviews and examination included extensive phenotypic characterization (detailed clinical data based on standardized questionnaire, skin prick tests, lung function tests, bronchial responsiveness, blood samples, white blood cell counts, total IgE), data on risk factors (environmental exposures, diet, physical activity, hormone-related events) and drug consumption. For the present study, cases with asthma were defined by a positive answer to the question "Have you ever had asthma attacks?" at EGEA1 or EGEA2. Detailed description of the study can be found in Kauffmann *et al*[65,664] and at http://egeanet.vjf.inserm.fr. After QC, a total of 1,928 EGEA subjects were retained in the GWAS analyses.

ALSPAC: is a population-based, prospective, longitudinal, birth-cohort study that was recruited during pregnancy. Pregnant women resident in Avon, United Kingdom and with estimated dates of delivery 1/4/1991-31/12/1992 were recruited through antenatal clinics.[67](www.bristol.ac.uk/alspac) Of 14,451 pregnancies recruited, there were 14,072 live births and 13,988 children remained alive at age 1 year. Children have been followed from birth using a combination of self-completion questionnaires sent at regular intervals to their mothers and hands-on assessments at annual dedicated research clinics from age 7 years. Asthma in children was defined as a positive response to the question, "Has a doctor ever told you that your child has asthma?" in a questionnaire sent to their mothers at 91 months after birth. A total of 5,231 children had data on asthma at 91 months with DNA available for genotyping. Of these, 650 (12.4%) had asthma. An equal number of controls were selected at random from the remaining population with questionnaire responses at 91 months and DNA available. After QC a total of 1,216 subjects were retained in the GWAS analyses.

ECRHS: Sixteen centres (eight countries) in the ECRHS contributed samples to the GWAS.[68,69] (www.ecrhs.org) In each centre, a representative community-based sample of at least 3000 adults aged 20-44 years were invited to complete a brief postal questionnaire asking about respiratory symptoms (ECRHS I - Stage 1) between 1991-1993. A random sample of these (600 per centre) underwent intensive further investigation (ECRHS I - Stage 2 – random sample). Participants who had symptoms highly suggestive of asthma but who had not been selected at random to take part in Stage 2 were also invited to undergo intensive investigations (ECRHS I - Stage 2- enriched sample). About ten years later all adults who had taken part in Stage 2 were re-contacted (ECRHS II) and again asked about respiratory symptoms. Samples suitable for DNA extraction were collected. For the GWAS initiative all cases of asthma were identified (participants from the random or enriched sample who said yes to the question 'Have you ever had asthma?' at either ECRHS Stage I or Stage II). Controls were a random sample (of the random sample) who answered 'no' to the same question in both surveys. After quality control (QC) criteria a total of 2,210 ECRHS subjects were retained in the GWAS analyses.

BAMSE: Between 1994 and 1996, 4,089 newborn infants were recruited in the BAMSE study, and questionnaire data on baseline study characteristics were obtained.[70,71] The catchment area included central and north-western parts of Stockholm. At approximately one, two, four, and eight years of age, parents completed questionnaires on their children's symptoms related to asthma and other allergic diseases. The response rates were 96%, 94%, 92% and 84%, respectively. At eight years of age, all children of the BAMSE study were invited to clinical testing, and blood samples were obtained from 2,480 children. DNA was extracted from 2,033 samples after exclusion of samples with too little blood, lack of questionnaire data, or if parental consent to genetic analysis of the sample was not obtained. From these samples, all children with a doctor's diagnosis of asthma (ever) were selected as cases and children with no history of asthma or other allergic diseases were selected as controls. After QC a total of 485 subjects were retained in the GWAS analyses.

BUSSELTON: Residents of the town of Busselton in the southwest of Western Australia have been involved in a series of health surveys since 1966. (www.busseltonhealthstudy.com) The population is predominantly of European origin. In 1994/95 there was a follow-up study involving a subset of those who had attended any of the previous surveys. Cases of asthma were defined as those who reported doctor-diagnosed asthma at any survey that they attend from 1966 to 1994 (answer 'Yes' to 'Has your doctor ever told you that you had asthma?').[72] Controls are those who have consistently answered 'No' to 'Has your doctor ever told you that you had asthma?' at all previous surveys that they have attended from 1996 to 1994. For the GWA study, a case control sample of unrelated individuals was selected. After QC a total of 1,207 subjects were retained in the GWAS analyses.

GABRIEL ADVANCED SURVEYS: Are cross-sectional population-based surveys conducted in rural areas of Austria, Germany, and Switzerland. In total, 135,359 children aged 6-12 years were addressed through schools. In a first stage in fall/winter 2006, asthma, allergic disease, and contact to farming environments were assessed using a short parental questionnaire (n=79,888). In a second stage in spring/summer 2007, 9,668 children were selected among families consenting in writing to blood sampling, genetic testing and collection of environmental samples by stratified random sampling to ensure representation of children with high exposure to farming environments.[73] Genomic DNA was purified from blood samples using the Puregene chemistry (QIAGEN, Hilden, Germany) on an Autopure LS instrument (QIAGEN, Hilden, Germany). Genomic DNA and questionnaire data were available for 7,303 children of whom 862 cases and 865 controls were selected for genotyping. A case was defined as a parental report of asthma diagnosed by a doctor at least once or asthmatic bronchitis diagnosed at least twice during lifetime. To account for the stratified random sampling, probability weights were introduced in the statistical analyses. After QC a total of 1,692 subjects were retained in the GWAS analyses.

KSMU: is a population-based case-control study of adult cases of asthma and controls matched for age and sex.[74,75] A total of 429 unrelated subjects were recruited in this study, (215 patients with asthma and 214 controls). The study subjects were of Russian origin from Central Russia. All patients were recruited at the Department of Pulmonology, Kursk Regional Clinical Hospital between 2003 and 2004. Additional adult patients with asthma and healthy subjects (>200 samples) from the same population were recruited between 2007 and 2008 specially in order to increase final sample size for the GWAS initiative. All patients were diagnosed with asthma by the presence of characteristic symptoms, reversibility of airway obstruction or airway hyperresponsiveness to methacholine. All control subjects were enrolled in accordance with the following criteria: (1) no symptoms and history of allergic diseases, (2) normal total serum IgE levels, (3) and normal pulmonary function test results. Personal data, including smoking status and age of the disease onset, was collected through in-person interviews. After QC a total of 568 subjects were retained in the GWAS analyses.

MRCA-UK: is a collection of nuclear families (207 families total number of subjects 783) ascertained through a proband with ≥Step 3 asthma according to British Thoracic Society guidelines[76] and four hundred and thirty seven non-asthmatic UK controls (UK-C)[77]. Probands and family members all answered a nurse-administered comprehensive respiratory questionnaire with asthma being defined as positive response to the question ''Has your doctor ever told you that you have asthma?''. The children from this collection together with those from MAGICs (below) formed the case control dataset genotyped in the first GWAS for asthma[77].

MAGICS consists of 655 asthmatic children (asthma diagnosed by a pulmonologist) were derived from the Multicenter Asthma Genetics In Childhood Study with a further 73 asthmatics and 694 unaffected individuals (randomly selected) from Phase One of the International Study of Asthma and Allergy in Childhood (ISAAC)[78,79]. For the 73 asthmatics from ISAAC, asthma was physician diagnosed and/or reports by parent of recurrent spastic or asthmatic bronchitis. MAGICS together with the children from the MRCA collection formed the case control dataset genotyped in the first GWAS for asthma[77] .

MAS: Consists of 1,314 healthy mature children born in 5 German cities in the year 1990. All children were followed at the age of 1, 3, 6, 12, 18, and 24 months and at yearly intervals thereafter until age 15 years.[80,81] Clinical and environmental assessment included standardized interviews, questionnaires, physical examinations, and environmental studies. Total and specific IgE antibodies to hen's egg, cow's milk, wheat, and soy were determined at the age of 1, 2, 3, 5, 7, and 10 years. DNAs from all children with a doctor diagnosis of asthma were provided for the GWA study. This dataset was combined with the MAGICS dataset.

PIAMA: Is a birth cohort study consisting of two parts: a placebo controlled intervention study in which the effect of mite impermeable mattress covers was studied and a natural history study in which no intervention took place. In this study, only data from the natural history part of the study are presented. Details of the study design have been published previously.[82-84] Recruitment took place in 1996-1997. A screening questionnaire was distributed to 10,232 pregnant women visiting one of 52 prenatal clinics. 10,232 pregnant women completed a validated screening questionnaire at their prenatal health care clinic. Based on this screening, 7,862 women were invited to participate, of whom 4,146 women agreed and gave informed consent. Mothers reporting a history of asthma, current hay fever or allergy to pets or house dust mite were defined as allergic. Follow-up of the children took place at 3 months of age and yearly from 1 to 8 years of age. The response rates to the annual questionnaires ranged from 3030 (92%) at age 1 to 2732 (83%) at age 8 years. For the GWA study, DNA from childhood asthma cases and a set of matched non-asthmatic controls were provided. After QC a total of 359 subjects were retained in the GWAS analyses.

SAPALDIA: Contributed all self-reported asthma cases as well as a random sample of controls. These subjects were obtained from among 6,055 SAPALDIA cohort subjects that participated in both, the baseline (1991) and follow-up (2002) examinations and agreed to providing blood for genetic analysis. SAPALDIA is a population-based cohort that originally recruited subjects aged 18 to 60 from population registries in eight Swiss communities representing the three largest language groups (German, French, Italian) as well as different levels of air pollution, altitude and degrees of urbanization.[85-87] At both baseline and follow-up examination subjects underwent spirometry as well as a detailed interview on respiratory health, smoking history, lifestyle factors and anthropometry. At follow-up, 8,047 of 9,651 baseline subjects re-participated in at least one part of the study and a formal biobank was established. SAPALDIA questions about smoking and asthma status were equivalent to those used by the ECRHS. Asthma status was defined by an affirmative answer to the question “Have you ever had asthma” at baseline and/or follow-up interview. After QC a total of 1,521 subjects were retained in the GWAS analyses.

TOMSK: Is a population-based family study conducted by the Research Institute of Medical Genetics and Siberian State Medical University (Tomsk, Russia) from 1998 onwards.[88,89] Both nuclear families and extended pedigrees were recruited through atopic bronchial asthmatic probands. All participants were Russians or of a mixed ethnic origin due to marriages between Russians and major East Slavonic populations (Ukrainians, Byelorussians). Altogether, 196 families were studied, out of which 150 families were recruited in Tomsk Region Children Hospital and Tomsk Region Hospital (Tomsk, Russia), and 46 families were recruited in the city of Irkutsk hospitals by the staff of the Irkutsk State Institute of Doctor’s Advanced Training (Irkutsk, Russia). Both probands and their relatives were clinically examined to establish diagnosis of asthma and atopy by the GINA criteria (Global Initiative for Asthma: Global Strategy for Asthma Management and Prevention. http://www.ginasthma.org). Besides the clinical examination, laboratory and functional testing were conducted to assess common IgE levels (solid-phase immune-enzyme assay), specific sensitization (skin-prick tests), lung volumes (spirometry), and airway responsiveness (bronchoprovocative tests with methacholine). After QC a total of 681 subjects were retained in the GWAS analyses.

UFA: Is a population-based case-control study of asthma cases and controls matched on age and sex. Cases are unrelated patients with physician-diagnosed asthma and controls disease-free. Subjects are of different ethnic origins (Russians, Tatars and Bashkirs) from Volga-Ural region of Russian Federation. The Volga-Ural region is located at the border between Europe and Asia and has been the arena of permanent genetic exchanges among Siberian, European, Central Asian and other populations. Anthropologically, Russians, Tatars and Bashkirs are Caucasians and have a varying Asian component. Recruitment of cases and controls was carried out by the Hospital of the Bashkir Medical State University and Ufa Municipal Hospital №21 between 1999 and the year 2007. Asthma patients were diagnosed by pulmonologists on the basis of clinical examination, family and medication history, objective tests of lung function. The controls were healthy subjects who met all the following criteria: (1) no symptoms or history of asthma or other pulmonary diseases; (2) no symptoms or history of atopy; and (3) absence of first-degree relatives with a history of asthma or atopy. After QC a total of 678 subjects were retained in the GWAS analyses.

INDUSTRIAL (the Industrial Cohorts Research Group)**:** The study base consists of several pooled surveys on occupational asthma from Denmark and The Netherlands. The populations come from industries with exposure to known major allergens and irritants; high molecular weight sensitizers (wheat flour, fungal alpha amylase, animal allergens), low molecular weight sensitizers (isocyanate monomers and oligomers) and irritants and inflammatory agents (isocyanates, organic dust, endotoxins, wood). Prevalent cases and industry, gender and age matched study-specific controls were included for the GWAS initiative. Briefly, cases and controls originate from the following population based or prospective cohort studies in agricultural dust and/or animal exposed environments: the Danish SUS study[90,91], the Dutch Omega[92,93] and Veterinarian's Health Study[94]; in wheat and amylase exposed environments: the bakers from the Dutch Bakers health surveillance project[95]; in wood dust exposed environments: workers in the Danish furniture industry of the Danish Wood Dust Cohort;[96,97] and for isocyanate exposed workers: a population of Dutch industrial spray painters.[98,99] Asthma, respiratory symptoms and potential confounders like smoking were primarily assessed from questionnaires. More objective health measures were also collated including lung function measurements, a specific bronchial hyperresponsiveness and specific IgE measurements. Exposure was assessed by taking job histories from questionnaires. For all studies extensive measurement series have been collected which have been used to create generic or study specific Job Exposure Matrices by which the exposure can be estimated quantitatively on the basis of job title and sometimes tasks performed[100]. After QC a total of 1,227 subjects were retained in the GWAS analyses.

SEVERE: Severe/refractory cases of asthma were recruited through three specialist severe asthma clinics; adult and childhood clinics based at the Royal Brompton Hospital, London and an adult clinic at the Glenfield Hospital, Leicester. Patients attending the Glenfield Hospital clinics had full characterisation and were deemed to have severe/refractory asthma according to a specialised protocol involving parameters of airway inflammation, airway physiology, as well as quality of life and control of symptoms.[101,102] Those attending Royal Brompton Hospital adult clinics were also fully characterised, with severe asthma defined according to the ATS and ERS definition of severe asthma.[103,104]

Severe asthma in the pediatric clinic was defined as one or more of the following criteria: (1) Persistent (most days, for at least 3 months) chronic symptoms (the necessity because of symptoms for short-acting β-2 agonists at least three times/week) of airways obstruction despite high dose inhaled corticosteroids

(Beclomethasone equivalent 800 mcg/day) and trials of every add-on medication available in the country of residence (these would include, if available, long acting β-2 agonist, leukotriene receptor antagonist, oral theophylline in the low, anti-inflammatory dose). This group includes Type 1 brittle asthma. (2) Recurrent severe asthma exacerbations despite attempts with medication including trials of allergen avoidance, low dose daily inhaled corticosteroids or intermittent high dose inhaled corticosteroids: *either* at least one admission to an intensive care unit, or at least two hospital admissions requiring intravenous medication/s, *or* $\geq$ 2 courses of oral steroids during the last year, despite the above therapy. This group includes Type 2 brittle asthma. (3) Persistent airflow obstruction: post oral steroid, post-bronchodilator Z score < -1.96 for FEV_1, with appropriate normative data despite the above therapy. (4) The necessity of prescription of alternate day or daily oral steroids to achieve control of asthma. Children were evaluated in detail to exclude as far as possible non-adherence to therapy, significant co-morbidity (for example, rhinosinusitis and gastroesophageal reflux), psychosocial issues and adverse environmental circumstances as contributing factors to the severity of asthma.[104-107] Because of the relatively small numbers of severe asthmatics, this group were not subdivided into childhood onset and adult onset groups. After QC a total of 290 subjects were retained in the GWAS analyses.

For the SEVERE cohorts, control data for analysis was obtained through the WTCCC (http://www.wtccc.org.uk). Data used was from 974 samples genotyped using an Illumina 1.2M custom chip.

Genotyping and QC for all GABRIEL datasets: All Gabriel consortium datasets, except for the MRCA and MAGICS datasets, were genotyped at Centre National de Génotypage (CNG, Evry, France) using the Illumina Human610-Quad array[6]. The MRCA and MAGICS datasets were genotyped using Illumina Sentrix Human-1 and Sentrix HumanHap300 BeadChips, as part of the first asthma GWAS[77]. QC of individuals and SNPs genotyped at CNG was done in each dataset following the same protocol[6]. Briefly, individuals were removed from analysis if they were not of European descent (principal component analysis of each GABRIEL datasets with all HapMap populations), had a low genotyping call rate (<95%) or were discrepant or ambiguous for genetic sex. Single Nucleotide Polymorphisms (SNPs) with call rate lower than 95% or minor allele frequency (MAF) lower than 0.01, or with Hardy-Weinberg equilibrium P-value $<10^{-4}$ were removed. QC for MRCA and MAGICS is detailed Moffatt *et al*.[77]

Imputation and analysis of all GABRIEL datasets: In each dataset, genome-wide imputations were performed using MACH 1.0 software and HapMap Phase 2 (Release 21) as reference panel. SNPs with imputation quality score (rsq) ≥ 0.5 and minor allele frequency ≥ 1% were kept for analysis. Association analysis between asthma and individual SNPs was performed using a logistic regression model that included allele dosage for each SNP and principal components to account for population structure. In family data, a robust sandwich estimation of the variance and a family cluster were used to take into account familial dependencies. Moreover, due to the complex sampling design of the GABRIELA study, survey regression techniques were used for this study to estimate robust standard errors ('svy' command in Stata). All analyses were performed using Stata® version 10 (distributed by Stata Corporation, College Station, Texas, USA).

NTR: The Netherlands Twin Register

Subjects: NTR [108,109] participants are ascertained because of the presence of twins or triplets in the family and consist of multiples, their parents, siblings and spouses. Twins are born in all strata of society and NTR represents a general sample from the Dutch population. In this study, 2,867 individuals were included (451 cases and 2,416 controls) with asthma definition: "ever doctor diagnosed asthma ignoring age of onset".

Genotyping and QC: [La table sup 2 indique "Illumina 660K, Illumina Omni Express 1 mil, Affymetrix Perlegen and Affymetrix 6.0"] Genotype data were checked for European ancestry, Mendelian errors, gender inconsistencies and high genome-wide homozygosity. Checks for relatedness were carried out and only unrelated individuals were used in the analysis. Genotype data were further checked based on Hardy-Weinberg Equilibrium (1×10^{-6} HWE), minor allele frequencies (MAF 0.01), SNP call rate (95% threshold of subjects with missing genotypes per SNP) and sample call rate (75% threshold of missing SNPs per subject).

Data Imputation and Analysis: The reference set used for imputation is HapMap phase II CEU data NCBI build 36 (UCSC hg18). Imputation was carried out using IMPUTE. Genome-wide association analysis was conducted using logistic regression (under an additive model) and including sex, age at examination and 4 principal components as covariates. Association analysis was conducted in PLINK, taking the uncertainty of the imputed genotypes into account.

Rotterdam Study (RS-I, RS-II, RS-III)

Subjects: The Rotterdam Study is a prospective population based cohort study ongoing since 1990 in the city of Rotterdam in The Netherlands. Study design and objectives have been described elsewhere[110]. The first cohort (RS I) consists of 7,983 participants, aged 55 years and over. The second cohort (RS II) was recruited in 2000 with the same inclusion criteria and consists of 3,011 participants. The third cohort (RS IIII) consists of 3,932 participants, aged 45 years and over and was recruited in 2006. As of 2008, 14,926 subjects aged 45 years or over comprise the Rotterdam Study cohort. Asthma cases were collected by chart review. Cases were ascertained by 1) Doctor's diagnosis of Asthma ***and*** 2) no conflicting respiratory diagnosis. Additionally, prescriptions for respiratory medicines were used for case finding. The number of cases and controls by study is shown in the Supplementary Table 1.

Genotyping and QC: Genotyping was done using the following arrays: Illumina Infinium II HumanHap550 chip v3.0 array (RS1), the HumanHap550 Duo Arrays and the Illumina Human610-Quad Arrays (RS-II), and the Human 610 Quad Arrays Illumina (RS-III). Exclusions were based on a call rate < 98%, Hardy-Weinberg p-value < 10^{-6} and MAF < 0.01%. SNP exclusions were based on a call rate < 98%, Hardy-Weinberg p-value < 10^{-6} and MAF < 0.01%.

Data Imputation and Analysis: We used the Markov Chain Haplotyping (MACH) package version 1.0.15 software (Rotterdam, The Netherlands; imputed to plus strand of NCBI build 36, HapMap release #22) for the analyses of RSI and RSII. RSIII was imputed using MACH 1.0.16. For the analyses we used a MACH2DAT implemented in GRIMP, a high-speed pipeline for Genome Wide Association analyses[34].

DAGC Dutch Asthma Genetics Consortium

Subjects : The Dutch Asthma GWAS (DAG) cohort consists of in total 915 asthma cases and 986 controls, all from the northern of the Netherlands. The DAG cohort was genotyped in two phases and meta-analysed afterwards. For the first phase, 463 cases were selected from a trio and family study. The 469 controls were non-asthmatic spouses or pseudo-controls of untransmitted alleles in our trio design (GWAS I). For the second phase (GWAS II), 452 asthmatics were selected from previous clinical and genetic studies performed by our research institute. The 517 controls were selected from the COPACETIC study, a geographically matched population-based study on lung cancer screening in male smokers. All asthmatics had a physician's diagnosis of asthma, asthma symptoms, and BHR to either histamine or methacholine. BHR was measured with a metacholine or histamine challenge test, and defined as PC20 histamine. Controls had no asthma or COPD, nor any evidence of significant airway obstruction.[111]

Genotyping: Genotyping was performed on two platforms, 1. the Illumina HAPMAP 317K platform and 2. HAPMAP Illumina 370 Duo Chip. Quality control was applied; subjects were removed for analysis if they were not of Caucasian descent, had a low genotyping call rate (< 95%) or were discrepant or ambiguous for genetic sex. SNPs were deleted if the call rates were low (95%), if they were not in Hardy-Weinberg Equilibrium (p < 10E-04), or if the minor allele frequency was < 0.05.

Data Imputation and Analysis: Imputation was performed using BEAGLE and the HapMap2 CEU reference panel. All statistical analyses have been performed using PLINK v1.07.

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