

Genome-wide association study of aspirin-exacerbated respiratory disease in a Korean population

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Abstract Aspirin-exacerbated respiratory disease (AERD) is a nonallergic clinical syndrome characterized by a severe decline in forced expiratory volume in one second (FEV1) following the ingestion of non-steroidal anti-inflammatory drugs (NSAIDs) such as aspirin. The effects of genetic variants have not fully explained all of the observed individual differences to an aspirin challenge despite previous attempts to identify AERD-related genes. In the present study, we performed genome-wide association study (GWAS) and targeted association study in Korean asthmatics to identify new genetic factors associated with AERD. A total of 685 asthmatic patients without AERD and 117 subjects with AERD were used for the GWAS of the first stage,

and 996 asthmatics without AERD and 142 subjects with AERD were used for a follow-up study. A total of 702 SNPs were genotyped using the GoldenGate assay with the Vera-Code microbead. GWAS revealed the top-ranked variants in 3' regions of the HLA-DPB1 gene. To investigate the detailed genetic effects of an associated region with the risk of AERD, a follow-up targeted association study with the 702 single nucleotide polymorphisms (SNPs) of 14 genes was performed on 802 Korean subjects. In a case-control analysis, HLA-DPB1 *rs1042151* (Met105Val) shows the most significant association with the susceptibility of AERD ($p = 5.11 \times 10^{-7}$; OR = 2.40). Moreover, *rs1042151* also shows a gene dose for the percent decline of FEV1 after an aspirin challenge ($p = 2.82 \times 10^{-7}$). Our findings show that the HLA-DPB1 gene polymorphism may be the most susceptible genetic factor for the risk of AERD in Korean

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asthmatics and confirm the importance of HLA-DPB1 in the genetic etiology of AERD.

Introduction

Aspirin-exacerbated respiratory disease (AERD) is characterized by asthma, nasal polyps, chronic rhinosinusitis, and exacerbated bronchial obstruction after the ingestion of non-steroidal anti-inflammatory drugs in about 10–20 % of adult asthmatics (Babu and Salvi 2000; Macy et al. 2007; Sturtevant 1999). The main pathophysiology of AERD is the inhibition of the cyclooxygenase (COX) pathway by aspirin that results in the decreased synthesis of prostaglandin E₂ (PGE₂) and the overproduction of cysteinyl leukotrienes (cysLTs) (Bennett 2000). Several genetic studies have shown that the polymorphisms of genes in the arachidonate pathways, such as cysteinyl leukotriene receptor 1 (Kim et al. 2007), cysteinyl leukotriene receptor 2 (Park et al. 2005), thromboxane A₂ receptor (Kim et al. 2005b), and prostaglandin E₂ receptor subtype 2 (Jinnai et al. 2004), leukotriene C₄ synthase (LTC₄S) (Sanak and Szczeklik 2001) and arachidonate 5-lipoxygenase (ALOX5) (Choi et al. 2004b), are associated with AERD. However, the effects of AERD-related gene variants have partly explained the individual differences in the airway obstruction following aspirin challenge.

Studies have identified alterations in immune responses (Delaney and Kay 1976; Lee et al. 2006), and alterations in the immune and inflammatory gene responses as predisposing factors of the disease; genetic variants such as FcεR1β (Kim et al. 2006), HLA (Choi et al. 2004a; Dekker et al. 1997; Park et al. 2004), TBX21 (Akahoshi et al. 2005), IL-4 (Kim et al. 2008), *NLRP3* (Hitomi et al. 2009) PPAR-γ (Oh et al. 2009) genes were reported to be associated with AERD. The data suggests that genetic variants on the extra-arachidonate pathways may be more related to the development of AERD than previously thought.

Since genome-wide association study (GWAS) emerged as a high throughput technology to genotype genomic nucleotide variations, several genes (e.g., *ORMDL3*, *PDE4D*, and *IL1RL1*) have been discovered to be susceptible to asthma and asthma-related phenotypes (Gudbjartsson et al. 2009; Himes et al. 2009; Moffatt et al. 2007). Our previous GWAS using a low-density BeadChip showed that a nonsynonymous single nucleotide polymorphism (SNP) of *CEP68*, rs7572857 G>A (Gly74Ser) could be an important marker of AERD susceptibility (Kim et al. 2010). However, this 100K BeadChip could cover a small portion of genetic variants over the whole genome. Recent technical improvements have developed a denser

BeadChip of 657,366 (660W) that cover a wider range of genetic variants. To identify new genetic variants associated with AERD, the present study performed GWAS using the 660W chip as well as a replication study to evaluate the associations between genetic variants and the risk of AERD in the Korean population.

Materials and methods

Ethics statement

A written informed consent was obtained from all subjects to participate in the study. The protocols used in this study were approved by the Soonchunhyang Bucheon Hospital's ethics committee. 1,138 DNA were obtained from the biobank at the Genome Research Center for Allergy and Respiratory Diseases (Soonchunhyang Bucheon Hospital), South Korea.

Subjects

Study subjects were recruited from the Asthma Genome Research Center; all subjects were ethnic Koreans and gave their informed consent to participate in the study. A total of 685 asthmatic patients without AERD and 117 subjects with AERD were used for the GWAS of the first stage, and 996 asthmatics without AERD and 142 subjects with AERD (including samples of GWAS) were used for a follow-up study (Table 1). All patients were diagnosed by physicians and met the criteria for asthma according to the Global Initiative for Asthma (GINA) guidelines (1995). All patients had a history of dyspnea and wheezing in the previous 12 months, plus one of the following: (1) >15 % increase in forced expiratory volume in 1 s (FEV₁) or >12 % increase plus 200 mL following inhalation of a short-acting bronchodilator; (2) <10 mg/mL PC₂₀ methacholine; and (3) >20 % increase in FEV₁ following 2 weeks of treatment with inhaled or systemic corticosteroids. Total IgE was measured by the CAP system (Pharmacia Diagnostics, Uppsala, Sweden). Twenty-four commonly inhaled allergens were used for a skin-prick test. Atopy was defined as a wheal reaction with a diameter of 3 mm or greater than the reaction to histamine.

Questions related to five specific elements of aspirin hypersensitivity (dyspnea, wheezing, nasal blockage, skin eruption, and loss of consciousness after aspirin ingestion) were incorporated in the questionnaires. Oral aspirin challenge (OAC) was performed to all study subjects. The asthmatic patients had experienced no exacerbation of asthma or respiratory tract infection in the 6 weeks preceding oral aspirin challenge (OAC). OAC was performed

Table 1 Clinical profiles of GWAS and replication study subjects

Description	First subjects for GWAS of AERD		Follow-up study of AERD	
	AERD	ATA	AERD	ATA
Number of subjects	117	685	142	996
Age, mean (range)	41.35 (17–72.4)	46.21 (10.8–77.4)	42.44 (17–72)	44.80 (11–77)
Onset age, mean (range)	34.33 (1–68)	39.71 (1–75)	35.79 (1–71)	38.77 (1–76)
Duration, mean (range)	6.97 (1–35)	6.57 (1–60)	6.40 (1–35)	6.08 (1–60)
Sex (male/female)	47/70	255/430	54/88	380/616
Current smoker/ex smoker (%)	15.38/5.98	14.60/17.81	15.49/4.93	13.76/16.57
Positive rate of skin test (%)	56.41	53.14	52.82	52.21
BMI (kg/m ²)	23.74 ± 3.67	23.46 ± 3.45	23.63 ± 3.53	24.38 ± 3.58
% decline of FEV1 by aspirin provocation	32.94 ± 12.12	3.56 ± 5.10	30.59 ± 15.37	3.81 ± 4.84
Blood eosinophil (%)	6.78 ± 6.25	5.74 ± 5.31	6.79 ± 6.05	5.59 ± 5.21
FVC %, predicted	83.52 ± 19.46	85.03 ± 17.46	85.01 ± 19.15	83.07 ± 17.88
FEV1 %, predicted	80.22 ± 20.04	83.94 ± 18.82	81.47 ± 20.12	83.38 ± 19.76
PC20, methacholine (mg/mL)	3.44 ± 6.55	5.60 ± 8.36	4.26 ± 7.43	6.50 ± 8.60
Total IgE (IU/mL)	431.30 ± 684.42	348.18 ± 549.38	408.78 ± 644.51	395.34 ± 635.53

The samples for follow-up study include the samples of GWAS

AERD aspirin-exacerbated respiratory disease, *ATA* aspirin-tolerant asthma

with increasing doses of aspirin using the methods previously described (Chang et al. 2011; Nizankowska-Mogilnicka et al. 2007). Patients having a history of aspirin hypersensitivity were given a dose of 30 mg and those with no history were started on 100 mg of aspirin orally. Symptoms, external signs (urticaria, angioedema, and rhinorrhea), blood pressure, and FEV1 were documented every 30 min for a period of 2 h. In the absence of any symptoms or signs suggestive of an adverse reaction, 100 mg of aspirin were administered and the same measurements were repeated every hour, with doses of 450 mg given until the patient developed a reaction. The test was deemed negative if no reaction occurred within 4 h after the final dose. Aspirin-induced bronchospasms were calculated as the pre-challenge FEV1 minus the post-challenge FEV1 divided by the pre-challenge FEV1. OAC reactions were categorized into two groups as follows: (1) a 15 % or greater decrease in FEV1 or naso-ocular reactions (AERD); and (2) a decrease of less than 15 % in FEV1 without naso-ocular or cutaneous reactions [aspirin-tolerant asthma (ATA)]. The protocols were approved by the Ethics Committee of the Soonchunhyang University Hospital.

Genome-wide SNP genotyping

Approximately 200 ng of genomic DNA was used to genotype each sample on the Illumina Human660W BeadChip® (Illumina, Inc., San Diego, CA). Samples were processed according to the Illumina Infinium assay manual. Each sample was whole-genome amplified, fragmented,

precipitated, and resuspended in an appropriate hybridization buffer. Denatured samples were hybridized on a prepared Human660W BeadChip® for a minimum of 16 h at 48 °C. Following hybridization, the BeadChips were processed for the single-base extension reaction, stained, and imaged on an Illumina Bead Array Reader. Normalized bead intensity data obtained for each sample were loaded into the GenomeStudio® software (Illumina, Inc.), which converted fluorescent intensities into SNP genotypes. SNP clusters for genotype calling were examined for all SNPs using the GenomeStudio® software. For quality control, SNPs that met the following criteria were retained: call rate ≥0.98, minor allele frequency ≥0.05 except for the SNPs of the X chromosome. The overall call rate for all SNPs was 99.89 %.

Fine-mapping study

A total of 14 genes (Supplementary Table 1), which included the SNPs showing significant association signals, were selected. SNPs on these genes were selected using the database of Asian populations from the International HapMap Project database (<http://hapmap.ncbi.nlm.nih.gov/>) and the NCBI database (<http://www.ncbi.nlm.nih.gov>). SNP selection was based on the following scheme. At first, candidate SNPs were extracted in the intragenic region including 2 kb of the 5' region of each gene using Asian data of International HapMap database, and then LD structures of each gene were analyzed using SNPs with over 5 % of minor allele frequencies. Among SNPs in almost absolute LD ($|D'| = 1$

and $r^2 > 0.95$), one representative SNP was selected. A total of 702 SNPs were selected from the sequential processing and genotyped using the GoldenGate assay with the VeraCode microbead (Illumina, Inc.) (Lin et al. 2009). This was followed by a scan using the BeadXpress[®] system (Illumina, Inc.).

Statistics

For association analysis, genotype distributions between asthmatics with and without AERD were compared using logistic regression analyses adjusted for age, sex, atopic status, smoking status, and BMI as covariates using the HelixTree[®] software (Golden Helix Inc., Bozeman, MT, USA). Regression models were used for an association analysis of the percent decrease of FEV1 after an aspirin challenge. Haploview v4.2 software downloaded from the Broad Institute (<http://www.broadinstitute.org/mpg/haploview>) was used to determine the LD of the candidate genes (Barrett et al. 2005). Haplotypes were first estimated using the PHASE software (Stephens et al. 2001) and then computed by logistic analyses using the HelixTree[®] software.

Results

Genome-wide associations

A total of 430,486 SNPs passed our quality control and were used for association analysis with the risk of AERD in 117 subjects with AERD and 685 ATA subjects. The results of the genome-wide association analyses of all SNPs with the risk of AERD are represented in a Manhattan plot (Fig. 1). *rs2281389* ($p = 5.6 \times 10^{-6}$; OR = 2.41; Table 2) on the intergenic area adjacent to the 3' region of *HLA-DPB1* was the most strongly associated SNP, although it failed to meet the statistical significance (1.17×10^{-7}) when adjusted by a Bonferroni correction (Table 2). The 49 top-ranked SNPs associated with the risk of AERD are listed in Table 2. In the association analysis with the percent decline of FEV1 after an aspirin challenge, all 49 SNPs showed significant associations with the percent decline of FEV1 after an aspirin challenge (Table 2); subsequently, a follow-up study selected 14 genes based on two kinds of association analyses (Supplementary Table 1, Table 2).

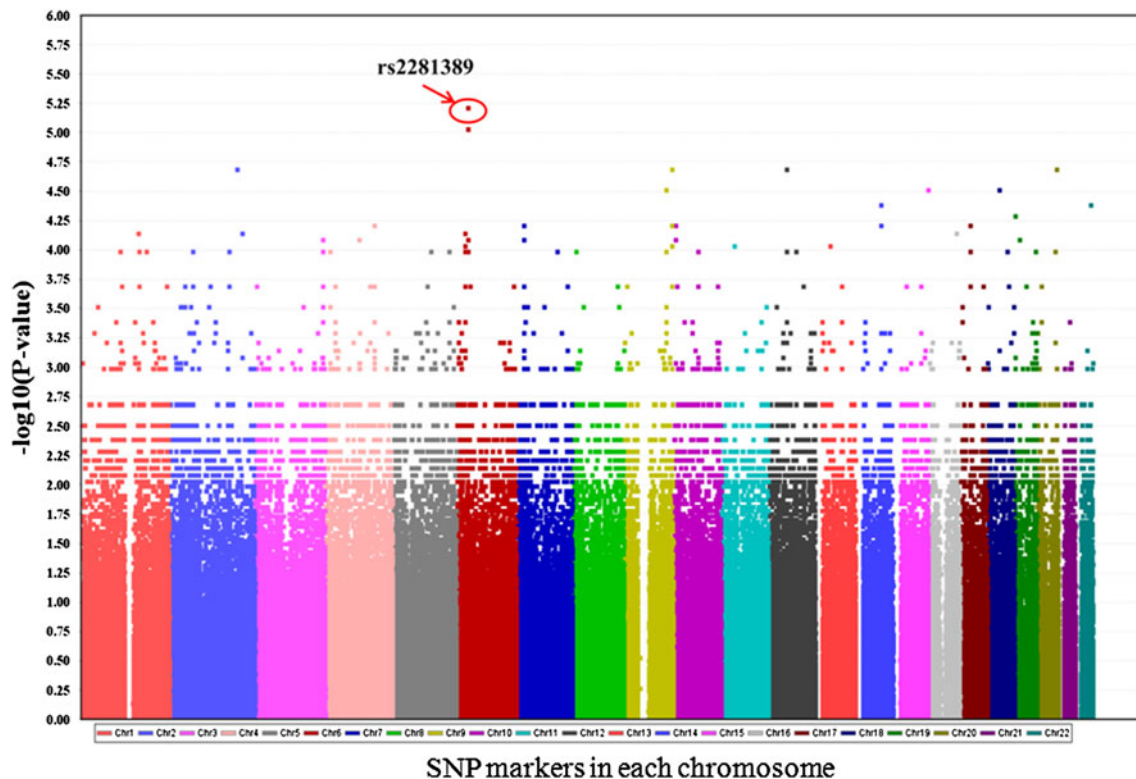


Fig. 1 p values of GWAS. The Manhattan plot shows p values for AERD versus ATA using the logistic regression analysis. X-axis represents the SNP markers in each chromosome. A total of 430,487

SNPs are presented. The highest p value ($p = 5.6 \times 10^{-6}$; OR = 2.41) was observed in *rs2281389* on the intergenic area adjacent to the 3' region of *HLA-DPB1* on 6p21.3

Table 2 49 top SNPs-associated loci on the GWAS with AERD and their % decline of FEV1 after aspirin challenge

Loci	Allele	Gene	Chromosome	Location	Amino acid change	AERD versus ATA		% decline of FEV1 after aspirin challenge						
						AERD (N = 117)	ATA (N = 685)	OR (95 % CI)	p of logistic model	CC [N (mean)]	CR [N (mean)]	RR [N (mean)]	p of regression model	P _{corr}
rs2281389	T>C	(HLA-DPB1)	6p21.3	3'		0.179	0.082	2.41 (1.63–3.57)	5.6E–06	654 (7.05)	137 (10.95)	9 (15.22)	1.8E–04	0.0005
rs2064478	G>A	(HLA-DPB1)	6p21.3	3'		0.179	0.084	2.37 (1.61–3.51)	8.8E–06	652 (7.07)	139 (10.80)	9 (15.22)	2.9E–04	0.0008
rs3117230	T>C	(HLA-DPB1)	6p21.3	3'		0.179	0.084	2.37 (1.61–3.51)	8.8E–06	652 (7.07)	139 (10.80)	9 (15.22)	2.9E–04	0.0008
rs1073123	C>T	TSC1	9q34	Coding	M322T	0.154	0.072	2.41 (1.58–3.68)	1.6E–05	671 (7.16)	124 (11.18)	5 (12.20)	4.6E–04	0.0018
rs10901219	A>G	TSC1	9q34	Intron		0.154	0.072	2.41 (1.58–3.68)	1.6E–05	671 (7.16)	124 (11.18)	5 (12.20)	4.6E–04	0.0018
rs10901220	G>A	TSC1	9q34	Intron		0.154	0.072	2.41 (1.58–3.68)	1.6E–05	671 (7.16)	124 (11.18)	5 (12.20)	4.6E–04	0.0018
rs11243929	T>C	TSC1	9q34	Intron		0.154	0.072	2.39 (1.57–3.64)	1.9E–05	670 (7.16)	125 (11.16)	5 (12.20)	4.8E–04	0.0019
rs4761880	C>T		12q13			0.162	0.078	2.41 (1.58–3.67)	1.9E–05	660 (7.22)	136 (10.63)	4 (9.75)	3.7E–03	0.0037
rs16980768	G>A		20q13			0.205	0.352	0.47 (0.34–0.66)	2.2E–05	358 (9.64)	353 (6.61)	88 (5.32)	4.3E–04	0.0004
rs2286896	A>G	NAB1	2q32.3–q33	Intron		0.547	0.390	1.87 (1.41–2.47)	2.2E–05	283 (6.23)	374 (7.77)	143 (11.06)	4.0E–04	0.0004
rs2771994	G>A	C9orf98	9q34.13	Intron		0.368	0.241	1.78 (1.34–2.38)	2.5E–05	447 (6.63)	292 (9.06)	61 (10.52)	1.1E–03	0.0011
rs3825915	G>T	PCSK6	15q26.3	Intron		0.248	0.389	0.52 (0.37–0.71)	2.5E–05	320 (9.82)	371 (6.85)	109 (5.19)	9.5E–05	0.0001
rs930026	G>A		18p12			0.261	0.155	1.99 (1.41–2.79)	2.9E–05	548 (6.77)	232 (9.88)	20 (12.35)	1.2E–04	0.0002
rs930027	G>A		18p12			0.261	0.155	1.99 (1.41–2.79)	2.9E–05	548 (6.77)	232 (9.88)	20 (12.35)	1.2E–04	0.0002
rs13057050	G>A		22q13.31			0.154	0.072	2.41 (1.58–3.67)	3.7E–05	670 (7.15)	124 (11.30)	5 (9.35)	1.1E–03	0.0011
rs12432987	A>C	ZFYVE1	14q24.2	Intron		0.342	0.220	1.85 (1.37–2.52)	4.4E–05	464 (6.21)	291 (9.90)	45 (10.82)	1.6E–05	0.00002
rs10403288	G>A	ATP8B3	19p13.3	Intron		0.222	0.364	0.50 (0.36–0.70)	4.6E–05	348 (9.21)	354 (6.87)	98 (6.26)	7.8E–03	0.0078
rs10904326	C>T		10p15.1			0.316	0.198	1.92 (1.40–2.64)	5.5E–05	490 (7.23)	277 (8.27)	33 (12.72)	2.8E–02	0.084
rs11252674	C>T		10p15.1			0.316	0.198	1.92 (1.40–2.64)	5.5E–05	490 (7.23)	277 (8.27)	33 (12.72)	2.8E–02	0.084
rs10904327	G>A		10p15.1			0.316	0.198	1.92 (1.40–2.64)	5.5E–05	490 (7.23)	277 (8.27)	33 (12.72)	2.8E–02	0.084
rs6821994	C>T		4q31			0.145	0.272	0.44 (0.30–0.66)	5.6E–05	441 (9.29)	311 (6.22)	48 (4.51)	2.3E–04	0.0002
rs1050700	A>G	TSC1	9q34	3'UTR		0.355	0.234	1.75 (1.31–2.35)	5.8E–05	457 (6.63)	285 (9.15)	58 (10.56)	1.0E–03	0.001
rs9639334	A>G	(TMEM196)	7p21.1			0.265	0.400	0.54 (0.39–0.74)	6.0E–05	309 (9.05)	374 (7.47)	117 (5.67)	8.4E–03	0.0084
rs3742829	G>A	ZFYVE1	14q24.2	Intron		0.329	0.210	1.84 (1.36–2.50)	6.1E–05	479 (6.32)	278 (9.89)	43 (10.98)	2.5E–05	0.00003
rs8005215	T>C	RBM25	14q24.3	Intron		0.342	0.223	1.82 (1.34–2.46)	6.1E–05	463 (6.24)	290 (9.88)	47 (10.53)	2.5E–05	0.00003
rs16969807	A>G		17q12			0.145	0.069	2.35 (1.52–3.63)	6.3E–05	675 (7.21)	121 (10.56)	4 (25.78)	3.5E–04	0.0003
rs9923415	A>G		16q23.2			0.132	0.057	2.49 (1.60–3.89)	6.6E–05	696 (7.19)	99 (12.10)	5 (10.40)	6.4E–04	0.0006
rs849530	T>G	NRP2	2q33.3	Intron		0.389	0.264	1.73 (1.30–2.30)	6.9E–05	422 (6.52)	305 (8.98)	73 (10.40)	1.1E–03	0.0011
rs870601	C>T	DCDC2	6p22.1	Intron		0.325	0.215	1.77 (1.30–2.40)	7.2E–05	474 (6.75)	283 (9.17)	43 (10.58)	1.3E–03	0.0013
rs4657015	G>A		1q23.3			0.418	0.295	1.72 (1.29–2.29)	7.2E–05	379 (7.02)	340 (7.80)	80 (11.40)	8.4E–03	0.0084
rs2240299	C>T	ILVBL	19p13.1	Intron		0.226	0.359	0.52 (0.37–0.72)	7.6E–05	348 (9.10)	359 (7.19)	93 (5.40)	3.7E–03	0.0037
rs6977660	T>C	TMEM196	7p21.1	Intron		0.256	0.393	0.53 (0.39–0.73)	8.1E–05	316 (9.15)	372 (7.24)	112 (5.94)	9.3E–03	0.0093
rs10904321	C>T		10p15.1			0.312	0.196	1.90 (1.39–2.62)	8.1E–05	492 (7.27)	276 (8.17)	32 (13.03)	3.5E–02	0.035
rs6809685	A>G	CLDN1	3q28–q29	Intron		0.120	0.052	2.41 (1.52–3.81)	8.2E–05	706 (7.24)	89 (12.35)	5 (8.50)	5.1E–04	0.0005
rs3789224	G>A	DCDC2	6p22.1	Intron		0.269	0.172	1.81 (1.30–2.51)	8.6E–05	529 (6.78)	245 (9.51)	26 (12.86)	1.1E–04	0.0002
rs7129384	C>T		11p12			0.222	0.123	2.05 (1.44–2.91)	8.6E–05	598 (7.01)	186 (10.85)	16 (2.39)	2.7E–02	0.027

Table 2 continued

Loci	Allele	Gene	Chromosome	Location	Amino acid change	AERD versus ATA		% decline of FEV1 after aspirin challenge						<i>P</i> _{corr}
						AERD (<i>N</i> = 117)	ATA (<i>N</i> = 685)	OR (95 % CI)	<i>p</i> of logistic model	CC [<i>N</i> (mean)]	CR [<i>N</i> (mean)]	RR [<i>N</i> (mean)]	<i>p</i> of regression model	
rs12055879	A>C	DCDC2	6p22.1	Intron		0.325	0.215	1.75 (1.29–2.38)	9.2E–05	472 (6.77)	280 (9.30)	44 (10.00)	2.0E–03	0.004
rs7874234	C>T	TSC1	9q34	Intron		0.171	0.091	2.12 (1.42–3.16)	9.2E–05	643 (7.20)	150 (10.24)	7 (11.74)	3.1E–03	0.0031
rs9533399	A>G		13q14.1			0.355	0.237	1.78 (1.32–2.40)	9.3E–05	444 (6.48)	304 (9.30)	52 (10.54)	4.8E–04	0.0004
rs11170121	T>G	(KRT6B)	12q13.13	3′		0.158	0.079	2.27 (1.49–3.44)	1.0E–04	661 (7.24)	134 (10.61)	5 (8.80)	7.0E–03	0.007
rs4571226	G>A	(CLDN1)	3q28-q29	3′		0.141	0.066	2.23 (1.47–3.40)	1.1E–04	685 (7.25)	107 (10.90)	8 (14.55)	1.2E–03	0.0012
rs6691127	C>T		1q23.3			0.423	0.301	1.72 (1.29–2.30)	1.1E–04	368 (6.37)	353 (8.82)	79 (10.03)	1.6E–03	0.0016
rs1402314	G>A		12q14.3			0.509	0.374	1.69 (1.28–2.23)	1.1E–04	303 (6.52)	362 (7.94)	134 (10.43)	2.0E–03	0.002
rs13180419	A>G		5q34			0.222	0.127	1.96 (1.38–2.78)	1.1E–04	593 (7.08)	190 (9.68)	17 (12.44)	3.1E–03	0.0031
rs4409627	T>C		1q23.3			0.444	0.319	1.70 (1.28–2.26)	1.1E–04	354 (6.24)	352 (8.92)	94 (9.58)	1.8E–03	0.0018
rs12619205	A>G	MEIS1	2p14	Intron		0.521	0.385	1.73 (1.31–2.29)	1.1E–04	287 (5.77)	379 (8.24)	134 (10.98)	3.2E–05	0.00003
rs17661177	G>A		17q12			0.150	0.074	2.23 (1.46–3.41)	1.2E–04	668 (7.28)	127 (9.95)	5 (24.62)	1.3E–03	0.0013
rs7852394	C>A		9q33.1			0.128	0.058	2.43 (1.54–3.85)	1.3E–04	693 (7.23)	104 (11.47)	3 (15.63)	6.4E–04	0.0006
rs775821	G>A	GP6 & RDH13	19q13.42	Intron		0.137	0.250	0.45 (0.30–0.68)	1.3E–04	459 (9.17)	308 (6.03)	33 (5.54)	6.5E–04	0.0006

AERD aspirin-exacerbated respiratory disease, ATA aspirin tolerant asthma, OR odd ratio, CI confidence interval

AERD aspirin-exacerbated respiratory disease, ATA aspirin tolerant asthma, OR odd ratio, CI confidence interval

Follow-up fine mapping study

Total 702 SNPs in the 14 genes were genotyped in 142 AERD and 996 ATA subjects. Their clinical characteristics are summarized in Table 1. Three SNPs were failed in genotyping. Among 699 SNPs, *HLA-DPB1* gene polymorphisms were most significantly associated with the risk of AERD. Among *HLA-DPB1* polymorphisms, *rs1042151* (Met105Val) in exon 2 showed the highest susceptibility to AERD ($p = 5.11 \times 10^{-7}$; OR = 2.40; Fig. 2; Supplementary Table 2). Two SNPs among the top ranked in the GWAS (*rs2281389* and *rs3117230* in 3' region of *HLA-DPB1*) were in almost absolute LDs ($|D'| = 1$ and $r^2 = 0.97$) with the *rs1042151* (Met105Val). The association of these two SNPs observed in GWAS analysis was well replicated in the follow-up analysis ($p = 8.85 \times 10^{-7}$ and 1.37×10^{-6} ; OR = 2.35 and 2.31, respectively; Fig. 2; Table 3). In addition, a nonsynonymous SNP (Met322Thr) of *TSC1* in GWAS and follow-up study showed significant association with the risk of AERD ($p = 1.57 \times 10^{-5}$ and 2.06×10^{-5} ; OR = 2.49 and 2.26, respectively; Supplementary Table 3).

The associations between genotype distribution of each SNP and the percent decline of FEV1 after aspirin challenge were also analyzed using the linear regression analyses. *HLA-DPB1 rs1042151* (Met105Val) showed the most significant association in gene dose-dependent manner, e.g. the mean values of percent decline of FEV1 after aspirin challenge were 6.28 % in Met/Met, 10.15 % in Met/Val, and 17.27 % in Val/Val ($p = 2.82 \times 10^{-7}$; Supplementary Table 4). SNPs in other candidate genes showed similar pattern in their associations of the percent decline of FEV1 after aspirin challenge to the analyses of the risk of AERD (Supplementary Table 5).

Discussion

In the present study to identify a new genetic predisposition for the risk of AERD, GWAS with 430,486 SNPs was tried in 802 asthmatics. In fine mapping, 702 SNPs were genotyped in 1,138 subjects. As a result, a nonsynonymous SNP in exon 2 of *HLA-DPB1*, *rs1042151* (Met105Val), showed the highest association with the risk of AERD. The significance remained after a Bonferroni correction.

The *HLA-DPB1* gene has been implicated in AERD. Dekker and colleagues (Dekker et al. 1997) first reported that the DPB1*0301 frequency increased in 118 AERD patients when compared with 114 ATA subjects (19.5 vs. 4.4 %, respectively). The association of DPB1*0301 with AERD was replicated in a Korean population study; 13.8 % in 76 AERD and 4.1 % in 73 ATA ($p = 0.004$) (Choi et al. 2004a). The reason for the high frequency in

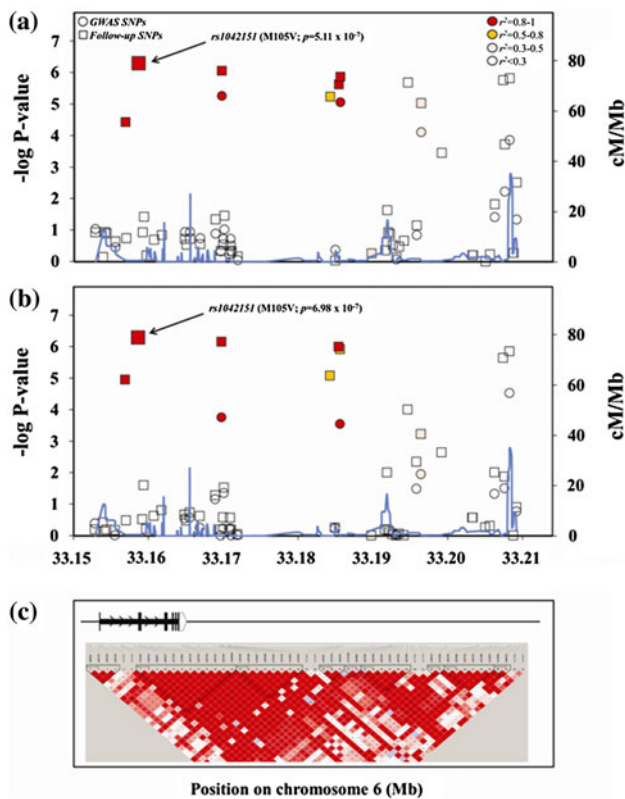


Fig. 2 Regional association plots showing signals in follow-up association study of *HLA-DPB1* and 3' expanded region. SNPs are plotted by position on chromosome against association with risk of AERD ($-\log_{10} p$ value). Circles mean the SNPs of GWAS and squares mean the added SNPs for follow-up study. The figures highlight the most significantly associated SNP after the follow-up study. Estimated recombination rates, averaged across populations from HapMap DB, are plotted in blue to reflect the local LD structure. SNPs surrounding the most significant SNP are color-coded to reflect their LD with this SNP as in the insert. Genes and the plotted SNPs, the direction of transcription, and the LDs among SNPs are noted below the plots. Haplotype blocks are parsed by $|D'|$ values ($|D'| > 0.9$) (color figure online)

the Caucasian population may be due to racial differences and the genotyping methods between the studies. Dekker and colleagues performed HLA-DPB1 typing of 19 recognized alleles (Bodmer et al. 1990) by a restriction enzyme analysis of the exon 2 amplified by PCR (Dekker and Eastaugh 1990). The Korean study (Dekker et al. 1997)

performed a high-resolution genotyping of HLA-DPB1 alleles on amplified gene products using 21 recognized locus specific primers (Van der Zwan and Tilanus 2000) and automatic direct sequencing. In the present study, the minor allele frequency of *rs1042151* A>G is 17.7 % in 142 AERD and 8.3 % in 996 ATA. The data indicates that the minor allele frequency of *rs1042151* A>G in the present study is higher than the frequency of DPB1*0301 in AERD (13.8 %) and in ATA (4.1 %) of the previous Korean population study (Choi et al. 2004a). The differences may originate from the HLA-DPB1 alleles other than HLA-DPB1*0301 having the minor allele of *rs1042151* A>G. Because more than hundred alleles have been described for DPB1 locus (http://hla.alleles.org/data/txt/dpb_prot.txt), frequency of other HLA-DPB1 alleles may be important information in the study of immune responses. There are 40 DPB1 alleles having valine at 76 AA in exon 2. Among them, the DPB1*0301 may be the most frequent allele having *rs1042151* (Met105Val) in exon 2 in Koreans (41) and Caucasians (22). Dekker and collaborators reported a higher frequency of DPB1*0101 allele and lower frequency of 0401 in AERD compared to ATA (22). HLA-DPB1*0101 have valine while HLA-DPB1*0401 have methionine in exon 2; subsequently, the summation of DPB1*0101 and DPB1*0301 may increase the frequency of the minor allele of *rs1042151* A>G. In addition, high-density sequencing analysis of HLA-DPB1 alleles would provide more detailed information on the immunogenetic mechanism of AERD. A Korean study of 152 subjects with AERD reported the frequency of 10 alleles in HLA-DPB1 (Kim et al. 2005a). The minor allele frequencies of HLA-DPB1* *rs1042151* A>G in AERD are 13.8 % (DPB1*0301), 2 % (DPB1*0901), and 2 % (DPB1*1401), respectively. The summation of the alleles frequency is 17.8 %, which is almost similar to the allele frequency of *rs1042151* A>G (17.7 %) in the present study. In addition, they genotyped DPB1*0301 in 188 subjects with aspirin-induced urticaria and found no difference in the frequency of DPB1*0301 compared to that of the normal control (Kim et al. 2005a). The data suggest that aspirin-induced urticaria may have different immunologic backgrounds from AERD.

Table 3 Association analysis of three variants of *HLA-DPB1* with the risk of AERD in GWAS and fine-mapping study

Locus	Alleles	Position (amino acid change)	GWAS				Fine-mapping study			
			AERD (n = 117)	ATA (n = 685)	OR (95 % CI)	p	AERD (n = 141)	ATA (n = 996)	OR (95 % CI)	p
rs1042151	A>G	Exon 2 (M105V)					0.177	0.083	2.40 (1.68–3.42)	5.11E–07
rs2281389	T>C	3'	0.179	0.082	2.40 (1.61–3.58)	5.60E–06	0.177	0.085	2.35 (1.65–3.34)	8.85E–07
rs3117230	T>C	3'	0.179	0.084	2.36 (1.58–3.51)	8.81E–06	0.177	0.086	2.31 (1.62–3.29)	1.37E–06

Bold values indicate statistically significant ($P < 0.00001$)

AERD aspirin-exacerbated respiratory disease, ATA aspirin-tolerant asthma, OR odd ratio, CI confidence interval

In our previous low-density BeadChip GWAS (Kim et al. 2010), we could not find any association of *HLA-DPB1* with AERD. This result is caused by the low SNP coverage of the region that includes the *HLA-DPB1* gene; *rs1042151* was excluded in the contents of the low-density BeadChip. In addition, CEP68 gene polymorphisms were not replicated in the present study. In our previous study, the nonsynonymous *rs7572857* G>A variant of the CEP68 gene showed the most significant association with AERD compared to ATA controls in co-dominant model ($p = 6.0 \times 10^{-5}$). In the present study, the Illumina Human660W contains *rs2302647* and *rs10496123* SNPs on the CEP68 gene instead of *rs7572857* SNP. The two SNPs *rs2302647* and *rs10496123* showed a statistically insignificant association with AERD both in the present and in the previous study. Because the 660 Chip includes only one-thirtieths of the SNP contents of the 100K chip (3,178 SNPs), combination of the two results would provide more additive information on the genetic variants related to human diseases.

Additional in silico analyses were performed to investigate the potential functions of the nonsynonymous *rs1042151* of *HLA-DPB1*. Using the ELM program (<http://elm.eu.org/index.html>), the amino acid change from the methionine to valine of the *rs1042151* was not predicted as a functional linear motif. We applied the eQTL browser (<http://eqtl.uchicago.edu/cgi-bin/gbrowse/eqtl/>) to expect whether *rs1042151* could regulate the expression of protein(s) and/or mRNA(s). Intriguingly, *rs1042151* was found to act as a potential *cis*-regulator for *HLA-DPB1* expression with a high eQTL score of 36.83 (Supplementary Fig. 1). In addition, the SNP function prediction (<http://snpinfo.niehs.nih.gov/snpfunc.htm>) indicates that the *rs1042151* could be located in an exonic splicing enhancer (ESE) region (Supplementary Table 6). The findings suggest that *HLA-DPB1 rs1042151* could be a functional nonsynonymous variant for AERD development.

In conclusion, we demonstrated that SNPs on 3' regions of the *HLA-DPB1* gene were significantly associated with the risk of AERD on a GWAS in a Korean asthmatic cohort. The genetic effects of *HLA-DPB1* polymorphisms were scrutinized for AERD via fine mapping and *rs1042151* (Met105Val) was revealed to be the most important genetic variant for the risk of AERD. The findings confirm previous studies and provide new insight into the genetic factors associated with AERD.

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Conflict of interest The authors declare that they have no conflicts of interest.

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Supplementary Table 1. Candidate SNPs and their regions for follow-up study

SNPID	Chr.	Gene (nearest gene)	Location	Amino acid change	Association of the risk of ARED			Associatic CC (mean)
					ARED (N=117)	ATA (N=685)	<i>p</i>	
rs2281389	6	HLA-DPB1	3'	.	0,179	0,082	6E-06	654(7.05)
rs1073123	9	TSC1 / AK8	coding	M322T	0,154	0,072	0,00002	671(7.16)
rs2286896	2	NAB1	intron	.	0,547	0,39	0,00002	283(6.23)
rs3825915	15	PCSK6	intron	.	0,248	0,389	0,00003	320(9.82)
rs12432987	14	ZFYVE1 / RBM25	intron	.	0,342	0,22	0,00004	464(6.21)
rs10403288	19	ATP8B3 / REXO1	intron	.	0,222	0,364	0,00005	348(9.21)
rs9639334	7	TMEM196	5'	.	0,265	0,4	0,00006	309(9.05)
rs849530	2	NRP2	intron	.	0,389	0,264	0,00007	422(6.52)
rs870601	6	DCDC2	intron	.	0,325	0,215	0,00007	474(6.75)
rs2240299	19	ILVBL	intron	.	0,226	0,359	0,00008	348(9.10)
rs6809685	3	CLDN1	intron	.	0,120	0,052	0,00008	709 (7.35)
rs11170121	12	KRT6B / KRT75	intergenic	.	0,158	0,079	0,0001	664 (7.38)
rs12619205	2	MEIS1	intron	.	0,521	0,385	0,0001	290 (6.11)
rs775821	19	GP6 / RDH13	intron	.	0,137	0,250	0,0001	462 (9.36)

on of the percent decline of FEV1 after aspirin challenge			Selected region for follow-up study	
CR (mean)	RR (mean)	<i>p</i>	Chromosome position	Size
137(10.95)	9(15.22)	0,0002	chr6:33140000..33180000	40kb
124(11.18)	5(12.20)	0,0005	chr9:134580786..134819841	239kb
374(7.77)	143(11.06)	0,0004	chr2:191222093..191265736	44kb
371(6.85)	109(5.19)	0,0001	chr15:99661657..99847710	186kb
291(9.90)	45(10.82)	0,00002	chr14:72500000..72660000	160kb
354(6.87)	98(6.26)	0,008	chr19:17300000..18000000	70kb
374(7.47)	117(5.67)	0,008	chr7:19724000..19821000	97kb
305(8.98)	73(10.40)	0,001	chr2:206254000..206372000	118kb
283(9.17)	43(10.58)	0,001	chr6:24,278,963..24,468,259	182kb
359(7.19)	93(5.40)	0,004	chr19:15085000..15098000	13kb
91 (12.88)	5 (8.50)	0,0002	chr3:191,505,197..191,524,909	19kb
136 (10.92)	5 (8.80)	0,006	chr12:51100000..51135000	35kb
380 (8.28)	135 (11.19)	0,00008	chr2:66,514,036..66,654,394	140kb
310 (6.19)	33 (5.54)	0,0006	chr19:60,215,889..60,274,709	60kb

Supplementary Table 2. Association analysis of polymorphisms in HLA-DPB1 and its 3' region on 6p21.3 with the risk of AERD

Locus	Alleles	Position (Amino acid change)	GWAS				Fine-mapping study		
			AERD (n=117)	ATA (n=685)	OR (95% CI)	p	AERD (n=141)	ATA (n=996)	OR(95% CI)
rs987870	T>C	5'	0,141	0,101	1.42(0.94-2.16)	0,09	0,135	0,104	1.35(0.92-1.97)
rs2071351	G>A	Intron1					0,450	0,441	1.05(0.81-1.35)
rs2071352	T>A	Intron1					0,138	0,107	1.35(0.92-1.97)
rs2071354	T>C	Intron1					0,135	0,104	1.34(0.91-1.96)
rs3135021	G>A	Intron1	0,419	0,456	0.88(0.67-1.17)	0,36	0,404	0,443	0.86(0.66-1.11)
rs1431402	T>A	Intron1					0,209	0,121	1.98(1.42-2.76)
rs1431403	C>T	Intron1					0,436	0,479	0.84(0.65-1.09)
rs1042151	A>G	Exon2 (M105V)					0,177	0,083	2.40(1.68-3.42)
rs928976	T>C	Intron2					0,443	0,497	0.82(0.63-1.06)
rs9378177	A>G	Intron2					0,284	0,342	0.74(0.56-0.98)
rs7772134	G>T	Intron2					0,067	0,060	1.12(0.68-1.86)
rs3128961	G>A	Intron2					0,532	0,487	1.18(0.91-1.52)
rs9277419	A>G	Intron2					0,539	0,488	1.21(0.93-1.56)
rs9277535	A>G	3'UTR	0,538	0,475	1.25(0.94-1.66)	0,12	0,532	0,486	1.18(0.92-1.52)
rs9277539	A>G	3'					0,461	0,425	1.14(0.88-1.47)
rs9277554	C>T	3'	0,538	0,475	1.25(0.94-1.67)	0,12	0,535	0,489	1.18(0.92-1.53)
rs9277565	C>T	3'	0,466	0,411	1.20(0.91-1.60)	0,18	0,465	0,427	1.15(0.89-1.48)
rs10484569	G>A	3'	0,286	0,330	0.78(0.57-1.07)	0,13	0,287	0,342	0.75(0.57-0.99)
rs2281390	C>A	3'	0,111	0,101	1.19(0.76-1.86)	0,48	0,114	0,102	1.16(0.78-1.74)
rs2281389	T>C	3'	0,179	0,082	2.40(1.61-3.58)	5,60E-06	0,177	0,085	2.35(1.65-3.34)
rs3128917	T>G	3'	0,466	0,412	1.20(0.90-1.59)	0,19	0,465	0,427	1.14(0.89-1.47)
rs2281388	C>T	3'	0,278	0,326	0.76(0.56-1.04)	0,10	0,280	0,340	0.74(0.56-0.98)
rs7764491	C>G	3'					0,071	0,061	1.16(0.71-1.90)
rs3117222	G>A	3'	0,466	0,412	1.20(0.90-1.59)	0,19	0,465	0,429	1.14(0.88-1.47)
rs3128918	T>C	3'	0,111	0,101	1.19(0.76-1.86)	0,48	0,113	0,102	1.16(0.78-1.73)
rs3130192	C>T	3'	0,075	0,079	1.04(0.61-1.76)	0,91	0,086	0,082	1.09(0.70-1.70)
rs3128927	C>T	3'					0,252	0,148	2.04(1.49-2.79)
rs3130215	G>A	3'	0,073	0,087	0.80(0.46-1.39)	0,43	0,082	0,082	0.98(0.61-1.57)
rs910320	G>A	3'					0,174	0,085	2.28(1.60-3.25)
rs3117230	T>C	3'	0,179	0,084	2.36(1.58-3.51)	8,81E-06	0,177	0,086	2.31(1.62-3.29)
rs6937061	A>G	3'					0,057	0,048	1.17(0.68-2.02)
rs11751659	A>G	3'					0,096	0,084	1.18(0.77-1.80)
rs9348907	C>A	3'					0,294	0,360	0.73(0.55-0.96)
rs9277628	A>C	3'					0,266	0,316	0.80(0.61-1.06)
rs9277630	C>A	3'					0,270	0,317	0.81(0.61-1.07)
rs9277637	C>T	3'					0,305	0,339	0.87(0.66-1.14)
rs1810472	A>G	3'	0,410	0,414	0.98(0.73-1.30)	0,86	0,394	0,405	0.96(0.74-1.24)
rs9277642	T>C	3'					0,309	0,340	0.88(0.67-1.15)
rs9277656	G>T	3'					0,304	0,343	0.85(0.64-1.11)
rs3129294	T>G	3'					0,316	0,188	1.91(1.45-2.52)
rs3117039	G>A	3'	0,500	0,450	1.24(0.94-1.65)	0,15	0,496	0,439	1.26(0.98-1.61)
rs1883414	C>T	3'	0,278	0,163	1.89(1.37-2.62)	7,86E-05	0,277	0,164	1.89(1.42-2.53)
rs3129286	C>T	3'					0,154	0,086	1.94(1.33-2.81)
rs6913744	A>G	3'					0,433	0,420	1.06(0.83-1.37)
rs6913896	A>T	3'					0,433	0,419	1.06(0.83-1.37)
rs9277756	G>A	3'					0,394	0,396	1.00(0.78-1.29)
rs9277761	G>C	3'					0,319	0,340	0.93(0.72-1.21)
rs3117008	T>C	3'	0,397	0,474	0.73(0.55-0.98)	3,93E-02	0,408	0,487	0.73(0.57-0.94)
rs3129270	G>A	3'					0,089	0,031	3.19(1.92-5.30)
rs3129269	G>T	3'	0,265	0,178	1.57(1.13-2.16)	6,05E-03	0,273	0,174	1.70(1.28-2.25)
rs6901221	A>C	3'	0,128	0,060	2.41(1.51-3.84)	1,41E-04	0,128	0,053	2.63(1.73-3.99)
rs3116994	T>C	3'					0,124	0,109	1.13(0.77-1.65)
rs2294472	C>T	3'	0,231	0,172	1.41(1.00-1.97)	4,68E-02	0,248	0,172	1.55(1.16-2.09)

p
0,12
0,73
0,12
0,13
0,23
3,76E-05
0,18
5,11E-07
0,12
3,84E-02
0,65
0,20
0,15
0,19
0,30
0,19
0,28
4,67E-02
0,46
8,85E-07
0,29
3,54E-02
0,55
0,32
0,47
0,71
5,86E-06
0,93
2,40E-06
1,37E-06
0,56
0,45
2,37E-02
0,12
0,13
0,30
0,75
0,34
0,22
2,09E-06
0,07
9,43E-06
3,58E-04
0,64
0,63
1,00
0,60
1,53E-02
1,76E-06
1,93E-04
1,53E-06
0,53
3,12E-03

Supplementary Table 3. Association analysis of polymorphisms in genes selected from GWAS with the risk of AERD

Gene	Chr.	Locus	Alleles	Coordinate	Position (Amino acid change)	GWAS			
						AERD (n=117)	ATA (n=685)	OR (95% CI)	p
AK8 (C9orf98)		rs306530	G>A	134588424	3'	0,218	0,200	1.11(0.79-1.56)	0,53
		rs306525	A>G	134590141	3'	0,427	0,458	0.91(0.69-1.20)	0,53
		rs396819	G>A	134591175	intron	0,419	0,446	0.92(0.70-1.22)	0,59
		rs10901205	G>A	134592277	intron				
		rs10901206	T>C	134593361	intron	0,299	0,341	0.86(0.63-1.16)	0,32
		rs12550888	C>T	134595260	intron				
		rs386472	A>G	134597934	intron	0,504	0,489	1.04(0.79-1.36)	0,81
		rs574544	C>T	134605130	intron				
		rs4962210	C>T	134606067	intron	0,359	0,376	0.90(0.67-1.20)	0,49
		rs13294558	G>A	134606199	intron				
		rs913705	T>C	134606521	intron	0,504	0,496	1.03(0.78-1.37)	0,83
		rs4962077	C>T	134607931	intron				
		rs13285450	G>A	134608020	intron				
		rs10901207	G>A	134608146	intron	0,423	0,474	0.81(0.61-1.07)	0,14
		rs11243898	G>A	134608281	intron				
		rs11243900	G>A	134614018	intron	0,410	0,361	1.23(0.93-1.63)	0,16
		rs12000803	T>C	134614724	intron	0,175	0,164	1.08(0.75-1.56)	0,67
		rs10901209	A>G	134616217	intron				
		rs954390	G>A	134621877	intron	0,115	0,066	1.88(1.16-3.03)	7,43E-03
		rs12552369	G>A	134622314	intron	0,350	0,371	0.90(0.67-1.21)	0,47
		rs4962078	C>T	134625673	intron	0,115	0,064	1.90(1.17-3.07)	6,26E-03
		rs10901212	A>C	134636842	intron				
		rs932887	T>C	134638726	intron	0,235	0,176	1.43(1.02-2.01)	3,27E-02
		rs7869905	C>G	134641205	intron				
		rs4962214	T>C	134641277	intron	0,115	0,071	1.77(1.10-2.83)	1,48E-02
		rs932886	G>A	134641701	intron				
		rs4962215	C>T	134646067	intron				
		rs2809249	T>G	134648385	intron				
		rs215156	G>A	134653342	intron				
		rs2772008	G>T	134653987	intron	0,120	0,105	1.14(0.74-1.74)	0,53
		rs215189	C>T	134660885	intron	0,376	0,447	0.75(0.56-1.00)	4,23E-02
		rs215188	T>A	134661006	intron				
		rs215187	G>A	134662401	intron	0,491	0,457	1.17(0.88-1.55)	0,28
		rs215185	T>C	134663711	intron	0,389	0,482	0.68(0.52-0.91)	6,98E-03
		rs2519083	G>A	134666011	intron				
		rs215184	G>C	134666101	intron				
		rs215180	C>T	134666693	intron				
		rs215163	C>T	134670397	intron	0,393	0,488	0.68(0.52-0.91)	7,10E-03
		rs451714	G>T	134674316	intron	0,393	0,488	0.68(0.52-0.91)	7,10E-03
		rs438369	C>T	134680115	intron				
		rs2809253	T>G	134682604	intron	0,248	0,180	1.55(1.12-2.15)	8,24E-03
		rs2771991	T>C	134701753	intron	0,397	0,498	0.67(0.51-0.89)	4,58E-03
		rs4962220	G>A	134702857	intron	0,235	0,260	0.85(0.61-1.18)	0,34
		rs17149822	A>G	134709579	intron	0,120	0,061	2.08(1.31-3.29)	1,27E-03
		rs1609597	C>T	134711248	intron	0,120	0,061	2.08(1.31-3.29)	1,27E-03
		rs2771997	T>G	134712473	intron	0,248	0,180	1.55(1.12-2.15)	7,94E-03
		rs214634	C>A	134713995	intron				
		rs2771994	G>A	134714722	intron	0,368	0,241	1.87(1.39-2.52)	2,48E-05
		rs2254289	G>A	134717230	intron	0,248	0,180	1.55(1.12-2.15)	7,94E-03
		rs10491535	A>G	134726909	intron	0,120	0,062	2.06(1.30-3.26)	1,48E-03
		rs2526004	G>A	134728634	intron	0,235	0,261	0.84(0.61-1.18)	0,32
C9orf9	9	rs10901218	C>T	134741680	intron	0,397	0,496	0.68(0.51-0.90)	5,25E-03
		rs2519760	G>A	134748242	intron	0,363	0,327	1.14(0.86-1.52)	0,34
		rs2231406	G>A	134752742	coding				
TSC1	9	rs2073869	C>T	134753637	coding				
		rs1050700	A>G	134757764	3'UTR	0,355	0,234	1.82(1.35-2.45)	5,82E-05
		rs2809244	C>A	134760168	3'UTR	0,410	0,396	1.07(0.81-1.41)	0,65
		rs11243929	T>C	134763985	intron	0,154	0,072	2.46(1.60-3.79)	1,93E-05
		rs2250057	T>G	134765024	intron	0,436	0,450	0.95(0.72-1.26)	0,74
		rs7020438	C>A	134766162	intron				
		rs10901219	C>T	134768648	intron	0,154	0,072	2.49(1.62-3.83)	1,57E-05
		rs12345576	T>C	134769351	intron				
		rs10901220	G>A	134771384	intron	0,154	0,072	2.49(1.62-3.83)	1,57E-05
		rs1073123	A>G	134776725	coding (M322T)	0,154	0,072	2.49(1.62-3.83)	1,57E-05
		rs3761840	A>G	134794556	intron	0,415	0,485	0.75(0.57-1.00)	4,78E-02
		rs10116061	C>T	134798682	intron				
		rs7874234	C>T	134802822	intron	0,171	0,091	2.19(1.46-3.28)	9,23E-05

NAB1	2	rs4419933	C>T	134805090	intron				
		rs10793948	G>C	134813798	5'				
		rs1860849	C>G	191227105	intron				
		rs929566	G>C	191229686	intron				
		rs1989344	C>T	191236153	intron	0,073	0,078	0.97(0.56-1.67)	0,89
		rs958770	C>T	191236407	intron	0,150	0,208	0.68(0.47-0.99)	4,35E-02
		rs1978273	T>C	191240284	intron				
		rs12612904	A>G	191243092	intron				
		rs2286896	A>G	191243821	intron	0,547	0,390	1.80(1.36-2.38)	2,21E-05
		rs12611764	T>C	191245388	intron				
		rs10931468	C>A	191246807	intron	0,457	0,363	1.45(1.09-1.93)	9,94E-03
		rs2356126	G>A	191250759	intron				
		rs3771317	A>G	191252207	intron				
		rs2192008	T>C	191253392	intron				
		rs10185029	T>C	191256472	intron				
PCSK6	15	rs17465200	C>T	191257881	intron				
		rs6716985	G>A	191260643	intron				
		rs4853516	G>A	191262176	intron	0,214	0,282	0.70(0.50-0.98)	3,76E-02
		rs1804116	C>T	99661795	3'				
		rs2073595	G>A	99662447	3'	0,107	0,099	1.06(0.67-1.67)	0,81
		rs4965825	T>C	99668442	intron	0,197	0,188	1.02(0.72-1.45)	0,91
		rs2073594	T>C	99670187	intron				
		rs3784515	C>A	99672421	intron	0,188	0,189	0.96(0.67-1.38)	0,83
		rs7168817	T>C	99674207	intron	0,107	0,108	1.01(0.63-1.60)	0,99
		rs12902381	A>G	99674306	intron				
		rs7169313	C>T	99675070	intron	0,124	0,122	1.01(0.65-1.56)	0,98
		rs3825921	G>A	99679686	intron	0,299	0,331	0.88(0.65-1.19)	0,41
		rs2277594	G>A	99680410	intron				
		rs1871975	T>C	99680493	intron				
		rs9806256	T>C	99681096	intron	0,158	0,199	0.77(0.53-1.12)	0,17
		rs4965830	A>T	99681512	intron				
		rs2277593	C>T	99682520	intron	0,235	0,231	0.99(0.70-1.40)	0,98
		rs7182874	C>T	99682995	intron				
		rs1471656	T>C	99685010	intron	0,449	0,486	0.87(0.66-1.15)	0,35
		rs12594500	C>T	99685405	intron				
		rs752028	C>T	99686708	intron	0,158	0,197	0.78(0.53-1.13)	0,19
		rs882422	A>G	99686778	intron				
		rs2073592	C>T	99689829	intron	0,308	0,320	0.94(0.69-1.28)	0,69
		rs12916087	A>G	99692286	intron				
		rs11855415	T>A	99692646	intron				
		rs2086678	T>C	99693939	intron	0,363	0,395	0.85(0.63-1.15)	0,30
		rs1976033	T>C	99694714	intron	0,393	0,463	0.73(0.54-0.98)	3,67E-02
		rs7162072	A>C	99698484	intron				
		rs6598451	A>G	99699903	intron				
		rs11854332	C>T	99700024	intron	0,021	0,065	0.31(0.13-0.79)	1,03E-02
		rs11852754	A>T	99700950	intron				
		rs7175368	A>G	99704278	intron	0,128	0,152	0.82(0.55-1.23)	0,36
		rs12914198	A>G	99704376	intron	0,274	0,262	1.09(0.80-1.50)	0,59
		rs2949	T>C	99705290	intron	0,299	0,354	0.77(0.57-1.06)	0,11
		rs8038528	A>G	99706116	intron	0,175	0,202	0.84(0.58-1.22)	0,35
		rs11630183	A>G	99707078	intron	0,338	0,328	1.03(0.76-1.38)	0,87
		rs10152458	T>G	99708334	intron	0,385	0,407	0.89(0.66-1.20)	0,46
		rs10152471	A>G	99708436	intron				
		rs11247283	C>T	99711161	intron				
		rs12591632	T>G	99711494	intron				
		rs4965831	C>T	99712558	intron	0,432	0,458	0.88(0.66-1.17)	0,39
		rs12593069	C>T	99713394	intron	0,162	0,129	1.26(0.86-1.84)	0,23
		rs8031210	C>A	99717726	intron				
		rs1077015	C>A	99718796	intron	0,303	0,309	0.96(0.70-1.31)	0,83
		rs1078988	G>A	99720223	intron	0,436	0,470	0.87(0.65-1.16)	0,34
		rs7167668	A>G	99720676	intron	0,376	0,320	1.31(0.97-1.77)	0,08
		rs963172	C>A	99720860	intron				
		rs4965833	A>G	99722607	intron	0,299	0,360	0.77(0.57-1.05)	0,09
		rs3784509	T>C	99724869	intron				
		rs3784507	T>C	99725117	intron	0,145	0,136	1.12(0.74-1.70)	0,62
		rs2955965	A>G	99727305	intron	0,470	0,460	1.03(0.78-1.35)	0,83
		rs20543	T>C	99728073	coding (L571L)				
		rs2073590	T>C	99728323	intron				
		rs2073589	A>G	99728405	intron				
		rs6598456	T>C	99729071	intron	0,444	0,415	1.16(0.87-1.55)	0,32
		rs4965836	G>C	99731727	intron				

rs739319	G>C	99732600	intron					
rs730557	G>C	99733151	intron					
rs8036466	C>T	99734170	intron					
rs8035763	G>C	99734412	intron					
rs2934996	T>C	99734832	intron					
rs3021420	A>G	99735187	intron					
rs7183455	C>G	99735590	intron					
rs3825915	G>T	99736820	intron	0,248	0,389	0.51(0.37-0.70)	2,50E-05	
rs3784493	G>A	99737023	intron					
rs3784492	C>G	99737161	intron					
rs3784491	A>G	99737809	intron	0,329	0,261	1.36(1.01-1.82)	4,56E-02	
rs3825914	C>G	99739287	intron					
rs2277590	A>T	99740119	intron					
rs10152309	C>T	99740808	intron	0,150	0,183	0.82(0.56-1.20)	0,31	
rs1135911	G>A	99742069	coding (V56V)	0,145	0,155	0.93(0.63-1.39)	0,75	
rs2277589	G>A	99742361	intron	0,158	0,186	0.86(0.59-1.25)	0,43	
rs10152164	T>C	99743186	intron	0,333	0,321	1.04(0.77-1.40)	0,77	
rs6598459	G>A	99744173	intron					
rs8042699	G>A	99744596	intron	0,043	0,080	0.52(0.27-1.01)	4,59E-02	
rs3784485	G>A	99745400	intron	0,470	0,453	1.06(0.80-1.42)	0,68	
rs6598460	C>G	99747348	intron					
rs6598464	G>A	99747759	intron					
rs6598465	G>A	99747837	intron	0,312	0,323	0.95(0.71-1.28)	0,74	
rs903556	A>G	99748130	intron					
rs1542807	T>G	99748248	intron					
rs1542808	T>C	99748505	intron	0,444	0,410	1.16(0.87-1.54)	0,31	
rs3784484	C>T	99749375	intron	0,201	0,180	1.15(0.81-1.63)	0,44	
rs3784481	C>T	99749687	intron	0,389	0,465	0.72(0.54-0.97)	2,90E-02	
rs4965381	A>G	99749985	intron	0,479	0,479	1.00(0.75-1.33)	0,97	
rs12903394	G>C	99750601	intron					
rs4965843	A>G	99750749	intron	0,432	0,381	1.25(0.93-1.68)	0,14	
rs2277586	T>C	99751389	intron					
rs7173569	G>A	99751548	intron					
rs10400809	C>T	99751809	intron					
rs1039037	A>G	99753680	intron					
rs903564	G>A	99753911	intron					
rs3784470	G>A	99754243	intron					
rs1982906	G>A	99757205	intron	0,466	0,448	1.05(0.78-1.39)	0,71	
rs1874274	C>T	99757441	intron	0,333	0,338	0.98(0.73-1.32)	0,84	
rs3784463	T>C	99762482	intron	0,504	0,499	1.04(0.78-1.37)	0,82	
rs3825902	G>C	99764587	intron					
rs8043118	A>C	99765470	intron					
rs12437510	G>A	99765735	intron	0,427	0,424	1.01(0.76-1.34)	0,92	
rs4965847	C>T	99765888	intron	0,237	0,239	1.00(0.71-1.40)	0,96	
rs3825901	G>A	99766691	intron	0,269	0,278	0.99(0.71-1.36)	0,97	
rs12901252	A>C	99767450	intron					
rs1532364	G>A	99768367	intron	0,197	0,187	1.05(0.73-1.51)	0,82	
rs1000914	A>G	99768456	intron	0,197	0,187	1.05(0.73-1.51)	0,82	
rs1108993	A>G	99768718	intron	0,197	0,188	1.04(0.73-1.50)	0,85	
rs11633098	A>C	99769346	intron	0,197	0,187	1.05(0.73-1.51)	0,82	
rs12916267	G>A	99770553	intron	0,197	0,188	1.05(0.73-1.50)	0,83	
rs4965853	C>T	99772477	intron	0,427	0,412	1.04(0.78-1.39)	0,74	
rs10152229	T>G	99780180	intron	0,329	0,334	0.96(0.71-1.29)	0,74	
rs1495271	C>T	99780246	intron	0,380	0,399	0.96(0.72-1.27)	0,73	
rs7168655	G>A	99782444	intron	0,137	0,148	0.90(0.60-1.34)	0,60	
rs7169026	G>A	99782644	intron	0,209	0,189	1.14(0.80-1.63)	0,48	
rs1006273	A>T	99782862	intron					
rs4965384	C>A	99785324	intron	0,350	0,366	0.94(0.70-1.25)	0,65	
rs2643350	A>G	99786575	intron	0,115	0,136	0.78(0.50-1.21)	0,25	
rs2643353	T>C	99787272	intron					
rs3825896	C>A	99787846	intron	0,274	0,246	1.14(0.83-1.55)	0,41	
rs2643356	T>C	99788911	intron	0,457	0,443	1.06(0.80-1.41)	0,65	
rs2643358	G>A	99789558	intron	0,137	0,158	0.87(0.58-1.29)	0,46	
rs8024621	A>G	99790454	intron					
rs7170232	C>T	99791016	intron	0,303	0,282	1.14(0.84-1.55)	0,42	
rs2412014	A>G	99791921	intron	0,329	0,319	1.07(0.79-1.46)	0,68	
rs2412013	A>G	99792040	intron					
rs11638524	G>C	99792419	intron					
rs10438489	C>A	99794134	intron	0,137	0,156	0.87(0.58-1.33)	0,52	
rs1466744	C>T	99794981	intron	0,295	0,338	0.78(0.58-1.06)	0,12	
rs11638957	T>G	99795312	intron	0,323	0,301	1.13(0.83-1.53)	0,45	

ZFYVE1	14	rs999102	T>C	99796636	intron				
		rs1466745	C>T	99796713	intron	0,470	0,480	0.92(0.70-1.22)	0,58
		rs6598472	G>C	99797673	intron				
		rs6598473	G>A	99798126	intron	0,346	0,372	0.86(0.64-1.15)	0,31
		rs12591689	C>T	99798898	intron				
		rs7176003	G>A	99800850	intron	0,415	0,393	1.14(0.85-1.53)	0,37
		rs11855154	C>T	99801559	intron	0,171	0,193	0.90(0.61-1.32)	0,57
		rs6598474	A>G	99801766	intron				
		rs6422008	C>T	99801928	intron				
		rs12101979	A>G	99803337	intron				
		rs7402924	G>A	99804329	intron	0,274	0,245	1.18(0.85-1.62)	0,33
		rs4965870	G>A	99807989	intron	0,385	0,432	0.80(0.60-1.07)	0,14
		rs12594107	G>A	99808104	intron				
		rs7172696	A>G	99808834	intron	0,470	0,407	1.33(0.99-1.78)	0,05
		rs7178458	T>C	99809296	intron				
		rs11639051	C>A	99810521	intron				
		rs7167996	T>C	99810927	intron				
		rs1552948	C>T	99811512	intron	0,282	0,252	1.18(0.86-1.61)	0,32
		rs4965385	A>G	99813557	intron				
		rs2047216	G>A	99813902	intron				
		rs4547317	A>T	99814092	intron				
		rs4246336	A>G	99815109	intron	0,303	0,285	1.11(0.81-1.52)	0,51
		rs903552	C>T	99815514	intron				
		rs12719737	G>C	99816649	intron				
		rs4965873	T>C	99821546	intron				
		rs8041582	A>G	99823374	intron	0,483	0,446	1.15(0.87-1.53)	0,30
		rs1587107	C>T	99824008	intron	0,483	0,446	1.16(0.87-1.53)	0,30
		rs6598481	C>T	99826171	intron	0,197	0,242	0.77(0.54-1.10)	0,14
		rs9806393	A>G	99826358	intron				
		rs4965877	G>A	99826664	intron	0,308	0,294	1.08(0.79-1.47)	0,65
		rs11853956	G>T	99830470	intron	0,175	0,220	0.76(0.52-1.11)	0,14
		rs765825	A>G	99831870	intron	0,462	0,492	0.90(0.68-1.20)	0,46
		rs12900435	C>A	99832222	intron	0,043	0,055	0.75(0.38-1.50)	0,41
		rs6598483	T>C	99832313	intron	0,401	0,401	0.99(0.77-1.28)	0,92
		rs924014	T>G	99834904	intron				
		rs11247297	G>T	99835575	intron				
		rs7174882	T>G	99836368	intron	0,128	0,113	1.17(0.76-1.80)	0,47
		rs7177024	C>T	99836753	intron				
		rs7166284	C>T	99838216	intron				
		rs7165319	G>C	99838398	intron				
		rs7166898	C>T	99838571	intron	0,368	0,360	1.03(0.77-1.37)	0,89
		rs6598484	G>A	99840279	intron	0,466	0,460	1.04(0.78-1.38)	0,77
		rs4965881	C>T	99841659	intron	0,239	0,256	0.92(0.67-1.27)	0,60
		rs11247300	G>A	99842741	intron	0,504	0,486	1.09(0.82-1.44)	0,54
		rs7166089	T>C	99845991	intron				
		rs12437484	C>G	99846206	intron				
		rs2012620	C>T	72504904	3'				
		rs2806028	C>G	72506558	3'UTR				
		rs12436416	C>T	72509112	intron				
		rs12931	G>A	72510617	coding (T675T)	0,389	0,324	1.37(1.01-1.86)	4,22E-02
		rs2286836	C>T	72511945	intron	0,218	0,137	1.74(1.22-2.48)	2,11E-03
		rs12887074	A>G	72517593	intron				
		rs4899452	C>G	72517677	intron				
		rs9671668	A>G	72519095	intron				
		rs1106301	G>A	72523335	intron				
		rs2535920	T>C	72529471	intron				
		rs1007934	G>A	72533232	intron	0,124	0,171	0.70(0.46-1.07)	0,09
		rs11625299	T>C	72533503	intron				
		rs997667	A>G	72534756	coding (F168F)				
		rs10142131	G>A	72537427	intron	0,372	0,307	1.36(1.00-1.84)	5,02E-02
		rs12880210	A>C	72537512	intron	0,141	0,160	0.86(0.57-1.30)	0,49
		rs7149207	G>A	72538638	intron	0,082	0,051	1.70(0.98-2.94)	4,94E-02
		rs2806057	G>A	72544366	intron				
		rs955329	A>G	72545011	intron	0,231	0,147	1.73(1.22-2.45)	1,97E-03
		rs17123359	C>T	72545229	intron				
		rs4903092	A>G	72549478	intron	0,393	0,325	1.40(1.03-1.89)	3,19E-02
		rs2333021	A>G	72554137	intron				
		rs3742829	G>A	72559021	intron	0,329	0,210	1.86(1.36-2.54)	6,07E-05
		rs3742828	G>T	72561060	UTR	0,256	0,162	1.82(1.30-2.55)	4,81E-04
		rs12432987	A>C	72562948	intron	0,342	0,220	1.88(1.38-2.57)	4,36E-05
RBM25	14	rs2333022	C>G	72569867	5'				

ATP8B3	19	rs12433952	C>A	72594294	5'	0,410	0,453	0.81(0.60-1.08)	0,15
		rs2806049	C>T	72596366	intron				
		rs8005215	T>C	72600431	intron	0,342	0,223	1.85(1.36-2.52)	6,05E-05
		rs17124039	T>C	72616497	intron				
		rs17182104	G>C	72627302	intron				
		rs1990059	T>C	72639228	intron	0,222	0,137	1.77(1.24-2.52)	1,37E-03
		rs362412	C>T	72641159	intron	0,098	0,069	1.58(0.95-2.62)	0,07
		rs3025768	A>G	72644999	intron				
		rs1054597	C>T	1733189	3'UTR				
		rs757528	G>A	1733798	3'UTR	0,449	0,501	0.83(0.63-1.10)	0,20
		rs2385387	G>A	1734261	coding (K1186K)				
		rs6510624	C>T	1734794	intron	0,278	0,259	1.07(0.78-1.47)	0,67
		rs3764606	A>G	1735944	coding (Y1141Y)	0,274	0,240	1.19(0.87-1.62)	0,30
		rs12461977	T>G	1739247	intron				
		rs8100003	T>C	1743997	intron	0,308	0,298	1.02(0.75-1.40)	0,90
		rs8100856	T>C	1747166	coding (V571I)	0,440	0,428	1.03(0.77-1.37)	0,88
		rs7253430	G>T	1754582	intron				
		rs45574836	C>T	1757667	coding (A160T)				
		rs17604735	A>G	1758018	intron	0,167	0,125	1.38(0.94-2.03)	0,10
		rs7249302	C>T	1759683	intron	0,171	0,126	1.42(0.97-2.07)	0,07
		rs10403288	G>A	1759863	intron	0,222	0,364	0.51(0.36-0.71)	4,58E-05
		rs9941464	T>C	1760598	intron				
		rs4807143	G>A	1762130	intron	0,282	0,209	1.52(1.09-2.11)	1,20E-02
		rs10421558	A>G	1763521	5'	0,321	0,447	0.61(0.45-0.82)	1,01E-03
REXO1	19	rs11668832	A>G	1763682	5'				
		rs11882337	C>T	1765743	3'				
		rs10415018	A>G	1778565	coding (V408A)				
		rs3746037	A>C	1779948	intron	0,346	0,466	0.63(0.47-0.85)	1,95E-03
		rs732310	C>A	1784338	intron	0,274	0,250	1.10(0.79-1.52)	0,59
		rs10422439	G>A	1788061	intron				
		rs893539	G>A	1794493	intron	0,295	0,214	1.55(1.13-2.14)	6,11E-03
		rs1609760	G>T	1798407	intron				
		rs1609761	A>C	1798698	intron	0,342	0,461	0.63(0.47-0.85)	2,18E-03
		rs7802120	G>A	19724887	3'	0,355	0,426	0.74(0.55-0.99)	3,67E-02
(TMEM196)	7	rs2285924	A>T	19726448	3'UTR				
		rs17141851	G>A	19729844	intron	0,380	0,447	0.76(0.57-1.02)	0,06
		rs10435066	T>C	19729952	intron				
		rs6946520	A>G	19732961	intron				
		rs10240229	G>A	19733687	intron	0,175	0,284	0.53(0.37-0.76)	4,92E-04
		rs6951739	A>T	19734069	intron				
		rs9886152	C>T	19735265	intron	0,231	0,349	0.54(0.39-0.76)	3,09E-04
		rs17141862	T>C	19737281	intron	0,406	0,491	0.71(0.54-0.94)	1,63E-02
		rs4721822	C>T	19738218	intron				
		rs2214552	C>T	19741745	intron				
		rs10263780	A>G	19744611	intron	0,325	0,422	0.65(0.49-0.88)	4,78E-03
		rs10950752	A>G	19748056	intron				
		rs12530799	G>A	19749318	intron				
		rs1468287	T>A	19750735	intron				
		rs2390156	A>T	19752663	intron				
		rs10239147	T>C	19753984	intron	0,496	0,398	1.49(1.12-1.97)	5,26E-03
		rs12534026	T>C	19755212	intron				
		rs16872383	A>T	19759795	intron				
		rs4719582	A>G	19765056	intron	0,047	0,093	0.48(0.25-0.90)	1,95E-02
		rs7791038	A>G	19765358	intron				
		rs17141931	T>C	19767541	intron				
		rs10486365	A>G	19767889	intron	0,526	0,423	1.52(1.15-2.02)	3,42E-03
		rs714238	C>T	19770450	intron	0,590	0,469	1.63(1.23-2.17)	6,96E-04
		rs17141945	T>A	19771581	intron				
		rs6977660	T>C	19772005	intron	0,256	0,393	0.53(0.39-0.73)	8,11E-05
		rs13230910	A>G	19772528	intron				
		rs12334267	A>G	19776790	intron	0,565	0,448	1.59(1.20-2.11)	1,19E-03
		rs3922342	A>G	19777482	intron	0,355	0,426	0.73(0.54-0.98)	3,90E-02
		rs12672257	C>T	19779991	5'				
		rs13233821	C>A	19780162	5'				
		rs10254427	T>C	19782765	5'	0,291	0,403	0.61(0.45-0.82)	1,16E-03
		rs10226962	C>T	19785989	5'				
		rs10270204	C>T	19786069	5'				
		rs10240816	C>A	19786145	5'				
		rs4721826	C>T	19790329	5'	0,286	0,401	0.60(0.44-0.81)	8,39E-04
		rs10239332	G>A	19790990	5'				
		rs4721827	A>G	19792180	5'				

NRP2	2	rs17142014	T>G	19794624	5'	0,154	0,138	1.14(0.76-1.70)	0,53
		rs17142018	G>A	19798177	5'				
		rs17142027	A>G	19803923	5'				
		rs9639334	A>G	19805335	5'	0,265	0,400	0.53(0.39-0.73)	5,99E-05
		rs9638765	A>G	19807141	5'				
		rs10267417	C>T	19810322	5'	0,496	0,399	1.48(1.12-1.96)	6,50E-03
		rs17142032	C>G	19811801	5'				
		rs10486371	T>C	19814462	5'	0,197	0,145	1.43(1.00-2.06)	4,81E-02
		rs17142041	A>G	19817102	5'				
		rs2097811	G>A	19818564	5'				
		rs10224061	C>G	19819144	5'				
		rs7785317	G>T	19820007	5'				
		rs12666616	A>G	19820666	5'	0,197	0,268	0.66(0.47-0.93)	1,63E-02
		rs3806577	A>G	206254395	5'	0,419	0,465	0.84(0.62-1.12)	0,24
		rs861078	A>G	206260223	intron	0,154	0,088	2.06(1.34-3.16)	7,71E-04
		rs698909	A>G	206262789	intron				
		rs849530	T>G	206264049	intron	0,389	0,264	1.80(1.35-2.41)	6,91E-05
		rs1533509	C>T	206266758	intron				
		rs950219	G>A	206268858	intron				
		rs849558	A>G	206270495	intron				
		rs849556	G>A	206271503	intron	0,081	0,072	1.16(0.69-1.96)	0,56
		rs3771051	G>A	206273745	intron				
		rs849555	T>C	206273987	intron	0,141	0,118	1.23(0.81-1.86)	0,30
		rs849554	C>T	206274668	intron				
		rs849553	C>A	206276655	intron				
		rs9636330	T>C	206276749	intron				
		rs3771048	T>C	206279380	intron				
		rs3771047	G>C	206280779	intron				
		rs863707	T>G	206284428	intron				
		rs3771045	C>T	206285359	intron				
		rs3771044	T>C	206285656	intron	0,226	0,192	1.24(0.89-1.75)	0,21
		rs2110875	C>T	206288070	intron	0,265	0,214	1.33(0.97-1.82)	0,08
		rs849543	C>T	206288397	intron				
		rs3771039	G>A	206292641	intron				
		rs3755243	A>G	206294189	intron				
		rs3755242	C>G	206294283	intron				
		rs3771038	C>T	206294657	intron				
		rs849538	T>C	206296221	intron				
		rs861079	C>T	206297366	intron	0,295	0,234	1.39(1.02-1.88)	3,54E-02
		rs849526	G>A	206300940	coding (Y357Y)				
		rs868196	G>T	206302386	intron				
		rs3771033	G>A	206304055	intron				
		rs849523	T>C	206304181	intron	0,444	0,452	1.03(0.77-1.37)	0,85
		rs849521	C>G	206306114	intron				
		rs849584	G>T	206309961	intron				
		rs849581	G>A	206311010	intron	0,389	0,377	1.03(0.77-1.37)	0,84
		rs849575	A>C	206313425	intron	0,432	0,438	0.96(0.72-1.27)	0,76
		rs3771021	C>T	206318233	intron	0,286	0,302	0.91(0.66-1.24)	0,56
		rs849565	T>C	206318296	intron				
		rs1996412	A>G	206320830	intron	0,440	0,473	0.82(0.62-1.09)	0,19
		rs12472412	G>A	206320959	intron				
		rs13026243	T>G	206322336	intron	0,453	0,497	0.84(0.64-1.10)	0,22
		rs2241155	T>C	206323311	intron	0,466	0,498	0.88(0.67-1.15)	0,36
		rs3771016	A>G	206323784	intron	0,474	0,495	0.92(0.70-1.20)	0,54
		rs849559	G>T	206324158	intron				
		rs3771013	C>G	206328277	intron				
		rs6733650	C>T	206329648	intron				
		rs3755238	C>T	206330233	intron				
		rs10180293	A>G	206330821	intron	0,098	0,102	1.01(0.64-1.61)	0,96
		rs3755237	T>C	206331191	intron				
		rs3771010	G>C	206331839	intron				
		rs7564637	G>A	206335254	intron				
		rs872943	T>C	206335718	intron	0,103	0,109	0.99(0.63-1.57)	0,98
		rs3771004	G>A	206339132	intron	0,295	0,355	0.75(0.55-1.02)	0,08
		rs16837637	G>A	206339499	intron	0,316	0,337	0.88(0.65-1.20)	0,42
		rs3771003	T>G	206342088	intron	0,449	0,475	0.92(0.70-1.21)	0,53
		rs16837641	A>G	206343114	intron	0,410	0,414	1.01(0.77-1.34)	0,95
		rs3755233	C>T	206348076	intron	0,269	0,212	1.32(0.97-1.81)	0,07
		rs2160328	C>T	206350582	intron	0,286	0,313	0.87(0.64-1.18)	0,37
		rs1547477	C>G	206351677	intron				
		rs3771002	C>G	206353019	intron				

DCDC2	6	rs3771000	G>A	206353411	intron	0,132	0,144	0.94(0.62-1.42)	0,76
		rs4675542	G>C	206353492	intron				
		rs3770997	A>G	206357583	intron				
		rs3770996	T>C	206357988	intron	0,440	0,461	0.95(0.72-1.25)	0,69
		rs10932125	C>G	206360545	intron				
		rs3755232	A>G	206361208	intron	0,145	0,153	0.97(0.65-1.45)	0,89
		rs1990708	G>T	206362368	intron	0,274	0,222	1.27(0.94-1.73)	0,12
		rs15994	C>G	206370542	3'UTR				
		rs9393535	G>C	24279358	3'				
		rs6937665	G>A	24280905	3'UTR				
		rs6456594	G>A	24282312	3'UTR				
		rs2996452	G>A	24288345	intron				
		rs2791972	T>G	24293200	intron	0,269	0,212	1.38(1.01-1.90)	4,36E-02
		rs1277190	T>C	24294569	intron				
		rs2799372	C>G	24295012	intron				
		rs793845	A>G	24296970	intron				
		rs2027584	C>A	24299438	intron	0,291	0,328	0.82(0.60-1.11)	0,21
		rs2799373	G>A	24303738	intron	0,293	0,298	0.94(0.69-1.28)	0,69
		rs793850	C>G	24303914	intron				
		rs9467075	G>A	24313215	coding	0,064	0,044	1.45(0.81-2.58)	0,21
		rs12153942	C>G	24316546	intron				
		rs9379648	G>A	24318063	intron				
		rs793843	G>A	24325195	intron				
		rs1770909	G>A	24330431	intron	0,269	0,312	0.79(0.57-1.08)	0,15
		rs4052671	T>C	24331558	intron				
		rs793842	A>G	24332467	intron	0,393	0,468	0.73(0.54-0.97)	2,72E-02
		rs707885	G>A	24332655	intron				
		rs793837	T>G	24338193	intron	0,543	0,480	1.31(0.99-1.73)	0,06
		rs9460980	G>A	24341267	intron	0,406	0,480	0.72(0.54-0.96)	2,60E-02
		rs793834	C>T	24342912	intron	0,321	0,345	0.87(0.64-1.18)	0,37
		rs1087287	G>C	24345268	intron				
		rs9295618	T>C	24356599	intron				
		rs9358760	A>G	24357872	intron				
		rs9295619	T>C	24358490	intron	0,393	0,484	0.68(0.51-0.91)	8,20E-03
		rs870601	C>T	24369039	intron	0,325	0,215	1.88(1.38-2.58)	7,17E-05
		rs6456601	T>C	24374718	intron				
		rs2792682	T>G	24380363	intron	0,056	0,045	1.21(0.66-2.22)	0,54
		rs12055879	A>C	24382096	intron	0,325	0,215	1.86(1.36-2.54)	9,21E-05
		rs807699	T>C	24383362	intron	0,056	0,045	1.21(0.66-2.22)	0,54
		rs3789224	G>A	24388080	intron	0,269	0,172	1.98(1.41-2.77)	8,55E-05
		rs2328208	T>C	24393550	intron	0,274	0,177	1.90(1.37-2.65)	1,39E-04
		rs9379650	C>T	24394931	intron				
		rs17302729	G>A	24396703	intron	0,269	0,174	1.91(1.37-2.67)	1,52E-04
		rs2274305	G>A	24399182	coding (G221S)	0,316	0,213	1.80(1.32-2.46)	2,01E-04
		rs3804326	G>A	24400164	intron				
		rs3846829	C>T	24411174	intron	0,440	0,506	1.29(0.98-1.70)	0,07
		rs33914824	G>C	24410025	coding (P152A)				
		rs3895346	G>T	24416014	intron				
		rs2185599	T>C	24422202	intron				
		rs10806987	A>C	24423722	intron	0,440	0,497	0.80(0.60-1.05)	0,11
		rs1340695	G>A	24424174	intron	0,534	0,473	1.27(0.96-1.67)	0,09
		rs7741108	A>G	24424795	intron				
		rs12192947	A>G	24426549	intron	0,299	0,207	1.71(1.25-2.34)	7,95E-04
		rs4269365	G>T	24428410	intron				
		rs9366567	G>A	24431837	intron	0,303	0,205	1.76(1.29-2.40)	3,75E-04
		rs9460992	T>C	24437709	intron	0,333	0,235	1.69(1.24-2.30)	7,33E-04
		rs12661152	T>G	24441283	intron				
		rs4504468	C>G	24441723	intron	0,415	0,501	0.71(0.53-0.94)	1,54E-02
		rs16889092	G>A	24442358	intron				
		rs1923168	A>C	24447277	intron	0,282	0,210	1.55(1.13-2.14)	7,18E-03
		rs9379655	T>C	24449359	intron				
		rs12192603	A>G	24450350	intron	0,303	0,221	1.60(1.17-2.19)	3,12E-03
		rs1535331	T>C	24450591	intron	0,303	0,309	0.95(0.70-1.29)	0,74
		rs9393551	T>C	24451694	intron				
		rs1277351	T>C	24454035	intron	0,393	0,476	0.71(0.53-0.94)	1,72E-02
		rs793674	G>A	24455862	intron	0,325	0,314	1.02(0.76-1.39)	0,87
		rs6922023	G>C	24456096	intron	0,325	0,311	1.04(0.77-1.41)	0,79
		rs9460999	G>A	24457677	intron				
		rs7775357	A>C	24459476	intron				
		rs10498720	T>C	24461415	intron				
		rs813227	A>G	24461721	intron				

ILVBL	19	rs3765502	C>G	24462024	5'	0,355	0,367	0.95(0.71-1.27)	0,73
		rs13301	C>T	15086348	3'				
		rs2074261	A>C	15087611	intron				
		rs1468198	T>C	15089178	intron				
		rs7507755	A>G	15089542	intron				
CLDN1	3	rs2074265	A>C	15094581	coding (L213L)	0,423	0,339	1.43(1.07-1.89)	1,25E-02
		rs718100	G>T	15095635	intron				
		rs4141356	A>G	15096932	5'UTR				
		rs2074267	A>C	15097342	intron	0,355	0,420	0.74(0.55-1.01)	5,10E-02
		rs2240299	C>T	15089982	intron	0,226	0,359	0.51(0.37-0.72)	7,61E-05
		rs9290927	T>A	191505210	3'				
		rs3864005	G>A	191505497	3'	0,179	0,174	1.11(0.77-1.60)	0,59
		rs8298	C>T	191506246	3'UTR				
		rs8798	G>A	191506531	3'UTR				
		rs9290928	G>A	191507151	3'UTR				
		rs1060679	C>T	191507550	3'UTR				
		rs12629166	T>C	191509077	intron				
		rs3774032	G>A	191509554	intron				
		rs3774028	T>A	191510966	intron				
		rs6800425	G>A	191513018	intron	0,239	0,196	1.37(0.98-1.91)	0,07
		rs6776378	G>A	191513220	intron				
		rs9869263	G>A	191513374	coding (G123G)				
		rs10513846	G>A	191513683	intron	0,415	0,500	0.68(0.51-0.91)	8,15E-03
		rs6809685	A>G	191515288	intron	0,120	0,052	2.47(1.55-3.94)	8,18E-05
		rs9866788	T>C	191515814	intron				
		rs9852326	T>C	191516913	intron				
		rs3732923	T>A	191517403	intron				
		rs6793070	C>T	191517664	intron				
		rs3774023	G>T	191518519	intron	0,094	0,105	0.93(0.58-1.48)	0,75
		rs3774022	A>G	191518799	intron				
		rs9839711	C>G	191519713	intron				
		rs3774019	C>T	191520108	intron	0,466	0,390	1.38(1.04-1.83)	2,48E-02
		rs893051	G>C	191522295	intron				
KRT75	12	rs12696600	A>C	191522901	5'UTR				
		rs1155884	A>C	191523648	5'				
		rs16865347	T>C	191524091	5'				
		rs16865352	A>G	191524474	5'	0,222	0,180	1.34(0.95-1.88)	0,10
		rs44637	A>G	51101732	3'	0,487	0,499	1.02(0.77-1.36)	0,87
		rs2293638	C>T	51106511	intron				
		rs664354	G>A	51108259	intron				
		rs3782486	T>C	51109540	intron				
		rs10876290	A>G	51110214	intron				
		rs2232399	C>A	51110473	intron				
		rs2232386	C>G	51114007	coding (P117A)				
		rs298109	G>A	51114085	coding (R91G)	0,175	0,260	0.58(0.40-0.84)	2,45E-03
		rs3759193	A>G	51114706	5'	0,175	0,164	1.08(0.74-1.57)	0,66
		rs4761880	C>T	51117336	5'	0,162	0,078	2.45(1.60-3.76)	1,93E-05
		rs400120	A>G	51117607	5'				
		rs371202	T>C	51118620	5'				
		rs1798642	C>T	51119419	5'	0,175	0,260	0.58(0.40-0.84)	2,45E-03
		rs409929	G>A	51120364	5'	0,487	0,498	1.02(0.77-1.36)	0,88
KRT6B	12	rs429561	G>C	51121588	3'				
		rs375539	G>A	51121667	3'				
		rs11170121	T>G	51121877	3'	0,158	0,079	2.23(1.46-3.41)	1,03E-04
		rs400774	C>A	51122489	3'	0,350	0,428	0.70(0.52-0.94)	1,60E-02
		rs597340	G>A	51123986	3'	0,167	0,264	0.53(0.37-0.77)	5,50E-04
		rs610794	A>G	51124748	3'				
		rs17717236	A>G	51125123	3'				
		rs417466	G>A	51128475	intron				
		rs3809178	A>C	51132219	5'				
		rs447003	C>T	51134659	5'				
MEIS1	2	rs2280334	A>G	66518650	intron	0,282	0,275	1.03(0.75-1.42)	0,84
		rs2049019	T>C	66525362	intron	0,308	0,312	0.99(0.73-1.35)	0,97
		rs1519103	C>A	66531385	intron	0,316	0,312	1.03(0.76-1.41)	0,81
		rs10865353	G>T	66538448	intron				
		rs6716792	G>A	66541347	intron	0,205	0,228	0.89(0.63-1.26)	0,54
		rs17032103	C>A	66546012	intron	0,081	0,058	1.50(0.87-2.59)	0,14
		rs6727352	C>T	66548825	intron	0,184	0,129	1.53(1.04-2.25)	2,43E-02
		rs10203407	G>A	66552300	intron	0,090	0,067	1.35(0.81-2.25)	0,22
		rs10192756	G>A	66556149	intron				
		rs11889571	A>G	66560468	intron				

GP6	19	rs6705285	T>A	66562972	intron	0,342	0,315	1.15(0.84-1.56)	0,35
		rs7578320	G>T	66564752	intron	0,184	0,129	1.53(1.04-2.25)	2,43E-02
		rs17032114	T>C	66568101	intron	0,090	0,067	1.35(0.81-2.25)	0,22
		rs17032119	A>G	66568776	intron				
		rs7563565	T>G	66570096	intron	0,090	0,067	1.35(0.81-2.25)	0,22
		rs4671729	C>T	66573603	intron				
		rs2139246	A>C	66575364	intron	0,090	0,067	1.35(0.81-2.25)	0,22
		rs1519106	G>A	66576315	intron				
		rs11692361	T>C	66577203	intron	0,145	0,116	1.32(0.89-1.97)	0,17
		rs11692504	T>C	66577567	intron				
		rs12619205	T>C	66579371	intron	0,521	0,385	1.72(1.30-2.28)	1,14E-04
		rs13023583	A>G	66579444	intron	0,483	0,357	1.67(1.26-2.22)	2,33E-04
		rs4547518	C>T	66580072	intron	0,081	0,072	1.22(0.72-2.08)	0,46
		rs12620754	C>T	66580626	intron				
		rs12713567	C>G	66582924	intron				
		rs4387782	G>A	66584114	intron				
		rs12373638	T>G	66584746	intron	0,214	0,222	0.96(0.69-1.35)	0,26
		rs4430927	C>T	66588624	intron				
		rs4605359	G>A	66589003	intron				
		rs7579466	G>C	66591871	intron				
		rs12713568	A>T	66595742	intron	0,538	0,469	1.34(1.01-1.79)	0,82
		rs6721499	C>T	66597095	intron	0,239	0,242	1.00(0.72-1.38)	0,70
		rs3890755	T>C	66598107	intron				
		rs7586211	C>T	66599167	intron				
		rs4586617	G>A	66601780	intron				
		rs4316926	G>T	66602612	intron				
		rs6742861	A>G	66603656	intron	0,077	0,070	1.13(0.66-1.94)	4,71E-02
		rs6728018	T>C	66603769	intron	0,077	0,069	1.15(0.67-1.97)	0,98
		rs12621998	C>T	66606598	intron				
		rs4480973	C>G	66607557	intron	0,184	0,229	0.76(0.53-1.08)	0,65
		rs3891585	C>A	66610480	intron	0,286	0,228	1.38(1.00-1.90)	0,62
		rs12621948	G>A	66612416	intron				
		rs11693646	C>G	66613347	intron				
		rs10865355	G>A	66618501	intron	0,286	0,227	1.39(1.01-1.92)	0,12
		rs9789535	G>A	66619082	intron	0,355	0,305	1.24(0.92-1.67)	4,99E-02
		rs12472245	A>G	66624057	intron				
		rs11897119	T>A	66625504	intron	0,289	0,228	1.40(1.01-1.93)	4,34E-02
		rs2216120	T>C	66630010	intron	0,214	0,158	1.47(1.02-2.11)	0,15
		rs2300477	T>C	66630233	intron	0,256	0,296	0.83(0.60-1.13)	4,15E-02
		rs2192954	A>G	66631025	intron	0,560	0,447	1.57(1.18-2.08)	3,78E-02
		rs2300478	A>G	66634957	intron	0,278	0,229	1.28(0.93-1.78)	0,25
		rs2300479	T>G	66635165	intron				
		rs2300481	A>C	66635971	intron				
		rs2300482	C>T	66636175	intron				
		rs6711787	T>G	66637184	intron	0,179	0,224	0.76(0.53-1.08)	1,99E-03
		rs2284706	G>A	66637444	intron	0,222	0,165	1.46(1.02-2.08)	0,14
		rs10202912	A>G	66639909	intron				
		rs2300484	A>G	66641818	intron	0,090	0,072	1.34(0.80-2.23)	0,13
		rs2110974	C>T	66642095	intron				
		rs2300486	A>G	66644908	intron				
		rs12614369	G>T	66645613	intron				
		rs6735071	A>G	66645795	intron				
		rs2216123	T>C	66646652	intron				
		rs1000756	A>G	66648338	intron	0,154	0,164	0.92(0.63-1.36)	3,85E-02
		rs2066927	C>T	66650112	intron				
		rs2216124	A>G	66650642	intron				
		rs1654410	T>C	60216625	3'	0,329	0,411	0.70(0.52-0.95)	2,16E-02
		rs10416380	G>A	60216717	3'	0,154	0,168	0.91(0.61-1.35)	0,64
		rs10417943	G>A	60217149	3'UTR				
		rs17836524	T>C	60219502	intron				
		rs17836526	T>A	60219919	intron				
		rs8106615	G>A	60220241	intron				
		rs12462907	C>T	60220912	intron				
		rs11669150	T>C	60227784	intron	0,179	0,243	0.68(0.47-0.98)	3,74E-02
		rs1613662	A>G	60228407	coding				
		rs2886412	G>A	60229754	intron				
		rs1671196	T>C	60231360	intron	0,158	0,173	0.90(0.61-1.32)	0,56
		rs10401614	T>G	60231969	intron				
		rs12610286	G>A	60233211	intron				
		rs1671207	G>C	60238123	intron				
		rs4806636	T>G	60240370	intron				

RDH13	19	rs1654431	A>G	60241570	5'				
		rs1671215	A>C	60244831	3'	0,132	0,231	0.49(0.32-0.74)	6,34E-04
		rs8113032	A>G	60245950	3'	0,346	0,466	0.61(0.45-0.82)	9,82E-04
		rs4806637	A>G	60247800	3'UTR	0,205	0,191	1.11(0.78-1.57)	0,58
		rs775821	C>T	60250380	intron	0,137	0,250	0.45(0.29-0.68)	1,26E-04
		rs3745912	G>A	60250410	intron				
		rs2124090	C>A	60256268	intron				
		rs2124089	C>G	60256427	intron				
		rs11084387	G>A	60257164	intron				
		rs11672111	G>C	60257446	intron				
		rs1671169	C>T	60265445	intron				
		rs1654464	C>T	60270192	intron				
		rs12462815	C>T	60270418	intron				
		rs1654467	T>C	60273323	5'	0,415	0,411	1.02(0.77-1.35)	0,90

Odd ratios and corresponding p-values were calculated from genotype distribution using logistic regression models adjusted by age, sex, atopy,

MAF (n=1,137)	HWE			Fine-mapping study			
	All	AERD	ATA	AERD (n=141)	ATA (n=996)	OR(95% CI)	p
0,206	0,590	0,487	0,398	0,213	0,205	1.04(0.77-1.41)	0,80
0,461	0,336	0,349	0,504	0,440	0,464	0.93(0.73-1.20)	0,58
0,450	0,844	0,216	0,796	0,433	0,452	0.95(0.73-1.22)	0,67
0,449	0,979	0,296	0,670	0,429	0,452	0.94(0.73-1.21)	0,62
0,340	0,521	0,646	0,388	0,314	0,343	0.90(0.68-1.18)	0,45
0,357	0,848	0,975	0,828	0,358	0,357	0.99(0.76-1.28)	0,92
0,481	0,350	0,053	0,790	0,493	0,480	1.03(0.81-1.32)	0,80
0,087	0,835	0,713	0,938	0,099	0,085	1.20(0.78-1.83)	0,40
0,367	0,339	0,738	0,252	0,358	0,368	0.96(0.73-1.25)	0,73
0,173	0,987	0,274	0,711	0,164	0,175	0.90(0.64-1.27)	0,55
0,487	0,888	0,800	0,955	0,496	0,486	1.04(0.81-1.33)	0,77
0,368	0,489	0,925	0,463	0,415	0,361	1.25(0.97-1.61)	0,08
0,296	0,025	0,837	0,020	0,298	0,296	1.01(0.76-1.35)	0,93
0,479	0,975	0,894	0,969	0,433	0,486	0.79(0.62-1.02)	0,07
0,373	0,696	0,925	0,675	0,415	0,367	1.22(0.95-1.57)	0,12
0,368	0,381	0,764	0,317	0,421	0,361	1.29(1.00-1.66)	4,62E-02
0,156	0,321	0,643	0,213	0,163	0,155	1.08(0.77-1.52)	0,65
0,226	0,739	0,828	0,737	0,273	0,219	1.36(1.02-1.81)	3,65E-02
0,074	0,595	0,321	0,186	0,113	0,069	1.73(1.14-2.63)	7,88E-03
0,356	0,877	0,332	0,843	0,351	0,357	0.96(0.74-1.25)	0,77
0,072	0,704	0,321	0,233	0,113	0,066	1.80(1.19-2.73)	4,31E-03
0,102	0,313	0,495	0,170	0,113	0,101	1.17(0.79-1.73)	0,45
0,181	0,381	0,277	0,589	0,227	0,175	1.42(1.04-1.94)	2,58E-02
0,181	0,297	0,277	0,470	0,227	0,175	1.43(1.05-1.95)	2,37E-02
0,078	0,429	0,807	0,269	0,111	0,074	1.59(1.04-2.41)	2,86E-02
0,103	0,510	0,495	0,322	0,113	0,101	1.16(0.78-1.73)	0,46
0,181	0,381	0,277	0,589	0,227	0,175	1.42(1.04-1.94)	2,58E-02
0,189	0,216	0,237	0,375	0,230	0,183	1.38(1.01-1.88)	4,16E-02
0,181	0,396	0,277	0,611	0,227	0,175	1.42(1.04-1.94)	2,47E-02
0,103	0,347	0,495	0,195	0,113	0,102	1.15(0.78-1.71)	0,48
0,441	0,783	0,126	0,764	0,401	0,446	0.81(0.63-1.05)	0,12
0,454	0,969	0,209	0,621	0,390	0,463	0.72(0.56-0.94)	1,45E-02
0,455	0,047	0,684	0,022	0,482	0,451	1.17(0.90-1.52)	0,24
0,476	0,848	0,166	0,686	0,404	0,486	0.70(0.54-0.90)	6,26E-03
0,191	0,630	0,105	0,750	0,245	0,184	1.46(1.09-1.97)	1,09E-02
0,257	0,893	0,479	0,933	0,230	0,261	0.85(0.63-1.15)	0,28
0,448	0,111	0,465	0,046	0,475	0,445	1.16(0.89-1.50)	0,26
0,481	0,625	0,074	0,817	0,411	0,491	0.71(0.55-0.92)	8,43E-03
0,482	0,582	0,074	0,867	0,411	0,492	0.71(0.55-0.91)	7,99E-03
0,248	0,985	0,277	0,697	0,227	0,251	0.87(0.65-1.18)	0,37
0,191	0,635	0,105	0,744	0,245	0,184	1.46(1.09-1.96)	1,13E-02
0,491	0,540	0,101	0,949	0,415	0,502	0.69(0.54-0.90)	4,82E-03
0,248	0,977	0,277	0,689	0,227	0,251	0.88(0.65-1.18)	0,38
0,069	0,470	0,321	0,972	0,113	0,063	1.89(1.25-2.85)	1,96E-03
0,070	0,491	0,321	0,997	0,113	0,063	1.88(1.25-2.83)	2,16E-03
0,192	0,430	0,105	0,979	0,245	0,185	1.45(1.08-1.95)	1,25E-02
0,457	0,393	0,068	0,898	0,376	0,468	0.67(0.52-0.87)	2,66E-03
0,261	0,131	0,483	0,278	0,358	0,247	1.70(1.31-2.22)	6,05E-05
0,191	0,618	0,111	0,768	0,246	0,183	1.48(1.10-1.99)	8,90E-03
0,070	0,493	0,321	0,999	0,113	0,063	1.88(1.25-2.83)	2,19E-03
0,248	0,928	0,277	0,784	0,227	0,251	0.88(0.65-1.18)	0,39
0,490	0,561	0,101	0,924	0,415	0,501	0.70(0.54-0.90)	5,27E-03
0,323	0,124	0,270	0,228	0,348	0,320	1.13(0.87-1.46)	0,37
0,034	0,802	0,180	0,302	0,046	0,032	1.45(0.78-2.69)	0,24
0,273	0,340	0,006	0,991	0,262	0,275	0.93(0.70-1.23)	0,60
0,254	0,078	0,464	0,172	0,348	0,240	1.67(1.28-2.17)	1,12E-04
0,404	0,641	0,456	0,830	0,411	0,403	1.03(0.80-1.33)	0,79
0,079	0,666	0,563	0,675	0,142	0,070	2.25(1.52-3.31)	2,35E-05
0,453	0,242	0,414	0,346	0,450	0,454	0.98(0.77-1.26)	0,89
0,078	0,686	0,563	0,697	0,142	0,069	2.26(1.53-3.33)	2,07E-05
0,078	0,686	0,563	0,697	0,142	0,069	2.26(1.53-3.33)	2,09E-05
0,078	0,688	0,563	0,698	0,142	0,069	2.26(1.53-3.33)	2,01E-05
0,078	0,688	0,563	0,698	0,142	0,069	2.26(1.53-3.33)	2,01E-05
0,078	0,686	0,563	0,697	0,142	0,069	2.26(1.53-3.33)	2,06E-05
0,471	0,159	0,765	0,124	0,411	0,480	0.77(0.60-0.99)	3,74E-02
0,498	0,000	0,001	0,000	0,514	0,495	0.94(0.75-1.19)	0,60
0,099	0,493	0,878	0,248	0,163	0,090	2.06(1.43-2.96)	6,70E-05

0,433	0,195	0,395	0,287	0,426	0,435	0.96(0.75-1.22)	0,72
0,434	0,342	0,720	0,379	0,429	0,435	0.97(0.75-1.24)	0,80
0,352	0,314	0,834	0,391	0,433	0,340	1.46(1.13-1.88)	3,14E-03
0,247	0,720	0,825	0,848	0,181	0,256	0.65(0.47-0.89)	7,58E-03
0,080	0,280	0,944	0,259	0,082	0,080	1.00(0.64-1.58)	0,99
0,196	0,215	0,878	0,222	0,163	0,200	0.79(0.57-1.10)	0,17
0,256	0,658	0,928	0,687	0,220	0,261	0.81(0.60-1.09)	0,17
0,247	0,640	0,743	0,792	0,177	0,257	0.63(0.46-0.87)	5,12E-03
0,347	0,975	0,333	0,753	0,299	0,354	0.78(0.59-1.03)	0,08
0,373	0,998	0,143	0,484	0,443	0,363	1.39(1.08-1.80)	1,05E-02
0,343	0,770	0,433	0,607	0,291	0,351	0.76(0.58-1.00)	5,39E-02
0,381	0,783	0,293	0,771	0,468	0,369	1.49(1.16-1.92)	1,73E-03
0,251	0,790	0,842	0,855	0,216	0,256	0.81(0.60-1.10)	0,18
0,199	0,264	0,878	0,279	0,163	0,204	0.77(0.55-1.08)	0,13
0,343	0,814	0,433	0,648	0,291	0,350	0.76(0.58-1.01)	0,06
0,052	0,550	0,315	0,803	0,053	0,051	1.05(0.60-1.83)	0,88
0,270	0,215	0,985	0,202	0,238	0,275	0.83(0.62-1.11)	0,20
0,089	0,483	0,910	0,429	0,089	0,090	1.00(0.65-1.56)	0,99
0,095	0,803	0,642	0,939	0,103	0,094	1.08(0.72-1.64)	0,71
0,185	0,988	0,380	0,739	0,195	0,184	1.07(0.78-1.47)	0,67
0,359	0,072	0,909	0,047	0,383	0,355	1.13(0.87-1.48)	0,37
0,185	0,673	0,500	0,843	0,184	0,185	0.99(0.72-1.37)	0,96
0,114	0,170	0,713	0,182	0,099	0,116	0.84(0.55-1.28)	0,40
0,131	0,727	0,822	0,773	0,128	0,131	0.96(0.66-1.40)	0,82
0,119	0,238	0,799	0,180	0,110	0,121	0.91(0.60-1.36)	0,64
0,329	0,064	0,746	0,039	0,301	0,332	0.87(0.67-1.14)	0,32
0,135	0,730	0,622	0,576	0,138	0,134	1.03(0.72-1.48)	0,89
0,380	0,183	0,988	0,155	0,404	0,376	1.13(0.88-1.45)	0,36
0,194	0,316	0,318	0,184	0,160	0,199	0.77(0.55-1.08)	0,14
0,190	0,256	0,360	0,150	0,156	0,195	0.77(0.55-1.08)	0,13
0,228	0,172	0,017	0,596	0,241	0,226	1.08(0.80-1.46)	0,61
0,149	0,513	0,125	0,278	0,115	0,154	0.72(0.49-1.06)	0,10
0,487	0,529	0,339	0,314	0,454	0,491	0.86(0.67-1.10)	0,23
0,108	0,237	0,969	0,197	0,121	0,106	1.18(0.80-1.73)	0,41
0,195	0,187	0,360	0,106	0,156	0,200	0.75(0.53-1.05)	0,09
0,362	0,722	0,007	0,156	0,372	0,360	1.05(0.81-1.36)	0,71
0,317	0,083	0,725	0,047	0,305	0,319	0.93(0.71-1.23)	0,62
0,267	0,506	0,369	0,289	0,294	0,263	1.16(0.88-1.53)	0,27
0,160	0,189	0,969	0,187	0,121	0,166	0.70(0.48-1.02)	0,06
0,390	0,035	0,002	0,254	0,362	0,394	0.86(0.66-1.13)	0,27
0,452	0,043	0,006	0,222	0,394	0,460	0.74(0.57-0.97)	2,74E-02
0,277	0,196	0,497	0,250	0,312	0,272	1.23(0.93-1.63)	0,14
0,419	0,280	0,673	0,191	0,407	0,421	0.96(0.74-1.23)	0,74
0,061	0,512	0,729	0,493	0,028	0,066	0.39(0.19-0.82)	9,71E-03
0,144	0,073	0,877	0,074	0,113	0,148	0.75(0.51-1.10)	0,14
0,151	0,101	0,384	0,160	0,117	0,156	0.73(0.50-1.07)	0,10
0,266	0,480	0,200	0,210	0,280	0,264	1.08(0.82-1.43)	0,57
0,351	0,437	0,622	0,359	0,294	0,360	0.74(0.56-0.97)	2,87E-02
0,201	0,605	0,360	0,806	0,181	0,204	0.84(0.61-1.17)	0,30
0,333	0,466	0,999	0,436	0,337	0,332	1.02(0.78-1.33)	0,90
0,397	0,066	0,058	0,206	0,379	0,399	0.92(0.70-1.20)	0,51
0,397	0,071	0,058	0,218	0,379	0,399	0.92(0.70-1.20)	0,52
0,200	0,552	0,267	0,812	0,189	0,202	0.91(0.65-1.25)	0,55
0,144	0,130	0,321	0,214	0,113	0,149	0.75(0.51-1.10)	0,13
0,447	0,897	0,145	0,494	0,440	0,448	0.95(0.73-1.22)	0,67
0,136	0,316	0,318	0,132	0,160	0,133	1.26(0.90-1.78)	0,18
0,137	0,198	0,454	0,276	0,149	0,135	1.11(0.77-1.60)	0,58
0,301	0,263	0,321	0,412	0,311	0,300	1.06(0.80-1.39)	0,70
0,467	0,282	0,613	0,171	0,426	0,472	0.82(0.64-1.07)	0,15
0,325	0,006	0,307	0,009	0,365	0,319	1.25(0.95-1.65)	0,11
0,314	0,238	0,466	0,324	0,327	0,312	1.08(0.82-1.42)	0,60
0,362	0,770	0,558	0,961	0,311	0,370	0.77(0.59-1.01)	0,06
0,203	0,133	0,511	0,061	0,245	0,197	1.32(0.99-1.77)	0,06
0,135	0,091	0,563	0,112	0,142	0,134	1.06(0.73-1.54)	0,76
0,454	0,175	0,708	0,192	0,468	0,452	1.06(0.83-1.36)	0,64
0,262	0,236	0,847	0,213	0,213	0,269	0.71(0.52-0.97)	2,92E-02
0,385	0,137	0,254	0,245	0,397	0,383	1.07(0.82-1.39)	0,62
0,117	0,685	0,955	0,680	0,117	0,117	1.00(0.68-1.48)	0,97
0,426	0,752	0,721	0,646	0,454	0,423	1.15(0.90-1.48)	0,26
0,401	0,360	0,439	0,475	0,440	0,395	1.24(0.95-1.60)	0,11

0,269	0,853	0,286	0,836	0,273	0,269	1.02(0.77-1.36)	0,87
0,281	0,218	0,816	0,199	0,230	0,288	0.71(0.52-0.96)	2,46E-02
0,451	0,509	0,555	0,598	0,496	0,444	1.27(0.99-1.64)	0,06
0,450	0,563	0,447	0,714	0,493	0,444	1.26(0.97-1.62)	0,08
0,339	0,655	0,981	0,600	0,387	0,332	1.27(0.98-1.65)	0,07
0,133	0,978	0,686	0,901	0,135	0,133	1.01(0.70-1.46)	0,98
0,275	0,295	0,029	0,781	0,323	0,269	1.34(1.01-1.76)	3,94E-02
0,362	0,716	0,660	0,521	0,291	0,372	0.69(0.52-0.90)	7,25E-03
0,220	0,374	0,656	0,284	0,280	0,212	1.44(1.09-1.90)	1,10E-02
0,307	0,322	0,315	0,475	0,355	0,301	1.29(0.99-1.69)	0,06
0,273	0,122	0,373	0,206	0,312	0,268	1.22(0.93-1.59)	0,14
0,182	0,604	0,430	0,395	0,181	0,182	0.98(0.71-1.37)	0,93
0,433	0,865	0,687	0,738	0,436	0,432	1.00(0.78-1.29)	0,99
0,170	0,293	0,578	0,185	0,167	0,171	0.99(0.71-1.37)	0,94
0,147	0,728	0,260	0,986	0,135	0,149	0.90(0.62-1.30)	0,59
0,173	0,099	0,186	0,024	0,174	0,173	1.02(0.74-1.41)	0,90
0,326	0,959	0,284	0,657	0,312	0,328	0.93(0.71-1.22)	0,62
0,052	0,503	0,598	0,583	0,043	0,054	0.80(0.43-1.48)	0,49
0,081	0,293	0,505	0,234	0,053	0,085	0.61(0.35-1.04)	0,07
0,451	0,283	0,424	0,392	0,472	0,448	1.09(0.84-1.41)	0,51
0,391	0,646	0,702	0,715	0,422	0,387	1.14(0.88-1.47)	0,33
0,400	0,476	0,501	0,602	0,429	0,396	1.13(0.87-1.46)	0,35
0,326	0,042	0,986	0,030	0,316	0,328	0.95(0.73-1.24)	0,71
0,326	0,887	0,543	0,727	0,298	0,330	0.88(0.67-1.15)	0,34
0,263	0,193	0,457	0,095	0,262	0,263	1.00(0.75-1.32)	0,98
0,410	0,425	0,265	0,656	0,440	0,405	1.14(0.88-1.47)	0,32
0,182	0,607	0,348	0,352	0,204	0,179	1.18(0.87-1.62)	0,29
0,462	0,275	0,190	0,411	0,383	0,473	0.69(0.53-0.89)	5,15E-03
0,476	0,601	0,424	0,796	0,472	0,477	0.99(0.77-1.28)	0,95
0,166	0,407	0,092	0,199	0,124	0,172	0.69(0.48-1.00)	5,22E-02
0,386	0,176	0,778	0,162	0,436	0,379	1.26(0.97-1.64)	0,08
0,379	0,104	0,778	0,086	0,436	0,371	1.33(1.02-1.73)	3,48E-02
0,334	0,052	0,662	0,044	0,397	0,325	1.40(1.07-1.83)	1,42E-02
0,355	0,117	0,765	0,100	0,411	0,347	1.33(1.02-1.73)	3,57E-02
0,288	0,909	0,369	0,642	0,294	0,287	1.03(0.78-1.36)	0,83
0,036	0,207	0,762	0,216	0,025	0,038	0.66(0.30-1.47)	0,30
0,375	0,717	0,701	0,595	0,368	0,376	0.96(0.74-1.24)	0,73
0,439	0,062	0,539	0,078	0,454	0,437	1.07(0.82-1.38)	0,61
0,341	0,721	0,332	0,993	0,351	0,340	1.04(0.80-1.35)	0,78
0,489	0,963	0,269	0,723	0,514	0,485	1.13(0.88-1.45)	0,34
0,226	0,828	0,754	0,921	0,245	0,223	1.15(0.85-1.54)	0,38
0,467	0,284	0,165	0,535	0,468	0,466	1.02(0.80-1.31)	0,87
0,433	0,702	0,687	0,798	0,436	0,433	1.02(0.80-1.32)	0,86
0,243	0,507	0,809	0,425	0,230	0,245	0.93(0.69-1.25)	0,62
0,283	0,951	0,238	0,712	0,270	0,284	0.94(0.71-1.25)	0,68
0,331	0,096	0,916	0,084	0,312	0,334	0.90(0.69-1.18)	0,46
0,190	0,429	0,930	0,406	0,209	0,188	1.16(0.85-1.59)	0,37
0,191	0,409	0,930	0,385	0,209	0,188	1.16(0.84-1.58)	0,38
0,191	0,389	0,930	0,365	0,209	0,189	1.15(0.84-1.58)	0,39
0,191	0,434	0,930	0,412	0,209	0,188	1.15(0.84-1.58)	0,39
0,191	0,526	0,930	0,509	0,209	0,188	1.15(0.84-1.58)	0,38
0,411	0,821	0,467	0,605	0,422	0,410	1.04(0.81-1.34)	0,74
0,336	0,689	0,332	0,419	0,351	0,334	1.07(0.82-1.39)	0,64
0,396	0,488	0,359	0,288	0,372	0,400	0.89(0.69-1.15)	0,39
0,147	0,406	0,171	0,706	0,145	0,147	0.95(0.67-1.35)	0,79
0,193	0,955	0,323	0,741	0,223	0,189	1.26(0.93-1.71)	0,15
0,304	0,826	0,445	0,583	0,326	0,300	1.11(0.85-1.46)	0,45
0,379	0,140	0,915	0,106	0,379	0,379	1.00(0.77-1.29)	0,98
0,132	0,661	0,894	0,674	0,124	0,133	0.92(0.63-1.34)	0,65
0,186	0,038	0,242	0,079	0,202	0,184	1.12(0.82-1.52)	0,48
0,253	0,460	0,595	0,554	0,270	0,251	1.11(0.83-1.48)	0,47
0,436	0,758	0,333	0,488	0,436	0,436	1.02(0.79-1.31)	0,91
0,136	0,464	0,067	0,171	0,113	0,139	0.81(0.55-1.20)	0,28
0,293	0,448	0,238	0,233	0,262	0,298	0.82(0.62-1.08)	0,16
0,289	0,914	0,700	0,811	0,326	0,283	1.24(0.94-1.62)	0,12
0,323	0,319	0,315	0,485	0,355	0,318	1.19(0.91-1.56)	0,19
0,462	0,897	0,902	0,855	0,472	0,460	1.07(0.83-1.37)	0,61
0,498	0,905	0,916	0,924	0,479	0,501	0.90(0.70-1.15)	0,39
0,139	0,472	0,092	0,189	0,117	0,142	0.82(0.55-1.20)	0,29
0,344	0,762	0,837	0,732	0,298	0,351	0.77(0.58-1.01)	0,06
0,306	0,588	0,992	0,532	0,348	0,300	1.26(0.96-1.65)	0,09

0,469	0,889	0,937	0,912	0,489	0,466	1.12(0.87-1.44)	0,37
0,490	0,849	0,744	0,921	0,461	0,494	0.85(0.66-1.10)	0,22
0,478	0,497	0,830	0,520	0,472	0,479	1.00(0.78-1.28)	0,97
0,375	0,828	0,992	0,826	0,348	0,379	0.86(0.66-1.12)	0,25
0,389	0,791	0,584	0,624	0,390	0,389	1.02(0.79-1.32)	0,90
0,391	0,797	0,536	0,610	0,397	0,390	1.05(0.81-1.36)	0,72
0,183	0,236	0,441	0,127	0,163	0,186	0.88(0.62-1.24)	0,45
0,225	0,348	0,756	0,265	0,213	0,227	0.95(0.69-1.29)	0,72
0,249	0,538	0,594	0,671	0,206	0,255	0.75(0.55-1.01)	0,06
0,356	0,913	0,252	0,752	0,326	0,361	0.85(0.65-1.11)	0,22
0,248	0,654	0,388	0,874	0,280	0,243	1.21(0.91-1.61)	0,18
0,435	0,360	0,822	0,359	0,401	0,440	0.85(0.65-1.10)	0,21
0,162	0,942	0,880	0,894	0,174	0,160	1.09(0.79-1.52)	0,60
0,417	0,175	0,256	0,280	0,472	0,409	1.30(1.00-1.68)	4,63E-02
0,457	0,381	0,545	0,433	0,518	0,449	1.33(1.03-1.71)	2,95E-02
0,255	0,864	0,369	0,604	0,294	0,250	1.25(0.95-1.65)	0,11
0,158	0,922	0,960	0,928	0,170	0,157	1.10(0.79-1.53)	0,60
0,256	0,710	0,543	0,540	0,298	0,251	1.27(0.96-1.67)	0,09
0,256	0,888	0,369	0,627	0,294	0,250	1.25(0.95-1.65)	0,11
0,295	0,869	0,799	0,821	0,344	0,289	1.30(0.99-1.69)	0,06
0,314	0,844	0,795	0,894	0,287	0,318	0.85(0.64-1.12)	0,25
0,290	0,374	0,312	0,553	0,333	0,283	1.27(0.97-1.67)	0,09
0,423	0,663	0,528	0,831	0,447	0,420	1.11(0.86-1.43)	0,42
0,422	0,677	0,528	0,847	0,447	0,419	1.11(0.86-1.43)	0,40
0,476	0,751	0,555	0,895	0,504	0,472	1.13(0.88-1.46)	0,33
0,455	0,944	0,442	0,844	0,486	0,450	1.15(0.89-1.48)	0,27
0,455	0,944	0,442	0,844	0,486	0,450	1.15(0.89-1.48)	0,27
0,230	0,967	0,728	0,996	0,181	0,237	0.71(0.52-0.98)	3,81E-02
0,304	0,303	0,442	0,414	0,326	0,301	1.14(0.87-1.49)	0,36
0,299	0,279	0,598	0,335	0,319	0,297	1.12(0.85-1.48)	0,41
0,209	0,812	0,892	0,727	0,164	0,215	0.72(0.52-1.01)	0,06
0,486	0,443	0,990	0,402	0,461	0,490	0.90(0.70-1.16)	0,40
0,056	0,151	0,505	0,198	0,053	0,056	0.95(0.54-1.68)	0,87
0,474	0,659	0,025	0,709	0,472	0,474	0.99(0.77-1.28)	0,95
0,114	0,924	0,989	0,962	0,145	0,109	1.40(0.97-2.01)	0,07
0,356	0,554	0,307	0,805	0,365	0,354	1.06(0.82-1.38)	0,67
0,126	0,818	0,989	0,820	0,145	0,124	1.21(0.85-1.73)	0,28
0,115	0,000	0,168	0,000	0,103	0,117	0.91(0.61-1.34)	0,62
0,109	0,000	0,214	0,000	0,106	0,109	1.01(0.69-1.49)	0,94
0,355	0,539	0,483	0,356	0,358	0,354	1.00(0.77-1.31)	0,97
0,359	0,494	0,571	0,344	0,362	0,359	1.00(0.77-1.30)	1,00
0,469	0,364	0,442	0,491	0,489	0,466	1.10(0.85-1.42)	0,47
0,250	0,054	0,554	0,066	0,248	0,250	1.00(0.75-1.32)	0,97
0,499	0,423	0,435	0,567	0,521	0,496	0.90(0.70-1.16)	0,43
0,270	0,407	0,658	0,472	0,266	0,270	0.98(0.74-1.30)	0,88
0,461	0,638	0,762	0,697	0,468	0,460	1.02(0.80-1.32)	0,84
0,056	0,151	0,982	0,085	0,085	0,052	1.76(1.09-2.85)	1,89E-02
0,155	0,340	0,326	0,471	0,128	0,159	0.79(0.54-1.14)	0,20
0,170	0,956	0,829	0,850	0,232	0,161	1.54(1.14-2.09)	4,86E-03
0,341	0,220	0,543	0,110	0,379	0,336	1.21(0.93-1.58)	0,15
0,153	0,447	0,756	0,584	0,213	0,145	1.54(1.13-2.10)	5,83E-03
0,341	0,160	0,699	0,090	0,376	0,336	1.20(0.92-1.56)	0,18
0,329	0,955	0,533	0,861	0,309	0,331	0.89(0.68-1.16)	0,38
0,164	0,611	0,986	0,659	0,223	0,156	1.51(1.11-2.05)	7,42E-03
0,075	0,052	0,944	0,039	0,082	0,074	1.10(0.70-1.72)	0,67
0,155	0,328	0,364	0,435	0,124	0,160	0.76(0.52-1.11)	0,14
0,163	0,195	0,230	0,320	0,138	0,166	0.82(0.57-1.18)	0,28
0,450	0,315	0,344	0,148	0,415	0,455	0.84(0.65-1.08)	0,18
0,323	0,261	0,571	0,140	0,362	0,317	1.22(0.94-1.60)	0,14
0,326	0,324	0,426	0,156	0,365	0,320	1.22(0.94-1.60)	0,14
0,161	0,099	0,050	0,274	0,142	0,164	0.85(0.59-1.22)	0,38
0,056	0,151	0,982	0,085	0,085	0,052	1.78(1.10-2.88)	1,71E-02
0,154	0,173	0,399	0,227	0,121	0,159	0.74(0.50-1.08)	0,12
0,164	0,585	0,900	0,604	0,227	0,155	1.56(1.15-2.11)	3,80E-03
0,119	0,813	0,776	0,759	0,096	0,123	0.76(0.50-1.16)	0,21
0,340	0,373	0,439	0,188	0,386	0,334	1.26(0.97-1.64)	0,08
0,398	0,655	0,580	0,413	0,472	0,387	1.42(1.10-1.83)	6,40E-03
0,228	0,713	0,517	0,651	0,323	0,214	1.73(1.31-2.27)	6,73E-05
0,180	0,840	0,756	0,831	0,248	0,171	1.58(1.17-2.12)	2,17E-03
0,238	0,892	0,312	0,713	0,333	0,224	1.72(1.31-2.26)	7,02E-05
0,156	0,324	0,928	0,371	0,220	0,147	1.58(1.16-2.14)	3,10E-03

0,445	0,573	0,274	0,304	0,411	0,450	0.84(0.65-1.09)	0,19
0,155	0,334	0,448	0,401	0,117	0,160	0.70(0.47-1.03)	0,07
0,240	0,767	0,312	0,578	0,333	0,226	1.69(1.29-2.22)	1,11E-04
0,449	0,951	0,196	0,572	0,415	0,453	0.85(0.66-1.09)	0,21
0,158	0,162	0,064	0,375	0,135	0,161	0.81(0.56-1.18)	0,27
0,154	0,466	0,928	0,554	0,220	0,144	1.62(1.19-2.20)	1,88E-03
0,070	0,039	0,776	0,026	0,096	0,066	1.58(1.00-2.49)	4,70E-02
0,059	0,110	0,982	0,062	0,085	0,056	1.62(1.01-2.62)	4,36E-02
0,257	0,449	0,452	0,606	0,270	0,256	1.07(0.81-1.41)	0,65
0,499	0,514	0,777	0,428	0,475	0,502	1.11(0.87-1.42)	0,42
0,248	0,340	0,319	0,530	0,262	0,246	1.08(0.81-1.43)	0,61
0,252	0,874	0,238	0,776	0,262	0,250	1.07(0.81-1.43)	0,64
0,249	0,307	0,319	0,483	0,262	0,247	1.07(0.81-1.42)	0,63
0,254	0,582	0,282	0,857	0,259	0,254	1.04(0.78-1.39)	0,80
0,294	0,184	0,481	0,248	0,289	0,295	0.98(0.74-1.30)	0,90
0,428	0,911	0,961	0,886	0,411	0,430	0.91(0.71-1.18)	0,49
0,254	0,211	0,634	0,273	0,301	0,247	1.33(1.01-1.74)	3,96E-02
0,093	0,527	0,944	0,486	0,082	0,094	0.86(0.54-1.36)	0,50
0,119	0,409	0,797	0,479	0,160	0,113	1.48(1.04-2.09)	2,64E-02
0,121	0,349	0,878	0,379	0,163	0,115	1.48(1.05-2.08)	2,38E-02
0,339	0,388	0,357	0,653	0,252	0,351	0.62(0.47-0.83)	1,05E-03
0,486	0,659	0,532	0,717	0,564	0,475	1.43(1.11-1.85)	5,71E-03
0,208	0,102	0,040	0,338	0,262	0,200	1.45(1.07-1.95)	1,42E-02
0,426	0,310	0,805	0,402	0,340	0,439	0.67(0.52-0.87)	2,39E-03
0,368	0,540	0,115	0,953	0,390	0,365	1.11(0.86-1.44)	0,42
0,218	0,594	0,388	0,757	0,280	0,210	1.48(1.11-1.97)	6,77E-03
0,305	0,664	0,049	0,800	0,261	0,311	0.79(0.59-1.04)	0,09
0,466	0,000	0,050	0,000	0,390	0,476	0.73(0.58-0.93)	1,11E-02
0,257	0,156	0,395	0,233	0,266	0,256	1.05(0.78-1.40)	0,76
0,210	0,699	0,595	0,770	0,270	0,202	1.47(1.10-1.96)	8,65E-03
0,218	0,661	0,577	0,719	0,284	0,208	1.53(1.15-2.04)	3,20E-03
0,213	0,646	0,675	0,687	0,266	0,206	1.41(1.05-1.88)	2,03E-02
0,429	0,301	0,380	0,494	0,356	0,439	0.72(0.55-0.93)	1,12E-02
0,415	0,479	0,949	0,464	0,369	0,421	0.81(0.62-1.05)	0,10
0,310	0,684	0,897	0,801	0,234	0,321	0.65(0.49-0.87)	3,89E-03
0,438	0,302	0,684	0,362	0,394	0,444	0.82(0.64-1.05)	0,12
0,431	0,013	0,409	0,021	0,383	0,438	0.81(0.63-1.04)	0,09
0,084	0,715	0,365	0,511	0,071	0,086	0.81(0.50-1.30)	0,36
0,266	0,480	0,446	0,695	0,199	0,276	0.66(0.48-0.89)	7,36E-03
0,267	0,370	0,446	0,556	0,199	0,277	0.65(0.48-0.89)	6,53E-03
0,328	0,943	0,756	0,979	0,248	0,340	0.64(0.48-0.85)	2,07E-03
0,480	0,210	0,136	0,475	0,418	0,488	0.76(0.59-0.97)	3,00E-02
0,495	0,124	0,071	0,358	0,443	0,502	0.79(0.62-1.02)	0,07
0,083	0,390	0,339	0,221	0,074	0,084	0.88(0.55-1.40)	0,56
0,404	0,257	0,229	0,468	0,355	0,410	0.79(0.61-1.02)	0,07
0,447	0,238	0,152	0,504	0,496	0,440	1.26(0.98-1.61)	0,07
0,433	0,299	0,242	0,538	0,482	0,426	1.26(0.98-1.62)	0,07
0,425	0,027	0,037	0,129	0,475	0,418	1.26(0.98-1.60)	0,07
0,414	0,423	0,285	0,715	0,475	0,405	1.34(1.04-1.72)	2,22E-02
0,422	0,264	0,079	0,659	0,482	0,414	1.32(1.03-1.70)	2,80E-02
0,443	0,192	0,154	0,420	0,489	0,436	1.24(0.97-1.59)	0,09
0,336	0,667	0,828	0,637	0,273	0,345	0.70(0.53-0.93)	1,47E-02
0,081	0,311	0,630	0,370	0,067	0,083	0.82(0.51-1.34)	0,44
0,353	0,907	0,929	0,777	0,277	0,364	0.66(0.50-0.87)	3,51E-03
0,207	0,974	0,323	0,672	0,223	0,205	1.11(0.82-1.51)	0,48
0,441	0,990	0,310	0,656	0,500	0,433	1.32(1.03-1.70)	3,15E-02
0,489	0,802	0,996	0,868	0,561	0,479	1.40(1.09-1.81)	9,36E-03
0,465	0,849	0,846	0,978	0,535	0,455	1.40(1.09-1.80)	9,40E-03
0,375	0,646	0,316	0,980	0,298	0,385	0.67(0.51-0.88)	3,98E-03
0,372	0,658	0,316	0,988	0,298	0,383	0.68(0.52-0.89)	5,22E-03
0,466	0,820	0,846	0,944	0,535	0,456	1.39(1.08-1.79)	1,05E-02
0,416	0,651	0,347	0,840	0,364	0,424	0.77(0.59-1.00)	4,90E-02
0,470	0,516	0,830	0,587	0,528	0,461	1.32(1.03-1.70)	2,87E-02
0,365	0,759	0,454	0,991	0,305	0,374	0.72(0.55-0.95)	1,94E-02
0,392	0,625	0,394	0,895	0,325	0,401	0.71(0.54-0.92)	1,05E-02
0,367	0,721	0,381	0,990	0,301	0,377	0.70(0.54-0.92)	1,09E-02
0,472	0,626	0,708	0,759	0,532	0,463	1.34(1.04-1.72)	2,46E-02
0,367	0,773	0,381	0,932	0,301	0,377	0.70(0.54-0.92)	1,08E-02
0,390	0,631	0,372	0,916	0,323	0,400	0.70(0.54-0.92)	9,03E-03
0,452	0,000	0,000	0,000	0,375	0,464	0.74(0.58-0.93)	9,57E-03
0,472	0,563	0,708	0,687	0,532	0,463	1.33(1.04-1.71)	2,47E-02

0,138	0,719	0,179	0,359	0,145	0,137	1.08(0.76-1.55)	0,66
0,138	0,719	0,179	0,359	0,145	0,137	1.08(0.76-1.55)	0,66
0,150	0,404	0,138	0,773	0,181	0,146	1.33(0.95-1.87)	0,10
0,390	0,996	0,249	0,608	0,316	0,400	0.68(0.52-0.88)	4,18E-03
0,386	0,846	0,158	0,419	0,309	0,397	0.66(0.51-0.87)	2,87E-03
0,405	0,928	0,762	0,896	0,468	0,396	1.35(1.05-1.74)	2,07E-02
0,150	0,547	0,138	0,973	0,181	0,146	1.32(0.95-1.85)	0,10
0,151	0,525	0,138	0,944	0,181	0,146	1.32(0.94-1.84)	0,11
0,114	0,944	0,204	0,528	0,142	0,110	1.37(0.94-1.98)	0,10
0,391	0,954	0,249	0,654	0,316	0,402	0.67(0.51-0.88)	3,75E-03
0,250	0,843	0,446	0,920	0,199	0,257	0.70(0.52-0.96)	2,59E-02
0,348	0,968	0,885	0,998	0,284	0,357	0.70(0.53-0.93)	1,28E-02
0,264	0,755	0,615	0,650	0,223	0,269	0.77(0.57-1.04)	0,09
0,453	0,140	0,030	0,412	0,407	0,459	0.80(0.61-1.03)	0,09
0,099	0,294	0,226	0,525	0,139	0,094	1.67(1.14-2.46)	9,03E-03
0,033	0,838	0,659	0,969	0,036	0,032	1.17(0.59-2.33)	0,65
0,284	0,277	0,788	0,240	0,355	0,274	1.46(1.13-1.90)	4,30E-03
0,042	0,992	0,535	0,775	0,050	0,041	1.30(0.72-2.33)	0,39
0,034	0,554	0,566	0,346	0,046	0,033	1.48(0.80-2.71)	0,21
0,092	0,215	0,799	0,221	0,110	0,089	1.27(0.85-1.89)	0,24
0,070	0,816	0,365	0,551	0,071	0,069	1.03(0.64-1.68)	0,88
0,045	0,841	0,535	0,968	0,050	0,044	1.16(0.65-2.09)	0,61
0,120	0,657	0,326	0,385	0,128	0,119	1.10(0.75-1.59)	0,63
0,033	0,113	0,729	0,077	0,028	0,034	0.83(0.40-1.72)	0,62
0,081	0,341	0,248	0,579	0,089	0,079	1.11(0.71-1.75)	0,65
0,078	0,366	0,292	0,165	0,082	0,077	1.06(0.67-1.67)	0,80
0,420	0,689	0,439	0,887	0,440	0,417	1.09(0.85-1.41)	0,51
0,182	0,727	0,594	0,535	0,206	0,179	1.19(0.87-1.62)	0,28
0,234	0,986	0,909	0,991	0,257	0,231	1.16(0.87-1.54)	0,32
0,225	0,958	0,841	0,899	0,245	0,223	1.13(0.85-1.52)	0,40
0,201	0,496	0,774	0,394	0,214	0,199	1.10(0.80-1.49)	0,56
0,223	0,911	0,841	0,851	0,245	0,220	1.15(0.86-1.54)	0,35
0,223	0,911	0,841	0,851	0,245	0,220	1.15(0.86-1.54)	0,35
0,060	0,969	0,868	0,875	0,078	0,057	1.38(0.86-2.23)	0,18
0,237	0,960	0,899	0,987	0,262	0,233	1.18(0.88-1.57)	0,26
0,204	0,436	0,986	0,398	0,223	0,201	1.15(0.85-1.56)	0,38
0,190	0,446	0,756	0,331	0,213	0,187	1.18(0.86-1.61)	0,29
0,252	0,874	0,880	0,788	0,287	0,247	1.24(0.94-1.64)	0,13
0,244	0,923	0,745	0,799	0,270	0,240	1.17(0.88-1.55)	0,27
0,235	0,944	0,745	0,925	0,270	0,230	1.24(0.93-1.65)	0,14
0,214	0,870	0,932	0,870	0,255	0,208	1.30(0.97-1.74)	0,08
0,360	0,689	0,612	0,830	0,323	0,365	0.85(0.65-1.11)	0,22
0,458	0,651	0,687	0,521	0,436	0,461	0.93(0.72-1.20)	0,58
0,411	0,877	0,377	0,852	0,372	0,416	0.85(0.66-1.10)	0,23
0,246	0,403	0,062	0,877	0,262	0,244	1.12(0.84-1.48)	0,44
0,367	0,235	0,456	0,325	0,376	0,365	1.04(0.81-1.34)	0,77
0,434	0,542	0,581	0,657	0,433	0,434	0.99(0.77-1.27)	0,94
0,306	0,716	0,940	0,677	0,301	0,307	0.96(0.73-1.27)	0,78
0,449	0,469	0,433	0,632	0,443	0,450	0.98(0.76-1.26)	0,85
0,473	0,103	0,081	0,279	0,475	0,473	0.99(0.77-1.26)	0,94
0,172	0,082	0,165	0,178	0,163	0,173	0.96(0.69-1.34)	0,83
0,493	0,005	0,117	0,017	0,472	0,496	0.90(0.71-1.15)	0,41
0,496	0,054	0,320	0,093	0,479	0,499	0.92(0.72-1.17)	0,51
0,496	0,033	0,214	0,071	0,479	0,498	0.93(0.73-1.18)	0,53
0,058	0,331	0,475	0,440	0,057	0,058	0.97(0.56-1.68)	0,91
0,153	0,027	0,856	0,022	0,152	0,153	0.98(0.68-1.40)	0,89
0,415	0,711	0,101	0,824	0,415	0,415	1.00(0.78-1.29)	0,99
0,102	0,213	0,157	0,434	0,106	0,102	1.06(0.70-1.60)	0,78
0,098	0,162	0,642	0,188	0,103	0,097	1.08(0.72-1.63)	0,70
0,098	0,174	0,642	0,202	0,103	0,097	1.08(0.72-1.62)	0,72
0,331	0,581	0,805	0,495	0,319	0,332	0.94(0.72-1.23)	0,66
0,412	0,865	0,274	0,553	0,411	0,412	1.00(0.77-1.29)	0,97
0,105	0,283	0,720	0,311	0,106	0,105	1.03(0.69-1.54)	0,87
0,348	0,964	0,868	0,981	0,309	0,353	0.82(0.62-1.07)	0,14
0,324	0,376	0,442	0,512	0,326	0,324	1.01(0.77-1.33)	0,94
0,463	0,032	0,973	0,023	0,446	0,465	0.94(0.74-1.20)	0,62
0,401	0,115	0,565	0,057	0,401	0,401	1.01(0.79-1.30)	0,93
0,226	0,097	0,528	0,140	0,273	0,220	1.31(0.99-1.73)	0,06
0,309	0,723	0,795	0,647	0,287	0,312	0.88(0.67-1.16)	0,35
0,244	0,177	0,469	0,276	0,294	0,237	1.32(1.01-1.74)	4,46E-02
0,248	0,249	0,469	0,376	0,294	0,241	1.29(0.98-1.70)	0,06

0,138	0,885	0,595	0,731	0,128	0,139	0.92(0.64-1.34)	0,68
0,246	0,728	0,673	0,850	0,209	0,252	0.80(0.59-1.09)	0,15
0,425	0,560	0,216	0,876	0,408	0,427	0.94(0.73-1.21)	0,65
0,450	0,554	0,296	0,815	0,429	0,453	0.92(0.72-1.19)	0,54
0,346	0,576	0,999	0,551	0,337	0,347	0.95(0.73-1.23)	0,67
0,149	0,974	0,357	0,716	0,138	0,150	0.92(0.64-1.33)	0,67
0,239	0,127	0,493	0,190	0,284	0,232	1.29(0.98-1.69)	0,07
0,419	0,956	0,050	0,426	0,390	0,423	0.89(0.69-1.15)	0,37
0,265	0,759	0,040	0,662	0,262	0,266	0.98(0.74-1.31)	0,91
0,462	0,334	0,206	0,137	0,496	0,457	1.18(0.92-1.51)	0,19
0,456	0,380	0,206	0,165	0,496	0,451	1.20(0.94-1.54)	0,14
0,345	0,606	0,235	0,887	0,316	0,349	0.85(0.65-1.12)	0,25
0,221	0,790	0,758	0,711	0,262	0,215	1.33(1.00-1.78)	5,23E-02
0,231	0,943	0,106	0,636	0,209	0,234	0.86(0.63-1.17)	0,34
0,447	0,484	0,138	0,204	0,415	0,452	0.86(0.67-1.10)	0,22
0,356	0,622	0,528	0,760	0,333	0,359	0.89(0.68-1.16)	0,39
0,319	0,842	0,696	0,703	0,280	0,324	0.81(0.61-1.07)	0,13
0,303	0,728	0,837	0,768	0,298	0,304	0.96(0.73-1.26)	0,75
0,447	0,484	0,138	0,204	0,415	0,452	0.85(0.66-1.10)	0,21
0,051	0,198	0,418	0,072	0,064	0,049	1.33(0.80-2.21)	0,27
0,355	0,257	0,204	0,448	0,330	0,358	0.87(0.67-1.14)	0,33
0,220	0,835	0,930	0,803	0,209	0,221	0.93(0.68-1.26)	0,61
0,253	0,962	0,038	0,393	0,319	0,244	1.50(1.14-1.98)	3,89E-03
0,305	0,330	0,758	0,334	0,262	0,311	0.78(0.58-1.04)	0,09
0,170	0,422	0,225	0,616	0,248	0,159	1.86(1.37-2.54)	6,83E-05
0,461	0,742	0,035	0,272	0,422	0,466	0.83(0.64-1.06)	0,14
0,301	0,424	0,758	0,439	0,262	0,306	0.80(0.60-1.06)	0,12
0,483	0,464	0,201	0,215	0,518	0,478	1.19(0.93-1.52)	0,17
0,473	0,707	0,011	0,191	0,433	0,478	0.82(0.64-1.05)	0,12
0,344	0,147	0,284	0,238	0,312	0,348	0.84(0.64-1.11)	0,22
0,474	0,722	0,011	0,199	0,433	0,480	0.81(0.63-1.05)	0,11
0,490	0,916	0,040	0,428	0,429	0,499	0.74(0.57-0.95)	1,81E-02
0,246	0,970	0,842	0,958	0,216	0,250	0.82(0.61-1.11)	0,19
0,477	0,644	0,017	0,184	0,429	0,483	0.79(0.62-1.02)	0,07
0,227	0,682	0,102	0,894	0,305	0,216	1.66(1.25-2.20)	3,88E-04
0,227	0,697	0,102	0,876	0,305	0,216	1.66(1.25-2.20)	3,96E-04
0,048	0,389	0,505	0,227	0,053	0,048	1.11(0.64-1.93)	0,70
0,229	0,673	0,102	0,900	0,305	0,218	1.63(1.23-2.17)	5,88E-04
0,048	0,389	0,505	0,227	0,053	0,048	1.11(0.64-1.93)	0,70
0,180	0,243	0,189	0,405	0,252	0,170	1.76(1.29-2.39)	3,07E-04
0,185	0,579	0,332	0,754	0,255	0,175	1.70(1.26-2.30)	5,10E-04
0,232	0,822	0,143	0,803	0,312	0,221	1.66(1.25-2.19)	3,63E-04
0,183	0,541	0,386	0,673	0,252	0,173	1.69(1.25-2.29)	6,61E-04
0,224	0,919	0,393	0,896	0,295	0,214	1.59(1.20-2.11)	1,31E-03
0,246	0,763	0,900	0,775	0,227	0,249	0.89(0.66-1.19)	0,42
0,499	0,327	0,721	0,255	0,454	0,506	1.23(0.96-1.58)	0,10
0,016	0,587	0,864	0,606	0,014	0,016	0.90(0.31-2.58)	0,84
0,489	0,292	0,221	0,121	0,450	0,495	0.83(0.65-1.06)	0,13
0,491	0,264	0,300	0,121	0,454	0,496	0.84(0.65-1.07)	0,15
0,492	0,303	0,267	0,137	0,457	0,496	0.84(0.66-1.08)	0,18
0,481	0,059	0,789	0,037	0,518	0,476	1.19(0.93-1.52)	0,16
0,215	0,676	0,918	0,679	0,270	0,208	1.44(1.08-1.92)	1,22E-02
0,222	0,716	0,978	0,625	0,280	0,214	1.47(1.11-1.96)	7,57E-03
0,222	0,716	0,978	0,625	0,280	0,214	1.47(1.11-1.96)	7,57E-03
0,221	0,772	0,787	0,575	0,284	0,213	1.51(1.14-2.01)	4,20E-03
0,254	0,637	0,916	0,511	0,312	0,245	1.43(1.09-1.89)	1,08E-02
0,314	0,169	0,709	0,107	0,316	0,314	1.00(0.76-1.32)	1,00
0,487	0,188	0,561	0,113	0,443	0,493	0.82(0.64-1.05)	0,11
0,190	0,346	0,927	0,278	0,241	0,182	1.48(1.09-2.00)	1,19E-02
0,225	0,334	0,395	0,461	0,266	0,220	1.33(0.99-1.78)	0,06
0,290	0,181	0,787	0,126	0,284	0,290	0.97(0.73-1.28)	0,81
0,235	0,266	0,952	0,211	0,282	0,229	1.36(1.02-1.82)	3,37E-02
0,302	0,157	0,750	0,104	0,294	0,303	0.96(0.72-1.27)	0,77
0,039	0,558	0,796	0,562	0,021	0,042	0.49(0.21-1.14)	0,09
0,467	0,298	0,598	0,204	0,426	0,472	0.82(0.64-1.05)	0,12
0,308	0,294	0,575	0,363	0,309	0,308	1.00(0.76-1.32)	0,98
0,305	0,282	0,575	0,348	0,309	0,305	1.02(0.77-1.34)	0,90
0,305	0,076	0,931	0,063	0,294	0,307	0.94(0.71-1.24)	0,65
0,216	0,365	0,899	0,386	0,262	0,209	1.34(1.01-1.78)	4,09E-02
0,196	0,544	0,051	0,934	0,195	0,196	0.99(0.73-1.36)	0,96
0,434	0,128	0,150	0,280	0,411	0,438	0.89(0.69-1.14)	0,35

0,349	0,597	0,056	0,205	0,326	0,352	0.90(0.69-1.18)	0,45
0,488	0,042	0,740	0,066	0,387	0,502	0.64(0.50-0.82)	3,82E-04
0,485	0,037	0,543	0,076	0,379	0,501	0.62(0.49-0.80)	2,02E-04
0,491	0,362	0,932	0,453	0,603	0,475	1.66(1.28-2.13)	7,92E-05
0,338	0,277	0,581	0,273	0,241	0,352	0.59(0.45-0.79)	3,28E-04
0,358	0,681	0,216	0,854	0,433	0,348	1.43(1.11-1.84)	5,68E-03
0,354	0,660	0,165	0,827	0,429	0,344	1.43(1.11-1.85)	5,19E-03
0,387	0,904	0,331	0,740	0,447	0,378	1.33(1.04-1.72)	2,57E-02
0,407	0,067	0,483	0,025	0,358	0,414	0.79(0.60-1.03)	0,08
0,338	0,284	0,581	0,281	0,241	0,352	0.59(0.44-0.79)	3,15E-04
0,470	0,977	0,545	0,879	0,518	0,464	1.26(0.98-1.62)	0,07
0,174	0,582	0,307	0,839	0,174	0,174	1.01(0.73-1.41)	0,94
0,154	0,616	0,797	0,663	0,160	0,153	1.07(0.76-1.50)	0,72
0,154	0,616	0,797	0,663	0,160	0,153	1.07(0.76-1.50)	0,72
0,154	0,616	0,797	0,663	0,160	0,153	1.07(0.76-1.50)	0,72
0,116	0,094	0,198	0,204	0,128	0,114	1.14(0.79-1.65)	0,48
0,153	0,543	0,729	0,605	0,157	0,152	1.05(0.74-1.48)	0,78
0,114	0,227	0,598	0,144	0,106	0,116	0.90(0.60-1.34)	0,62
0,067	0,692	0,418	0,480	0,064	0,068	0.91(0.55-1.51)	0,70
0,208	0,996	0,712	0,843	0,241	0,203	1.27(0.94-1.71)	0,12
0,196	0,229	0,588	0,141	0,188	0,197	0.93(0.68-1.28)	0,68
0,132	0,294	0,856	0,230	0,152	0,130	1.22(0.86-1.73)	0,25
0,482	0,893	0,559	0,783	0,418	0,491	0.74(0.57-0.95)	1,92E-02
.							
0,203	0,682	0,087	0,259	0,266	0,194	1.52(1.14-2.03)	4,11E-03
0,408	0,702	0,629	0,771	0,465	0,400	1.31(1.02-1.69)	3,75E-02
0,219	0,420	0,266	0,190	0,245	0,215	1.17(0.88-1.57)	0,27
0,189	0,603	0,167	0,996	0,220	0,185	1.26(0.92-1.71)	0,15
0,109	0,433	0,598	0,303	0,106	0,109	0.99(0.66-1.48)	0,96
0,109	0,613	0,598	0,463	0,106	0,109	0.99(0.66-1.48)	0,97
0,141	0,195	0,622	0,118	0,138	0,142	0.96(0.67-1.37)	0,83
0,408	0,702	0,629	0,771	0,465	0,400	1.31(1.02-1.69)	3,75E-02
0,186	0,815	0,756	0,682	0,213	0,182	1.24(0.91-1.69)	0,18
0,183	0,679	0,486	0,428	0,216	0,178	1.31(0.96-1.79)	0,09
0,257	0,109	0,517	0,114	0,323	0,248	1.50(1.13-1.98)	4,75E-03
0,188	0,855	0,167	0,717	0,220	0,183	1.27(0.94-1.73)	0,12
0,191	0,633	0,140	0,936	0,223	0,187	1.27(0.93-1.72)	0,13
0,494	0,340	0,052	0,769	0,511	0,492	1.09(0.85-1.41)	0,50
0,094	0,996	0,230	0,580	0,138	0,087	1.68(1.15-2.44)	5,89E-03
0,248	0,873	0,360	0,984	0,181	0,258	0.63(0.46-0.87)	4,29E-03
0,195	0,164	0,033	0,525	0,230	0,190	1.29(0.95-1.76)	0,10
0,093	0,943	0,230	0,529	0,138	0,086	1.69(1.16-2.47)	4,88E-03
0,105	0,627	0,910	0,595	0,089	0,107	0.80(0.52-1.24)	0,29
0,164	0,765	0,511	0,945	0,167	0,164	1.00(0.72-1.40)	0,97
0,247	0,935	0,360	0,948	0,181	0,257	0.64(0.46-0.88)	4,76E-03
0,164	0,742	0,511	0,920	0,167	0,163	1.01(0.72-1.41)	0,95
0,094	0,976	0,204	0,582	0,142	0,088	1.73(1.19-2.51)	3,19E-03
0,494	0,283	0,108	0,584	0,511	0,492	1.09(0.85-1.41)	0,49
0,342	0,642	0,793	0,684	0,323	0,344	0.90(0.69-1.18)	0,45
0,248	0,945	0,360	0,826	0,181	0,257	0.64(0.46-0.88)	4,72E-03
0,494	0,258	0,108	0,541	0,511	0,492	1.10(0.85-1.41)	0,49
0,350	0,753	0,965	0,742	0,329	0,352	0.89(0.68-1.17)	0,41
0,490	0,218	0,075	0,510	0,514	0,486	1.14(0.88-1.48)	0,31
0,096	0,574	0,230	0,237	0,138	0,089	1.60(1.10-2.32)	1,08E-02
0,414	0,979	0,703	0,988	0,348	0,423	0.71(0.55-0.93)	1,14E-02
0,244	0,729	0,880	0,789	0,174	0,255	0.61(0.44-0.85)	2,57E-03
0,454	0,781	0,900	0,847	0,401	0,461	0.77(0.59-0.99)	4,09E-02
0,161	0,580	0,878	0,594	0,163	0,161	1.00(0.72-1.40)	0,98
0,248	0,843	0,880	0,918	0,174	0,258	0.60(0.43-0.83)	1,65E-03
0,162	0,631	0,960	0,621	0,167	0,161	1.03(0.74-1.43)	0,87
0,409	0,895	0,706	0,872	0,337	0,419	0.69(0.53-0.90)	5,99E-03
0,273	0,984	0,166	0,591	0,270	0,274	0.96(0.72-1.28)	0,80
0,308	0,908	0,433	0,878	0,291	0,311	0.90(0.68-1.18)	0,45
0,308	0,705	0,543	0,856	0,298	0,310	0.93(0.71-1.23)	0,62
0,236	0,800	0,673	0,918	0,209	0,240	0.83(0.61-1.12)	0,23
0,226	0,372	0,217	0,620	0,184	0,231	0.74(0.54-1.02)	0,07
0,056	0,384	0,292	0,646	0,082	0,052	1.65(1.02-2.68)	3,99E-02
0,125	0,307	0,803	0,249	0,177	0,118	1.65(1.17-2.33)	3,85E-03
0,065	0,905	0,982	0,913	0,085	0,062	1.41(0.89-2.23)	0,14
0,065	0,908	0,982	0,917	0,085	0,062	1.41(0.89-2.23)	0,14
0,048	0,348	0,630	0,454	0,067	0,045	1.50(0.90-2.49)	0,11

0,317	0,035	0,528	0,043	0,333	0,315	1.08(0.82-1.42)	0,57
0,125	0,309	0,803	0,251	0,177	0,118	1.65(1.17-2.33)	3,75E-03
0,065	0,905	0,982	0,913	0,085	0,062	1.41(0.89-2.23)	0,14
0,061	0,254	0,228	0,491	0,092	0,056	1.76(1.11-2.79)	1,56E-02
0,064	0,837	0,982	0,841	0,085	0,061	1.44(0.91-2.28)	0,11
0,063	0,217	0,228	0,425	0,092	0,058	1.70(1.07-2.69)	2,31E-02
0,065	0,905	0,982	0,913	0,085	0,062	1.41(0.89-2.23)	0,14
0,150	0,417	0,985	0,295	0,206	0,142	1.59(1.15-2.19)	4,27E-03
0,117	0,682	0,751	0,769	0,135	0,115	1.22(0.84-1.76)	0,29
0,319	0,854	0,739	0,748	0,318	0,319	1.02(0.77-1.33)	0,90
0,401	0,859	0,933	0,971	0,496	0,388	1.56(1.21-2.01)	4,64E-04
0,374	0,764	0,846	0,948	0,465	0,361	1.54(1.20-1.99)	6,84E-04
0,066	0,149	0,868	0,096	0,078	0,065	1.25(0.77-2.03)	0,36
0,357	0,923	0,746	0,953	0,301	0,365	0.75(0.57-0.98)	3,72E-02
0,371	0,869	0,367	0,595	0,390	0,369	1.09(0.84-1.42)	0,50
0,268	0,922	0,725	0,939	0,305	0,262	1.24(0.95-1.64)	0,12
0,210	0,851	0,003	0,361	0,209	0,210	0.99(0.73-1.35)	0,95
0,251	0,906	0,750	0,753	0,294	0,245	1.29(0.98-1.71)	0,07
0,148	0,521	0,057	0,184	0,131	0,150	0.84(0.58-1.22)	0,35
0,361	0,597	0,658	0,633	0,305	0,369	0.74(0.57-0.98)	3,37E-02
0,478	0,509	0,666	0,569	0,514	0,473	1.19(0.92-1.53)	0,19
0,233	0,759	0,027	0,620	0,230	0,233	0.98(0.73-1.32)	0,90
0,428	0,799	0,891	0,737	0,450	0,425	1.11(0.86-1.43)	0,41
0,185	0,555	0,689	0,610	0,220	0,180	1.30(0.95-1.77)	0,10
0,188	0,520	0,986	0,462	0,223	0,183	1.31(0.96-1.78)	0,09
0,256	0,534	0,746	0,552	0,301	0,249	1.32(1.00-1.74)	5,27E-02
0,067	0,321	0,868	0,243	0,078	0,065	1.22(0.75-1.97)	0,42
0,066	0,348	0,874	0,266	0,079	0,065	1.24(0.76-2.00)	0,38
0,112	0,199	0,643	0,180	0,163	0,105	1.71(1.19-2.45)	3,42E-03
0,223	0,531	0,691	0,430	0,202	0,226	0.87(0.64-1.18)	0,36
0,236	0,305	0,795	0,279	0,287	0,229	1.38(1.04-1.84)	2,45E-02
0,195	0,471	0,960	0,474	0,167	0,199	0.80(0.58-1.11)	0,18
0,066	0,335	0,868	0,254	0,078	0,065	1.23(0.76-1.99)	0,40
0,233	0,354	0,795	0,324	0,287	0,225	1.41(1.06-1.87)	1,75E-02
0,312	0,183	0,530	0,228	0,344	0,308	1.19(0.91-1.57)	0,20
0,218	0,669	0,830	0,608	0,196	0,221	0.86(0.63-1.18)	0,35
0,235	0,265	0,707	0,253	0,291	0,227	1.42(1.06-1.88)	1,56E-02
0,169	0,263	0,847	0,224	0,213	0,162	1.42(1.03-1.95)	3,06E-02
0,287	0,319	0,452	0,182	0,277	0,288	0.95(0.72-1.24)	0,69
0,465	0,599	0,891	0,445	0,550	0,453	1.50(1.16-1.94)	1,70E-03
0,240	0,140	0,439	0,194	0,264	0,236	1.18(0.88-1.58)	0,27
0,011	0,719	0,898	0,737	0,011	0,011	0.97(0.28-3.32)	0,98
0,234	0,243	0,707	0,227	0,291	0,226	1.43(1.07-1.90)	1,31E-02
0,226	0,724	0,551	0,563	0,209	0,228	0.90(0.66-1.22)	0,49
0,217	0,929	0,465	0,740	0,195	0,220	0.86(0.63-1.17)	0,34
0,176	0,140	0,928	0,083	0,220	0,170	1.41(1.03-1.94)	3,27E-02
0,288	0,283	0,371	0,140	0,282	0,288	0.98(0.74-1.28)	0,86
0,070	0,233	0,910	0,196	0,089	0,068	1.37(0.87-2.17)	0,17
0,474	0,886	0,077	0,424	0,507	0,469	1.17(0.91-1.51)	0,21
0,228	0,849	0,619	0,719	0,206	0,231	0.87(0.64-1.18)	0,35
0,269	0,322	0,598	0,217	0,319	0,262	1.29(0.99-1.69)	0,06
0,296	0,236	0,554	0,319	0,248	0,303	0.76(0.57-1.01)	0,06
0,247	0,217	0,135	0,450	0,248	0,247	1.01(0.76-1.34)	0,94
0,160	0,531	0,856	0,466	0,152	0,161	0.95(0.67-1.34)	0,78
0,216	0,119	0,233	0,224	0,216	0,216	1.00(0.74-1.35)	0,98
0,116	0,949	0,672	0,793	0,131	0,114	1.17(0.81-1.70)	0,41
0,405	0,780	0,106	0,830	0,351	0,413	0.78(0.60-1.02)	0,07
0,167	0,421	0,578	0,515	0,167	0,167	1.01(0.71-1.42)	0,97
0,155	0,459	0,578	0,562	0,167	0,153	1.13(0.80-1.59)	0,49
0,206	0,857	0,638	0,682	0,152	0,213	0.67(0.47-0.95)	2,37E-02
0,158	0,598	0,518	0,754	0,170	0,156	1.13(0.80-1.58)	0,48
0,486	0,747	0,256	0,973	0,415	0,496	0.72(0.56-0.94)	1,46E-02
0,242	0,305	0,581	0,375	0,241	0,242	1.01(0.75-1.36)	0,96
0,237	0,871	0,588	0,944	0,188	0,244	0.73(0.53-1.00)	4,98E-02
0,012	0,674	1,000	0,652	0,000	0,014	.	.
0,172	0,732	0,518	0,901	0,170	0,172	0.99(0.71-1.39)	0,95
0,172	0,732	0,518	0,901	0,170	0,172	0.99(0.71-1.39)	0,95
0,397	0,847	0,062	0,400	0,358	0,403	0.84(0.65-1.10)	0,20
0,484	0,948	0,256	0,804	0,415	0,493	0.73(0.57-0.95)	1,74E-02
0,233	0,724	0,985	0,711	0,238	0,233	1.04(0.77-1.39)	0,81
0,449	0,814	0,159	0,888	0,376	0,459	0.72(0.55-0.93)	1,24E-02

0,449	0,814	0,159	0,888	0,376	0,459	0.72(0.55-0.93)	1,24E-02
0,216	0,763	0,298	0,447	0,135	0,227	0.53(0.37-0.76)	5,77E-04
0,453	0,718	0,124	0,958	0,379	0,463	0.72(0.55-0.93)	1,21E-02
0,196	0,884	0,986	0,861	0,223	0,192	1.23(0.91-1.67)	0,19
						.	.
0,196	0,487	0,751	0,355	0,135	0,205	0.60(0.42-0.87)	7,10E-03
0,187	0,612	0,427	0,808	0,216	0,183	1.26(0.92-1.72)	0,14
0,187	0,750	0,689	0,833	0,220	0,182	1.29(0.95-1.76)	0,11
0,183	0,865	0,427	0,902	0,216	0,178	1.30(0.95-1.77)	0,10
0,187	0,592	0,427	0,784	0,216	0,183	1.26(0.92-1.72)	0,15
0,330	0,836	0,081	0,400	0,309	0,333	0.92(0.70-1.21)	0,57
0,257	0,116	0,842	0,077	0,216	0,263	0.78(0.57-1.05)	0,10
0,142	0,206	0,960	0,183	0,167	0,138	1.20(0.86-1.68)	0,28
0,418	0,867	0,114	0,432	0,433	0,416	1.07(0.83-1.38)	0,60

smoking status and/or BMI as covariates.

Supplementary Table 4. Association analysis of polymorphisms in HLA-DPB1 and its 3' region on 6p21.3 with the the percent decrease of FEV f

Locus	Alleles	Position (Amino acid change)	GWAS				C/C
			C/C	C/R	R/R	p	
rs987870	T>C	5'	639(7.67±12.52)	152(8.16±10.76)	9(12.40±16.31)	0,41	894(7.03±11.52)
rs2071351	G>A	Intron1					342(6.87±11.26)
rs2071352	T>A	Intron1					886(7.06±11.55)
rs2071354	T>C	Intron1					893(7.03±11.52)
rs3135021	G>A	Intron1	250(8.23±12.57)	378(7.41±12.28)	171(8.13±11.71)	0,98	355(7.63±12.32)
rs1431402	T>A	Intron1					840(6.23±9.65)
rs1431403	C>T	Intron1					296(7.56±12.23)
rs1042151	A>G	Exon2 (M105V)					920(6.28±9.91)
rs928976	T>C	Intron2					285(7.55±12.27)
rs9378177	A>G	Intron2					495(7.53±11.46)
rs7772134	G>T	Intron2					988(7.02±11.17)
rs3128961	G>A	Intron2					282(6.40±9.27)
rs9277419	A>G	Intron2					277(6.19±9.00)
rs9277535	A>G	3'UTR	208(6.60±10.31)	409(8.28±13.14)	183(8.16±12.22)	0,29	285(6.35±9.23)
rs9277539	A>G	3'					363(6.68±9.99)
rs9277554	C>T	3'	207(6.63±10.02)	410(8.26±13.21)	182(8.24±12.22)	0,27	278(6.24±9.02)
rs9277565	C>T	3'	270(7.19±10.95)	389(8.18±13.09)	141(8.01±12.17)	0,56	359(6.53±9.83)
rs10484569	G>A	3'	369(8.24±12.62)	344(8.00±12.39)	87(5.26±9.77)	0,07	491(7.39±11.36)
rs2281390	C>A	3'	645(7.90±12.27)	147(7.28±11.87)	8(10.89±10.00)	0,99	903(7.14±11.37)
rs2281389	T>C	3'	654(7.06±11.30)	137(10.95±15.39)	9(15.22±15.17)	1,76E-04	917(6.29±9.92)
rs3128917	T>G	3'	269(7.21±10.96)	390(8.16±13.09)	141(8.01±12.13)	0,59	358(6.56±9.84)
rs2281388	C>T	3'	375(8.35±12.71)	339(7.89±12.23)	86(5.21±9.76)	4,45E-02	500(7.48±11.42)
rs7764491	C>G	3'					986(7.01±11.19)
rs3117222	G>A	3'	269(7.21±11.00)	390(8.16±13.09)	141(8.01±12.13)	0,59	355(6.58±9.87)
rs3128918	T>C	3'	645(7.90±12.36)	147(7.28±11.87)	8(10.89±10.00)	0,99	904(7.18±11.43)
rs3130192	C>T	3'	676(7.76±12.23)	110(7.66±12.48)	7(5.44±8.69)	0,96	946(7.06±11.32)
rs3128927	C>T	3'					783(6.15±9.67)
rs3130215	G>A	3'	665(7.94±12.36)	134(7.08±11.61)	1(24.00)	0,58	941(7.14±11.34)
rs910320	G>A	3'					917(6.31±9.92)
rs3117230	T>C	3'	652(7.08±11.32)	139(10.80±15.33)	9(15.22±15.17)	2,86E-04	915(6.31±9.93)
rs6937061	A>G	3'					1017(7.06±11.38)
rs11751659	A>G	3'					939(7.02±11.35)
rs9348907	C>A	3'					472(7.72±11.53)
rs9277628	A>C	3'					536(7.23±11.80)
rs9277630	C>A	3'					536(7.14±11.69)
rs9277637	C>T	3'					498(7.00±11.64)
rs1810472	A>G	3'	272(7.73±12.74)	395(7.99±12.37)	133(7.47±10.83)	0,95	401(7.06±12.20)
rs9277642	T>C	3'					495(6.97±11.62)
rs9277656	G>T	3'					486(7.06±11.71)
rs3129294	T>G	3'					722(6.00±9.67)
rs3117039	G>A	3'	244(7.33±11.70)	378(7.05±11.68)	176(10.08±13.81)	3,27E-02	354(6.27±10.07)
rs1883414	C>T	3'	542(6.86±11.21)	229(10.08±14.35)	29(7.88±10.42)	1,12E-02	762(6.15±9.83)
rs3129286	C>T	3'					918(6.52±10.43)
rs6913744	A>G	3'					382(6.52±11.19)
rs6913896	A>T	3'					381(6.53±11.20)
rs9277756	G>A	3'					417(6.81±11.46)
rs9277761	G>C	3'					503(6.84±11.10)
rs3117008	T>C	3'	235(9.45±13.41)	389(7.12±11.33)	175(7.19±12.42)	4,72E-02	320(8.45±12.07)
rs3129270	G>A	3'					1036(6.60±10.45)
rs3129269	G>T	3'	531(7.00±11.39)	233(9.50±14.02)	36(8.93±11.18)	3,14E-02	755(6.43±10.57)
rs6901221	A>C	3'	691(7.10±11.24)	106(12.19±16.89)	3(19.00±16.09)	2,97E-05	984(6.44±10.35)
rs3116994	T>C	3'					889(7.09±11.28)
rs2294472	C>T	3'	539(7.21±11.26)	233(9.41±14.36)	28(6.21±9.89)	0,17	756(6.59±10.52)

for 1 month after aspirin challenge

Fine-mapping study			Coefficients
C/R	R/R	p	(R square)
218(6.83±9.50)	11(12.42±15.62)	0,63	0,0049
561(6.92±11.08)	216(7.65±11.55)	0,38	0,0053
226(6.71±9.40)	11(12.42±15.62)	0,73	0,0048
219(6.82±9.48)	11(12.42±15.62)	0,65	0,0048
550(6.57±10.68)	218(7.28±10.55)	0,67	0,0048
268(9.25±14.75)	15(13.53±12.32)	1,11E-05	0,0216
589(7.02±11.39)	238(6.46±9.24)	0,33	0,0055
193(10.15±15.40)	10(17.27±13.50)	2,82E-07	0,0277
573(7.08±11.43)	265(6.42±9.37)	0,30	0,0056
503(7.13±11.49)	124(4.76±8.45)	2,50E-02	0,009
129(7.06±11.14)	4(15.45±21.17)	0,61	0,0049
574(7.06±11.48)	266(7.69±12.42)	0,24	0,0059
578(7.17±11.57)	265(7.72±12.44)	0,16	0,0064
571(7.09±11.50)	267(7.69±12.40)	0,22	0,006
554(6.99±11.32)	204(7.84±12.87)	0,34	0,0055
578(7.13±11.56)	267(7.69±12.40)	0,18	0,0062
560(7.08±11.38)	204(7.84±12.87)	0,24	0,0059
506(7.30±11.60)	122(4.74±8.51)	5,24E-02	0,0077
209(6.32±10.23)	10(9.51±9.48)	0,64	0,0052
194(10.11±15.37)	11(15.52±14.07)	6,98E-07	0,0262
559(7.08±11.39)	205(7.81±12.84)	0,26	0,0058
501(7.17±11.51)	122(4.72±8.50)	2,99E-02	0,0088
133(7.03±10.99)	4(15.45±21.17)	0,63	0,0049
560(7.07±11.38)	205(7.81±12.84)	0,27	0,0057
208(6.38±10.23)	10(9.51±9.48)	0,65	0,0049
166(6.90±10.68)	8(6.24±7.77)	0,90	0,0047
318(8.74±13.82)	22(14.22±14.53)	8,34E-06	0,0221
178(6.52±10.47)	3(10.00±13.53)	0,56	0,0049
194(10.05±15.37)	11(15.52±14.07)	1,01E-06	0,0255
197(10.00±15.28)	11(15.52±14.07)	1,21E-06	0,0252
102(6.71±9.20)	4(10.75±13.74)	0,99	0,0046
171(6.99±10.28)	9(10.68±15.10)	0,64	0,0049
511(7.02±11.47)	140(4.86±8.57)	9,97E-03	0,0105
472(6.98±10.84)	111(6.62±9.72)	0,67	0,0049
474(7.04±11.00)	113(6.59±9.65)	0,77	0,0047
498(7.14±11.14)	127(6.84±9.65)	0,91	0,0047
538(7.07±10.84)	184(6.92±9.95)	1,00	0,0046
500(7.17±11.18)	128(6.85±9.61)	0,86	0,0047
501(7.16±11.16)	127(6.75±9.58)	0,98	0,0046
346(8.89±13.69)	55(9.11±11.00)	9,97E-05	0,0181
534(6.67±11.21)	235(9.05±12.55)	4,51E-03	0,0117
322(9.03±13.81)	39(8.08±10.44)	5,91E-04	0,0151
196(9.15±13.88)	8(10.98±12.33)	2,28E-03	0,0131
538(7.31±11.42)	203(7.33±10.64)	0,27	0,0057
537(7.32±11.43)	203(7.33±10.64)	0,27	0,0057
521(7.16±11.18)	183(7.19±10.79)	0,55	0,005
482(7.17±11.40)	138(7.35±10.95)	0,49	0,005
533(6.63±10.87)	268(6.17±10.69)	9,83E-03	0,0105
85(12.41±17.18)	1(21.00)	2,27E-06	0,0243
319(8.23±12.56)	49(8.71±10.69)	1,34E-02	0,0101
132(11.28±15.59)	4(15.75±14.66)	1,41E-06	0,0253
217(6.69±10.94)	16(9.74±11.00)	0,99	0,0046
327(8.14±12.74)	40(6.70±9.83)	0,13	0,0068

Supplementary Table 5. Association analysis of polymorphisms in genes selected from GWAS with the the percent decrease of FEV for 1 month after a

Gene	Chr.	Locus	Allele	Position (Amino acid change)	GWAS		
					C/C	C/R	R/R
AK8 (C9orf98)	9	rs306530	G>A	3'	510(7.51±11.62)	254(8.33±13.38)	35(8.55±12.46)
		rs306525	A>G	3'	248(8.04±12.59)	378(7.91±11.50)	174(7.30±13.33)
		rs396819	G>A	intron	255(8.18±12.79)	383(7.62±11.20)	162(7.71±13.68)
		rs10901205	G>A	intron			
		rs10901206	T>C	intron	350(8.45±12.77)	364(7.35±11.00)	86(7.18±15.05)
		rs12550888	C>T	intron			
		rs386472	A>G	intron	221(8.26±13.49)	370(7.19±11.21)	208(8.53±12.61)
		rs574544	C>T	intron			
		rs4962210	C>T	intron	310(8.07±12.37)	384(7.20±11.69)	106(9.30±13.72)
		rs13294558	G>A	intron			
		rs913705	T>C	intron	201(7.15±11.33)	402(8.37±13.01)	196(7.39±11.54)
		rs4962077	C>T	intron			
		rs13285450	G>A	intron			
		rs10901207	G>A	intron	234(8.08±12.06)	385(8.26±12.69)	181(6.52±11.43)
		rs11243898	G>A	intron			
		rs11243900	G>A	intron	327(7.03±11.37)	356(8.45±12.74)	117(8.06±12.96)
		rs12000803	T>C	intron	562(7.73±12.58)	212(8.04±11.49)	26(7.83±11.16)
		rs10901209	A>G	intron			
		rs954390	G>A	intron	685(7.33±11.62)	113(10.38±14.98)	2(29.00±24.04)
		rs12552369	G>A	intron	321(8.21±12.18)	369(7.56±12.73)	110(7.50±10.75)
		rs4962078	C>T	intron	687(7.31±11.60)	111(10.58±15.03)	2(29.00±24.04)
		rs10901212	A>C	intron			
		rs932887	T>C	intron	531(7.12±11.43)	241(9.56±13.87)	27(6.49±10.96)
		rs7869905	C>G	intron			
		rs4962214	T>C	intron	679(7.38±11.63)	118(10.46±15.25)	3(2.00±3.61)
		rs932886	G>A	intron			
		rs4962215	C>T	intron			
		rs2809249	T>G	intron			
		rs215156	G>A	intron			
		rs2772008	G>T	intron	643(7.68±12.28)	142(8.65±12.11)	14(6.36±12.48)
		rs215189	C>T	intron	261(9.75±13.96)	380(6.64±10.68)	159(7.46±12.45)
		rs215188	T>A	intron			
		rs215187	G>A	intron	227(7.69±12.13)	408(7.16±11.82)	165(9.61±13.29)
		rs215185	T>C	intron	235(9.97±14.25)	379(6.71±10.65)	186(7.36±12.24)
		rs2519083	G>A	intron			
		rs215184	G>C	intron			
		rs215180	C>T	intron			
		rs215163	C>T	intron	231(10.01±14.18)	379(6.63±10.76)	190(7.52±12.17)
		rs451714	G>T	intron	231(10.01±14.18)	379(6.63±10.76)	190(7.52±12.17)
		rs438369	C>T	intron			
		rs2809253	T>G	intron	529(7.21±11.54)	238(8.63±13.22)	32(11.93±14.96)
		rs2771991	T>C	intron	224(10.02±14.16)	378(6.80±10.92)	198(7.27±12.03)
		rs4962220	G>A	intron	442(7.81±12.25)	304(8.12±12.89)	53(6.23±7.63)
		rs17149822	A>G	intron	693(7.48±11.85)	102(10.04±14.43)	5(8.64±15.92)
		rs1609597	C>T	intron	693(7.48±11.85)	102(10.04±14.43)	5(8.64±15.92)
		rs2771997	T>G	intron	530(7.20±11.53)	238(8.63±13.23)	32(11.93±14.93)
		rs214634	C>A	intron			
		rs2771994	G>A	intron	447(6.64±10.72)	292(9.06±13.73)	61(10.52±14.12)
		rs2254289	G>A	intron	530(7.20±11.30)	238(8.63±13.22)	32(11.93±14.96)
		rs10491535	A>G	intron	692(7.50±11.85)	103(9.92±14.40)	5(8.64±15.92)
		rs2526004	G>A	intron	442(7.81±12.25)	305(8.09±12.88)	53(6.26±7.62)
		rs10901218	C>T	intron	225(9.96±14.16)	379(6.83±10.90)	196(7.27±12.08)
C9orf9	9	rs2519760	G>A	intron	368(7.50±12.21)	331(7.97±12.01)	100(8.52±13.19)
		rs2231406	G>A	coding			
		rs2073869	C>T	coding			
TSC1	9	rs1050700	A>G	3'UTR	457(6.63±10.68)	285(9.15±13.88)	58(10.56±14.09)
		rs2809244	C>A	3'UTR	298(7.48±11.68)	366(8.14±12.63)	135(7.73±12.46)
		rs11243929	T>C	intron	670(7.16±11.52)	125(11.16±15.13)	5(12.20±14.18)
		rs2250057	T>G	intron	251(7.71±11.22)	368(8.27±13.10)	169(7.24±11.82)
		rs7020438	C>A	intron			
		rs10901219	C>T	intron	671(7.16±11.51)	124(11.18±15.19)	5(12.20±14.18)
		rs12345576	T>C	intron			
		rs10901220	G>A	intron	671(7.16±11.51)	124(11.18±15.19)	5(12.20±14.18)
		rs1073123	A>G	coding (M322T)	671(7.16±11.51)	124(11.18±15.19)	5(12.20±14.18)
		rs3761840	A>G	intron	234(8.10±12.64)	373(8.53±13.46)	193(6.09±8.61)
		rs10116061	C>T	intron			
		rs7874234	C>T	intron	643(7.21±11.39)	150(10.24±15.08)	7(11.74±14.69)
		rs4419933	C>T	intron			

NAB1	2	rs10793948	G>C	5'			
		rs1860849	C>G	intron			
		rs929566	G>C	intron			
		rs1989344	C>T	intron	681(8.05±12.64)	115(6.47±9.76)	4(6.00±5.87)
		rs958770	C>T	intron	519(8.34±12.90)	242(6.78±10.87)	39(7.35±10.98)
		rs1978273	T>C	intron			
		rs12612904	A>G	intron			
		rs2286896	A>G	intron	283(6.23±10.31)	374(7.78±12.70)	143(11.06±14.69)
		rs12611764	T>C	intron			
		rs10931468	C>A	intron	311(6.92±10.31)	373(7.66±12.70)	114(10.87±14.96)
		rs2356126	G>A	intron			
		rs3771317	A>G	intron			
		rs2192008	T>C	intron			
		rs10185029	T>C	intron			
		rs17465200	C>T	intron			
PCSK6	15	rs6716985	G>A	intron			
		rs4853516	G>A	intron	429(8.66±13.47)	307(6.92±10.77)	64(6.42±9.62)
		rs1804116	C>T	3'			
		rs2073595	G>A	3'	648(7.91±12.44)	143(7.24±11.32)	8(10.41±12.72)
		rs4965825	T>C	intron	525(8.04±12.41)	246(7.28±11.91)	28(8.30±12.71)
		rs2073594	T>C	intron			
		rs3784515	C>A	intron	525(8.11±12.48)	246(7.23±11.71)	28(7.59±12.59)
		rs7168817	T>C	intron	634(8.00±12.48)	159(7.07±11.19)	7(8.54±14.32)
		rs12902381	A>G	intron			
		rs7169313	C>T	intron	614(7.95±12.32)	177(7.01±10.75)	9(14.72±27.08)
		rs3825921	G>A	intron	372(8.28±13.20)	333(7.87±11.86)	95(5.80±9.31)
		rs2277594	G>A	intron			
		rs1871975	T>C	intron			
		rs9806256	T>C	intron	524(8.23±13.04)	242(7.20±10.99)	34(5.86±6.95)
		rs4965830	A>T	intron			
		rs2277593	C>T	intron	466(7.17±10.81)	297(8.82±14.20)	37(7.84±12.31)
		rs7182874	C>T	intron			
		rs1471656	T>C	intron	220(8.45±13.93)	387(8.01±12.30)	191(6.76±9.82)
		rs12594500	C>T	intron			
		rs752028	C>T	intron	529(8.19±12.99)	235(7.40±11.02)	36(5.05±7.39)
		rs882422	A>G	intron			
		rs2073592	C>T	intron	367(8.17±12.42)	358(7.58±12.36)	75(7.19±10.87)
		rs12916087	A>G	intron			
		rs11855415	T>A	intron			
		rs2086678	T>C	intron	286(7.29±11.00)	402(8.41±13.46)	112(7.00±10.59)
		rs1976033	T>C	intron	230(7.52±11.68)	413(8.45±12.93)	156(6.61±11.12)
		rs7162072	A>C	intron			
		rs6598451	A>G	intron			
		rs11854332	C>T	intron	708(8.16±12.61)	90(5.15±8.94)	2(7.00±1.41)
		rs11852754	A>T	intron			
		rs7175368	A>G	intron	587(8.08±12.84)	188(7.25±10.65)	25(5.90±8.69)
		rs12914198	A>G	intron	433(7.64±12.10)	312(8.45±12.80)	55(5.65±9.85)
		rs2949	T>C	intron	343(8.49±13.33)	360(7.66±11.94)	97(6.01±8.78)
		rs8038528	A>G	intron	513(8.06±12.48)	257(7.56±12.18)	30(5.82±7.95)
		rs11630183	A>G	intron	357(7.88±12.38)	360(7.87±12.31)	83(7.32±11.62)
		rs10152458	T>G	intron	273(7.29±11.30)	407(8.30±13.10)	120(7.37±11.29)
		rs10152471	A>G	intron			
		rs11247283	C>T	intron			
		rs12591632	T>G	intron			
		rs4965831	C>T	intron	240(7.15±10.87)	391(8.42±12.94)	168(7.41±12.44)
		rs12593069	C>T	intron	604(7.57±11.94)	179(8.87±13.51)	17(5.34±7.65)
		rs8031210	C>A	intron			
		rs1077015	C>A	intron	376(7.16±10.89)	353(8.41±13.32)	71(8.33±13.03)
		rs1078988	G>A	intron	226(7.72±11.37)	403(7.94±12.73)	171(7.65±12.25)
		rs7167668	A>G	intron	349(7.14±11.80)	377(8.24±12.62)	74(8.83±12.61)
		rs963172	C>A	intron			
		rs4965833	A>G	intron	336(9.24±13.25)	367(6.78±11.71)	97(6.83±9.08)
		rs3784509	T>C	intron			
		rs3784507	T>C	intron	591(7.69±12.25)	199(8.20±12.28)	10(7.30±12.37)
		rs2955965	A>G	intron	246(7.11±10.84)	366(8.02±12.60)	186(8.46±13.25)
		rs20543	T>C	coding (L571L)			
		rs2073590	T>C	intron			
		rs2073589	A>G	intron			
		rs6598456	T>C	intron	271(7.70±12.61)	387(8.04±11.93)	142(7.43±12.44)
		rs4965836	G>C	intron			
		rs739319	G>C	intron			

rs730557	G>C	intron			
rs8036466	C>T	intron			
rs8035763	G>C	intron			
rs2934996	T>C	intron			
rs3021420	A>G	intron			
rs7183455	C>G	intron			
rs3825915	G>T	intron	320(9.82±13.78)	371(6.86±10.65)	109(5.19±11.67)
rs3784493	G>A	intron			
rs3784492	C>G	intron			
rs3784491	A>G	intron	430(7.01±11.38)	305(8.21±12.45)	65(11.30±15.85)
rs3825914	C>G	intron			
rs2277590	A>T	intron			
rs10152309	C>T	intron	544(8.38±12.87)	227(6.71±11.00)	29(5.89±8.35)
rs1135911	G>A	coding (V56V)	576(7.85±12.59)	203(7.98±11.78)	21(5.45±6.41)
rs2277589	G>A	intron	541(8.26±12.88)	227(7.09±11.17)	32(5.40±7.32)
rs10152164	T>C	intron	364(7.34±12.12)	354(8.58±12.68)	82(6.65±10.71)
rs6598459	G>A	intron			
rs8042699	G>A	intron	689(8.03±12.27)	104(6.61±12.42)	7(4.57±4.16)
rs3784485	G>A	intron	231(6.98±10.68)	408(8.14±12.74)	161(8.20±13.06)
rs6598460	C>G	intron			
rs6598464	G>A	intron			
rs6598465	G>A	intron	382(8.07±12.87)	323(7.97±12.07)	95(6.26±10.09)
rs903556	A>G	intron			
rs1542807	T>G	intron			
rs1542808	T>C	intron	270(6.74±10.70)	396(8.50±12.82)	134(7.96±13.34)
rs3784484	C>T	intron	537(7.89±12.68)	233(7.70±11.61)	30(7.40±8.99)
rs3784481	C>T	intron	231(8.69±12.86)	411(7.93±12.65)	158(6.23±10.01)
rs4965381	A>G	intron	213(8.38±13.20)	406(7.82±12.54)	180(7.18±10.27)
rs12903394	G>C	intron			
rs4965843	A>G	intron	291(6.86±10.32)	397(8.04±12.63)	112(9.48±15.11)
rs2277586	T>C	intron			
rs7173569	G>A	intron			
rs10400809	C>T	intron			
rs1039037	A>G	intron			
rs903564	G>A	intron			
rs3784470	G>A	intron			
rs1982906	G>A	intron	234(7.91±12.80)	411(7.47±11.45)	155(8.59±13.48)
rs1874274	C>T	intron	355(8.14±12.56)	349(7.14±10.96)	96(9.07±15.14)
rs3784463	T>C	intron	202(7.89±10.81)	397(8.15±13.30)	201(7.08±11.39)
rs3825902	G>C	intron			
rs8043118	A>C	intron			
rs12437510	G>A	intron	271(8.15±12.83)	378(7.65±11.88)	151(7.63±12.12)
rs4965847	C>T	intron	457(7.77±12.15)	302(7.71±12.19)	40(8.64±13.89)
rs3825901	G>A	intron	411(7.93±12.15)	333(7.39±12.13)	55(9.66±13.68)
rs12901252	A>C	intron			
rs1532364	G>A	intron	525(8.10±12.76)	249(7.16±11.09)	26(8.39±12.43)
rs1000914	A>G	intron	525(8.10±12.76)	249(7.16±11.09)	26(8.39±12.43)
rs1108993	A>G	intron	524(8.09±12.77)	250(7.17±11.07)	26(8.39±12.43)
rs11633098	A>C	intron	525(8.10±12.79)	249(7.16±11.11)	26(8.39±12.43)
rs12916267	G>A	intron	524(8.08±12.72)	250(7.19±11.19)	26(8.39±12.43)
rs4965853	C>T	intron	269(7.38±11.90)	398(7.95±12.21)	133(8.29±13.06)
rs10152229	T>G	intron	351(8.42±12.94)	364(7.09±11.54)	85(8.45±12.27)
rs1495271	C>T	intron	298(7.66±12.26)	372(8.20±12.02)	130(7.08±12.86)
rs7168655	G>A	intron	587(7.90±12.13)	191(7.37±12.61)	22(9.48±12.87)
rs7169026	G>A	intron	519(7.71±12.29)	255(8.15±12.48)	26(6.70±9.21)
rs1006273	A>T	intron			
rs4965384	C>A	intron	333(8.13±12.57)	353(7.77±12.12)	114(7.05±11.73)
rs2643350	A>G	intron	601(8.19±12.81)	186(6.48±10.36)	13(9.83±8.88)
rs2643353	T>C	intron			
rs3825896	C>A	intron	452(7.44±11.54)	294(8.44±13.38)	53(7.68±11.67)
rs2643356	T>C	intron	250(6.77±10.42)	388(9.03±13.49)	162(6.53±11.44)
rs2643358	G>A	intron	575(8.15±12.00)	200(7.00±12.92)	23(7.43±11.94)
rs8024621	A>G	intron			
rs7170232	C>T	intron	408(7.44±11.61)	323(8.01±12.71)	66(9.42±13.72)
rs2412014	A>G	intron	363(7.45±11.51)	361(7.96±12.82)	76(8.85±12.96)
rs2412013	A>G	intron			
rs11638524	G>C	intron			
rs10438489	C>A	intron	569(8.17±12.06)	218(6.81±12.75)	13(9.28±12.07)
rs1466744	C>T	intron	358(8.07±12.54)	348(7.90±12.47)	90(6.56±9.98)
rs11638957	T>G	intron	383(7.36±11.56)	345(7.86±12.70)	71(9.70±13.51)
rs999102	T>C	intron			

rs1466745	C>T	intron	218(8.11±12.53)	397(7.79±12.63)	185(7.53±11.06)
rs6598472	G>C	intron			
rs6598473	G>A	intron	319(8.16±12.74)	372(7.73±12.37)	109(7.09±10.29)
rs12591689	C>T	intron			
rs7176003	G>A	intron	284(7.68±12.33)	397(8.04±12.09)	119(7.40±12.61)
rs11855154	C>T	intron	519(8.03±11.88)	259(7.42±12.82)	22(7.47±14.04)
rs6598474	A>G	intron			
rs6422008	C>T	intron			
rs12101979	A>G	intron			
rs7402924	G>A	intron	448(7.33±11.80)	306(8.36±12.85)	46(8.89±12.45)
rs4965870	G>A	intron	256(8.29±13.32)	407(7.73±11.95)	137(7.20±10.98)
rs12594107	G>A	intron			
rs7172696	A>G	intron	262(7.03±11.57)	411(8.09±12.48)	127(8.55±12.82)
rs7178458	T>C	intron			
rs11639051	C>A	intron			
rs7167996	T>C	intron			
rs1552948	C>T	intron	443(7.38±11.80)	305(8.43±12.82)	52(7.94±12.64)
rs4965385	A>G	intron			
rs2047216	G>A	intron			
rs4547317	A>T	intron			
rs4246336	A>G	intron	402(7.61±12.30)	337(8.11±12.38)	61(7.54±11.30)
rs903552	C>T	intron			
rs12719737	G>C	intron			
rs4965873	T>C	intron			
rs8041582	A>G	intron	240(6.72±12.16)	373(8.76±12.36)	164(7.91±12.05)
rs1587107	C>T	intron	242(6.69±12.16)	394(8.47±12.36)	164(7.91±12.05)
rs6598481	C>T	intron	464(8.43±12.00)	295(7.23±12.79)	41(5.09±10.56)
rs9806393	A>G	intron			
rs4965877	G>A	intron	392(7.57±12.36)	341(7.96±12.13)	66(8.59±12.37)
rs11853956	G>T	intron	491(8.45±12.08)	276(6.98±12.50)	33(5.39±11.70)
rs765825	A>G	intron	206(8.50±12.12)	407(7.92±12.29)	187(6.85±12.27)
rs12900435	C>A	intron	715(8.00±12.37)	84(6.31±11.10)	1(5.00)
rs6598483	T>C	intron	329(8.52±12.83)	283(7.14±11.51)	174(7.94±13.05)
rs924014	T>G	intron			
rs11247297	G>T	intron			
rs7174882	T>G	intron	618(7.59±11.94)	162(8.81±13.15)	10(10.20±14.97)
rs7177024	C>T	intron			
rs7166284	C>T	intron			
rs7165319	G>C	intron			
rs7166898	C>T	intron	327(7.70±12.88)	371(8.16±12.00)	102(6.96±11.02)
rs6598484	G>A	intron	230(7.00±12.06)	401(8.38±12.04)	169(7.60±12.37)
rs4965881	C>T	intron	452(8.20±12.69)	289(7.50±11.57)	59(6.44±11.94)
rs11247300	G>A	intron	209(7.02±12.63)	397(8.36±12.00)	193(7.60±12.35)
rs7166089	T>C	intron			
rs12437484	C>G	intron			
rs2012620	C>T	3'			
rs2806028	C>G	3'UTR			
rs12436416	C>T	intron			
rs12931	G>A	coding (T675T)	344(7.30±11.89)	379(7.52±11.74)	77(11.56±15.39)
rs2286836	C>T	intron	581(7.17±11.65)	199(9.09±13.01)	19(14.53±18.12)
rs12887074	A>G	intron			
rs4899452	C>G	intron			
rs9671668	A>G	intron			
rs1106301	G>A	intron			
rs2535920	T>C	intron			
rs1007934	G>A	intron	552(8.40±12.78)	233(6.58±11.10)	15(5.32±7.61)
rs11625299	T>C	intron			
rs997667	A>G	coding (F168F)			
rs10142131	G>A	intron	366(7.41±11.97)	362(7.48±11.73)	72(11.56±15.31)
rs12880210	A>C	intron	563(7.95±12.35)	223(7.71±12.22)	14(4.21±7.56)
rs7149207	G>A	intron	708(7.47±11.85)	87(10.27±14.72)	1(23.00)
rs2806057	G>A	intron			
rs955329	A>G	intron	566(7.08±11.58)	213(9.16±13.13)	21(13.86±17.32)
rs17123359	C>T	intron			
rs4903092	A>G	intron	343(7.33±11.87)	379(7.46±11.78)	78(11.67±15.32)
rs2333021	A>G	intron			
rs3742829	G>A	intron	479(6.33±10.55)	278(9.89±14.09)	43(10.98±14.47)
rs3742828	G>T	UTR	539(6.89±11.40)	228(9.60±13.32)	25(13.20±16.31)
rs12432987	A>C	intron	464(6.22±10.44)	291(9.90±14.09)	45(10.82±14.15)
rs2333022	C>G	5'			
rs12433952	C>A	5'	236(8.78±13.29)	414(7.31±11.74)	150(7.69±11.92)

ATP8B3	19	rs2806049	C>T	intron			
		rs8005215	T>C	intron	463(6.25±10.45)	290(9.88±14.12)	47(10.53±13.92)
		rs17124039	T>C	intron			
		rs17182104	G>C	intron			
		rs1990059	T>C	intron	581(7.14±11.56)	199(9.16±13.27)	20(14.21±17.70)
		rs362412	C>T	intron	684(7.47±11.88)	115(9.76±14.04)	1(23.00)
		rs3025768	A>G	intron			
		rs1054597	C>T	3'UTR			
		rs757528	G>A	3'UTR	208(8.17±11.68)	393(7.76±12.54)	198(7.58±12.26)
		rs2385387	G>A	coding (K1186K)			
		rs6510624	C>T	intron	436(7.84±12.44)	308(7.99±12.05)	56(6.71±11.88)
		rs3764606	A>G	coding (Y1141Y)	463(7.75±12.08)	284(7.34±12.03)	53(10.94±14.42)
		rs12461977	T>G	intron			
		rs8100003	T>C	intron	385(8.17±12.85)	352(7.48±11.37)	63(7.54±13.09)
		rs8100856	T>C	coding (V571I)	258(8.29±12.66)	396(7.51±11.58)	145(7.91±13.27)
		rs7253430	G>T	intron			
		rs45574836	C>T	coding (A160T)			
		rs17604735	A>G	intron	606(7.71±12.10)	179(8.10±12.93)	15(8.71±10.89)
		rs7249302	C>T	intron	603(7.69±12.08)	182(8.17±12.92)	15(8.71±10.89)
		rs10403288	G>A	intron	348(9.22±13.77)	354(6.87±11.59)	98(6.26±7.42)
		rs9941464	T>C	intron			
		rs4807143	G>A	intron	482(7.23±11.45)	286(8.71±13.52)	32(8.59±11.53)
		rs10421558	A>G	5'	264(9.19±13.48)	386(7.32±12.58)	150(6.68±8.25)
		rs11668832	A>G	5'			
		rs11882337	C>T	3'			
		rs10415018	A>G	coding (V408A)			
		rs3746037	A>C	intron	248(9.09±13.19)	385(7.36±12.41)	167(6.98±10.52)
		rs732310	C>A	intron	439(7.44±11.42)	316(8.27±12.84)	45(8.28±15.52)
		rs10422439	G>A	intron			
		rs893539	G>A	intron	478(7.24±11.77)	284(8.43±12.78)	38(10.50±14.06)
		rs1609760	G>T	intron			
		rs1609761	A>C	intron	250(9.19±13.34)	390(7.23±12.52)	160(7.10±9.22)
(TMEM196)	7	rs7802120	G>A	3'	276(8.55±13.70)	383(7.82±11.90)	141(6.37±9.93)
		rs2285924	A>T	3'UTR			
		rs17141851	G>A	intron	257(8.50±13.93)	386(7.59±11.19)	157(7.24±11.77)
		rs10435066	T>C	intron			
		rs6946520	A>G	intron			
		rs10240229	G>A	intron	430(8.95±13.80)	311(6.46±10.11)	59(6.69±9.68)
		rs6951739	A>T	intron			
		rs9886152	C>T	intron	356(9.35±13.92)	357(6.76±10.96)	87(5.91±8.94)
		rs17141862	T>C	intron	228(9.43±14.19)	376(7.38±11.68)	195(6.81±10.71)
		rs4721822	C>T	intron			
		rs2214552	C>T	intron			
		rs10263780	A>G	intron	285(8.97±14.20)	378(7.28±10.81)	137(6.91±11.47)
		rs10950752	A>G	intron			
		rs12530799	G>A	intron			
		rs1468287	T>A	intron			
		rs2390156	A>T	intron			
		rs10239147	T>C	intron	280(6.99±11.20)	379(7.89±11.79)	141(9.25±14.95)
		rs12534026	T>C	intron			
		rs16872383	A>T	intron			
		rs4719582	A>G	intron	671(8.08±12.55)	121(6.56±10.75)	8(4.88±3.00)
		rs7791038	A>G	intron			
		rs17141931	T>C	intron			
		rs10486365	A>G	intron	251(6.85±10.56)	395(7.95±12.30)	154(9.03±14.07)
		rs714238	C>T	intron	212(6.00±8.87)	395(8.11±12.61)	193(9.21±14.33)
		rs17141945	T>A	intron			
		rs6977660	T>C	intron	316(9.15±14.15)	372(7.24±11.11)	112(5.94±9.44)
		rs13230910	A>G	intron			
		rs12334267	A>G	intron	230(6.25±9.53)	386(8.09±12.62)	177(9.09±14.21)
		rs3922342	A>G	intron	272(8.17±13.54)	393(8.41±12.45)	135(5.36±7.88)
		rs12672257	C>T	5'			
		rs13233821	C>A	5'			
		rs10254427	T>C	5'	305(8.85±13.89)	372(7.50±11.06)	123(6.21±10.65)
		rs10226962	C>T	5'			
		rs10270204	C>T	5'			
		rs10240816	C>A	5'			
		rs4721826	C>T	5'	307(8.88±13.87)	371(7.43±11.22)	122(6.31±10.64)
		rs10239332	G>A	5'			
		rs4721827	A>G	5'			
		rs17142014	T>G	5'	590(7.77±12.37)	197(7.99±12.08)	13(7.18±9.24)

NRP2	2	rs17142018	G>A	5'			
		rs17142027	A>G	5'			
		rs9639334	A>G	5'	309(9.05±13.97)	374(7.47±11.52)	117(5.69±9.24)
		rs9638765	A>G	5'			
		rs10267417	C>T	5'	278(6.46±9.63)	382(8.47±13.42)	140(8.73±13.31)
		rs17142032	C>G	5'			
		rs10486371	T>C	5'	576(7.45±11.96)	205(9.00±13.17)	19(6.13±10.15)
		rs17142041	A>G	5'			
		rs2097811	G>A	5'			
		rs10224061	C>G	5'			
		rs7785317	G>T	5'			
		rs12666616	A>G	5'	449(8.16±13.00)	290(7.72±11.73)	61(5.74±8.17)
		rs3806577	A>G	5'	222(8.34±11.03)	422(7.90±13.17)	156(6.85±11.23)
		rs861078	A>G	intron	647(7.27±11.49)	149(10.12±14.69)	4(10.85±24.78)
		rs698909	A>G	intron			
		rs849530	T>G	intron	422(6.53±11.28)	305(8.98±13.43)	73(10.40±11.77)
		rs1533509	C>T	intron			
		rs950219	G>A	intron			
		rs849558	A>G	intron			
		rs849556	G>A	intron	687(7.51±11.83)	109(9.80±14.71)	4(6.58±4.59)
		rs3771051	G>A	intron			
		rs849555	T>C	intron	615(7.42±12.02)	175(9.04±12.89)	10(10.47±13.68)
		rs849554	C>T	intron			
		rs849553	C>A	intron			
		rs9636330	T>C	intron			
		rs3771048	T>C	intron			
		rs3771047	G>C	intron			
		rs863707	T>G	intron			
		rs3771045	C>T	intron			
		rs3771044	T>C	intron	517(7.81±12.74)	251(7.45±10.95)	32(10.85±12.56)
		rs2110875	C>T	intron	493(7.36±12.07)	260(8.44±12.70)	47(9.11±11.48)
		rs849543	C>T	intron			
		rs3771039	G>A	intron			
		rs3755243	A>G	intron			
		rs3755242	C>G	intron			
		rs3771038	C>T	intron			
		rs849538	T>C	intron			
		rs861079	C>T	intron	466(7.45±12.15)	280(7.73±11.61)	54(11.38±15.80)
		rs849526	G>A	coding (Y357Y)			
		rs868196	G>T	intron			
		rs3771033	G>A	intron			
		rs849523	T>C	intron	238(7.75±10.65)	401(7.46±12.44)	161(8.79±13.87)
		rs849521	C>G	intron			
		rs849584	G>T	intron			
		rs849581	G>A	intron	315(8.57±13.54)	366(7.09±11.54)	119(8.05±10.55)
		rs849575	A>C	intron	257(8.65±13.58)	388(7.41±11.96)	155(7.44±10.44)
		rs3771021	C>T	intron	389(7.74±12.73)	342(7.64±11.59)	69(9.08±12.68)
		rs849565	T>C	intron			
		rs1996412	A>G	intron	229(9.01±14.16)	394(7.05±11.43)	177(7.98±11.20)
		rs12472412	G>A	intron			
		rs13026243	T>G	intron	226(8.85±13.95)	364(7.34±11.82)	210(7.53±10.95)
		rs2241155	T>C	intron	219(8.42±13.73)	374(7.80±11.96)	207(7.22±10.70)
		rs3771016	A>G	intron	221(8.25±13.67)	371(7.76±12.18)	207(7.39±10.72)
		rs849559	G>T	intron			
		rs3771013	C>G	intron			
		rs6733650	C>T	intron			
		rs3755238	C>T	intron			
		rs10180293	A>G	intron	649(7.68±12.17)	140(8.55±12.69)	11(6.58±11.03)
		rs3755237	T>C	intron			
		rs3771010	G>C	intron			
		rs7564637	G>A	intron			
		rs872943	T>C	intron	640(7.67±12.19)	148(8.60±12.67)	12(6.03±10.69)
		rs3771004	G>A	intron	339(8.39±12.83)	366(7.62±12.42)	95(6.50±8.99)
		rs16837637	G>A	intron	348(8.14±12.09)	369(7.75±12.54)	83(6.72±11.57)
		rs3771003	T>G	intron	240(7.59±11.42)	365(8.26±12.63)	195(7.25±12.23)
		rs16837641	A>G	intron	288(7.20±10.92)	362(8.52±13.10)	150(7.30±12.52)
		rs3755233	C>T	intron	499(7.44±12.54)	252(8.27±11.10)	49(9.29±14.74)
		rs2160328	C>T	intron	386(7.90±12.35)	333(7.84±12.20)	81(7.33±12.03)
		rs1547477	C>G	intron			
		rs3771002	C>G	intron			
		rs3771000	G>A	intron	586(7.88±12.09)	200(7.43±12.21)	14(10.85±18.40)

DCDC2	6	rs4675542	G>C	intron			
		rs3770997	A>G	intron			
		rs3770996	T>C	intron	238(8.68±12.32)	389(7.09±11.61)	173(8.26±13.42)
		rs10932125	C>G	intron			
		rs3755232	A>G	intron	573(7.99±12.19)	209(7.05±11.99)	17(11.87±16.14)
		rs1990708	G>T	intron	484(7.54±12.70)	255(8.26±10.91)	53(9.15±14.20)
		rs15994	C>G	3'UTR			
		rs9393535	G>C	3'			
		rs6937665	G>A	3'UTR			
		rs6456594	G>A	3'UTR			
		rs2996452	G>A	intron			
		rs2791972	T>G	intron	492(7.37±11.71)	263(8.37±12.84)	45(9.41±14.29)
		rs1277190	T>C	intron			
		rs2799372	C>G	intron			
		rs793845	A>G	intron			
		rs2027584	C>A	intron	367(8.20±12.29)	350(7.75±12.61)	83(6.43±10.53)
		rs2799373	G>A	intron	392(7.99±11.93)	338(7.75±12.88)	68(6.76±10.97)
		rs793850	C>G	intron			
		rs9467075	G>A	coding	728(7.76±12.26)	69(8.53±12.52)	3(4.83±5.84)
		rs12153942	C>G	intron			
		rs9379648	G>A	intron			
		rs793843	G>A	intron			
		rs1770909	G>A	intron	380(8.17±11.87)	352(7.88±13.13)	68(5.55±9.70)
		rs4052671	T>C	intron			
		rs793842	A>G	intron	234(7.84±12.33)	400(8.84±13.41)	166(5.30±8.30)
		rs707885	G>A	intron			
		rs793837	T>G	intron	212(5.78±8.95)	391(8.91±13.44)	194(7.93±12.63)
		rs9460980	G>A	intron	224(7.63±12.25)	400(9.01±13.56)	176(5.34±8.13)
		rs793834	C>T	intron	337(8.13±11.86)	380(7.97±13.13)	83(5.83±9.35)
		rs1087287	G>C	intron			
		rs9295618	T>C	intron			
		rs9358760	A>G	intron			
		rs9295619	T>C	intron	225(7.96±12.57)	396(8.85±13.46)	179(5.36±8.05)
		rs870601	C>T	intron	474(6.75±11.44)	283(9.18±13.15)	43(10.58±13.71)
		rs6456601	T>C	intron			
		rs2792682	T>G	intron	729(7.92±12.37)	68(6.84±11.19)	3(4.83±5.84)
		rs12055879	A>C	intron	472(6.77±11.46)	280(9.31±13.06)	44(10.00±14.09)
		rs807699	T>C	intron	729(7.92±12.37)	68(6.84±11.19)	3(4.83±5.84)
		rs3789224	G>A	intron	529(6.78±11.37)	245(9.52±13.40)	26(12.86±15.32)
		rs2328208	T>C	intron	525(6.79±11.41)	245(9.48±13.19)	30(12.19±16.04)
		rs9379650	C>T	intron			
		rs17302729	G>A	intron	527(6.87±11.57)	244(9.22±12.98)	28(13.14±15.47)
		rs2274305	G>A	coding (G221S)	479(6.87±11.64)	277(8.94±12.56)	44(11.08±14.50)
		rs3804326	G>A	intron			
		rs3846829	C>T	intron	208(8.38±9.40)	388(8.46±13.18)	203(6.07±12.77)
		rs33914824	C>G	coding (P152A)			
		rs3895346	G>C	intron			
		rs2185599	G>T	intron			
		rs10806987	T>C	intron	215(7.98±12.60)	387(8.55±13.00)	198(6.19±10.02)
		rs1340695	A>C	intron	226(6.40±9.94)	378(8.38±13.09)	196(8.36±12.87)
		rs7741108	G>A	intron			
		rs12192947	A>G	intron	489(6.87±11.27)	269(8.74±13.18)	42(12.90±15.15)
		rs4269365	A>G	intron			
		rs9366567	G>T	intron	491(6.85±11.26)	267(8.64±13.08)	42(13.86±15.57)
		rs9460992	G>A	intron	453(6.77±11.40)	295(8.58±12.63)	52(12.54±15.59)
		rs12661152	T>C	intron			
		rs4504468	T>G	intron	214(8.86±13.25)	390(8.12±12.73)	196(6.06±9.88)
		rs16889092	C>G	intron			
		rs1923168	G>A	intron	486(7.01±11.56)	275(8.79±13.04)	39(10.97±14.08)
		rs9379655	A>C	intron			
		rs12192603	T>C	intron	472(6.87±11.40)	283(8.70±12.90)	45(12.20±15.27)
		rs1535331	A>G	intron	378(8.06±11.80)	351(7.50±12.50)	71(8.08±13.64)
		rs9393551	T>C	intron			
		rs1277351	T>C	intron	230(9.32±14.25)	397(7.72±11.75)	173(6.05±10.11)
		rs793674	T>C	intron	370(7.52±11.24)	356(8.04±13.04)	74(8.21±13.27)
		rs6922023	G>A	intron	374(7.55±11.20)	352(8.02±13.09)	74(8.21±13.27)
		rs9460999	G>C	intron			
		rs7775357	G>A	intron			
		rs10498720	A>C	intron			
		rs813227	T>C	intron			
		rs3765502	A>G	intron	319(8.19±12.53)	376(7.24±11.89)	105(8.72±12.68)

ILVBL	19	rs13301	C>T	3'			
		rs2074261	A>C	intron			
		rs1468198	T>C	intron			
		rs7507755	A>G	intron			
		rs2074265	A>C	coding (L213L)	341(7.16±11.60)	358(7.78±12.48)	101(10.18±13.33)
		rs718100	G>T	intron			
		rs4141356	A>G	5'UTR			
		rs2074267	A>C	intron	265(9.01±12.54)	409(7.23±12.52)	124(7.31±10.52)
		rs2240299	C>T	intron	348(9.10±13.26)	359(7.19±12.09)	93(5.40±7.53)
		rs9290927	T>A	3'			
CLDN1	3	rs3864005	G>A	3'	548(7.68±12.28)	225(7.92±12.02)	27(9.63±13.86)
		rs8298	C>T	3'UTR			
		rs8798	G>A	3'UTR			
		rs9290928	G>A	3'UTR			
		rs1060679	C>T	3'UTR			
		rs12629166	T>C	intron			
		rs3774032	G>A	intron			
		rs3774028	T>A	intron			
		rs6800425	G>A	intron	511(7.11±11.24)	253(9.24±14.12)	36(7.81±11.37)
		rs6776378	G>A	intron			
		rs9869263	G>A	coding (G123G)			
		rs10513846	G>A	intron	213(8.55±13.44)	394(8.80±12.64)	193(5.00±9.38)
		rs6809685	A>G	intron	706(7.24±11.60)	89(12.35±14.12)	5(8.50±12.68)
		rs9866788	T>C	intron			
		rs9852326	T>C	intron			
		rs3732923	T>A	intron			
		rs6793070	C>T	intron			
		rs3774023	G>T	intron	645(7.73±12.20)	144(8.48±12.88)	11(4.15±5.62)
		rs3774022	A>G	intron			
		rs9839711	C>G	intron			
		rs3774019	C>T	intron	289(5.99±10.35)	379(8.85±12.72)	132(8.84±14.24)
		rs893051	G>C	intron			
		rs12696600	A>C	5'UTR			
		rs1155884	A>C	5'			
		rs16865347	T>C	5'			
		rs16865352	A>G	5'	529(7.41±12.21)	243(8.69±12.34)	28(7.86±12.34)
		rs44637	A>G	3'	196(7.46±11.65)	412(8.46±12.71)	192(6.80±11.82)
		rs2293638	C>T	intron			
		rs664354	G>A	intron			
		rs3782486	T>C	intron			
KRT75	12	rs10876290	A>G	intron			
		rs2232399	C>A	intron			
		rs2232386	C>G	coding (P117A)			
		rs298109	G>A	coding (R91G)	451(8.25±12.51)	303(7.55±12.39)	46(5.35±7.65)
		rs3759193	A>G	5'	552(7.95±12.41)	228(7.21±11.86)	19(11.28±12.52)
		rs4761880	C>T	5'	660(7.22±11.91)	136(10.63±13.50)	4(9.75±16.70)
		rs400120	A>G	5'			
		rs371202	T>C	5'			
		rs1798642	C>T	5'	451(8.25±12.51)	303(7.55±12.40)	46(5.35±7.65)
		rs409929	G>A	5'	196(7.53±11.73)	413(8.29±12.43)	191(7.09±12.39)
KRT6B	12	rs429561	G>C	3'			
		rs375539	G>A	3'			
		rs11170121	T>G	3'	661(7.24±11.94)	134(10.61±13.42)	5(8.80±14.62)
		rs400774	C>A	3'	269(8.51±13.25)	395(7.76±11.90)	136(6.62±11.13)
		rs597340	G>A	3'	449(8.57±12.86)	303(6.91±11.57)	48(6.51±9.94)
		rs610794	A>G	3'			
		rs17717236	A>G	3'			
		rs417466	G>A	intron			
		rs3809178	A>C	5'			
		rs447003	C>T	5'			
MEIS1	2	rs2280334	T>C	intron	415(7.25±11.31)	328(8.76±13.73)	57(6.47±9.11)
		rs2049019	C>A	intron	370(7.61±11.65)	361(8.25±13.22)	69(6.64±9.88)
		rs1519103	G>T	intron	367(7.54±11.60)	366(8.18±12.98)	67(7.36±11.80)
		rs10865353	G>A	intron			
		rs6716792	C>A	intron	480(8.43±13.26)	280(6.76±10.42)	40(7.82±11.16)
		rs17032103	C>T	intron	704(7.41±11.46)	95(10.84±16.86)	1(8.00)
		rs6727352	G>A	intron	591(7.25±11.45)	199(9.34±14.34)	10(11.10±11.57)
		rs10203407	G>A	intron	690(7.81±12.38)	107(7.80±11.51)	3(9.57±11.36)
		rs10192756	A>G	intron			
		rs11889571	T>A	intron			
		rs6705285	G>T	intron	357(7.82±11.87)	376(7.49±12.42)	67(9.67±13.26)

GP6	19	rs7578320	T>C	intron	591(7.25±11.44)	199(9.34±14.34)	10(11.10±11.57)
		rs17032114	A>G	intron	690(7.81±12.38)	107(7.80±11.51)	3(9.57±11.36)
		rs17032119	T>G	intron			
		rs7563565	C>T	intron	690(7.81±12.39)	107(7.80±11.53)	3(9.57±11.36)
		rs4671729	A>C	intron			
		rs2139246	G>A	intron	690(7.81±12.38)	107(7.80±11.51)	3(9.57±11.36)
		rs1519106	T>C	intron			
		rs11692361	T>C	intron	623(7.29±11.47)	162(9.62±14.46)	15(10.10±15.97)
		rs11692504	T>C	intron			
		rs12619205	A>G	intron	287(5.77±10.13)	379(8.24±12.64)	134(10.98±14.37)
		rs13023583	C>T	intron	317(6.16±10.50)	367(8.05±12.38)	116(11.62±15.09)
		rs4547518	C>T	intron	686(7.70±11.96)	112(8.48±13.96)	2(11.50±14.85)
		rs12620754	C>G	intron			
		rs12713567	G>A	intron			
		rs4387782	T>G	intron			
		rs12373638	C>T	intron	489(8.27±12.72)	269(6.46±10.99)	42(11.23±13.78)
		rs4430927	G>A	intron			
		rs4605359	G>C	intron			
		rs7579466	A>T	intron			
		rs12713568	C>T	intron	212(6.92±11.50)	410(7.57±12.50)	178(9.45±12.45)
		rs6721499	T>C	intron	463(8.05±12.30)	288(6.89±11.79)	49(11.06±13.11)
		rs3890755	C>T	intron			
		rs7586211	G>A	intron			
		rs4586617	G>T	intron			
		rs4316926	A>G	intron			
		rs6742861	T>C	intron	690(7.69±11.95)	107(8.53±14.15)	3(10.33±10.69)
		rs6728018	C>T	intron	691(7.69±12.00)	106(8.55±14.27)	3(10.33±10.69)
		rs12621998	C>G	intron			
		rs4480973	C>A	intron	488(7.92±11.43)	267(7.99±13.88)	45(5.64±10.25)
		rs3891585	G>A	intron	464(7.24±11.74)	293(8.62±13.04)	43(8.53±11.91)
		rs12621948	C>G	intron			
		rs11693646	G>A	intron			
		rs10865355	G>A	intron	465(7.24±11.73)	293(8.58±13.01)	42(8.84±12.24)
		rs9789535	A>G	intron	376(6.90±11.58)	350(8.60±12.92)	74(8.75±12.08)
		rs12472245	T>A	intron			
		rs11897119	T>C	intron	462(7.17±11.63)	294(8.64±13.13)	42(8.84±12.24)
		rs2216120	T>C	intron	551(7.45±12.14)	231(8.43±12.49)	18(11.13±12.40)
		rs2300477	A>G	intron	405(7.81±11.25)	325(8.11±13.14)	70(6.49±13.48)
		rs2192954	A>G	intron	231(6.23±10.80)	396(7.98±12.91)	172(9.64±12.29)
		rs2300478	T>G	intron	462(7.06±12.08)	299(8.94±12.36)	39(8.15±11.90)
		rs2300479	A>C	intron			
		rs2300481	C>T	intron			
		rs2300482	T>G	intron			
		rs6711787	G>A	intron	491(7.93±11.36)	269(7.94±13.93)	40(5.65±10.51)
		rs2284706	A>G	intron	541(7.41±12.20)	240(8.33±12.27)	19(12.86±12.56)
		rs10202912	A>G	intron			
		rs2300484	C>T	intron	684(7.60±11.81)	113(9.07±14.69)	3(10.33±10.69)
		rs2110974	A>G	intron			
		rs2300486	G>T	intron			
		rs12614369	A>G	intron			
		rs6735071	T>C	intron			
		rs2216123	A>G	intron			
		rs1000756	C>T	intron	564(7.82±12.02)	213(7.71±12.58)	23(8.62±15.12)
		rs2066927	A>G	intron			
		rs2216124	G>A	intron			
		rs1654410	T>C	3'	285(8.98±13.49)	391(7.57±12.28)	124(5.93±8.36)
		rs10416380	G>A	3'	554(8.09±12.22)	227(7.01±12.20)	19(9.59±13.70)
		rs10417943	G>A	3'UTR			
		rs17836524	T>C	intron			
		rs17836526	T>A	intron			
		rs8106615	G>A	intron			
		rs12462907	C>T	intron			
		rs11669150	T>C	intron	464(8.57±13.58)	297(6.92±10.26)	39(5.73±8.52)
		rs1613662	A>G	coding			
		rs2886412	G>A	intron			
		rs1671196	T>C	intron	549(8.05±12.22)	229(7.19±12.29)	22(8.58±13.00)
		rs10401614	T>G	intron			
		rs12610286	G>A	intron			
		rs1671207	G>C	intron			
		rs4806636	T>G	intron			
		rs1654431	A>G	5'			

RDH13	19	rs1671215	A>C	3'	483(8.99±13.92)	286(6.11±8.83)	31(5.30±9.43)
		rs8113032	A>G	3'	242(9.40±13.95)	397(7.70±12.26)	161(5.72±8.72)
		rs4806637	A>G	3'UTR	521(7.66±11.78)	249(8.04±13.05)	30(8.75±13.66)
		rs775821	C>T	intron	459(9.18±13.93)	308(6.03±10.99)	33(5.54±10.25)
		rs3745912	G>A	intron			
		rs2124090	C>A	intron			
		rs2124089	C>G	intron			
		rs11084387	G>A	intron			
		rs11672111	G>C	intron			
		rs1671169	C>T	intron			
		rs1654464	C>T	intron			
		rs12462815	C>T	intron			
		rs1654467	T>C	5'	279(8.42±12.54)	383(6.87±11.14)	138(9.23±14.36)

ispirin challenge

Fine-mapping study				
p	C/C	C/R	R/R	p
0,40	714(6.94±10.90)	358(7.33±11.87)	51(6.51±10.64)	0,90
0,65	336(7.31±11.50)	539(7.00±10.91)	246(6.76±11.51)	0,60
0,74	344(7.44±11.68)	550(6.81±10.64)	228(7.01±11.85)	0,62
	343(7.45±11.69)	553(6.83±10.66)	225(6.97±11.81)	0,59
0,28	482(7.71±12.25)	508(6.47±9.70)	122(6.86±12.82)	0,20
	464(6.91±11.01)	513(7.34±11.57)	146(6.42±10.52)	0,87
0,88	310(7.54±11.78)	543(6.43±10.61)	270(7.72±11.65)	0,92
	935(6.80±10.82)	179(8.28±12.98)	8(7.74±12.47)	0,13
0,83	442(7.14±10.89)	538(6.54±10.45)	143(8.63±14.38)	0,48
	766(7.35±11.50)	322(6.59±10.85)	33(3.89±5.87)	0,06
0,82	291(6.41±9.88)	564(7.66±12.18)	267(6.46±10.37)	0,89
	452(6.36±10.08)	513(7.65±12.00)	158(7.05±11.54)	0,23
	539(7.23±11.18)	500(7.00±11.37)	84(6.10±10.44)	0,45
0,24	306(7.52±12.11)	561(7.21±11.20)	256(6.12±10.01)	0,16
	441(6.49±10.14)	520(7.54±11.97)	160(7.00±11.48)	0,35
0,23	451(6.30±10.03)	508(7.69±12.04)	159(6.99±11.56)	0,20
0,85	804(6.89±11.12)	287(7.41±11.58)	32(7.65±10.11)	0,50
	671(6.54±10.51)	396(7.56±12.17)	56(9.43±11.83)	3,86E-02
3,54E-03	959(6.74±10.78)	157(8.71±13.18)	5(14.60±19.28)	1,64E-02
0,47	467(7.22±11.49)	511(6.92±11.33)	145(6.93±9.78)	0,70
2,24E-03	966(6.71±10.75)	152(8.94±13.32)	5(14.60±19.28)	8,36E-03
	906(6.88±10.91)	200(7.81±12.45)	15(6.61±12.06)	0,41
0,08	747(6.52±10.26)	343(8.23±13.04)	33(6.59±10.26)	0,07
	747(6.52±10.26)	344(8.22±13.02)	32(6.73±10.39)	0,06
3,02E-02	949(6.78±10.81)	166(8.62±13.29)	5(4.20±7.79)	0,10
	906(6.89±10.91)	203(7.74±12.38)	14(6.94±12.45)	0,42
	747(6.52±10.26)	343(8.23±13.04)	33(6.59±10.26)	0,07
	731(6.48±10.20)	357(8.24±13.06)	34(6.63±10.11)	5,29E-02
	747(6.53±10.26)	342(8.25±13.05)	33(6.59±10.26)	0,06
0,67	905(6.90±10.92)	202(7.77±12.40)	15(6.61±12.06)	0,45
2,90E-02	355(8.50±12.50)	547(6.24±10.29)	217(6.75±11.06)	3,39E-02
	338(8.64±12.66)	555(6.26±10.30)	230(6.58±10.80)	1,58E-02
0,21	316(6.82±10.76)	589(6.57±11.04)	218(8.64±12.14)	0,11
2,06E-02	312(8.72±12.92)	556(6.31±10.17)	255(6.58±10.91)	1,70E-02
	735(6.62±10.84)	344(7.50±11.46)	44(10.50±14.33)	2,61E-02
	619(7.01±10.89)	430(7.20±12.09)	74(6.39±8.04)	0,83
	327(6.82±10.67)	581(6.54±11.08)	215(8.74±12.19)	0,10
3,08E-02	308(8.74±12.85)	551(6.27±10.28)	263(6.67±10.84)	2,27E-02
3,08E-02	308(8.74±12.85)	550(6.27±10.29)	264(6.67±10.82)	2,27E-02
	634(6.89±10.81)	418(7.46±12.33)	70(6.01±6.84)	1,00
1,44E-02	734(6.63±10.85)	344(7.50±11.46)	44(10.50±14.33)	2,66E-02
2,14E-02	298(8.78±12.84)	550(6.40±10.39)	275(6.45±10.70)	1,31E-02
0,56	635(6.88±10.81)	418(7.46±12.33)	70(6.01±6.84)	0,99
0,06	974(6.84±10.94)	141(8.43±12.78)	7(6.74±13.60)	0,16
0,06	974(6.84±10.94)	142(8.42±12.74)	7(6.74±13.60)	0,16
1,38E-02	735(6.62±10.84)	342(7.52±11.48)	46(10.17±14.13)	2,95E-02
	339(8.72±12.75)	543(6.27±10.28)	241(6.44±10.66)	8,74E-03
1,10E-03	622(6.22±10.31)	414(7.93±11.97)	87(8.68±13.02)	5,65E-03
1,38E-02	733(6.56±10.66)	343(7.51±11.47)	44(10.50±14.33)	1,86E-02
0,07	973(6.85±10.94)	142(8.35±12.77)	7(6.74±13.60)	0,18
0,54	635(6.88±10.81)	419(7.44±12.32)	69(6.13±6.82)	0,96
2,38E-02	298(8.74±12.85)	549(6.44±10.38)	273(6.44±10.72)	1,47E-02
0,55	525(6.70±10.81)	469(7.24±11.45)	129(7.73±11.88)	0,34
	1047(6.97±11.13)	74(8.00±12.16)	1(20.00)	0,34
	598(7.21±11.21)	433(6.64±11.16)	89(7.99±11.53)	0,98
9,95E-04	634(6.30±10.26)	402(7.92±12.14)	84(8.69±12.97)	8,37E-03
0,70	401(7.07±11.52)	533(7.00±10.93)	189(7.12±11.33)	0,98
4,79E-04	950(6.58±10.67)	167(9.55±13.56)	6(11.17±12.94)	9,38E-04
0,83	345(7.30±11.33)	538(7.11±11.35)	240(6.52±10.70)	0,43
	950(6.57±10.67)	166(9.56±13.60)	6(11.17±12.94)	9,31E-04
4,64E-04	950(6.58±10.67)	166(9.56±13.60)	6(11.17±12.94)	9,48E-04
	951(6.58±10.67)	166(9.56±13.60)	6(11.17±12.94)	9,36E-04
4,64E-04	951(6.58±10.67)	166(9.56±13.60)	6(11.17±12.94)	9,36E-04
4,64E-04	950(6.58±10.67)	166(9.56±13.60)	6(11.17±12.94)	9,66E-04
0,10	326(7.04±11.37)	537(7.53±11.67)	260(6.04±9.90)	0,33
	329(6.92±11.26)	454(6.91±11.05)	333(7.25±11.38)	0,72
3,15E-03	909(6.65±10.61)	205(8.70±13.36)	9(9.58±13.58)	1,21E-02
	371(7.28±11.53)	530(7.02±11.14)	222(6.71±10.82)	0,53

	368(7.25±11.54)	537(7.12±11.21)	218(6.49±10.61)	0,45
	481(6.23±9.47)	496(7.22±12.16)	146(9.13±12.75)	9,76E-03
	635(7.38±11.28)	412(6.95±11.40)	69(4.69±9.53)	0,13
0,23	950(7.20±11.62)	160(6.21±8.83)	10(5.91±4.43)	0,28
0,17	732(7.44±11.77)	341(6.28±10.04)	50(6.40±10.08)	0,15
	624(7.72±12.17)	421(6.20±9.92)	77(6.17±9.28)	4,23E-02
	640(7.39±11.25)	413(6.91±11.37)	70(4.63±9.48)	0,11
4,03E-04	.	.	.	.
	477(7.27±11.00)	506(7.02±11.61)	134(5.92±9.30)	0,27
1,22E-02	442(6.34±9.28)	524(6.90±11.95)	157(9.50±13.15)	7,85E-03
	486(7.40±11.26)	502(7.00±11.62)	134(5.92±9.30)	0,20
	434(6.13±9.03)	523(6.99±12.11)	166(9.59±12.91)	2,10E-03
	632(7.68±12.13)	418(6.21±9.93)	73(6.25±9.32)	5,28E-02
	725(7.49±11.81)	347(6.24±9.95)	51(6.20±10.08)	0,11
	486(7.42±11.25)	502(7.00±11.62)	133(5.93±9.33)	0,20
	1012(7.13±11.41)	107(6.32±9.24)	4(4.70±4.41)	0,40
5,00E-02	606(7.68±12.33)	426(6.32±9.85)	91(6.16±8.85)	0,06
	934(7.13±11.19)	178(6.59±11.43)	11(6.75±9.03)	0,52
0,77	918(6.98±10.95)	194(7.18±12.38)	11(9.93±11.21)	0,61
0,47	743(7.05±10.90)	339(6.98±11.90)	39(7.54±11.12)	0,99
	447(7.22±11.56)	545(6.57±10.42)	131(8.38±12.92)	0,77
0,32	747(7.10±10.97)	335(6.91±11.80)	41(7.00±10.71)	0,75
0,49	877(7.27±11.54)	236(6.19±9.79)	10(7.38±12.44)	0,25
	843(6.95±10.89)	260(7.26±12.34)	18(8.15±9.18)	0,62
0,80	866(7.18±11.39)	245(6.29±9.52)	12(12.88±23.35)	0,76
0,14	517(7.21±11.65)	468(7.19±11.35)	135(5.93±8.82)	0,37
	838(6.99±10.88)	262(7.37±12.34)	22(5.38±9.65)	0,95
	444(6.42±9.53)	508(7.39±12.05)	170(7.63±12.57)	0,12
0,16	734(7.26±11.96)	340(6.82±9.96)	47(5.34±6.65)	0,27
	742(7.20±11.92)	335(6.93±9.98)	46(5.30±6.72)	0,35
0,13	664(6.57±9.69)	408(7.88±13.29)	51(6.46±11.15)	0,15
	816(7.36±11.84)	279(6.23±9.14)	27(4.17±5.37)	0,06
0,16	300(7.75±13.43)	551(7.08±10.94)	271(6.14±8.71)	0,07
	895(6.99±11.16)	207(7.52±11.69)	16(5.61±7.85)	0,78
0,14	735(7.24±11.97)	339(6.92±9.87)	49(4.87±7.04)	0,23
	459(6.93±11.50)	514(7.60±11.91)	149(5.51±6.82)	0,43
0,44	507(7.14±10.98)	512(7.11±11.71)	100(6.28±9.86)	0,59
	608(6.92±11.43)	432(7.46±11.37)	83(5.81±8.23)	0,81
	797(7.20±11.82)	290(6.94±9.72)	35(4.41±7.82)	0,27
0,79	402(6.44±9.77)	567(7.76±12.47)	154(5.98±9.55)	0,66
0,68	321(6.75±10.36)	589(7.65±12.03)	213(5.82±9.92)	0,60
	575(6.71±10.52)	466(7.48±12.14)	77(6.96±10.65)	0,42
	386(7.15±12.03)	530(7.35±11.58)	205(5.97±8.17)	0,29
4,20E-02	983(7.36±11.59)	133(4.78±7.78)	3(4.67±4.16)	1,23E-02
	830(7.13±11.77)	262(7.03±9.57)	31(4.80±8.10)	0,44
0,22	815(7.22±11.84)	275(6.76±9.42)	33(5.11±8.33)	0,27
0,89	609(6.98±11.35)	431(7.45±11.45)	83(5.37±8.43)	0,62
0,08	473(7.44±11.82)	503(7.05±11.31)	146(5.77±8.41)	0,13
0,39	710(7.16±11.04)	370(7.02±11.87)	43(5.32±7.22)	0,45
0,73	492(6.95±10.92)	510(7.35±11.72)	119(6.20±10.15)	0,81
0,72	395(6.45±10.03)	566(7.64±12.21)	162(6.41±10.13)	0,54
	395(6.46±10.03)	565(7.64±12.22)	162(6.41±10.13)	0,56
	705(7.05±10.78)	367(7.26±12.33)	42(5.33±7.26)	0,72
	828(7.21±11.79)	265(6.70±9.45)	30(5.58±8.60)	0,32
0,65	344(6.69±9.72)	551(7.26±11.41)	228(7.06±12.72)	0,58
0,67	844(6.86±11.07)	255(7.87±11.92)	24(4.90±6.96)	0,57
	827(6.91±10.71)	276(7.47±12.72)	16(7.61±9.89)	0,46
0,17	540(6.40±9.66)	486(7.61±12.52)	95(7.52±11.77)	0,09
0,94	309(7.01±10.37)	578(7.14±11.82)	236(6.84±10.72)	0,98
0,17	492(6.43±10.33)	529(7.47±11.97)	98(7.84±11.28)	0,12
	521(6.43±9.67)	497(7.53±12.36)	103(7.40±12.15)	0,12
1,31E-02	455(8.23±12.62)	517(6.17±10.42)	149(6.13±7.79)	4,89E-03
	725(6.67±10.98)	344(7.81±11.76)	54(7.15±10.53)	0,22
0,58	831(6.88±10.81)	277(7.49±12.38)	14(7.99±10.54)	0,39
0,20	346(6.66±9.71)	533(6.71±10.94)	244(8.31±13.47)	0,08
	602(7.43±11.57)	451(6.66±11.23)	70(6.18±7.07)	0,16
	415(6.82±11.21)	553(7.23±11.34)	155(6.98±10.71)	0,82
	876(7.01±11.19)	231(7.11±11.36)	16(7.79±10.53)	0,87
0,94	373(7.32±12.27)	544(6.90±10.45)	206(6.91±11.15)	0,61
	396(7.01±11.92)	554(6.93±10.54)	173(7.46±11.62)	0,73
	601(6.75±10.16)	443(7.61±12.62)	79(6.07±10.23)	0,58

	571(7.53±11.58)	472(6.61±11.24)	80(6.16±7.54)	0,10
	332(6.61±11.68)	568(7.12±10.74)	223(7.51±11.66)	0,33
	333(6.61±11.66)	566(7.17±10.78)	223(7.39±11.62)	0,37
	485(6.53±10.53)	510(7.30±11.67)	127(7.99±11.78)	0,16
	846(6.99±11.45)	256(7.41±10.35)	20(4.57±11.43)	0,98
	584(6.38±11.02)	462(7.92±11.41)	77(6.86±11.10)	0,09
9,52E-05	457(8.34±12.05)	524(6.45±10.43)	142(5.07±10.73)	6,46E-04
	685(6.13±10.65)	374(8.37±11.62)	59(9.04±13.94)	7,27E-04
	528(6.37±10.27)	494(7.65±12.16)	100(7.58±10.95)	0,10
1,10E-02	604(6.44±10.25)	425(7.47±11.83)	94(8.96±13.71)	2,68E-02
	746(6.99±11.06)	341(7.05±11.61)	35(8.35±10.52)	0,70
	361(6.69±9.60)	553(7.10±11.87)	209(7.52±11.96)	0,43
0,07	780(7.44±11.77)	305(6.25±10.00)	38(5.25±7.56)	0,07
0,78	815(7.01±11.49)	283(7.27±10.72)	23(5.48±6.12)	0,98
0,11	777(7.36±11.75)	305(6.50±10.18)	41(5.04±6.71)	0,12
0,75	508(6.78±11.63)	494(7.62±11.18)	121(5.81±9.23)	0,94
	1005(7.07±11.31)	115(6.90±10.35)	2(2.00±7.07)	0,81
0,19	952(7.22±11.35)	161(6.19±10.61)	10(4.18±3.88)	0,18
0,30	329(6.38±9.64)	573(7.14±11.15)	221(7.77±13.30)	0,15
	413(6.37±9.78)	541(7.29±11.14)	169(7.91±14.22)	0,12
	398(6.37±9.77)	549(7.27±11.18)	175(7.86±13.99)	0,13
0,28	526(7.34±12.10)	464(7.06±10.70)	133(5.80±8.95)	0,22
	508(6.99±11.70)	493(7.40±11.06)	122(5.81±9.51)	0,66
	621(7.24±11.72)	418(7.14±11.04)	84(5.14±7.28)	0,25
0,20	385(6.20±9.63)	555(7.39±11.24)	183(7.75±13.82)	0,09
0,78	758(7.14±11.66)	325(6.86±10.40)	39(6.36±8.40)	0,62
0,07	313(7.84±12.70)	576(7.13±11.20)	233(5.75±8.73)	3,55E-02
0,35	305(7.53±12.85)	567(7.09±10.95)	251(6.36±9.49)	0,24
	785(7.24±11.55)	303(6.95±10.80)	35(3.52±4.05)	0,18
4,95E-02	413(6.28±9.32)	552(7.17±11.07)	157(8.63±15.36)	3,05E-02
	421(6.33±9.36)	553(7.20±11.14)	149(8.50±15.36)	4,01E-02
	484(6.32±9.23)	528(7.34±11.68)	111(8.79±15.71)	2,50E-02
	456(6.29±9.28)	537(7.40±11.54)	130(8.21±15.18)	4,95E-02
	569(7.06±11.49)	460(7.27±11.11)	94(5.87±9.84)	0,59
	1040(7.05±11.23)	82(6.79±10.76)	.	0,83
	432(7.38±12.03)	530(6.66±10.12)	155(7.42±12.44)	0,74
0,83	337(6.95±10.97)	582(6.82±10.34)	202(7.80±13.74)	0,52
0,94	490(7.27±11.93)	499(6.56±9.82)	134(8.01±13.12)	0,92
0,49	296(6.36±9.44)	559(7.26±12.26)	268(7.34±10.69)	0,25
	675(7.20±11.81)	387(6.81±10.33)	58(6.67±9.66)	0,58
	329(7.87±12.40)	541(6.63±10.68)	253(6.86±10.63)	0,25
0,64	365(7.69±12.39)	544(6.72±10.53)	214(6.78±10.71)	0,27
0,75	638(7.26±11.31)	422(6.78±11.01)	63(6.65±11.52)	0,49
0,66	576(7.41±11.34)	456(6.57±11.02)	90(7.16±11.34)	0,44
	514(6.72±10.48)	472(7.45±11.85)	137(6.87±11.55)	0,61
0,42	734(7.20±11.81)	353(6.68±9.89)	36(7.53±10.68)	0,65
0,42	733(7.20±11.82)	354(6.67±9.88)	36(7.53±10.68)	0,64
0,42	732(7.20±11.83)	355(6.67±9.87)	36(7.53±10.68)	0,65
0,42	727(7.22±11.86)	351(6.68±9.91)	36(7.53±10.68)	0,64
0,44	734(7.18±11.78)	352(6.73±10.00)	37(7.40±10.56)	0,68
0,43	390(6.79±10.38)	540(7.32±11.67)	193(6.77±11.51)	0,86
0,36	493(7.21±11.48)	506(6.73±11.06)	123(7.72±10.75)	0,94
0,85	415(6.78±10.93)	525(7.39±11.39)	183(6.63±11.30)	0,92
0,84	818(7.00±10.78)	274(7.01±12.41)	28(8.97±11.58)	0,69
0,98	732(6.90±11.41)	348(7.45±11.17)	42(6.07±7.52)	0,81
	545(7.04±11.09)	475(6.80±11.34)	103(8.17±11.22)	0,72
0,36	447(7.12±11.35)	503(7.08±11.37)	173(6.73±10.34)	0,69
0,14	846(7.23±11.74)	259(6.32±9.47)	18(8.48±7.91)	0,42
	754(6.98±11.56)	320(7.02±9.69)	49(8.12±14.50)	0,65
0,49	620(6.65±10.19)	433(7.60±12.61)	68(7.18±10.67)	0,27
0,80	359(6.06±9.11)	547(8.10±12.62)	217(6.00±10.29)	0,59
0,37	834(7.25±11.08)	271(6.24±11.60)	18(9.42±10.61)	0,55
	568(7.38±12.24)	454(7.03±10.47)	101(5.22±7.63)	0,09
0,18	566(6.78±10.36)	459(7.32±12.03)	94(7.80±11.90)	0,27
0,31	506(6.61±10.17)	507(7.21±11.44)	110(8.28±14.23)	0,13
	323(6.76±9.36)	559(7.03±11.47)	241(7.45±12.76)	0,38
	282(7.50±12.48)	566(6.96±11.23)	274(6.73±9.71)	0,34
0,39	826(7.30±11.11)	276(6.22±11.52)	19(8.71±10.76)	0,44
0,28	487(7.36±11.95)	503(6.99±11.08)	133(6.07±8.51)	0,20
0,16	536(6.62±10.29)	485(7.11±11.27)	101(8.92±14.90)	0,08
	314(6.68±9.39)	560(6.99±11.37)	249(7.62±12.82)	0,25

0,48	290(7.61±12.45)	567(6.96±11.23)	265(6.60±9.63)	0,21
	308(6.82±9.66)	549(7.09±11.46)	262(7.35±12.35)	0,46
0,29	442(7.37±12.13)	522(7.00±11.04)	158(6.27±8.84)	0,24
	416(6.95±10.74)	538(7.35±11.65)	169(6.29±10.87)	0,82
0,87	414(6.92±10.74)	538(7.36±11.60)	170(6.34±11.08)	0,89
0,74	743(7.14±10.54)	347(6.85±12.45)	32(7.00±12.31)	0,87
	669(7.07±10.68)	403(7.09±12.12)	51(6.31±10.56)	0,93
	640(7.56±12.20)	410(6.61±9.81)	72(5.05±8.94)	3,33E-02
	468(7.40±11.99)	513(6.85±10.72)	142(6.54±10.22)	0,29
0,21	631(6.50±10.46)	425(7.71±12.27)	67(7.94±10.67)	0,08
0,33	354(7.33±11.81)	568(7.16±11.40)	201(6.19±9.41)	0,26
	788(7.03±11.24)	305(7.10±11.16)	30(6.83±11.03)	0,97
0,20	369(6.31±10.13)	569(7.42±11.82)	185(7.35±11.26)	0,20
	322(6.31±10.55)	573(7.26±11.58)	228(7.54±11.12)	0,18
	623(6.55±10.44)	424(7.79±12.36)	75(7.03±10.35)	0,17
	792(7.02±11.23)	301(7.19±11.16)	28(6.75±11.62)	0,95
0,32	623(6.54±10.45)	423(7.70±12.25)	77(7.45±11.02)	0,14
	623(6.53±10.45)	425(7.80±12.33)	75(7.03±10.35)	0,16
	557(6.59±10.78)	464(7.42±11.78)	99(8.05±10.82)	0,13
	527(7.24±12.10)	483(7.12±10.50)	109(6.06±9.76)	0,36
0,78	564(6.84±10.78)	470(7.38±11.87)	88(6.62±10.27)	0,73
	379(6.49±11.49)	539(7.29±10.74)	205(7.43±11.86)	0,30
	380(6.48±11.45)	539(7.24±10.78)	204(7.58±11.82)	0,25
	309(6.00±10.75)	562(7.63±11.55)	251(7.04±10.92)	0,25
0,26	336(6.05±10.73)	555(7.71±11.71)	232(6.88±10.54)	0,29
0,25	336(6.05±10.73)	555(7.71±11.71)	232(6.88±10.54)	0,29
0,06	661(7.45±11.18)	402(6.69±11.51)	60(4.90±9.07)	0,09
	539(6.90±11.01)	483(7.27±11.55)	97(6.91±10.77)	0,74
0,47	546(6.90±11.04)	482(7.21±11.47)	94(7.06±10.89)	0,70
0,06	698(7.42±11.20)	376(6.54±11.27)	48(5.06±10.06)	0,10
0,23	289(7.51±10.82)	573(7.24±11.52)	261(6.10±10.91)	0,17
0,26	998(7.18±11.38)	123(6.01±9.71)	1(5.00)	0,29
0,40	312(7.47±11.48)	555(6.87±10.84)	255(6.89±11.68)	0,51
	883(6.64±10.57)	224(8.49±13.30)	15(8.80±12.59)	2,52E-02
	460(7.05±11.42)	525(7.27±11.26)	137(6.15±10.28)	0,62
0,19	859(6.78±10.64)	245(7.86±12.97)	19(8.18±11.38)	0,16
	891(7.08±11.17)	201(7.05±11.46)	30(5.67±10.88)	0,71
	903(7.02±11.05)	193(7.30±11.93)	27(6.06±11.27)	0,93
	463(7.03±12.18)	523(7.26±10.52)	137(6.27±10.28)	0,64
0,78	456(7.08±12.22)	527(7.21±10.54)	140(6.31±10.17)	0,58
0,44	307(6.51±10.88)	571(7.28±11.21)	237(6.85±11.18)	0,64
0,28	644(7.45±11.81)	399(6.68±10.19)	80(5.60±10.92)	0,12
0,51	273(6.81±11.33)	576(7.39±11.17)	274(6.55±11.17)	0,75
	604(7.53±11.93)	433(6.70±10.11)	86(5.31±11.00)	0,07
	318(6.86±11.22)	563(7.32±11.38)	234(6.73±10.89)	1,00
	998(6.82±10.90)	123(8.76±13.36)	1(23.00)	3,52E-02
	795(7.33±11.17)	302(6.58±11.55)	23(4.50±6.48)	0,19
	775(6.53±10.78)	313(7.91±11.69)	32(10.82±15.11)	1,12E-02
3,45E-02	479(6.78±11.44)	525(6.88±10.48)	119(8.81±13.12)	0,19
4,34E-03	811(6.60±10.87)	283(7.92±11.54)	29(10.87±15.53)	1,80E-02
	477(6.80±11.46)	526(6.98±10.70)	117(8.41±12.44)	0,27
	504(7.43±11.28)	497(6.88±11.53)	122(6.12±9.40)	0,19
	789(6.56±10.85)	302(7.95±11.59)	32(10.38±14.86)	1,65E-02
	963(7.07±11.36)	149(7.06±10.56)	11(4.18±3.70)	0,63
	796(7.33±11.19)	303(6.51±11.49)	23(4.50±6.48)	0,16
4,69E-02	778(7.27±11.16)	317(6.72±11.63)	24(4.95±6.39)	0,33
	328(7.64±11.81)	574(6.88±11.16)	220(6.61±10.38)	0,24
	505(6.89±11.49)	504(6.88±10.51)	106(8.90±13.15)	0,25
0,07	505(6.89±11.49)	508(6.79±10.44)	110(8.94±13.05)	0,26
0,48	783(7.23±11.51)	318(6.74±10.70)	22(4.68±6.25)	0,29
2,10E-02	999(6.81±10.89)	123(8.81±13.33)	1(23.00)	3,15E-02
	796(7.30±11.13)	305(6.33±11.39)	21(4.95±6.62)	0,15
3,01E-03	790(6.53±10.83)	300(8.00±11.63)	32(10.38±14.86)	1,26E-02
	871(7.00±11.29)	235(7.30±11.07)	17(4.72±7.31)	0,94
3,41E-02	482(6.77±11.34)	516(6.80±10.54)	120(8.90±13.10)	0,17
	405(6.28±10.57)	546(7.09±11.17)	171(8.64±12.56)	2,40E-02
2,48E-05	676(6.07±10.05)	388(8.35±12.59)	59(9.36±12.80)	4,16E-04
3,27E-04	759(6.39±10.67)	327(8.19±11.85)	37(9.85±14.40)	4,40E-03
1,59E-05	657(5.99±9.98)	403(8.43±12.59)	63(8.93±12.59)	3,71E-04
	806(6.58±10.82)	284(7.96±11.67)	31(10.85±15.02)	1,28E-02
0,24	338(7.48±11.71)	566(6.82±11.22)	218(6.86±10.32)	0,42

	797(7.41±11.24)	303(6.21±11.32)	23(4.78±6.48)	0,08
2,50E-05	654(6.00±10.01)	403(8.44±12.57)	65(8.77±12.43)	4,72E-04
	338(7.52±11.70)	559(6.76±11.25)	226(6.97±10.28)	0,45
	789(7.27±11.48)	310(6.61±10.75)	22(4.71±6.24)	0,22
3,48E-03	811(6.56±10.80)	283(7.98±11.70)	29(10.87±15.53)	1,26E-02
2,74E-02	968(6.81±10.91)	154(8.30±12.75)	1(23.00)	0,07
	991(6.84±10.92)	131(8.33±13.04)	1(23.00)	0,09
	624(7.05±10.89)	420(6.66±11.41)	78(8.90±12.42)	0,60
0,71	284(6.76±10.43)	552(7.08±11.78)	287(7.19±10.79)	0,68
	641(7.17±11.40)	408(6.44±10.54)	74(9.13±12.70)	0,81
0,66	627(6.86±10.95)	425(7.37±11.64)	71(6.44±10.70)	0,79
0,36	639(7.18±11.41)	408(6.42±10.54)	75(9.18±12.62)	0,80
	620(6.92±11.03)	433(7.27±11.52)	70(6.50±10.74)	0,89
0,41	549(7.30±12.02)	485(6.72±10.15)	88(6.90±11.33)	0,49
0,45	364(7.39±11.26)	553(6.85±11.07)	206(6.89±11.44)	0,45
	637(6.67±10.91)	407(7.33±11.19)	79(8.34±13.32)	0,12
	922(7.20±11.43)	193(6.33±10.10)	8(3.99±8.44)	0,21
0,74	872(6.89±10.66)	229(7.61±13.19)	19(7.23±10.07)	0,46
0,67	871(6.86±10.64)	232(7.65±13.20)	20(7.11±9.81)	0,44
7,83E-03	496(7.75±12.19)	491(6.59±11.09)	136(6.00±6.83)	5,38E-02
	293(6.30±8.67)	569(7.21±12.06)	261(7.46±11.74)	0,25
0,15	695(6.48±10.02)	388(8.04±13.07)	39(6.92±10.46)	0,07
4,65E-02	377(7.80±11.97)	532(6.77±11.86)	214(6.33±7.38)	0,12
	444(6.77±10.39)	532(7.38±11.91)	147(6.57±10.89)	0,91
	682(6.49±10.11)	388(7.87±12.92)	50(7.93±11.00)	0,06
	540(7.41±11.70)	467(6.43±10.94)	108(7.49±9.45)	0,53
0,10	357(7.63±11.60)	483(6.50±11.16)	283(7.17±10.72)	0,59
0,44	608(6.88±10.79)	450(7.28±11.44)	64(6.78±13.28)	0,79
	698(6.74±10.94)	376(7.41±11.67)	47(8.31±11.25)	0,23
0,07	684(6.72±10.98)	384(7.32±11.43)	51(9.19±12.57)	0,14
	693(6.73±11.00)	381(7.44±11.57)	48(8.18±11.18)	0,23
0,09	372(7.68±11.74)	529(6.49±11.16)	215(7.17±10.37)	0,49
0,11	391(7.45±11.89)	531(7.26±11.39)	199(5.63±9.04)	0,12
	540(7.74±11.76)	473(6.60±11.13)	110(5.40±7.94)	3,16E-02
0,31	365(7.39±12.08)	534(7.10±10.84)	224(6.27±10.53)	0,29
	385(7.50±11.97)	507(7.01±10.95)	229(6.29±10.42)	0,23
	938(7.10±11.31)	173(6.71±10.89)	9(5.24±5.44)	0,56
1,27E-02	611(7.70±11.97)	428(6.39±10.44)	83(5.48±8.59)	3,14E-02
	611(7.70±11.96)	427(6.40±10.45)	85(5.39±8.54)	2,73E-02
2,49E-03	508(7.97±12.10)	495(6.52±10.82)	120(5.13±7.96)	6,05E-03
3,07E-02	314(8.17±12.46)	537(6.85±11.11)	268(6.05±9.69)	2,84E-02
	300(7.98±12.55)	535(6.78±10.58)	288(6.50±10.79)	0,13
	942(7.08±11.27)	168(6.94±11.16)	10(5.02±5.18)	0,70
0,07	411(7.73±12.20)	521(6.89±10.72)	190(5.95±10.11)	0,07
	349(6.61±11.18)	539(6.76±10.43)	235(8.27±12.77)	0,11
	365(6.56±10.95)	538(6.86±10.68)	219(8.04±12.47)	0,15
	383(6.70±11.58)	515(6.75±10.18)	221(8.30±12.72)	0,13
	388(6.50±11.05)	536(6.98±10.72)	199(8.22±12.61)	0,10
0,07	378(6.65±11.21)	532(6.75±10.39)	209(8.50±13.03)	0,09
	352(6.75±11.51)	533(6.75±10.42)	230(8.17±12.52)	0,19
	492(7.53±11.66)	509(6.97±11.38)	121(5.24±7.93)	0,07
0,14	953(7.11±11.07)	161(6.73±12.22)	9(4.33±3.24)	0,55
	470(7.75±12.11)	516(6.90±11.00)	137(5.07±8.01)	1,96E-02
	707(6.75±10.54)	367(7.57±12.41)	49(7.06±10.80)	0,39
0,07	345(6.54±10.86)	558(6.90±10.83)	218(7.98±12.29)	0,15
7,52E-03	290(6.01±9.99)	561(7.06±11.09)	269(8.12±12.54)	2,44E-02
	319(6.10±10.25)	561(7.08±11.08)	243(8.13±12.52)	3,20E-02
9,35E-03	444(7.89±12.33)	519(6.70±10.10)	160(5.74±11.16)	2,55E-02
	447(7.86±12.29)	518(6.69±10.11)	158(5.80±11.20)	3,16E-02
1,59E-02	318(6.10±10.24)	560(7.12±11.08)	244(8.08±12.51)	3,47E-02
0,07	378(7.41±11.91)	554(7.32±11.61)	190(5.32±7.80)	0,07
	317(6.10±10.34)	554(7.18±11.12)	252(7.87±12.31)	0,06
	456(7.72±12.15)	516(6.80±10.16)	151(5.73±11.47)	4,82E-02
3,55E-02	420(7.77±12.19)	527(6.74±10.01)	175(5.92±11.67)	4,77E-02
	453(7.79±12.21)	516(6.77±10.14)	153(5.71±11.39)	3,68E-02
	313(6.20±10.36)	557(7.08±11.09)	253(7.93±12.33)	0,06
	452(7.81±12.22)	516(6.77±10.14)	152(5.72±11.42)	3,57E-02
3,63E-02	422(7.80±12.18)	527(6.76±10.14)	174(5.98±11.68)	5,25E-02
	400(7.90±12.39)	412(6.83±10.51)	290(6.19±10.57)	4,67E-02
	313(6.20±10.36)	554(7.07±11.12)	253(7.93±12.33)	0,06
0,98	838(6.99±11.34)	262(7.23±11.01)	23(6.32±7.54)	0,94

	838(6.99±11.34)	262(7.23±11.01)	23(6.32±7.54)	0,94
	810(6.80±11.14)	291(7.75±11.44)	22(6.04±9.73)	0,36
8,36E-03	418(7.89±12.30)	533(6.73±10.20)	169(5.91±11.31)	3,54E-02
	422(8.04±12.58)	534(6.59±9.86)	164(5.98±11.45)	2,15E-02
4,35E-02	394(6.16±9.94)	545(7.38±11.74)	184(7.87±11.98)	0,06
	811(6.79±11.14)	289(7.79±11.48)	23(5.91±9.53)	0,37
0,33	810(6.80±11.14)	290(7.75±11.47)	23(5.91±9.53)	0,40
	884(6.87±11.18)	224(7.62±11.46)	15(7.86±8.33)	0,35
	418(7.91±12.49)	534(6.72±10.00)	171(5.87±11.29)	3,00E-02
	636(7.45±11.77)	416(6.51±10.38)	71(6.34±10.47)	0,16
	477(7.45±11.75)	510(7.06±11.19)	136(5.42±8.94)	0,10
0,17	612(7.31±11.50)	430(6.72±10.38)	81(6.54±12.95)	0,35
0,28	320(7.14±9.81)	581(7.42±12.25)	215(5.75±10.14)	0,20
5,58E-03	906(6.65±10.70)	207(8.58±12.87)	8(8.66±16.43)	1,68E-02
	1039(6.82±10.91)	71(9.28±14.14)	1(4.00)	0,07
1,12E-03	583(6.17±10.20)	443(7.91±12.43)	97(8.21±10.62)	1,13E-02
	1032(6.89±10.95)	89(8.69±13.78)	2(6.30±3.25)	0,15
	1048(6.86±10.94)	73(9.53±14.39)	2(6.30±3.25)	0,06
	930(6.89±11.23)	180(7.61±10.90)	13(8.86±13.08)	0,29
0,09	974(6.88±10.91)	143(8.15±13.11)	6(5.44±4.00)	0,26
	1024(6.85±11.00)	97(8.91±13.05)	2(6.30±3.25)	0,09
0,09	870(6.82±11.10)	234(7.78±11.60)	18(7.43±10.78)	0,24
	1052(7.05±11.17)	68(6.73±11.84)	3(6.79±3.83)	0,86
	947(7.01±11.07)	170(7.33±12.00)	5(1.60±4.67)	0,98
	958(7.01±11.29)	155(7.37±10.93)	9(4.46±4.58)	0,96
	375(6.76±11.31)	552(7.24±11.46)	196(6.95±10.22)	0,75
	748(7.06±11.27)	340(6.81±10.92)	34(8.84±12.50)	0,88
	659(6.75±10.84)	403(7.32±11.72)	60(7.58±10.43)	0,40
	675(6.78±10.88)	392(7.40±11.82)	56(7.42±10.60)	0,43
0,64	711(7.05±11.35)	369(6.74±10.71)	40(8.39±11.67)	0,99
0,19	679(6.75±10.86)	389(7.48±11.84)	55(7.35±10.68)	0,38
	679(6.75±10.86)	389(7.48±11.84)	55(7.35±10.68)	0,38
	993(7.04±11.16)	125(6.71±10.84)	4(15.65±26.94)	0,83
	654(6.72±10.71)	407(7.20±11.32)	62(9.21±14.75)	0,15
	705(6.90±10.86)	375(7.06±11.64)	41(9.06±12.96)	0,45
	731(6.91±10.78)	355(7.09±11.74)	35(9.24±13.97)	0,46
	627(6.68±10.81)	427(7.15±11.17)	69(9.48±14.23)	0,10
0,09	641(6.81±10.95)	416(7.03±10.96)	65(9.23±14.58)	0,23
	657(6.73±10.86)	404(7.14±11.07)	61(9.48±14.99)	0,14
	693(6.62±10.75)	377(7.67±11.98)	51(8.13±11.23)	0,13
	463(6.82±9.55)	511(7.08±12.15)	149(7.51±12.50)	0,40
0,28	326(6.94±9.60)	563(6.83±11.67)	233(7.64±12.10)	0,41
	391(7.04±9.77)	539(6.90±11.76)	192(7.37±12.31)	0,68
	642(6.60±9.67)	407(7.39±12.74)	74(8.81±14.02)	5,26E-02
0,26	459(7.67±12.56)	504(6.53±10.36)	160(6.78±9.41)	0,15
0,18	364(7.74±12.77)	544(6.78±10.73)	215(6.47±9.33)	0,12
0,61	537(7.06±11.27)	486(6.88±11.14)	100(7.64±11.10)	0,85
	346(7.82±13.03)	546(6.86±10.63)	231(6.25±9.33)	0,07
0,21	323(7.82±12.29)	537(6.60±11.14)	263(6.94±9.79)	0,25
	777(6.97±10.98)	305(6.87±10.76)	41(9.32±17.11)	0,37
0,25	310(7.78±12.30)	518(6.75±11.28)	295(6.73±9.74)	0,21
0,32	299(7.49±12.12)	532(6.95±11.36)	291(6.55±9.51)	0,28
0,48	302(7.38±12.10)	529(7.05±11.52)	292(6.64±9.53)	0,40
	995(6.99±11.33)	125(7.46±10.20)	2(3.00±0.00)	0,81
	794(7.20±11.21)	312(6.55±11.32)	16(8.11±8.46)	0,49
	384(7.28±10.42)	542(6.68±11.11)	194(7.62±12.87)	0,93
	904(7.01±11.28)	211(7.24±11.02)	8(4.03±2.60)	0,98
0,51	918(6.94±11.24)	191(7.58±11.07)	14(5.53±10.00)	0,65
	917(6.86±11.20)	192(7.93±11.27)	14(5.76±10.00)	0,36
	497(7.20±11.41)	507(6.91±11.36)	119(6.86±9.55)	0,69
	385(7.09±10.39)	551(6.81±11.18)	187(7.57±12.77)	0,75
0,54	900(6.93±11.27)	206(7.65±11.00)	15(5.16±9.74)	0,64
0,18	475(7.39±11.48)	513(7.03±11.62)	135(5.79±8.06)	0,17
0,31	506(7.01±10.48)	506(7.05±11.88)	111(7.02±11.22)	0,97
0,85	339(6.77±10.14)	523(7.17±11.70)	259(6.93±11.26)	0,78
0,65	415(6.40±9.65)	515(7.60±12.18)	193(6.88±11.51)	0,36
0,24	684(6.94±11.74)	372(7.11±9.74)	66(7.53±13.18)	0,72
0,70	538(7.07±11.05)	475(7.11±11.52)	110(6.50±10.53)	0,70
	652(6.73±11.20)	397(7.42±10.93)	73(7.60±12.67)	0,35
	646(6.77±11.23)	403(7.36±10.88)	74(7.54±12.59)	0,41
0,84	832(7.01±11.07)	270(7.00±11.24)	20(8.99±15.56)	0,64

	638(7.39±11.66)	413(6.72±10.57)	71(5.75±10.49)	0,19
	374(7.51±11.72)	539(6.43±10.25)	207(7.72±12.56)	0,98
0,72	342(7.61±11.95)	547(6.45±10.31)	233(7.56±12.02)	0,87
	485(6.96±11.10)	498(7.07±11.13)	139(7.20±11.84)	0,87
0,99	811(7.06±11.18)	288(6.72±10.98)	24(9.58±14.24)	0,78
0,32	663(6.80±11.24)	388(7.32±10.83)	72(7.57±12.72)	0,45
	376(7.82±12.30)	549(6.05±9.68)	198(8.25±12.64)	0,92
	603(6.67±10.27)	443(7.69±12.60)	77(6.05±9.33)	0,56
	334(5.88±8.72)	540(7.60±12.42)	248(7.38±11.29)	0,07
	340(5.88±8.66)	541(7.59±12.41)	242(7.40±11.41)	0,07
	479(7.07±10.68)	513(7.46±12.25)	131(5.24±8.23)	0,28
0,12	682(6.81±11.02)	384(7.17±11.23)	57(8.72±12.96)	0,21
	664(6.84±10.20)	401(7.65±13.11)	58(5.01±6.51)	0,99
	349(6.75±10.76)	545(7.91±12.49)	229(5.38±7.93)	0,27
	460(7.09±10.65)	524(7.31±12.05)	138(5.78±9.52)	0,39
0,22	518(7.18±10.93)	492(7.15±11.84)	112(5.83±9.42)	0,36
0,39	541(7.07±10.73)	482(7.13±12.02)	100(6.33±9.48)	0,65
	349(6.77±10.74)	545(7.91±12.50)	229(5.36±7.93)	0,25
0,84	1012(7.03±11.29)	105(7.17±10.60)	5(6.14±4.54)	0,99
	457(7.06±10.57)	533(7.37±12.22)	132(5.60±8.69)	0,38
	686(7.35±12.12)	381(6.69±9.89)	56(5.50±6.73)	0,17
	624(6.34±10.83)	423(8.05±11.64)	73(7.24±11.50)	3,56E-02
0,16	533(7.17±10.60)	489(7.27±12.26)	96(5.16±8.58)	0,26
	769(6.30±10.55)	324(8.38±12.08)	29(11.77±14.82)	1,73E-04
0,07	329(6.84±10.75)	554(8.00±12.62)	240(5.07±7.44)	0,11
	543(7.09±10.56)	485(7.32±12.27)	95(5.24±8.63)	0,35
5,05E-02	306(5.35±7.98)	550(8.03±12.57)	267(6.90±11.13)	0,06
0,09	315(6.67±10.68)	555(8.13±12.72)	253(5.06±7.32)	0,13
0,19	471(7.16±10.66)	530(7.27±12.21)	121(5.47±8.16)	0,27
	313(6.76±10.64)	555(8.09±12.76)	254(5.05±7.30)	0,10
	292(7.34±11.14)	561(7.71±12.00)	270(5.29±9.21)	2,91E-02
	639(7.73±12.63)	415(6.16±9.20)	69(5.79±6.72)	2,01E-02
4,73E-02	312(6.89±11.03)	553(8.05±12.61)	258(5.03±7.24)	0,07
1,26E-03	668(6.35±10.73)	398(7.86±11.72)	56(9.36±12.31)	5,10E-03
	667(6.36±10.74)	397(7.85±11.74)	56(9.36±12.31)	5,48E-03
0,38	1017(7.13±11.37)	102(6.14±9.50)	4(5.43±4.91)	0,36
2,01E-03	665(6.37±10.75)	401(7.86±11.64)	57(8.94±12.62)	9,21E-03
0,38	1017(7.13±11.37)	102(6.14±9.50)	4(5.43±4.91)	0,36
1,10E-04	750(6.35±10.58)	342(8.10±12.01)	31(11.73±14.34)	5,74E-04
1,93E-04	744(6.37±10.61)	343(8.04±11.83)	36(11.06±14.93)	1,05E-03
	660(6.26±10.38)	403(7.97±12.09)	60(9.31±12.89)	2,39E-03
2,98E-04	747(6.42±10.74)	341(7.87±11.65)	35(11.80±14.45)	1,34E-03
2,05E-03	673(6.44±10.88)	389(7.51±11.21)	56(9.76±13.18)	1,28E-02
	635(7.52±12.32)	419(6.56±9.86)	67(5.54±6.94)	0,09
0,06	286(5.58±8.38)	547(7.68±12.29)	289(7.26±11.38)	0,07
	1087(7.05±11.23)	36(6.56±10.29)	.	0,81
	301(6.85±11.04)	546(7.90±12.29)	276(5.51±8.66)	0,16
	300(6.87±11.05)	545(7.85±12.23)	278(5.61±8.87)	0,18
0,15	298(6.82±11.04)	546(7.84±12.22)	278(5.61±8.87)	0,20
0,09	315(5.74±8.82)	531(7.78±12.33)	274(7.11±11.29)	0,10
	692(6.49±10.97)	376(7.50±11.12)	55(10.68±13.66)	6,43E-03
5,96E-04	675(6.45±10.66)	394(7.48±11.57)	54(11.14±13.89)	3,54E-03
	675(6.45±10.66)	394(7.48±11.57)	54(11.14±13.89)	3,54E-03
2,51E-04	677(6.43±10.65)	392(7.40±11.48)	54(11.88±14.34)	1,75E-03
4,73E-04	621(6.46±10.85)	432(7.24±11.10)	70(10.77±13.89)	5,36E-03
	516(6.94±10.47)	505(7.05±11.66)	101(7.35±12.52)	0,79
2,26E-02	305(7.40±11.46)	540(7.54±12.05)	273(5.63±8.91)	0,06
	732(6.53±10.64)	355(7.56±11.83)	36(12.04±14.24)	5,73E-03
7,27E-03	667(6.59±10.92)	404(7.45±11.42)	52(9.42±12.61)	4,46E-02
	556(6.96±10.55)	482(7.06±11.67)	85(7.36±12.59)	0,78
1,21E-03	646(6.52±10.82)	417(7.31±11.33)	56(10.64±13.76)	1,42E-02
0,66	535(7.04±10.55)	493(7.02±11.72)	91(7.10±12.26)	1,00
	1035(7.15±11.44)	87(5.63±7.71)	1(6.00)	0,23
7,21E-03	328(7.81±12.36)	545(7.23±11.32)	250(5.58±9.02)	1,81E-02
0,62	530(6.66±10.07)	494(7.41±12.18)	99(7.11±11.79)	0,41
0,64	533(6.65±10.05)	493(7.42±12.19)	97(7.16±11.90)	0,38
	526(6.96±10.58)	502(7.12±11.67)	92(7.15±12.18)	0,84
	694(6.42±10.00)	372(7.86±12.95)	57(9.07±12.18)	1,33E-02
	730(7.35±11.95)	348(6.40±9.73)	45(6.78±8.90)	0,25
	374(7.76±11.91)	529(6.99±11.16)	220(5.90±9.89)	3,96E-02
0,97	469(7.27±11.84)	520(6.62±10.52)	134(7.79±11.42)	0,96

	307(8.03±12.04)	530(6.87±10.81)	285(6.25±10.93)	5,18E-02
	310(8.29±12.37)	529(6.72±10.54)	283(6.24±10.97)	2,44E-02
	299(6.12±10.69)	547(6.86±10.76)	274(8.42±12.48)	1,55E-02
	497(7.82±11.71)	490(6.78±11.59)	136(5.08±6.69)	1,06E-02
5,15E-02	469(6.80±11.15)	507(6.80±10.91)	147(8.57±12.22)	0,20
	475(6.87±11.24)	504(6.71±10.79)	144(8.71±12.31)	0,22
	426(6.86±11.33)	528(6.90±10.99)	169(7.89±11.54)	0,38
0,14	378(7.64±11.25)	574(6.65±11.55)	171(7.00±9.77)	0,43
3,72E-03	496(7.83±11.72)	490(6.78±11.59)	136(5.08±6.69)	1,03E-02
	315(6.27±11.18)	558(7.37±10.87)	249(7.28±11.92)	0,19
0,33	771(7.03±11.35)	315(6.85±10.71)	37(8.75±12.08)	0,61
	807(6.90±11.19)	287(7.40±11.45)	29(7.13±8.77)	0,46
	807(6.90±11.19)	287(7.40±11.45)	29(7.13±8.77)	0,46
	807(6.90±11.19)	287(7.40±11.45)	29(7.13±8.77)	0,46
	883(7.09±11.34)	219(6.86±10.68)	21(6.30±10.75)	0,70
	804(6.90±11.21)	283(7.27±11.37)	29(7.13±8.77)	0,54
	885(6.96±11.16)	220(7.48±11.59)	18(4.84±7.77)	0,93
	974(7.08±11.36)	141(6.90±10.29)	6(3.90±5.23)	0,68
3,00E-02	704(6.66±10.61)	370(7.73±12.36)	49(7.16±10.04)	0,15
	733(6.92±11.00)	341(7.66±11.93)	48(4.46±8.17)	0,83
	850(6.83±10.88)	250(7.76±12.46)	23(6.72±7.83)	0,30
1,77E-03	303(7.33±11.83)	558(7.58±11.11)	262(5.53±10.51)	4,99E-02
5,09E-04				
	714(6.36±10.40)	360(8.46±12.76)	49(6.42±9.03)	2,86E-02
	390(6.04±9.38)	551(7.53±11.86)	182(7.66±12.53)	5,40E-02
	689(6.68±10.71)	377(7.63±11.48)	57(7.39±14.57)	0,25
	736(6.68±10.69)	350(7.81±12.21)	37(6.56±11.04)	0,23
0,80	894(7.02±11.23)	213(7.27±11.40)	15(4.09±4.96)	0,88
	892(7.04±11.23)	214(7.25±11.38)	14(4.24±5.11)	0,89
	832(6.93±11.06)	264(7.66±11.94)	26(4.20±6.60)	0,96
6,04E-03	390(6.04±9.38)	551(7.53±11.86)	182(7.66±12.53)	5,40E-02
	743(6.70±10.54)	343(7.84±12.61)	37(6.22±9.89)	0,27
	747(6.78±10.51)	341(7.51±12.39)	35(7.72±13.13)	0,28
	609(6.39±9.71)	450(7.72±12.69)	64(8.32±12.86)	3,45E-02
	741(6.69±10.80)	344(7.83±12.03)	38(6.44±10.91)	0,24
0,23	732(6.77±10.82)	352(7.66±11.98)	38(6.44±10.91)	0,38
0,68	279(6.65±10.36)	577(7.36±11.21)	265(6.75±12.04)	0,86
	923(6.71±11.02)	190(8.55±12.00)	10(7.87±10.34)	4,11E-02
	636(7.32±11.66)	418(6.89±11.08)	69(5.27±6.56)	0,17
	720(6.55±10.46)	367(8.00±12.66)	36(6.74±8.94)	0,09
	925(6.69±11.01)	188(8.66±12.00)	10(7.87±10.34)	3,04E-02
	901(7.12±11.41)	208(6.72±10.42)	14(5.91±8.93)	0,48
	783(7.21±11.39)	308(6.46±10.72)	32(8.19±11.03)	0,57
0,11	638(7.32±11.64)	416(6.87±11.10)	69(5.30±6.54)	0,16
0,97	783(7.21±11.39)	307(6.46±10.74)	32(8.19±11.03)	0,57
3,75E-03	921(6.68±11.02)	191(8.71±11.97)	10(7.87±10.34)	2,49E-02
	278(6.73±10.44)	579(7.21±10.98)	264(6.98±12.44)	0,75
	484(7.00±11.61)	513(7.03±11.18)	126(7.15±9.62)	0,91
0,11	638(7.32±11.64)	414(6.89±11.12)	70(5.33±6.49)	0,17
0,81	278(6.73±10.44)	581(7.20±10.96)	264(6.98±12.44)	0,74
	472(7.03±11.71)	515(6.92±10.96)	133(7.38±10.22)	0,89
	282(6.66±10.27)	582(7.16±10.96)	258(7.16±12.65)	0,54
6,96E-03	921(6.69±11.05)	190(8.68±11.85)	12(6.97±9.64)	4,35E-02
0,12	386(7.77±12.57)	542(6.81±10.49)	194(6.23±10.15)	0,07
3,69E-02	645(7.51±11.90)	407(6.46±10.43)	70(5.93±8.44)	0,07
	337(7.73±12.81)	551(6.78±10.29)	234(6.64±10.75)	0,17
	790(7.17±11.42)	301(6.70±10.80)	32(6.76±9.35)	0,51
	639(7.54±11.94)	413(6.42±10.38)	71(5.98±8.39)	0,07
	788(7.16±11.42)	303(6.73±10.81)	32(6.76±9.35)	0,55
	394(7.92±12.74)	538(6.70±10.38)	191(6.15±9.83)	3,44E-02
0,46	595(6.82±10.79)	445(7.56±12.21)	83(5.75±7.77)	0,96
0,92	538(7.17±11.10)	482(7.13±11.82)	103(5.87±8.34)	0,42
0,66	535(7.10±11.06)	485(7.10±11.64)	101(6.33±9.83)	0,64
	655(7.45±12.13)	403(6.41±9.82)	65(6.71±9.10)	0,19
0,20	677(7.63±12.27)	382(5.99±9.32)	63(6.96±9.13)	0,07
1,05E-02	1004(6.77±10.58)	117(9.33±15.42)	2(3.90±5.80)	2,65E-02
2,65E-02	859(6.66±10.59)	249(8.20±13.09)	14(9.06±10.36)	4,33E-02
0,95	982(7.02±11.31)	136(7.08±10.51)	5(8.14±8.53)	0,89
	980(7.02±11.32)	136(7.08±10.51)	5(8.14±8.53)	0,89
	1020(7.03±11.34)	99(6.95±9.80)	4(9.43±9.28)	0,94
0,50	511(7.32±11.28)	516(6.56±11.06)	96(8.04±11.51)	0,86

2,65E-02	860(6.66±10.58)	249(8.20±13.09)	14(9.06±10.36)	4,30E-02
0,95	982(7.02±11.31)	136(7.08±10.51)	5(8.14±8.53)	0,89
	992(6.71±10.54)	128(9.73±15.16)	2(3.90±5.80)	6,74E-03
0,95	979(7.03±11.32)	133(7.27±10.54)	5(8.14±8.53)	0,77
	989(6.73±10.55)	132(9.32±15.08)	2(3.90±5.80)	1,83E-02
0,95	982(7.02±11.31)	136(7.08±10.51)	5(8.14±8.53)	0,89
	810(6.64±10.49)	289(8.03±12.94)	22(8.88±11.24)	4,65E-02
2,28E-02	880(6.77±10.68)	226(7.91±12.71)	17(9.14±15.20)	0,11
	518(7.10±11.00)	489(6.65±10.15)	113(8.11±15.48)	0,66
3,20E-05	403(5.35±8.98)	536(7.44±11.88)	182(9.56±12.93)	1,12E-05
4,66E-05	441(5.62±9.44)	523(7.33±11.58)	159(9.98±13.55)	1,94E-05
0,40	977(6.95±10.98)	144(7.54±12.61)	2(11.50±14.85)	0,47
	463(7.87±10.91)	517(6.67±11.73)	143(5.63±9.93)	2,13E-02
	442(6.99±12.12)	528(7.04±10.38)	151(7.14±11.27)	0,92
	602(6.28±10.43)	440(7.75±12.03)	81(8.67±11.70)	1,38E-02
0,75	703(7.32±11.63)	369(6.13±9.98)	49(9.93±13.04)	0,80
	627(6.30±10.37)	426(7.74±12.09)	70(9.29±12.22)	7,90E-03
	814(7.29±11.78)	287(6.12±9.22)	21(9.40±12.47)	0,37
	453(7.89±10.97)	526(6.69±11.66)	143(5.57±9.96)	1,97E-02
4,99E-02	302(6.26±10.17)	571(6.93±11.73)	250(8.19±11.07)	4,88E-02
0,74	662(7.14±11.34)	395(6.33±10.62)	61(9.53±12.10)	0,79
	365(6.36±10.25)	551(7.33±11.51)	206(7.45±11.94)	0,21
	742(6.77±11.30)	345(7.56±11.08)	36(7.45±10.09)	0,30
	736(6.80±11.34)	350(7.42±10.95)	37(8.11±10.72)	0,30
	614(6.51±10.99)	433(7.86±11.57)	69(6.97±10.78)	0,16
0,44	976(6.93±10.95)	143(7.64±12.85)	3(10.33±10.69)	0,41
0,43	965(6.94±10.99)	140(7.67±12.97)	3(10.33±10.69)	0,41
	880(6.60±11.06)	233(8.52±11.65)	10(10.01±9.51)	1,42E-02
0,45	680(6.99±10.21)	383(7.45±12.99)	60(4.86±9.20)	0,64
0,17	650(6.50±10.93)	417(7.77±11.63)	56(7.72±10.79)	0,09
	729(7.19±10.55)	347(6.94±12.58)	47(5.22±10.04)	0,32
	978(6.93±10.94)	142(7.64±12.89)	3(10.33±10.69)	0,41
0,15	656(6.49±10.89)	412(7.78±11.66)	55(7.95±11.07)	0,07
0,07	523(6.51±11.14)	500(7.34±11.26)	100(8.20±11.09)	0,10
	683(7.02±10.22)	378(7.30±12.93)	56(5.07±9.47)	0,61
0,12	651(6.42±10.81)	417(7.86±11.75)	55(7.95±11.07)	4,93E-02
0,18	771(6.66±11.21)	325(7.71±11.16)	27(9.42±10.83)	0,09
0,70	577(6.81±9.91)	444(7.68±12.58)	100(5.46±11.62)	0,91
7,55E-03	317(5.82±10.92)	568(7.04±11.36)	238(8.64±11.01)	3,99E-03
0,09	639(6.56±11.38)	425(7.61±10.91)	56(7.35±10.18)	0,17
	1100(7.07±11.24)	23(5.35±8.91)	.	0,42
	653(6.43±10.80)	416(7.85±11.76)	54(8.06±11.14)	4,58E-02
	672(6.98±10.10)	391(7.43±13.09)	60(5.03±9.28)	0,71
0,48	686(7.00±10.13)	383(7.39±13.08)	54(4.87±9.37)	0,64
0,10	755(6.66±11.31)	340(7.56±10.90)	28(10.66±11.24)	0,06
	574(6.72±9.78)	445(7.81±12.64)	100(5.21±11.92)	0,97
0,19	969(6.88±10.83)	151(7.95±13.32)	3(10.33±10.69)	0,22
	311(5.80±8.39)	559(8.06±12.48)	253(6.28±11.02)	0,48
	669(7.14±10.34)	393(7.29±12.68)	60(4.27±9.73)	0,29
	606(6.36±11.01)	428(7.98±11.86)	89(7.06±8.65)	0,10
	564(7.32±11.52)	453(6.92±11.35)	106(5.99±8.48)	0,27
	646(7.28±11.76)	400(6.29±10.17)	77(8.80±11.24)	0,98
0,99	797(7.02±11.11)	294(7.02±11.25)	32(7.45±13.13)	0,93
	697(7.12±11.55)	363(6.57±10.57)	62(8.82±10.80)	0,76
	878(6.89±11.06)	230(7.67±11.65)	15(5.91±12.11)	0,52
2,64E-02	393(7.94±12.05)	546(6.84±11.50)	184(5.65±7.71)	2,79E-02
0,58	774(7.11±10.83)	321(6.73±12.04)	28(8.30±11.53)	0,96
	798(6.98±10.73)	301(7.05±12.28)	24(8.58±12.45)	0,60
	706(7.76±12.44)	370(5.79±8.67)	47(5.90±7.67)	1,13E-02
	793(6.94±10.70)	304(7.16±12.36)	26(8.21±12.04)	0,54
	291(8.44±12.79)	568(6.93±11.40)	264(5.70±8.36)	6,27E-03
	638(7.13±10.79)	425(6.78±11.98)	60(7.80±9.78)	0,97
4,75E-02	649(7.73±12.52)	410(6.22±9.27)	63(5.21±7.08)	1,78E-02
	1092(7.11±11.27)	28(3.28±5.35)	.	0,07
	767(7.08±10.82)	324(6.91±12.05)	32(7.19±11.35)	0,92
0,57	767(7.08±10.82)	324(6.91±12.05)	32(7.19±11.35)	0,92
	407(7.61±11.75)	535(7.08±11.70)	181(5.60±7.80)	0,08
	296(8.22±12.66)	563(7.07±11.46)	263(5.62±8.43)	9,86E-03
	660(7.05±10.98)	398(7.00±11.51)	64(7.17±11.60)	0,94
	337(8.14±12.44)	560(6.99±11.43)	226(5.48±8.05)	9,12E-03
	337(8.14±12.44)	560(6.99±11.43)	226(5.48±8.05)	9,12E-03

1,60E-03	687(8.03±12.76)	383(5.53±7.95)	51(5.16±7.75)	5,74E-04
5,68E-03	331(8.08±12.49)	563(7.06±11.44)	229(5.46±8.02)	1,11E-02
0,50	722(6.75±10.49)	358(7.47±12.31)	43(8.16±12.90)	0,20
6,49E-04				
	719(7.83±12.52)	361(5.59±8.21)	40(5.64±8.01)	3,80E-03
	737(6.67±10.42)	348(7.71±12.52)	37(7.70±12.92)	0,14
	737(6.69±10.42)	346(7.75±12.54)	38(7.36±12.87)	0,16
	744(6.65±10.39)	338(7.81±12.67)	37(7.70±12.92)	0,11
	737(6.69±10.42)	349(7.69±12.51)	37(7.70±12.92)	0,15
	504(6.99±11.12)	494(7.31±12.05)	125(6.10±7.30)	0,83
	608(7.28±11.82)	449(6.66±10.62)	65(7.30±9.02)	0,60
	833(6.97±11.29)	262(7.17±10.66)	28(7.65±13.55)	0,79
0,95	380(7.41±11.17)	548(6.49±10.75)	194(7.87±12.38)	0,98

Supplementary Table 6. A result of *rs1042151* for functional prediction.

Allele	Position	Prediction Strand	Forward Sequence	Matrix	Score	Method
A	7	+	GACAGGA	SF2ASF2	2,3	ESEfind
G	7	+	GACAGGG	SF2ASF2	1,87	ESEfind
A	7	+	GACAGGA	SF2ASF1	4,4	ESEfind
G	7	+	GACAGGG	SF2ASF1	3,67	ESEfind
A	7	+	GACAGGA	SF2ASF1	2,3	ESEfind
G	7	+	GACAGGG	SF2ASF1	1,87	ESEfind
A	7	+	GACAGGA	SF2ASF1	4,4	ESEfind
G	7	+	GACAGGG	SF2ASF1	3,67	ESEfind
G	4	+	AGG	NA	NA	FAS-ESS
G	4	+	AGG	NA	NA	FAS-ESS

Based on the SNP Function Prediction (<http://snpinfo.niehs.nih.gov/snptunc.htm>) website, two exonic splicing enhancers (ESEs) including the polymorphic site of *rs1042151* of HLA-DPB1 are predicted for binding of splicing factors including SF2/ASF2 and SF2/ASF1.

Verfahren zur Ermittlung

1. Bestimmung der zu untersuchenden Stoffe

2. Ermittlung

3. Bestimmung der Konzentration

Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden? (z.B. in einem bestimmten Stoff) (z.B. in einem bestimmten Stoff) (z.B. in einem bestimmten Stoff)

Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden?

Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden?

Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden?

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Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden? (z.B. in einem bestimmten Stoff) (z.B. in einem bestimmten Stoff) (z.B. in einem bestimmten Stoff)

Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden?

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Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden?

Bestimmung der Konzentration: Wie oft ist ein Stoff in einem bestimmten Stoff vorhanden?



HAW - Hochschule für Angewandte Wissenschaften

Supplement Data

Genome-wide Association Study of Aspirin Exacerbated Respiratory Disease in a Korean Population

Materials and Methods

Materials and Methods

Exclusion Criteria of OAC were 1) a history of very severe anaphylactic reactions precipitated by aspirin or other NSAIDs, 2) Severe disease of the heart, digestive tract, liver, kidney, 3) Infection of respiratory tract within 4 weeks prior to the challenge, 4) Pregnancy, and 5) Current treatment with b-receptor blocker.