

Importance of hedgehog interacting protein and other lung function genes in asthma

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Background: Two recent large meta-analyses of genome-wide association studies of lung function in general populations of European descent identified 11 candidate genes/regions. The importance of these genes in lung function in white and African American subjects with asthma is unknown.

Objectives: To determine whether genes that regulate lung function in general populations are associated with lung function abnormalities in subjects with asthma from different racial groups.

Methods: Single nucleotide polymorphisms (SNPs) were tested in 5 asthma populations (N = 1441) for association with pulmonary function, and meta-analysis was performed across populations. The SNPs with the highest significance were then tested for association with bronchodilator reversibility and bronchial hyperresponsiveness to methacholine. A joint analysis of consistently replicated SNPs was performed to predict lung function in asthma.

Results: Hedgehog interacting protein (*HHIP*) on chromosome 4q31 was associated with lung function in all 5 populations (rs1512288: $P_{\text{meta}} = 9.62\text{E-}05$ and $3.23\text{E-}05$ for percent predicted FEV₁ [ppFEV₁] and percent predicted forced vital capacity [ppFVC], respectively). The SNPs in *HHIP* were also associated with reversibility ($P < .05$) but not bronchial

hyperresponsiveness to methacholine. Because of differences in linkage disequilibrium in the African American subjects, the most relevant SNPs in *HHIP* were identified. A subset of normal lung function genes, including *HHIP*, family with sequence similarity 13, member A (*FAM13A*), and patched homolog 1 (*PTCH1*), together predict lung function abnormalities, a measure of severity in white and African American subjects with asthma.

Conclusion: A subset of the genes, including *HHIP*, that regulate lung function in general populations are associated with abnormal lung function in asthma in non-Hispanic white and African American subjects. (J Allergy Clin Immunol 2011;■■■:■■■-■■■.)

Key words: Asthma, genetics, asthma severity, meta-analysis, FEV₁, FVC, FEV₁/FVC, *HHIP*, *FAM13A*, *PTCH1*

Asthma is a heterogeneous disease that is classified phenotypically as mild, moderate, or severe on the basis of National Asthma Education and Prevention Program (NAEPP), Global Initiative for Asthma (GINA), or American Thoracic Society (ATS) guidelines,¹⁻³ and more recently, 5 asthma severity

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Abbreviations used

ATS:	American Thoracic Society
COPD:	Chronic obstructive pulmonary disease
CSGA:	Collaborative Studies on the Genetics of Asthma
FAM13A:	Family with sequence similarity 13, member A
FVC:	Forced vital capacity
GWAS:	Genome-wide association study
HHIP:	Hedgehog interacting protein
LD:	Linkage disequilibrium
PTCH1:	Patched homolog 1
pp:	Percent predicted
SARP:	Severe Asthma Research Program
SNP:	Single nucleotide polymorphism
TENOR:	The Epidemiology and Natural History of Asthma: Outcomes and Treatment Regimens

phenotypes were identified by using cluster analysis.⁴ The majority of morbidity and health care use occurs in severe asthma, a phenotype largely determined by pulmonary function (baseline lung function: percent predicted [pp] FEV₁, pp forced vital capacity [FVC], and FEV₁/FVC).^{3,4} Quantitative phenotypes such as ppFEV₁ are essential for categorizing asthma severity for current guidelines classification or with cluster methodologies.⁵

A recent genome-wide association study (GWAS) meta-analysis for pulmonary function in 20,890 participants from general populations of European white ancestry (CHARGE consortium) found that genes in the *INTS12-GSTCD-NPNT* region were associated with FEV₁, and 8 genes (hedgehog interacting protein [*HHIP*], *GPR126*, *ADAM19*, *AGER-PPT2*, family with sequence similarity 13, member A [*FAM13A*], patched homolog 1 [*PTCH1*], *PID1*, and *HTR4*) were associated with FEV₁/FVC.⁶ A second GWAS meta-analysis for lung function in general populations (20,288 participants of European white ancestry: SpiroMeta consortium) identified 4 genes (*HHIP*, *GSTCD*, *TNSI*, and *HTR4*) associated with FEV₁ and 3 loci (*HHIP*, *NOTCH4-AGER-PPT2*, *THSD4*) associated with FEV₁/FVC.⁷ Although these genes may only influence lung function in subjects without respiratory diseases, we hypothesize that some of these genes are important in determining lung function in subjects with asthma. Identifying the genetic variants that influence pulmonary function in asthma is of major importance because these genomic approaches will lead to improved understanding of biologic factors that regulate lung function in asthma, a fundamental determinant of asthma severity.⁸

In this study, we performed meta-analysis of ppFEV₁, ppFVC, and FEV₁/FVC in 5 asthma populations including non-Hispanic whites and African Americans to determine whether the genes previously identified in the 2 GWASs for normal variation of lung function are important in determining lung function in subjects with asthma. Our primary hypothesis was to determine whether the previously identified single nucleotide polymorphism (SNP) in each gene that was significant in the general population is important in asthma; therefore, we analyzed 1 SNP in each of the 11 genes (3 additional SNPs were analyzed in *HHIP* because they are in strong linkage disequilibrium (LD) with the previously identified SNP). To present a more comprehensive view of each gene, the additional SNPs already genotyped in the 11 genes were analyzed as a secondary analysis. Importantly, the previous studies did not include subjects of African descent, a population with increased frequency and severity of asthma.^{3,5,9,10}

METHODS**Study subjects**

Subjects with mild to severe asthma were recruited at the National Heart, Lung, and Blood Institute–funded Severe Asthma Research Program (SARP) centers and carefully characterized including baseline spirometry with a medication withhold before testing.^{3,4} Similar baseline spirometry was performed in subjects with severe or difficult-to-treat asthma from The Epidemiology and Natural History of Asthma: Outcomes and Treatment Regimens (TENOR) multicenter study.^{11,12} In addition, subjects with asthma who were studied in the National Heart, Lung, and Blood Institute Collaborative Studies on the Genetics of Asthma (CSGA) by the Wake Forest investigators using similar protocol were included in the analyses.⁹ TENOR, SARP, and CSGA studies were approved by the appropriate institutional review board at the participating sites including appropriate informed consent.

DNA was isolated by using standard protocols, and SNP genotyping was performed by using the Illumina HumanCNV370 BeadChip (Illumina, Inc, San Diego, Calif) for TENOR.¹² SARP and CSGA samples were genotyped using the Illumina HumanHap1M BeadChip (unpublished data). Genotyping for both studies was performed by using BeadStudio (Illumina, Inc).

Statistical analysis

SARP cases were removed if they (1) had low genotyping call rates (<95%), (2) were discrepant or ambiguous for genetic sex (heterozygous haploid genotype percentage ≥ 0.01 or X chromosome homozygosity $F \geq 0.9$), (3) were different from described race, (4) failed the check for family relatedness (PI_HAT > 0.125), or (5) were detected as an outlier (>6 SDs for the first or second principal component). After subjects meeting these criteria were excluded, SNPs were removed if (1) the call rates were still low (95%), (2) inconsistent with Hardy-Weinberg equilibrium ($P < 10E-04$), or (3) the minor allele frequency was less than 0.05. Quality control of TENOR and CSGA cases was performed in a similar manner.

A linear additive model was used for analysis of ppFEV₁, ppFVC, FEV₁/FVC, and gene-gene interaction analysis with PLINK (version 1.06; <http://pngu.mgh.harvard.edu/purcell/plink/>),¹³ adjusted for age, sex, and significant principal components (EIGENSTRAT, version 3.0; <http://genepath.med.harvard.edu/~reich/Software.htm>).¹⁴ Haploview (<http://www.broad.mit.edu/mpg/haploview/>) was used to generate linkage disequilibrium plots,¹⁵ and 95% CIs on D' were used to define blocks.¹⁶ For the primary analysis, 14 SNPs in 11 candidate genes/regions were analyzed for replication at the SNP level (rs6845536, rs720485, rs1828591, and rs1512288 in *HHIP*; rs2571445 in *TNSI*; rs10516526 in *INTS12-GSTCD-NPNT*; rs3995090 in *HTR4*; rs2070600 in *NOTCH4-AGER-PPT2*; rs1913768 in *THSD4*; rs11155242 in *GPR126*; rs2277027 in *ADAM19*; rs2869967 in *FAM13A*; rs10512249 in *PTCH1*; and rs1358443 in *PID1*). Using a more relaxed replication standard,¹⁷ assuming gene as a unit and related phenotypes as similar, the most significant SNPs were reported for each candidate genes.

Meta-analysis of *P* values from 3 non-Hispanic white populations, 2 African American populations, or all of 5 populations was performed with weights proportional to the square-root of the sample size by using METAL software (<http://www.sph.umich.edu/csg/abecasis/metal/>). Meta-analysis of effect size (regression slope) of the identified candidate SNPs was performed with weights proportional to sample size using the rmeta package based on the random effects model (<http://cran.r-project.org/web/packages/rmeta/index.html>). To reduce genomic inflation, *P* values with genomic control adjustment from each population were used for meta-analysis.

Joint analysis of the 3 most consistent SNPs (rs1512288 in *HHIP*, rs576594 in *PTCH1*, and rs2869967 in *FAM13A*) or 5 SNPs (rs1512288 in *HHIP*, rs576594 in *PTCH1*, rs2869967 in *FAM13A*, rs3845823 in *PID1*, and rs206015 in *NOTCH4*) was performed in SARP non-Hispanic white subjects, SARP African American subjects, and TENOR white subjects. Genotypes with 1 or 2 minor alleles were merged together and recoded as 0 (if minor allele was protective allele) or 1 (if minor allele was risk allele). A linear additive model was used for analysis of ppFEV₁, ppFVC, and FEV₁/FVC with the number of risk SNPs. A logistic regression model was used for analysis of the percentage of subjects with severe asthma by using ATS and cluster classification^{3,4} with the number of risk SNPs.

TABLE I. Meta-analysis results of 34 SNPs in the *HHIP* region in 5 populations with asthma

No.	SNP	Minor (risk) allele C/A§	Coordinate	Location	ppFEV ₁			ppFVC			FEV ₁ /FVC		
					<i>P</i> _{meta} *	<i>P</i> _{meta_C} †	<i>P</i> _{meta_A} ‡	<i>P</i> _{meta} *	<i>P</i> _{meta_C} †	<i>P</i> _{meta_A} ‡	<i>P</i> _{meta} *	<i>P</i> _{meta_C} †	<i>P</i> _{meta_A} ‡
1	rs4362772	C	145549252	5'UTR									
2	rs749316	G	145590796		.029	7.3E-03	.752	.046	.047	.597	.734	.437	.478
3	rs7684769	T	145638960										
4	rs12641251	G/A	145644293										
5	rs6827794	T	145649747										
6	rs1512282	C	145650947										
7	rs6845536	C (C)	145672233	Intron	2.8E-04	1.1E-04	.600	2.5E-04	3.2E-04	.288	.109	.077	.911
8	rs720485	C (A)	145682038		4.4E-04	2.6E-03	.067	1.1E-04	1.2E-03	.035	.141	.201	.462
9	rs1828591	G (A)	145700230		1.5E-04	1.6E-03	.036	8.6E-05	1.2E-03	.023	.175	.140	.901
10	rs1512288	T (C)	145710731		9.6E-05	9.5E-03	7.7E-04	3.2E-05	4.5E-03	5.1E-04	.112	.214	.300
11	rs2175586	A	145716391										
12	rs1996020	C	145730644										
13	rs7670758	A	145731325		.010	1.8E-04	.149	6.9E-03	1.8E-04	.224	.242	.090	.510
14	rs7677662	G	145732503										
15	rs2353397	C	145737028		.022	5.9E-03	.820	.044	.012	.701	.086	.089	.640
16	rs4835180	G	145740058										
17	rs2035901	G/A	145741317		.340	.232	.854	.054	.033	.920	.721	.485	.593
18	rs11947381	T	145757300		.851	.651	.232	.022	1.8E-03	.356	.097	.100	.651
19	rs2575570	T	145768383										
20	rs1398244	T	145781907		.258	.464	.314	.734	.600	.804	.005	.007	.355
21	rs6845999	T	145785276										
22	rs1812175	T	145794294										
23	rs2220514	T	145796008										
24	rs2306924	A	145801986										
25	rs6537307	G	145821313										
26	rs2575580	C	145824475		.936	.600	.270	.270	.929	.033	.099	.132	.496
27	rs6537310	T	145856182		.275	.108	.523	.074	7.3E-03	.240	.996	.934	.872
28	rs6854783	G	145862529		.264	.107	.552	.055	7.3E-03	.373	.960	.895	.729
29	rs11944404	C	145890321	3'UTR	.034	.142	.088	.297	.535	.300	.133	.211	.396
30	rs4835186	T	145906597										
31	rs2353934	T	145916490		.446	.911	.173	.125	.516	.045	.928	.876	.922
32	rs12647866	C	145928136										
33	rs12651029	A	145989617		.040	.020	.963	.013	3.2E-03	.822	.852	.651	.662
34	rs13102609	T	145990671										

UTR, Untranslated region.

Only rows with at least 1 entry with a *P* value less than .05 are shown.**P*_{meta} is the meta-analysis *P* value for all 5 populations with asthma.†*P*_{meta_C} is the meta-analysis *P* value for 3 non-Hispanic white populations.‡*P*_{meta_A} is the meta-analysis *P* value for 2 African American populations.

§Minor (risk) allele C/A represents the minor (risk) allele of non-Hispanic white and African American populations, respectively. Risk alleles are labeled for SNPs 7 to 10 only. See Tables E2 and E3 for other risk alleles.

||SNPs 7 to 10 are the 4 SNPs studied for strict replication because they are in strong LD with the previously identified SNP. Results from the other previously genotyped SNPs are presented for completeness but are the results of a secondary analysis.

RESULTS

Although the 3 studies used similar clinical approaches to phenotype cases carefully, they differ in the proportion of subjects with severe asthma because SARP is a cohort that is enriched for subjects with severe asthma, TENOR focused on difficult-to-treat or severe asthma, and CSGA recruited a cohort including all levels of severity but primarily focused on milder levels of asthma severity. These differences are reflected in baseline lung function (see this article's Table E1 in the Online Repository at www.jacionline.org). The cohorts have a broad range of lung function with slightly lower levels in the SARP and TENOR subjects with asthma, consistent with the recruitment of subjects with more severe asthma in these studies.

After quality control analysis was completed as described, data from 1441 subjects with asthma (SARP non-Hispanic white subjects, *n* = 438; TENOR non-Hispanic white subjects, *n* = 431; CSGA non-Hispanic white subjects, *n* = 230; SARP African

American subjects, *n* = 206; and CSGA African American subjects, *n* = 136) were analyzed for association with spirometric measures of lung function: ppFEV₁, ppFVC, and FEV₁/FVC, and the SNPs in 11 genes identified through 2 recent meta-analyses of GWAS of normal lung function. The issue of multiple testing was minimized because only 14 SNPs in 11 previously identified genes were analyzed for replication at the SNP level (*P* value for Bonferroni adjustment was 3.57E-03; *P* = .05/14 SNPs).

The SNP rs1512288 at the 5' flanking region of *HHIP* showed the most consistent association in all 5 cohorts of subjects with asthma (*P*_{meta} = 9.62E-05, 3.23E-05, and .11 for ppFEV₁, ppFVC, and FEV₁/FVC, respectively; Table I; Fig 1, A; see this article's Tables E2 and E3 in the Online Repository at www.jacionline.org). The LD structure of the *HHIP* region was different between non-Hispanic white and African American subjects (Fig 1, B and C). The SNPs with the lowest *P* values

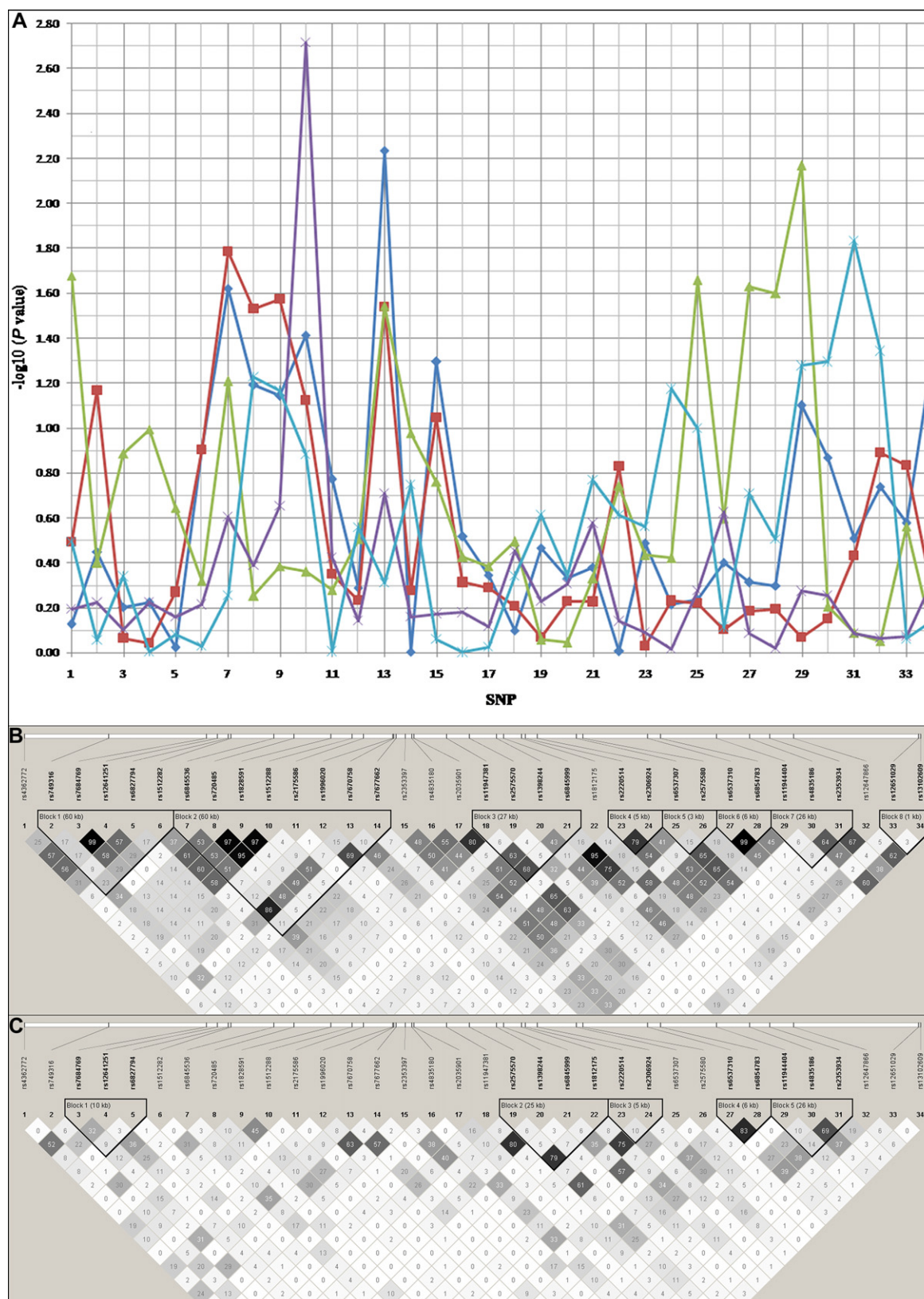


FIG 1. LD and association plot of 34 SNPs in *HHIP*. **A**, Association plot: blue diamond, TENOR subjects; red square, SARP non-Hispanic white subjects; green triangle, CSGA non-Hispanic white subjects; purple cross, SARP African American subjects; cyan asterisk, CSGA African American subjects. **B**, LD plot of non-Hispanic white subjects. **C**, LD plot of African American subjects: r^2 color scheme was used and labeled. 95% CIs on D' were used to set up blocks.

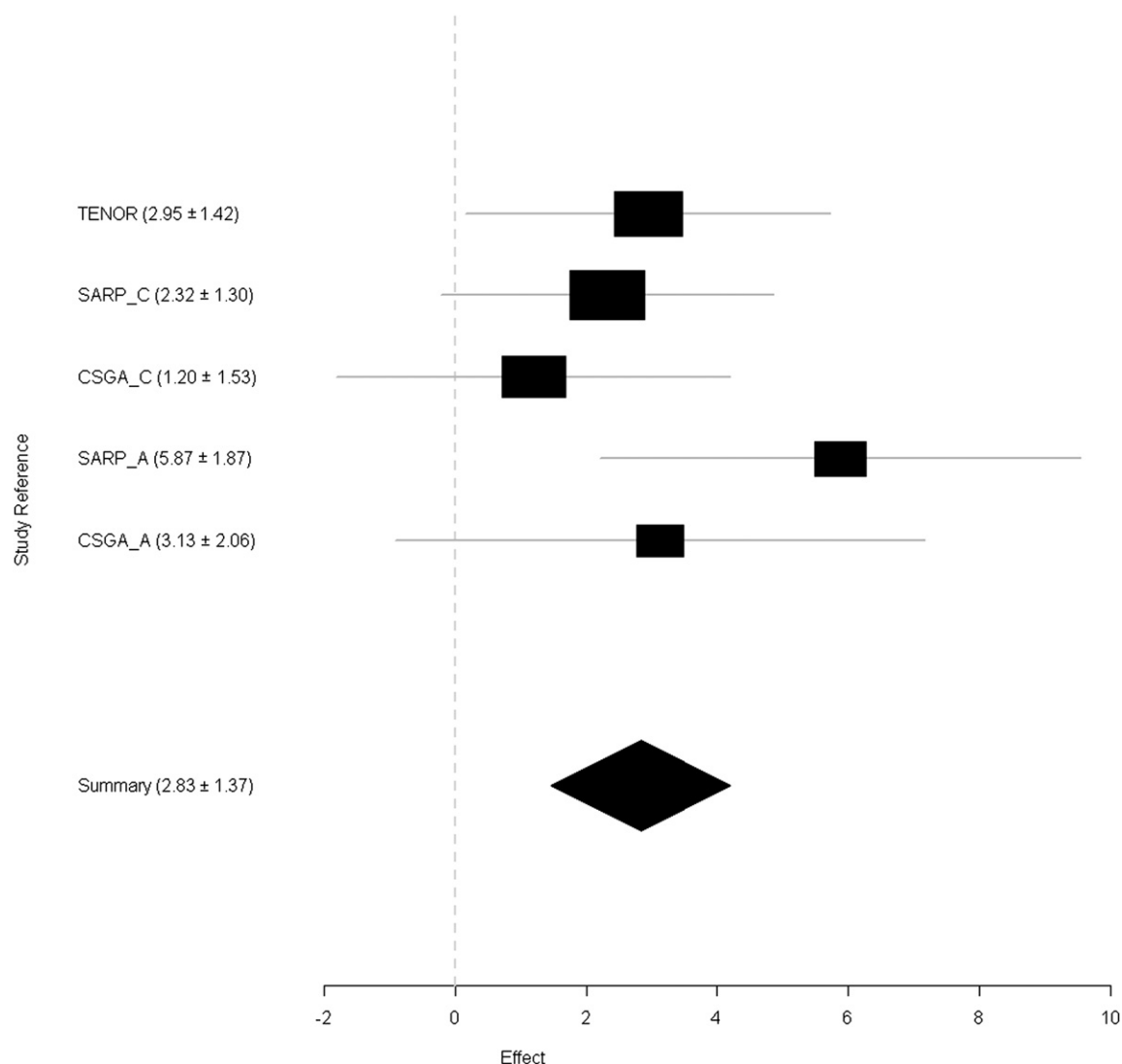


FIG 2. Forest plot of rs1512288 of *HHIP* with ppFEV₁. Random effects model are applied on effect size of regression slope. *SARP_C*, SARP non-Hispanic white subjects; *CSGA_C*, CSGA non-Hispanic white subjects; *SARP_A*, SARP African American subjects; *CSGA_A*, CSGA African American subjects.

—rs6845536, rs720485, rs1828591, and rs1512288—were in strong LD in non-Hispanic white subjects ($R^2 > 0.5$), but in weak LD in African American subjects ($R^2 < 0.5$). SNP rs6845536 at the 5' flanking region of *HHIP*, in LD with rs1512288 ($R^2 = 0.63$), showed the strongest signal in non-Hispanic white populations ($P_{\text{meta}} = 1.08\text{E-}04$, $3.20\text{E-}04$, and $.08$ for ppFEV₁, ppFVC, and FEV₁/FVC, respectively), whereas SNP rs1512288 had the strongest signal in African American subjects ($P_{\text{meta}} = 7.74\text{E-}04$, $5.11\text{E-}04$, and $.30$ for ppFEV₁, ppFVC, and FEV₁/FVC, respectively). Thus, we conclude on the basis of the LD structure in African American subjects that rs1512288 is either the causal SNP or in LD with a smaller set of SNPs (Table I; Fig 1).

The effect size (regression slope) of rs1512288 was consistent among 5 asthma populations (heterogeneity P value = $.41$; Fig 2). The summary effect size was 2.83 (SD = 1.37), and ppFEV₁ increased 2.83% on average with every copy of the minor allele T. For non-Hispanic white subjects from the SARP cohort, the effect size was 2.32 (SD = 1.30) for ppFEV₁ or 0.085 (SD = 0.056) for

baseline FEV₁, and FEV₁ differed by 85 mL on average with every copy of the minor allele T; for African American subjects from SARP, the effect size was 5.87 (SD = 1.87) for ppFEV₁ or 0.252 (SD = 0.077) for baseline FEV₁, and FEV₁ differed by 252 mL on average with every copy of the minor allele T.

Single nucleotide polymorphisms in *HHIP* were associated with bronchodilator reversibility (rs720485: $P = .024$ and $.057$ for non-Hispanic white and African American subjects, respectively) but not with bronchial hyperresponsiveness to methacholine (logPC₂₀; see this article's Table E4 in the Online Repository at www.jacionline.org).

Analysis results from the other genes previously identified for lung function in general populations identified 5 genes (*FAM13A*, *NOTCH4*, *THSD4*, *PTCHI*, and *PIDI*) that were associated significantly with lung function in asthma at the SNP or gene level (Table II; see this article's Tables E5 and E6 in the Online Repository at www.jacionline.org). At the SNP level, rs2869967, in the intron of *FAM13A* on chromosome 4q22, was significant ($P_{\text{meta}} = 2.9\text{E-}03$ for FVC) using strict replication standards and after

TABLE II. Meta-analysis results of 10 candidate genes in 5 populations with asthma

Previously identified SNPs	Tested SNPs	LD C/A§	Minor (risk) allele C/A§	ppFEV ₁			ppFVC			FEV ₁ /FVC		
				<i>P</i> _{meta} *	<i>P</i> _{meta_C} †	<i>P</i> _{meta_A} ‡	<i>P</i> _{meta} *	<i>P</i> _{meta_C} †	<i>P</i> _{meta_A} ‡	<i>P</i> _{meta} *	<i>P</i> _{meta_C} †	<i>P</i> _{meta_A} ‡
<i>TNSI</i> : rs2571445	rs2571445	1	T	.14	.47	.08	.11	.47	.05	.71	.76	.83
	rs929937	0/0	C/T	.32	.64	.22	.01	.06	.02	.56	.43	.80
<i>INTS12-GSTCD-NPNT</i> : rs10516526	rs10516526	1	G	.80	.96	.68	.61	.91	.21	.68	.79	.70
	rs3960769	0/0	A	.08	.12	.41	.47	.81	.28	.01	.06	.05
<i>HTR4</i> : rs3995090	rs3995090	1	C	.10	.14	.45	.43	.37	1.00	.24	.51	.22
	rs1833710	0/0	C	.04	.01	.63	.02	.01	.97	.67	.24	.20
<i>NOTCH4-AGER-PPT2</i> : rs2070600	rs2070600	1	A	.33	.91	.07	.74	.43	.45	.36	.79	.02
	rs206015	0.7/NA	T	3.2E-03	2.0E-04	.51	.01	9.0E-04	.63	.47	.22	.47
<i>THSD4</i> : rs12899618	rs1913768	1/0.8	A	.32	.41	.58	.69	.96	.36	.04	.07	.41
	rs1568010	0.2/0	C	.09	.12	.50	.82	.83	.38	2.9E-03	.05	.01
<i>GPR126</i> : rs11155242	rs11155242	1	C	.16	.16	.70	.95	.75	.65	.25	.22	.87
	rs171891	0.9/0.6	A	.02	.02	.59	.91	.95	.91	.36	.37	.81
<i>ADAM19</i> : rs2277027	rs2277027	1	C/A	.59	.46	.83	.54	.82	.40	.98	.64	.36
	rs6890282	0/0	G/T	.03	.18	.05	.69	.71	.88	.16	.57	.06
<i>FAM13A</i> : rs2869967	rs2869967	1	C/T (C/T)	.26	.17	.88	2.9E-03	4.9E-03	.29	.20	.09	.69
	rs6830970	0.6/0.2	G	.10	.15	.44	1.6E-03	.01	.09	.36	.12	.34
<i>PTCH1</i> : rs16909898	rs10512249	1/0.6	T	.72	.93	.57	.22	.24	.69	.51	.76	.41
	rs576594	0.1/0.2	T (T/C)	9.0E-04	6.5E-07	.04	.01	1.9E-05	.03	.01	1.1E-03	.90
<i>PID1</i> : rs1435867	rs1358443	0.3/0.1	C	.18	.44	.16	.31	.20	.84	.04	.36	.01
	rs3845823	0/0	T	.02	.01	.81	3.8E-04	1.0E-03	.17	.86	.56	.48

The first SNP in each gene was tested under our primary hypothesis of testing the previously reported SNP (or one in strong LD) for strict replication of the results in the general population. The second SNP listed for each gene is the SNP with the strongest *P* value across the gene to present a more comprehensive view of each gene (secondary analysis).

**P*_{meta} is the meta-analysis *P* value for all 5 populations with asthma.

†*P*_{meta_C} is the meta-analysis *P* value for 3 non-Hispanic white populations.

‡*P*_{meta_A} is the meta-analysis *P* value for 2 African American populations.

§LD C/A and minor (risk) allele C/A represent *R*² of LD between tested SNPs and candidate SNPs and minor (risk) allele of non-Hispanic white and African American populations, respectively. Risk alleles are labeled for rs2869967 and rs576594 only. See Tables E5 and E6 for other risk alleles.

correction for multiple testing. This signal was driven mainly by non-Hispanic white subjects. *NOTCH4* on chromosome 6p21, *THSD4* on chromosome 15q23, *PTCH1* on chromosome 9q22-q31, and *PID1* on chromosome 2q36 were significant (Table II) using a more relaxed replication standard at the gene level. *TNSI* on chromosome 2q35-q36, *GSTCD* on chromosome 4q24, *HTR4* on chromosome 5q31-q33, *GPR126* on chromosome 6q23-q24, and *ADAM19* on chromosome 5q33 were not significant after correcting for multiple testing.

Among these 11 genes, *PTCH1* is another gene involved in the hedgehog signaling pathway. SNP rs576594 was associated with ppFEV₁ (*P*_{meta} = 6.5E-07), ppFVC (*P*_{meta} = 1.9E-05), and FEV₁/FVC (*P*_{meta} = 1.1E-03) in the white populations, specifically the extensively phenotyped SARP cohort with broader ranges of asthma severity and lung function (Tables II, E5, and E6). The association of rs576594 was observed in the African American subjects, although weaker (*P* < .05) and, interestingly, in the opposite direction. Because HHIP and PTCH1 had overlapping functions in the hedgehog signaling pathway, the gene-gene interaction between them was analyzed. Interactions were tested between rs1512288 of *HHIP* and 14 *PTCH1* SNPs (LD *R*² < 0.3). No interaction was found in 3 white populations; however, interaction (*P* < .05) was observed in the 2 African American populations (rs3824491: *P* = 8.5E-03, .071, and .051 for meta-analysis, SARP, and CSGA African American subjects, respectively; see this article's Table E7 in the Online Repository at www.jacionline.org). This interaction needs to be replicated in other populations because the 2 African American populations have smaller sample sizes.

Joint analysis of the most consistently associated SNPs, based on our/previous study and biological function^{6,7} (rs1512288 in *HHIP*, rs576594 in *PTCH1*, and rs2869967 in *FAM13A*), was performed. With the increase in the number of risk SNPs, ppFEV₁, ppFVC, and FEV₁/FVC decreased (range of *P* values, .08-.003; Table III). The results were consistent for SARP non-Hispanic white subjects, SARP African American subjects, and TENOR, and may be generalized to other populations. Modeling with the 3 best SNPs, limited variance (0.7% to 4%) was explained (Table III), indicating there may be more genes involved. Joint analysis of SNPs from 5 replicated genes (*HHIP*, *PTCH1*, *FAM13A*, *PID1*, and *NOTCH4*) generated a more significant trend in SARP non-Hispanic white subjects, a cohort that was recruited for a wide range of asthma severity and pulmonary function (*P* = 9.8E-06 for ppFEV₁; Fig 3, A; see this article's Table E8 in the Online Repository at www.jacionline.org), and less significant in TENOR, a cohort with a narrower range of lung function (*P* = .01 for ppFEV₁). In SARP non-Hispanic white subjects, ppFEV₁ decreased significantly from 85.4 to 80.8, then to 78.5, 74.5, and finally to 62.9 when the number of risk SNPs increased from 0 to 5 (Fig 3, A). Because of this relationship, we analyzed 2 measures of asthma severity in the SARP non-Hispanic white subjects. The first was based on ATS criteria for severe asthma³ by comparing severe asthma (group 5) and mild asthma (groups 1 and 2), whereas the second used our newer approach to asthma phenotypic classification based on cluster analysis⁴ by comparing the more severe clusters (clusters 3, 4, and 5) with the less severe clusters (clusters 1 and 2). As seen in Fig 3, B, there is an increase in severity as the number of

TABLE III. Joint analysis of 3 SNPs in *HHIP*, *PTCH1*, and *FAM13A*

No. of risk SNPs*	0	1	2	3	P value	R ²
SARP non-Hispanic white subjects						
n	42	141	175	71		
ppFEV ₁	83 ± 22	80 ± 21	74 ± 23	73 ± 22	.003	0.02
ppFVC	92 ± 19	90 ± 17	85 ± 20	84 ± 17	.004	0.02
FEV ₁ /FVC	0.75 ± 0.1	0.72 ± 0.1	0.71 ± 0.1	0.70 ± 0.1	.03	0.01
TENOR non-Hispanic white subjects						
n	47	137	192	60		
ppFEV ₁	87 ± 26	78 ± 19	78 ± 20	72 ± 23	.003	0.02
ppFVC	91 ± 21	89 ± 17	90 ± 17	84 ± 19	.08	0.007
FEV ₁ /FVC	0.77 ± 0.1	0.72 ± 0.1	0.72 ± 0.1	0.71 ± 0.1	.007	0.02
SARP African American subjects						
n	15	78	82	30		
ppFEV ₁	85 ± 26	80 ± 20	75 ± 20	71 ± 17	.005	0.04
ppFVC	97 ± 23	91 ± 19	88 ± 17	88 ± 16	.06	0.02
FEV ₁ /FVC	0.72 ± 0.1	0.74 ± 0.1	0.71 ± 0.1	0.69 ± 0.1	.07	0.02

*No. of risk SNPs is the sum of risk SNPs in *HHIP* (rs1512288), *PTCH1* (rs576594), and *FAM13A* (rs2869967).

risk SNPs increases ($P = 6.0\text{E-}04$ and $2.7\text{E-}03$ for ATS and cluster classification, respectively).

DISCUSSION

In this study, a meta-analysis of 1441 extensively phenotyped subjects with a broad range of asthma severity from 5 asthma cohorts was performed. These studies differ in the proportion of subjects with severe asthma. However, these studies used similar comprehensive approaches to characterize subjects with asthma; thus, their combined use in a meta-analysis is an appropriate approach. Genomic inflation was weak (inflation factor <1.1 for every phenotype/population tested) and was adjusted in every population before meta-analysis.

HHIP was the most consistently replicated gene in the 5 asthmatic populations. *HHIP* protein is a regulatory factor of the hedgehog signaling pathway, interacting directly with all 3 hedgehog family members: sonic hedgehog, Indian hedgehog, and desert hedgehog.¹⁸ *HHIP* protein attenuates hedgehog signaling through a negative feedback mechanism by interacting with hedgehog proteins.¹⁸ Patched protein prevents hedgehog signaling through binding to smoothened in the absence of hedgehog; however, hedgehog protein together with cholesterol releases patched and transduces signals through smoothened.^{19,20} In mouse studies, *HHIP* and *PTCH1* proteins had been shown with a partially overlapping feedback function for hedgehog signaling pathway.²¹ Hedgehog protein regulates branching morphogenesis of tracheal-bronchial mesenchyme²² and influences embryonic lung morphogenesis.²³ *HHIP* and *PTCH1* are significantly associated with human height.^{24,25} However, in studies involving measures of lung function such as ppFEV₁ and ppFVC, adjustments for height are used in the calculation of percent predicted values. In GWASs of lung functions primarily in subjects without pulmonary diseases, *HHIP* was associated with FEV₁ and FEV₁/FVC.^{6,7,26} In a GWAS of chronic obstructive pulmonary disease (COPD), *HHIP* was associated with the risk of developing COPD²⁷; however, because the definition of COPD includes an abnormal level of lung function in a long-term smoker, this association may primarily reflect the association with pulmonary function.

The SNPs in *HHIP* most frequently identified in the previous GWAS in non-Hispanic white subjects were all in strong LD,

and thus, causal SNPs could not be determined. The SNPs identified previously were either the same or in very strong LD ($R^2 > 0.9$) with the SNPs found in this study.^{6,7} Very importantly, the differences in LD structure between African American and non-Hispanic white subjects allowed identification of a single SNP, rs1512288 (Table I; Fig 1). In our study, the association of *HHIP* with lung functions in non-Hispanic white populations was consistent with the previous GWAS, including SNPs in a large range from the 5' flanking region to introns. In African American populations, the association was primarily a result of rs1512288, indicating it was either the causal SNP or in LD with causal SNPs; however, only functional studies can determine the true causal SNPs. The effect directions of rs1512288 were the same for non-Hispanic white and African American subjects—that is, ppFEV₁ increased with copy numbers of minor allele T. The effect size of rs1512288 was larger in African American than non-Hispanic white subjects (Fig 2). Our results confirmed the importance of cross-validation by using more than 1 population with different LD structures. Second-generation sequencing to identify rare SNPs and causal SNPs of *HHIP* in larger African American populations, such as SARP, is warranted in the future.

The SNPs in *HHIP* were also associated with reversibility but not with bronchial hyperresponsiveness (logPC₂₀; Table E4). Bronchodilator reversibility is a measure of the ability of the lung to return or improve to more nearly normal function. Hence, the association of *HHIP* with bronchodilator reversibility is consistent with the association with baseline lung function. Furthermore, SNPs in *HHIP* were not identified by several other GWASs of asthma susceptibility^{28–31} and were not associated with asthma susceptibility in TENOR (see this article's Table E9 in the Online Repository at www.jacionline.org). On the basis of these data, variation in *HHIP* is important in determining level of lung function in subjects with asthma, which represents an important determinant of asthma severity.

Five genes (*FAM13A*, *NOTCH4-AGER-PPT2*, *THSD4*, *PTCH1*, and *PID1*) were also significantly associated with lung function at the SNP or gene level (Tables II, E5, and E6). *FAM13A* was the only gene (except *HHIP*) replicated at SNP levels, although in FVC instead of FEV₁/FVC as in previous findings.⁶ Interestingly, a recent GWAS of COPD susceptibility identified variants in *FAM13A* (rs7671167 and rs1903003; both in moderate LD [$R^2 > 0.5$] with rs2869967).³² Both *HHIP* and

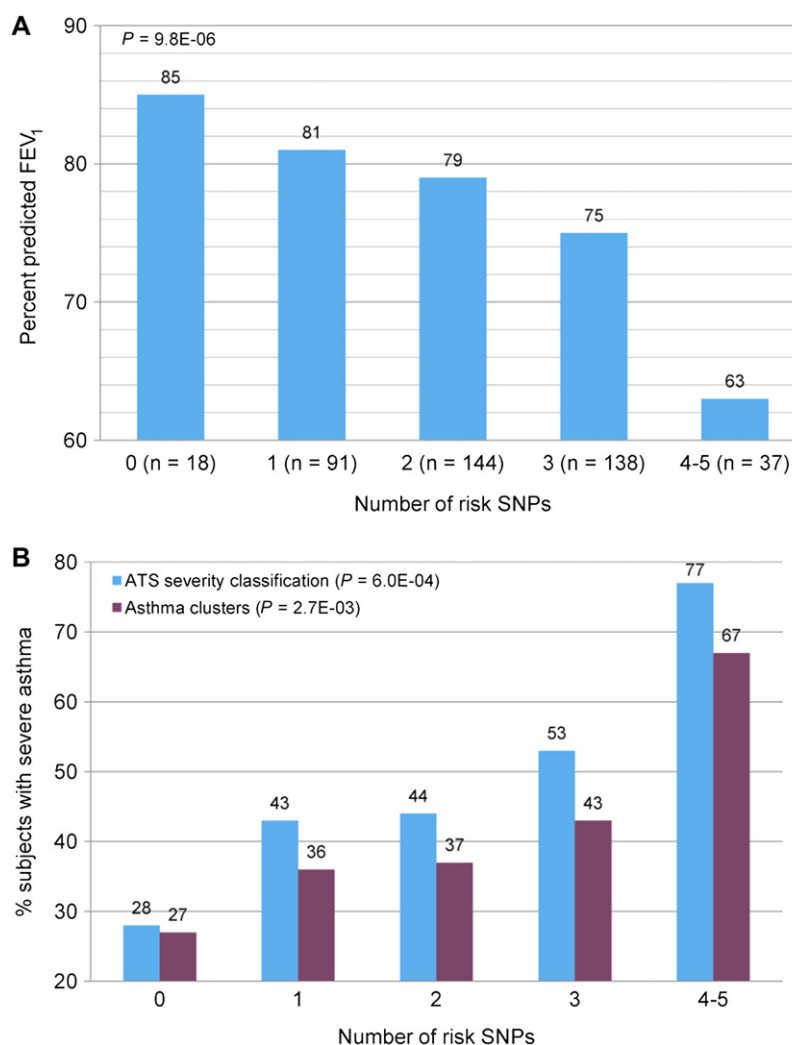


FIG 3. Joint analysis of 5 SNPs in *HHIP*, *PTCH1*, *FAM13A*, *PID1*, and *NOTCH4* in SARP non-Hispanic white subjects for ppFEV₁ (**A**) and percentage of subjects with severe asthma (**B**) on the basis of ATS and cluster classification.^{3,4}

FAM13A were associated with level of lung function in subjects with and without asthma^{6,7} and were associated with COPD susceptibility^{27,32} but not asthma susceptibility in previous GWASs, which may suggest genetic differences between the development of asthma and COPD. However, it is important to remember that the definition of COPD is based on abnormal levels of lung function, whereas subjects with asthma may have normal or abnormal levels of baseline lung function, especially those subjects with mild asthma. On the other hand, asthma, COPD, and other lung diseases may share some common genetic pathways. For example, *MMP12* and *ADAM33* have been shown to be associated with lung function, COPD, and asthma.³³⁻³⁵ Genes including *HHIP* and *FAM13A* are associated with normal lung function,^{6,7} COPD susceptibility,^{27,32} and asthma severity; therefore, further study of these candidates with lung function in COPD populations is warranted.³⁵

Normally, a single SNP/gene has limited predictive power for common diseases, and thus, joint analysis of the most consistent SNPs in *HHIP*, *PTCH1*, and *FAM13A* was performed. With the increase in the number of risk SNPs, ppFEV₁, ppFVC, and

FEV₁/FVC decreased significantly and consistently for SARP non-Hispanic white subjects, SARP African American subjects, and TENOR, and may be generalized to other populations (Table III). Joint analysis of SNPs from 5 replicated genes (*HHIP*, *PTCH1*, *FAM13A*, *PID1*, and *NOTCH4*) generated a more significant trend in SARP non-Hispanic white subjects, a cohort that was recruited for a wide range of asthma severity (Fig 3, A; Table E8). Asthma severity is strongly related to levels of lung function,^{3,4} and there was a significant relationship between the number of risk SNPs and the percentage of patients with severe asthma on the basis of either ATS criteria or cluster analysis (Fig 3, B). Although model overfitting might be a problem, the results should be generalizable because the SNPs used in the joint analysis were common for normal lung function, COPD susceptibility, and asthma severity, and the effect directions were consistent for SARP, TENOR, and CSGA populations.

In summary, these results demonstrate important associations between variation in *HHIP* with lung function in 5 cohorts of well characterized subjects with asthma (N = 1441). Because of LD among *HHIP* SNPs in white populations, multiple SNPs were

significant. However, in the 2 African American cohorts, we narrowed the signal to 1 SNP (rs1512288). Pulmonary function is a major determinant of asthma severity.¹⁻⁴ Combinations of risk lung function SNPs identified patients with asthma with increasing reductions in lung function (Table III; Fig 3). Thus, lung function in these asthma cohorts tracked with the number of risk genotypes, and this additive genetic approach could be useful in predicting lung function decline and asthma severity. However, longitudinal studies evaluating changes in asthma lung function in relationship to these genes are needed.

We acknowledge all investigators, staff, and participants in the SARP, TENOR, and CSGA studies.

Clinical implications: Lung function is a major determinant of asthma severity. Combinations of risk lung function SNPs in *HHIP*, *PTCH1*, and *FAM13A* identified patients with asthma with lower levels of lung function.

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Original Article

Importance of *HHIP* and other lung function genes in asthma

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Table E1. Demographics (Mean $\pm$ SD) of subjects in TENOR, SARP, and CSGA

	SARP White*	TENOR*	CSGA White*	SARP AA†	CSGA AA†
N	431	438	230	206	136
Age (yrs)	37.2 $\pm$ 14.3	47.0 $\pm$ 18.1	25.6 $\pm$ 13.6	29.8 $\pm$ 13.8	24.3 $\pm$ 13.4
Gender (% Female)	67	63	62	61	58
ppFEV₁	76.6 $\pm$ 22.4	78.4 $\pm$ 21.0	85.3 $\pm$ 16.7	77.0 $\pm$ 20.3	80.1 $\pm$ 20.9
ppFVC	87.0 $\pm$ 18.5	89.0 $\pm$ 17.8	92.8 $\pm$ 13.9	89.8 $\pm$ 17.8	91.6 $\pm$ 16.3
FEV₁/FVC	0.71 $\pm$ 0.13	0.72 $\pm$ 0.12	0.78 $\pm$ 0.11	0.72 $\pm$ 0.12	0.75 $\pm$ 0.13

*SARP White, TENOR, and CSGA White are non-Hispanic Whites from SARP, TENOR, and CSGA.

†SARP AA and CSGA AA are African Americans from SARP and CSGA.

Table E2. Meta-analysis results of *HHIP* region in three non-Hispanic white asthmatic populations.

SNP	P _{meta_FEV1}	FEV1 _{meta_Direction}	P _{TENOR_FEV1}	P _{SARP_FEV1}	P _{CSGA_FEV1}	P _{meta_FVC}	FVC _{meta_Direction}	P _{TENOR_FVC}	P _{SARP_FVC}	P _{CSGA_FVC}	P _{meta_FEV1/FVC}	FEV1/FVC _{meta_Direction}	P _{TENOR_FEV1/FVC}	P _{SARP_FEV1/FVC}	P _{CSGA_FEV1/FVC}	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs4362772	8.E-01	++	7.E-01	3.E-01	2.E-02	8.E-01	+/-	8.E-01	1.E-01	5.E-01	7.E-01	++	2.E-01	7.E-01	1.E-01	4	145549252	HHIP	flanking_5UTR	a	c	C	C	C
rs749316	7.E-03	+++	4.E-01	7.E-02	4.E-01	5.E-02	++	4.E-01	1.E-01	9.E-01	4.E-01	++	9.E-01	3.E-01	6.E-01	4	145590796	HHIP	flanking_5UTR	a	g	G	G	G
rs7684769	6.E-01	++	6.E-01	9.E-01	1.E-01	8.E-01	++	8.E-01	7.E-01	6.E-01	7.E-01	++	3.E-01	1.E+00	5.E-01	4	145638960	HHIP	flanking_5UTR	t	c	T	T	T
rs12641251	6.E-01	++	6.E-01	9.E-01	1.E-01	1.E+00	++	7.E-01	8.E-01	5.E-01	7.E-01	+/-	3.E-01	1.E+00	5.E-01	4	145644293	HHIP	flanking_5UTR	a	g	G	G	G
rs6827794	6.E-01	++	9.E-01	5.E-01	2.E-01	7.E-01	++	1.E+00	5.E-01	4.E-01	1.E+00	+/-	1.E+00	9.E-01	8.E-01	4	145649747	HHIP	flanking_5UTR	t	c	T	T	T
rs1512282	1.E-01	++	1.E-01	1.E-01	5.E-01	7.E-02	++	2.E-01	1.E-01	6.E-01	4.E-01	++	3.E-01	5.E-01	7.E-01	4	145650947	HHIP	flanking_5UTR	t	c	C	C	C
rs6845536	1.E-04	+++	2.E-02	2.E-02	6.E-02	3.E-04	+++	4.E-02	6.E-03	8.E-01	8.E-02	+++	6.E-01	4.E-01	4.E-02	4	145672233	HHIP	flanking_5UTR	t	c	C	C	C
rs720485	3.E-03	---	6.E-02	3.E-02	6.E-01	1.E-03	++	1.E-01	8.E-03	8.E-01	2.E-01	---	5.E-01	5.E-01	4.E-01	4	145682038	HHIP	flanking_5UTR	a	c	C	C	C
rs1828591	2.E-03	---	7.E-02	3.E-02	4.E-01	1.E-03	++	1.E-01	9.E-03	9.E-01	1.E-01	---	4.E-01	4.E-01	3.E-01	4	145700230	HHIP	flanking_5UTR	a	g	G	G	G
rs1512288	9.E-03	+++	4.E-02	8.E-02	4.E-01	5.E-03	+++	6.E-02	2.E-02	1.E+00	2.E-01	+++	4.E-01	6.E-01	4.E-01	4	145710731	HHIP	flanking_5UTR	t	c	T	T	T
rs2175586	5.E-01	++	2.E-01	4.E-01	5.E-01	1.E+00	++	9.E-03	6.E-01	2.E-01	1.E+00	+/-	4.E-01	9.E-01	3.E-01	4	145716391	HHIP	flanking_5UTR	a	g	A	A	A
rs1996020	2.E-01	---	5.E-01	6.E-01	3.E-01	5.E-01	---	6.E-01	7.E-01	7.E-01	5.E-01	+/-	1.E+00	7.E-01	4.E-01	4	145730644	HHIP	flanking_5UTR	a	c	C	C	C
rs7670758	2.E-04	---	6.E-03	3.E-02	3.E-02	2.E-04	---	1.E-02	9.E-03	3.E-01	9.E-02	---	4.E-01	6.E-01	9.E-02	4	145731325	HHIP	flanking_5UTR	a	g	A	A	A
rs7677662	1.E-01	---	1.E+00	5.E-01	1.E-01	2.E-01	---	1.E+00	4.E-01	6.E-01	5.E-01	+/-	8.E-01	8.E-01	2.E-01	4	145732503	HHIP	flanking_5UTR	a	g	G	G	G
rs2353397	6.E-03	+++	5.E-02	9.E-02	2.E-01	1.E-02	+++	1.E-01	5.E-02	1.E+00	9.E-02	+++	2.E-01	8.E-01	7.E-02	4	145737028	HHIP	flanking_5UTR	t	c	C	C	C
rs4835180	2.E-01	---	3.E-01	5.E-01	4.E-01	1.E-01	---	5.E-01	2.E-01	1.E+00	6.E-01	+/-	4.E-01	6.E-01	4.E-01	4	145740058	HHIP	flanking_5UTR	a	g	G	G	G
rs2035901	2.E-01	---	5.E-01	5.E-01	4.E-01	3.E-02	---	1.E-01	9.E-02	1.E+00	5.E-01	++	6.E-01	2.E-01	3.E-01	4	145741317	HHIP	flanking_5UTR	a	g	G	G	G
rs11947381	7.E-01	+/-	8.E-01	6.E-01	3.E-01	2.E-03	---	6.E-01	4.E-02	2.E-01	1.E-01	++	3.E-01	1.E-01	1.E+00	4	145757300	HHIP	flanking_5UTR	t	c	T	T	T
rs2575570	9.E-01	++	3.E-01	9.E-01	9.E-01	9.E-01	++	2.E-01	9.E-01	7.E-01	8.E-01	++	9.E-01	7.E-01	9.E-01	4	145768383	HHIP	flanking_5UTR	t	g	T	T	T
rs1398244	5.E-01	+++	5.E-01	6.E-01	9.E-01	6.E-01	+/-	1.E+00	4.E-01	2.E-01	7.E-03	+++	2.E-01	4.E-02	2.E-01	4	145781907	HHIP	flanking_5UTR	t	c	T	T	T
rs6845999	7.E-01	++	4.E-01	6.E-01	5.E-01	7.E-01	++	8.E-01	5.E-02	3.E-01	1.E-01	---	3.E-01	2.E-01	9.E-01	4	145785276	HHIP	flanking_5UTR	t	c	T	T	T

rs1812175	5.E-01	+-	1.E+00	1.E-01	2.E-01	9.E-01	+-	9.E-01	2.E-01	8.E-01	8.E-02	---	7.E-01	2.E-01	1.E-01	4	145794294	HHIP	intron	t	c	T	T	T
rs2220514	7.E-01	++	3.E-01	9.E-01	4.E-01	7.E-01	++	7.E-01	2.E-01	3.E-01	1.E-01	++	3.E-01	2.E-01	9.E-01	4	145796008	HHIP	intron	t	c	T	T	T
rs2306924	7.E-01	+-	6.E-01	6.E-01	4.E-01	7.E-01	+-	8.E-01	2.E-02	4.E-01	2.E-01	+++	7.E-01	1.E-01	1.E+00	4	145801986	HHIP	intron	a	g	A	A	A
rs6537307	3.E-01	+-	6.E-01	6.E-01	2.E-02	4.E-01	+-	6.E-01	1.E+00	6.E-02	1.E+00	+-	8.E-01	4.E-01	5.E-01	4	145821313	HHIP	intron	a	g	G	G	G
rs2575580	6.E-01	+-	4.E-01	8.E-01	3.E-01	9.E-01	+-	7.E-01	6.E-01	8.E-01	1.E-01	+++	3.E-01	8.E-01	2.E-01	4	145824475	HHIP	intron	t	c	C	C	C
rs6537310	1.E-01	---	5.E-01	7.E-01	2.E-02	7.E-03	---	4.E-01	1.E-01	2.E-01	9.E-01	+-	8.E-01	3.E-01	3.E-01	4	145856182	HHIP	intron	t	c	T	T	T
rs6854783	1.E-01	+++	5.E-01	6.E-01	3.E-02	7.E-03	+++	4.E-01	1.E-01	2.E-01	9.E-01	+-	9.E-01	3.E-01	3.E-01	4	145862529	HHIP	intron	a	g	G	G	G
rs11944404	1.E-01	---	8.E-02	9.E-01	7.E-03	5.E-01	+-	5.E-02	1.E+00	2.E-01	2.E-01	---	6.E-01	8.E-01	9.E-02	4	145890321	HHIP	flanking_3UTR	t	c	C	C	C
rs4835186	8.E-01	+-	1.E-01	7.E-01	6.E-01	6.E-01	+-	2.E-01	4.E-01	2.E-01	8.E-01	++	5.E-01	9.E-01	6.E-01	4	145906597	HHIP	flanking_3UTR	t	c	T	T	T
rs2353934	9.E-01	+-	3.E-01	4.E-01	8.E-01	5.E-01	+-	2.E-01	3.E-02	2.E-01	9.E-01	++	1.E+00	4.E-01	4.E-01	4	145916490	HHIP	flanking_3UTR	t	c	T	T	T
rs12647866	9.E-01	+-	2.E-01	1.E-01	9.E-01	7.E-01	+-	1.E-01	7.E-03	5.E-01	8.E-01	++	1.E+00	7.E-01	1.E+00	4	145928136	HHIP	flanking_3UTR	t	c	C	C	C
rs12651029	2.E-02	---	3.E-01	1.E-01	3.E-01	3.E-03	---	4.E-01	5.E-02	3.E-01	7.E-01	++	4.E-01	9.E-01	9.E-01	4	145989617	HHIP	flanking_3UTR	a	g	A	A	A
rs13102609	9.E-01	+-	5.E-02	5.E-01	8.E-01	7.E-01	+-	5.E-02	1.E-01	4.E-01	6.E-01	++	6.E-01	7.E-01	8.E-01	4	145990671	HHIP	flanking_3UTR	t	g	T	T	T

Table E3. Meta-analysis results of *HHIP* region in two African American asthmatic populations.

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs4362772	8.E-01	+	6.E-01	3.E-01	1.E+00	+	7.E-01	7.E-01	6.E-01	+	3.E-01	6.E-01	4	145549252	HHIP	flanking_5UTR	a	c	C	C
rs749316	8.E-01	+	6.E-01	9.E-01	6.E-01	++	1.E+00	4.E-01	5.E-01	--	6.E-01	6.E-01	4	145590796	HHIP	flanking_5UTR	a	g	G	G
rs7684769	5.E-01	-	8.E-01	5.E-01	6.E-01	--	8.E-01	7.E-01	7.E-01	+-	2.E-01	4.E-01	4	145638960	HHIP	flanking_5UTR	t	c	T	T
rs12641251	7.E-01	--	6.E-01	1.E+00	3.E-01	--	4.E-01	7.E-01	1.E+00	+	4.E-01	3.E-01	4	145644293	HHIP	flanking_5UTR	a	g	A	A
rs6827794	7.E-01	++	7.E-01	8.E-01	3.E-01	++	4.E-01	4.E-01	8.E-01	+-	7.E-01	3.E-01	4	145649747	HHIP	flanking_5UTR	t	c	T	T
rs1512282	7.E-01	+-	6.E-01	9.E-01	9.E-01	+-	7.E-01	8.E-01	6.E-01	+-	2.E-01	5.E-01	4	145650947	HHIP	flanking_5UTR	t	c	C	C
rs6845536	6.E-01	+-	2.E-01	6.E-01	3.E-01	++	4.E-01	5.E-01	9.E-01	+-	4.E-01	3.E-01	4	145672233	HHIP	flanking_5UTR	t	c	C	C
rs720485	7.E-02	--	4.E-01	6.E-02	4.E-02	--	3.E-01	3.E-02	5.E-01	--	8.E-01	4.E-01	4	145682038	HHIP	flanking_5UTR	a	c	C	C
rs1828591	4.E-02	-	2.E-01	7.E-02	2.E-02	--	1.E-01	8.E-02	9.E-01	+-	1.E+00	8.E-01	4	145700230	HHIP	flanking_5UTR	a	g	G	G
rs1512288	8.E-04	++	2.E-03	1.E-01	5.E-04	++	9.E-04	2.E-01	3.E-01	++	3.E-01	8.E-01	4	145710731	HHIP	flanking_5UTR	t	c	T	T
rs2175586	5.E-01	++	4.E-01	1.E+00	3.E-01	++	4.E-01	6.E-01	6.E-01	+-	5.E-01	1.E+00	4	145716391	HHIP	flanking_5UTR	a	g	A	A
rs1996020	7.E-01	+	7.E-01	3.E-01	9.E-01	+	7.E-01	8.E-01	8.E-01	+	3.E-01	4.E-01	4	145730644	HHIP	flanking_5UTR	a	c	C	C
rs7670758	1.E-01	++	2.E-01	5.E-01	2.E-01	++	3.E-01	5.E-01	5.E-01	++	9.E-01	4.E-01	4	145731325	HHIP	flanking_5UTR	a	g	A	A
rs7677662	2.E-01	++	7.E-01	2.E-01	7.E-01	++	7.E-01	8.E-01	9.E-01	+	4.E-01	5.E-01	4	145732503	HHIP	flanking_5UTR	a	g	G	G
rs2353397	8.E-01	+	7.E-01	9.E-01	7.E-01	--	7.E-01	9.E-01	6.E-01	++	6.E-01	9.E-01	4	145737028	HHIP	flanking_5UTR	t	c	C	C
rs4835180	7.E-01	++	7.E-01	1.E+00	1.E-01	++	1.E-01	5.E-01	7.E-01	--	8.E-01	8.E-01	4	145740058	HHIP	flanking_5UTR	a	g	G	G
rs2035901	9.E-01	+-	8.E-01	9.E-01	9.E-01	+-	6.E-01	4.E-01	6.E-01	+	4.E-01	8.E-01	4	145741317	HHIP	flanking_5UTR	a	g	A	A
rs11947381	2.E-01	++	4.E-01	5.E-01	4.E-01	++	3.E-01	9.E-01	7.E-01	+	8.E-01	3.E-01	4	145757300	HHIP	flanking_5UTR	t	c	T	T
rs2575570	8.E-01	+	6.E-01	2.E-01	6.E-01	+	1.E+00	4.E-01	5.E-01	+	9.E-01	2.E-01	4	145768383	HHIP	flanking_5UTR	t	g	T	T
rs1398244	3.E-01	++	5.E-01	5.E-01	8.E-01	+-	6.E-01	8.E-01	4.E-01	+	1.E+00	1.E-01	4	145781907	HHIP	flanking_5UTR	t	c	T	T
rs6845999	8.E-02	++	3.E-01	2.E-01	2.E-01	++	5.E-01	3.E-01	3.E-01	++	5.E-01	4.E-01	4	145785276	HHIP	flanking_5UTR	t	c	T	T
rs1812175	3.E-01	++	7.E-01	2.E-01	9.E-02	++	4.E-01	9.E-02	5.E-01	++	8.E-01	5.E-01	4	145794294	HHIP	intron	t	c	T	T

rs2220514	6.E-01	-+	8.E-01	3.E-01	9.E-01	-+	3.E-01	3.E-01	8.E-01	+-	7.E-01	1.E+00	4	145796008	HHIP	intron	t	c	T	T
rs2306924	2.E-01	++	1.E+00	7.E-02	7.E-02	++	3.E-01	7.E-02	7.E-01	-+	6.E-01	2.E-01	4	145801986	HHIP	intron	a	g	A	A
rs6537307	1.E-01	--	5.E-01	1.E-01	4.E-01	--	9.E-01	3.E-01	7.E-01	--	8.E-01	7.E-01	4	145821313	HHIP	intron	a	g	G	G
rs2575580	3.E-01	--	2.E-01	8.E-01	3.E-02	--	7.E-02	3.E-01	5.E-01	++	9.E-01	3.E-01	4	145824475	HHIP	intron	t	c	C	C
rs6537310	5.E-01	-+	8.E-01	2.E-01	2.E-01	++	5.E-01	3.E-01	9.E-01	-+	6.E-01	7.E-01	4	145856182	HHIP	intron	t	c	T	T
rs6854783	6.E-01	+-	1.E+00	3.E-01	4.E-01	--	5.E-01	6.E-01	7.E-01	+-	6.E-01	9.E-01	4	145862529	HHIP	intron	a	g	G	A
rs11944404	9.E-02	--	5.E-01	5.E-02	3.E-01	--	6.E-01	3.E-01	4.E-01	--	9.E-01	2.E-01	4	145890321	HHIP	flanking_3UTR	t	c	C	C
rs4835186	4.E-01	+-	6.E-01	5.E-02	7.E-02	--	6.E-01	2.E-02	5.E-01	++	5.E-01	9.E-01	4	145906597	HHIP	flanking_3UTR	t	c	T	T
rs2353934	2.E-01	+-	8.E-01	1.E-02	4.E-02	--	4.E-01	3.E-02	9.E-01	+-	5.E-01	5.E-01	4	145916490	HHIP	flanking_3UTR	t	c	T	T
rs12647866	3.E-01	-+	9.E-01	5.E-02	8.E-02	++	8.E-01	1.E-02	6.E-01	--	9.E-01	5.E-01	4	145928136	HHIP	flanking_3UTR	t	c	C	C
rs12651029	1.E+00	-+	8.E-01	9.E-01	8.E-01	++	9.E-01	8.E-01	7.E-01	++	6.E-01	9.E-01	4	145989617	HHIP	flanking_3UTR	a	g	A	A
rs13102609	7.E-01	-+	5.E-01	7.E-01	1.E+00	-+	6.E-01	5.E-01	5.E-01	-+	3.E-01	8.E-01	4	145990671	HHIP	flanking_3UTR	t	g	T	T

Table E4. Association results of top 4 SNPs of *HHIP* region with reversibility and logPC20 in SARP & CSGA combined dataset.

SNP	Reversibility*		LogPC20†	
	White** (n = 584)	AA†† (n = 306)	White** (n = 538)	AA†† (n = 251)
rs6845536	0.072	0.878	0.971	0.657
rs720485	0.024	0.057	0.670	0.341
rs1828591	0.031	0.132	0.674	0.622
rs1512288	0.038	0.474	0.815	0.231

*Reversibility is the P value of reversibility in cases only with age, sex, and ppFEV₁ as covariates.

†LogPC20 is the P value of logPC20 in cases only with age and sex as covariates.

**White represents combined non-Hispanic Whites of SARP and CSGA.

††AA represents combined African Americans of SARP and CSGA.

Table E5. Meta-analysis results of 10 candidate genes in three non-Hispanic white asthmatic populations.

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_TENOR_FEV1	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_TENOR_FVC	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_TENOR_FEV1/FVC	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_AI	SARP_AI	CSGA_AI
rs2373078	7.E-01	+++	8.E-01	8.E-01	9.E-01	4.E-01	++	9.E-01	4.E-01	6.E-01	9.E-01	++	7.E-01	4.E-01	7.E-01	2	218100800	TNS1	flanking_3UTR	t	c	T	T	T
rs1002353	7.E-01	++	9.E-01	5.E-01	5.E-01	3.E-01	++	4.E-01	3.E-01	5.E-01	4.E-01	++	6.E-01	1.E+00	3.E-01	2	218103390	TNS1	flanking_3UTR	t	c	C	C	C
rs2373079	6.E-01	++	1.E+00	7.E-01	3.E-01	4.E-01	++	2.E-01	1.E+00	5.E-02	6.E-01	++	2.E-01	7.E-01	9.E-01	2	218106382	TNS1	flanking_3UTR	a	g	A	A	A
rs3796025	4.E-01	++	8.E-01	6.E-01	6.E-02	8.E-01	++	6.E-01	5.E-01	2.E-02	1.E+00	++	3.E-01	3.E-01	9.E-01	2	218112318	TNS1	flanking_3UTR	t	c	T	T	T
rs17203333	6.E-01	++	7.E-01	4.E-01	3.E-01	7.E-01	++	7.E-01	4.E-01	5.E-01	8.E-01	++	9.E-01	5.E-01	9.E-01	2	218112453	TNS1	flanking_3UTR	t	c	C	C	C
rs4672833	6.E-01	++	7.E-01	7.E-01	2.E-01	7.E-01	++	6.E-01	7.E-01	8.E-02	1.E+00	++	3.E-01	3.E-01	8.E-01	2	218118260	TNS1	flanking_3UTR	t	c	C	C	C
rs4674189	4.E-01	++	9.E-01	6.E-01	8.E-01	6.E-01	++	3.E-01	7.E-01	2.E-01	6.E-01	++	1.E-01	8.E-01	7.E-01	2	218122227	TNS1	flanking_3UTR	t	c	T	T	T
rs6714500	7.E-01	++	1.E-01	1.E+00	4.E-01	6.E-01	++	9.E-02	4.E-01	2.E-01	8.E-01	++	6.E-01	9.E-01	7.E-01	2	218147088	TNS1	flanking_3UTR	t	c	T	T	T
rs6719545	7.E-01	++	8.E-02	9.E-01	2.E-01	1.E+00	++	2.E-02	9.E-01	6.E-01	1.E+00	++	1.E+00	5.E-01	3.E-01	2	218160079	TNS1	flanking_3UTR	t	g	G	G	G
rs2565686	3.E-01	++	2.E-01	2.E-01	2.E-02	6.E-01	++	4.E-02	8.E-02	2.E-01	3.E-01	++	9.E-01	9.E-01	8.E-02	2	218168866	TNS1	flanking_3UTR	t	c	C	C	C
rs2568177	6.E-01	++	8.E-01	9.E-01	3.E-01	9.E-01	++	6.E-01	6.E-01	3.E-01	1.E+00	++	9.E-01	9.E-01	8.E-01	2	218172299	TNS1	flanking_3UTR	t	c	C	C	C
rs1549733	7.E-01	++	8.E-01	5.E-01	3.E-01	6.E-01	++	4.E-01	4.E-01	2.E-01	6.E-01	++	9.E-01	3.E-01	9.E-01	2	218180417	TNS1	flanking_3UTR	t	c	T	T	T
rs7563651	7.E-01	++	7.E-01	9.E-01	2.E-01	7.E-01	++	4.E-01	8.E-01	3.E-01	9.E-01	++	7.E-01	8.E-01	1.E+00	2	218192012	TNS1	flanking_3UTR	a	g	A	A	A
rs6733585	5.E-01	++	3.E-01	4.E-01	5.E-01	1.E+00	++	1.E-01	9.E-01	9.E-01	6.E-01	++	9.E-01	2.E-01	6.E-01	2	218220843	TNS1	flanking_3UTR	a	g	A	A	A
rs6759238	1.E-01	+++	8.E-01	4.E-01	2.E-01	8.E-01	++	7.E-01	9.E-01	5.E-01	3.E-01	+++	7.E-01	5.E-01	5.E-01	2	218244694	TNS1	flanking_3UTR	a	g	G	G	G
rs6761086	9.E-01	++	3.E-01	6.E-01	2.E-01	9.E-01	++	1.E-01	8.E-01	8.E-01	8.E-01	++	1.E+00	3.E-01	4.E-01	2	218251675	TNS1	flanking_3UTR	t	c	T	T	T
rs4674200	8.E-01	++	2.E-01	5.E-01	2.E-01	9.E-01	++	1.E-01	1.E+00	9.E-01	7.E-01	++	7.E-01	4.E-01	4.E-01	2	218264996	TNS1	flanking_3UTR	a	c	C	C	C
rs10932725	4.E-01	++	2.E-01	1.E+00	5.E-02	6.E-01	++	3.E-01	1.E+00	2.E-01	3.E-01	++	2.E-01	4.E-01	4.E-01	2	218270341	TNS1	flanking_3UTR	t	c	T	T	T
rs934241	7.E-01	++	6.E-01	7.E-01	4.E-01	7.E-01	++	8.E-01	9.E-01	3.E-01	3.E-01	++	1.E-01	8.E-01	9.E-01	2	218271711	TNS1	flanking_3UTR	t	c	T	T	T
rs11688171	7.E-01	++	6.E-01	4.E-01	1.E-01	7.E-01	++	5.E-01	5.E-01	3.E-01	6.E-01	++	7.E-01	5.E-01	7.E-01	2	218282177	TNS1	flanking_3UTR	a	c	A	A	A
rs10168801	4.E-01	++	2.E-01	8.E-01	4.E-02	5.E-01	++	1.E-01	6.E-01	1.E-01	4.E-01	++	4.E-01	3.E-01	4.E-01	2	218288795	TNS1	flanking_3UTR	a	g	G	G	G
rs10932727	5.E-01	++	6.E-01	9.E-01	7.E-02	5.E-01	++	6.E-01	9.E-01	1.E-01	8.E-01	++	7.E-01	9.E-01	8.E-01	2	218313957	TNS1	flanking_3UTR	a	g	A	A	A
rs2052928	8.E-01	++	1.E-02	3.E-01	5.E-01	8.E-01	++	2.E-03	4.E-01	5.E-01	6.E-01	++	5.E-01	3.E-01	4.E-01	2	218328797	TNS1	flanking_3UTR	t	c	C	C	C
rs11677547	6.E-01	++	6.E-01	6.E-01	1.E-02	5.E-01	++	5.E-01	3.E-01	3.E-01	5.E-01	++	7.E-01	8.E-01	1.E-01	2	218331734	TNS1	flanking_3UTR	t	c	C	C	C
rs7560625	6.E-01	++	8.E-01	7.E-01	2.E-01	7.E-01	++	6.E-01	7.E-01	6.E-01	4.E-01	++	5.E-01	8.E-01	7.E-01	2	218334032	TNS1	flanking_3UTR	a	g	G	G	G
rs1835338	5.E-01	++	8.E-01	7.E-01	1.E-01	7.E-01	++	6.E-01	7.E-01	7.E-01	3.E-01	+++	5.E-01	8.E-01	4.E-01	2	218338844	TNS1	flanking_3UTR	a	g	A	A	A
rs1583109	4.E-01	++	3.E-01	9.E-01	7.E-02	7.E-01	++	9.E-01	5.E-01	3.E-01	9.E-01	++	6.E-02	6.E-01	1.E-01	2	218342264	TNS1	flanking_3UTR	a	g	G	G	G
rs10197943	2.E-01	++	4.E-01	6.E-01	4.E-03	5.E-01	++	3.E-01	6.E-01	2.E-01	6.E-01	++	1.E+00	9.E-01	2.E-01	2	218344279	TNS1	flanking_3UTR	t	c	T	T	T
rs2373146	2.E-01	++	9.E-01	1.E+00	6.E-03	8.E-01	++	8.E-01	6.E-01	3.E-01	2.E-01	++	9.E-01	4.E-01	8.E-02	2	218346421	TNS1	flanking_3UTR	t	c	C	C	C
rs7577167	9.E-01	++	9.E-03	1.E-01	8.E-01	9.E-01	++	3.E-03	4.E-01	7.E-01	5.E-01	++	3.E-01	1.E-01	5.E-01	2	218357732	TNS1	flanking_3UTR	t	g	G	G	G
rs11677208	4.E-01	++	4.E-01	1.E-01	8.E-02	5.E-01	++	4.E-01	2.E-01	1.E-01	5.E-01	++	5.E-01	3.E-01	3.E-01	2	218361192	TNS1	flanking_3UTR	t	c	C	C	C
rs2571460	5.E-01	++	7.E-02	3.E-01	2.E-01	8.E-01	++	7.E-02	3.E-01	5.E-01	9.E-01	++	5.E-01	7.E-01	9.E-01	2	218362333	TNS1	flanking_3UTR	a	g	A	A	A
rs2571457	7.E-01	++	6.E-01	5.E-01	4.E-01	1.E+00	++	6.E-01	3.E-01	1.E+00	7.E-01	++	1.E+00	7.E-01	7.E-01	2	218367229	TNS1	flanking_3UTR	t	c	C	C	C
rs3747	6.E-01	++	2.E-01	5.E-01	2.E-01	9.E-01	++	2.E-01	3.E-01	8.E-01	5.E-01	+++	7.E-01	7.E-01	8.E-01	2	218372878	TNS1	flanking_3UTR	t	g	G	G	G
rs918949	6.E-01	++	7.E-01	8.E-01	3.E-01	7.E-01	+++	6.E-01	9.E-01	6.E-01	8.E-01	++	5.E-01	7.E-01	3.E-01	2	218382942	TNS1	coding	t	c	C	C	C
rs1035672	6.E-01	++	7.E-01	8.E-01	3.E-01	6.E-01	+++	6.E-01	8.E-01	6.E-01	9.E-01	++	5.E-01	7.E-01	3.E-01	2	218383444	TNS1	intron	a	g	G	G	G
rs2059408	3.E-01	++	8.E-01	5.E-01	6.E-01	6.E-02	++	8.E-01	2.E-01	4.E-01	8.E-01	++	9.E-01	4.E-01	9.E-01	2	218387844	TNS1	intron	t	c	C	C	C
rs2161969	1.E+00	++	7.E-01	6.E-01	1.E+00	4.E-01	++	8.E-01	4.E-01	8.E-01	5.E-01	++	9.E-02	8.E-01	6.E-01	2	218388815	TNS1	intron	a	g	A	A	G
rs2571445	5.E-01	++	6.E-01	9.E-01	3.E-01	5.E-01	++	6.E-01	7.E-01	7.E-01	8.E-01	++	6.E-01	9.E-01	2.E-01	2	218391399	TNS1	coding	t	c	T	T	T
rs2552527	8.E-01	+++	5.E-01	9.E-01	1.E+00	3.E-01	+++	6.E-01	5.E-01	7.E-01	8.E-01	++	2.E-01	6.E-01	7.E-01	2	218396841	TNS1	intron	t	g	G	G	G
rs2571435	8.E-01	++	9.E-01	6.E-01	5.E-01	8.E-01	++	4.E-01	7.E-01	6.E-01	7.E-01	+++	7.E-01	9.E-01	1.E+00	2	218400004	TNS1	intron	t	c	T	T	T
rs1008835	5.E-01	++	2.E-01	9.E-01	1.E-01	7.E-01	++	5.E-01	6.E-01	4.E-01	2.E-01	+++	1.E-01	9.E-01	5.E-01	2	218412483	TNS1	intron	t	c	C	C	C
rs929937	6.E-01	+++	9.E-01	8.E-01	7.E-01	6.E-02	+++	1.E+00	2.E-01	4.E-01	4.E-01	++	9.E-01	3.E-01	7.E-01	2	218417460	TNS1	intron	t	c	C	C	C

rs3796033	7.E-01	--+	6.E-01	6.E-01	6.E-01	2.E-01	---	4.E-01	4.E-01	9.E-01	3.E-01	+++	7.E-01	5.E-01	5.E-01	2	218421527	TNS1	coding	a	g	A	A	A
rs3791978	7.E-01	+/-	6.E-01	7.E-01	4.E-01	6.E-01	+++	3.E-01	7.E-01	9.E-01	2.E-01	---	6.E-01	3.E-01	5.E-01	2	218422931	TNS1	intron	t	g	G	G	G
rs1035674	5.E-01	+++	5.E-01	3.E-01	1.E-01	3.E-01	++	2.E-01	5.E-01	4.E-02	5.E-01	---	7.E-01	8.E-01	6.E-01	2	218441371	TNS1	intron	a	g	A	A	A
rs2042542	7.E-01	+/-	3.E-01	3.E-01	4.E-01	7.E-01	+/-	9.E-02	8.E-01	4.E-01	3.E-01	---	8.E-01	2.E-01	8.E-01	2	218444537	TNS1	intron	a	g	G	G	G
rs1424916	8.E-01	+++	4.E-01	5.E-01	6.E-01	5.E-01	+++	3.E-01	9.E-01	4.E-01	4.E-01	+++	9.E-01	2.E-01	1.E+00	2	218447545	TNS1	intron	t	c	T	T	T
rs4674220	8.E-01	+/-	4.E-01	6.E-01	5.E-01	7.E-01	---	3.E-01	1.E+00	5.E-01	6.E-01	++	7.E-01	4.E-01	7.E-01	2	218450247	TNS1	intron	a	g	G	G	G
rs890049	4.E-01	++	9.E-01	5.E-01	1.E+00	2.E-01	++	5.E-01	3.E-01	6.E-01	8.E-01	++	4.E-01	9.E-01	4.E-01	2	218453131	TNS1	intron	t	c	T	T	T
rs3791940	3.E-01	---	3.E-01	5.E-01	7.E-01	9.E-01	---	5.E-01	1.E+00	8.E-01	6.E-01	+++	5.E-01	7.E-01	7.E-01	2	218457624	TNS1	intron	t	c	T	T	T
rs3791936	9.E-02	+++	2.E-01	5.E-01	6.E-02	4.E-01	+++	3.E-02	6.E-01	5.E-01	6.E-01	++	3.E-01	6.E-01	8.E-02	2	218476667	TNS1	intron	a	c	C	C	C
rs6755375	4.E-01	+/-	2.E-01	5.E-01	6.E-02	9.E-01	+/-	8.E-02	6.E-01	7.E-01	4.E-01	++	8.E-01	1.E+00	3.E-02	2	218484617	TNS1	intron	t	c	T	T	T
rs3791913	9.E-01	+++	6.E-01	6.E-01	7.E-01	7.E-01	++	2.E-01	6.E-01	4.E-01	3.E-01	+/-	1.E-01	3.E-01	2.E-01	2	218495921	TNS1	intron	t	c	C	C	C
rs3791911	9.E-01	++	1.E-01	5.E-01	7.E-01	4.E-01	++	9.E-01	5.E-01	1.E+00	4.E-01	++	2.E-02	7.E-02	3.E-01	2	218502228	TNS1	intron	t	c	T	T	T
rs3791906	3.E-01	---	1.E-01	7.E-01	3.E-01	2.E-01	---	6.E-01	4.E-01	5.E-01	3.E-01	++	3.E-02	2.E-01	4.E-01	2	218511574	TNS1	intron	a	g	G	G	G
rs1549589	6.E-01	+++	7.E-01	6.E-01	2.E-01	4.E-01	++	9.E-01	5.E-01	6.E-02	8.E-01	++	6.E-01	9.E-01	8.E-01	2	218519380	TNS1	flanking_5UTR	t	c	T	T	T
rs744753	9.E-01	+++	4.E-01	2.E-01	7.E-01	9.E-01	++	1.E-01	5.E-01	8.E-01	8.E-02	+++	6.E-01	2.E-01	2.E-01	2	218524323	TNS1	flanking_5UTR	a	g	A	A	A
rs3791890	2.E-02	---	6.E-01	1.E-01	3.E-01	3.E-02	---	9.E-01	2.E-01	3.E-01	3.E-01	---	3.E-01	9.E-01	5.E-01	2	218529831	TNS1	flanking_5UTR	t	c	C	C	C
rs3791884	6.E-01	+/-	8.E-01	7.E-01	3.E-01	6.E-01	+/-	1.E-01	9.E-01	3.E-01	5.E-01	++	1.E-01	8.E-01	4.E-01	2	218534627	TNS1	flanking_5UTR	a	g	G	G	G
rs11694996	8.E-01	+++	3.E-01	3.E-01	7.E-01	8.E-01	++	8.E-02	5.E-01	6.E-01	2.E-01	---	8.E-01	3.E-01	4.E-01	2	218536158	TNS1	flanking_5UTR	t	c	C	C	C
rs12619872	5.E-01	+/-	6.E-01	3.E-01	2.E-01	7.E-01	+/-	6.E-01	5.E-01	3.E-01	9.E-01	+/-	8.E-01	4.E-01	5.E-01	2	218541196	TNS1	flanking_5UTR	t	c	T	T	T
rs11674313	7.E-01	+/-	6.E-01	3.E-01	4.E-01	8.E-01	+/-	6.E-01	6.E-01	6.E-01	8.E-01	+/-	9.E-01	4.E-01	6.E-01	2	218546592	TNS1	flanking_5UTR	t	c	T	T	T
rs750132	9.E-01	+++	5.E-01	7.E-01	8.E-01	9.E-01	++	9.E-01	8.E-01	2.E-01	4.E-01	++	3.E-01	6.E-01	2.E-01	2	218548607	TNS1	flanking_5UTR	a	g	A	A	A
rs934039	9.E-01	+/-	6.E-01	6.E-01	9.E-01	1.E+00	+/-	7.E-01	8.E-01	9.E-01	9.E-01	+/-	6.E-01	5.E-01	9.E-01	2	218561636	TNS1	flanking_5UTR	t	c	T	T	T

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_TENOR_FEV1	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_TENOR_FVC	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_TENOR_FEV1/FVC	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs9307305	3.E-01	---	5.E-01	6.E-01	6.E-01	8.E-01	++	3.E-01	6.E-01	5.E-01	2.E-01	---	9.E-01	3.E-01	2.E-01	4	106661967	FLJ20184	flanking_5UTR	t	c	C	C	C
rs4082504	6.E-01	+/-	9.E-01	2.E-01	3.E-01	4.E-01	+/-	8.E-01	5.E-01	7.E-02	2.E-01	+++	9.E-01	3.E-01	4.E-01	4	106668349	FLJ20184	flanking_5UTR	a	c	A	A	A
rs12499086	8.E-01	---	9.E-01	8.E-01	1.E+00	7.E-01	+++	9.E-01	9.E-01	7.E-01	4.E-01	---	7.E-01	9.E-01	3.E-01	4	106670760	FLJ20184	flanking_5UTR	a	g	G	G	G
rs3960769	1.E-01	++	6.E-01	2.E-01	1.E+00	8.E-01	++	8.E-01	8.E-01	3.E-01	6.E-02	+++	5.E-01	2.E-01	2.E-01	4	106671248	FLJ20184	flanking_5UTR	a	c	A	A	A
rs730850	8.E-01	+++	5.E-01	2.E-01	6.E-01	1.E+00	+/-	4.E-01	3.E-01	9.E-01	4.E-01	++	8.E-01	4.E-01	3.E-01	4	106686037	FLJ20184	flanking_5UTR	t	g	T	T	T
rs2189228	4.E-01	+++	2.E-01	6.E-01	9.E-01	7.E-01	++	3.E-01	5.E-01	3.E-01	6.E-02	+++	3.E-01	3.E-01	2.E-01	4	106692026	FLJ20184	flanking_5UTR	a	c	A	A	A
rs17584487	2.E-02	---	8.E-01	1.E-01	5.E-01	5.E-01	++	7.E-01	5.E-01	8.E-01	1.E-01	---	9.E-01	1.E-01	3.E-01	4	106703347	FLJ20184	intron	a	g	G	G	G
rs7684945	8.E-01	++	9.E-01	8.E-01	7.E-01	9.E-01	++	9.E-01	3.E-01	7.E-01	8.E-01	++	9.E-01	8.E-01	2.E-01	4	106706033	FLJ20184	intron	a	c	C	C	C
rs2593305	6.E-01	+/-	9.E-01	9.E-01	2.E-01	9.E-01	++	7.E-01	3.E-01	8.E-01	5.E-01	++	6.E-01	7.E-01	8.E-02	4	106723939	FLJ20184	intron	a	g	G	G	G
rs199330	8.E-02	+++	3.E-01	5.E-01	6.E-02	8.E-01	++	4.E-01	6.E-01	6.E-01	3.E-02	+++	5.E-01	2.E-01	7.E-02	4	106724392	FLJ20184	intron	t	c	T	T	T
rs199332	9.E-01	++	4.E-02	7.E-01	8.E-01	8.E-01	+++	3.E-02	1.E+00	7.E-01	8.E-01	++	5.E-01	5.E-01	8.E-01	4	106727975	FLJ20184	intron	a	g	A	A	A
rs715706	7.E-01	+++	9.E-01	9.E-01	6.E-01	5.E-01	+++	5.E-01	9.E-01	4.E-01	7.E-01	+/-	6.E-01	9.E-01	7.E-01	4	106735477	FLJ20184	intron	t	c	T	T	T
rs1374530	8.E-01	+++	9.E-01	7.E-01	6.E-01	9.E-01	+/-	6.E-01	8.E-01	7.E-01	6.E-01	++	9.E-01	1.E+00	3.E-01	4	106743426	FLJ20184	intron	a	g	G	G	G
rs7687176	3.E-01	---	4.E-01	4.E-01	9.E-01	9.E-01	++	4.E-01	9.E-01	5.E-01	2.E-01	---	7.E-01	3.E-01	3.E-01	4	106746555	FLJ20184	intron	t	c	T	T	T
rs4326019	9.E-01	+++	4.E-01	3.E-01	9.E-01	7.E-01	++	2.E-01	6.E-01	4.E-01	2.E-01	+++	9.E-01	3.E-01	4.E-01	4	106746830	FLJ20184	intron	a	g	G	G	G
rs17035960	9.E-01	+/-	3.E-02	6.E-01	9.E-01	8.E-01	++	7.E-03	7.E-01	6.E-01	9.E-01	+/-	8.E-01	7.E-01	9.E-01	4	106751295	FLJ20184	intron	t	c	T	T	T
rs1447096	7.E-01	+/-	9.E-02	4.E-01	5.E-01	9.E-01	++	2.E-01	8.E-01	7.E-01	6.E-01	++	3.E-01	5.E-01	1.E-01	4	106778827	FLJ20184	flanking_3UTR	t	g	T	T	T
rs1447098	8.E-01	+++	1.E-01	3.E-01	5.E-01	9.E-01	++	2.E-01	8.E-01	8.E-01	6.E-01	++	4.E-01	5.E-01	2.E-01	4	106783049	FLJ20184	flanking_3UTR	t	c	C	C	C
rs1374534	8.E-01	+/-	5.E-03	9.E-01	6.E-01	7.E-01	++	4.E-03	5.E-01	5.E-01	9.E-01	+/-	1.E-01	9.E-01	1.E-01	4	106791905	FLJ20184	flanking_3UTR	a	g	A	A	A
rs4235415	9.E-01	++	1.E-02	9.E-01	7.E-01	9.E-01	++	2.E-02	9.E-01	8.E-01	3.E-01	---	2.E-01	7.E-01	8.E-01	4	106813299	PHF22	flanking_3UTR	a	g	G	G	G
rs6820671	8.E-01	+++	7.E-05	6.E-01	6.E-01	9.E-01	++	1.E-03	7.E-01	8.E-01	9.E-02	+/-	2.E-02	1.E+00	7.E-01	4	106833270	PHF22	intron	a	g	G	G	G
rs11727735	1.E+00	+++	2.E-02	5.E-01	9.E-01	9.E-01	+/-	6.E-03	7.E-01	8.E-01	9.E-01	+/-	5.E-01	5.E-01	7.E-01	4	106851319	FLJ13273	intron	a	g	G	G	G
rs4698951	1.E+00	++	7.E-03	9.E-01	7.E-01	7.E-01	++	8.E-02	1.E+00	4.E-01	7.E-02	---	5.E-02	6.E-01	6.E-01	4	106891647	FLJ13273	intron	t	c	C	C	C
rs10516526	1.E+00	+++	1.E-02	4.E-01	9.E-01	9.E-01	+/-	6.E-03	7.E-01	8.E-01	8.E-01	+/-	4.E-01	5.E-01	7.E-01	4	106908353	FLJ13273	intron	a	g	G	G	G
rs2553449	8.E-01	+/-	5.E-05	1.E-01	5.E-01	8.E-01	+++	7.E-05	2.E-01	5.E-01	1.E+00	+/-	6.E-02	3.E-01	2.E-01	4	106918341	FLJ13273	intron	t	c	T	T	T

rs2553463	9.E-01	+-	2.E-01	5.E-02	9.E-01	7.E-01	+-	8.E-02	3.E-01	5.E-01	2.E-01	++	1.E+00	8.E-02	8.E-01	4	106950112	FLJ13273	intron	t	c	C	C	C
rs2553435	8.E-01	++	7.E-01	2.E-01	6.E-01	1.E+00	++	7.E-01	4.E-01	1.E+00	3.E-01	++	9.E-01	2.E-01	6.E-01	4	107016314	NPNT	flanking_5UTR	a	c	C	C	C
rs2544408	7.E-01	+-	5.E-02	2.E-01	4.E-01	1.E+00	+-	2.E-01	6.E-01	9.E-01	9.E-01	+-	1.E-01	3.E-01	4.E-01	4	107027489	NPNT	flanking_5UTR	t	g	A	A	A
rs2553453	7.E-01	+-	6.E-02	2.E-01	3.E-01	1.E+00	+-	2.E-01	7.E-01	1.E+00	8.E-01	+-	2.E-01	3.E-01	4.E-01	4	107027621	NPNT	flanking_5UTR	a	g	A	A	A
rs11933466	8.E-01	+-	3.E-03	1.E-01	6.E-01	1.E+00	+-	8.E-03	5.E-01	9.E-01	9.E-01	+-	1.E-01	2.E-01	7.E-01	4	107032181	NPNT	flanking_5UTR	a	g	A	A	A
rs10470990	7.E-01	+-	8.E-01	6.E-01	3.E-01	9.E-01	+-	6.E-01	9.E-01	9.E-01	6.E-01	--	1.E+00	4.E-01	9.E-01	4	107041027	NPNT	intron	t	c	T	T	T
rs4600917	7.E-01	++	3.E-02	6.E-01	4.E-01	7.E-01	--	2.E-02	8.E-01	9.E-01	8.E-01	+-	4.E-01	2.E-01	1.E+00	4	107049094	NPNT	intron	t	c	C	C	C
rs4340795	4.E-01	--	2.E-01	7.E-01	4.E-01	9.E-01	+-	6.E-01	6.E-01	7.E-01	5.E-02	--	1.E-01	2.E-01	1.E+00	4	107081179	NPNT	coding	a	g	A	A	A
rs4074127	5.E-01	--	2.E-01	9.E-01	4.E-01	9.E-01	+-	7.E-01	6.E-01	7.E-01	8.E-02	--	1.E-01	3.E-01	1.E+00	4	107086429	NPNT	intron	a	g	A	A	A
rs6817700	6.E-01	+-	2.E-01	5.E-01	3.E-01	8.E-01	+-	1.E-01	3.E-01	5.E-01	8.E-01	+-	6.E-01	9.E-01	8.E-01	4	107110980	NPNT	3UTR	a	g	A	A	A
rs7691244	9.E-01	++	6.E-01	1.E-01	8.E-01	7.E-01	++	2.E-01	3.E-02	5.E-01	9.E-01	+-	7.E-01	8.E-01	5.E-01	4	107120677	NPNT	flanking_3UTR	a	g	G	G	G
rs13125117	8.E-01	+-	5.E-01	3.E-01	6.E-01	8.E-01	+-	3.E-01	2.E-01	6.E-01	8.E-01	+-	9.E-01	5.E-01	5.E-01	4	107129147	NPNT	flanking_3UTR	t	c	C	C	C
rs2156507	1.E-01	+-	4.E-01	6.E-01	7.E-02	3.E-01	+-	4.E-01	1.E+00	3.E-02	4.E-01	--	9.E-01	7.E-01	3.E-01	4	107133446	NPNT	flanking_3UTR	a	g	G	G	G
rs11730681	1.E+00	+-	2.E-01	4.E-01	9.E-01	9.E-01	+-	1.E-01	5.E-01	8.E-01	8.E-01	+-	5.E-01	5.E-01	6.E-01	4	107142409	NPNT	flanking_3UTR	a	g	A	A	A

SNP	pmeta_FEV1	FEV1_meta_Direction	p_TENOR_FEV1	p_SARP_FEV1	p_CSGA_FEV1	pmeta_FVC	FVC_meta_Direction	p_TENOR_FVC	p_SARP_FVC	p_CSGA_FVC	p_meta_FEV1/FVC	FEV1/FVC_meta_Direction	p_TENOR_FEV1/FVC	p_SARP_FEV1/FVC	p_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs3995090	1.E-01	--	2.E-01	4.E-01	4.E-01	4.E-01	++	4.E-02	4.E-01	6.E-01	5.E-01	+-	7.E-01	9.E-01	5.E-02	5	147826008	HTR4	intron	a	c	C	C	C
rs7723153	1.E-01	+-	2.E-01	2.E-01	6.E-01	6.E-01	--	3.E-01	9.E-01	4.E-01	3.E-02	+-	4.E-01	5.E-04	3.E-01	5	147857917	HTR4	intron	a	g	A	A	A
rs1368384	5.E-01	--	7.E-02	7.E-01	9.E-01	8.E-01	++	2.E-02	1.E+00	5.E-01	2.E-01	+-	9.E-01	1.E-01	4.E-01	5	147875141	HTR4	intron	t	c	C	C	C
rs1368386	9.E-02	+-	2.E-01	1.E-01	5.E-01	5.E-01	--	3.E-01	8.E-01	4.E-01	3.E-02	+-	4.E-01	4.E-04	2.E-01	5	147875331	HTR4	intron	t	g	T	T	T
rs2277049	4.E-02	+-	6.E-02	9.E-02	1.E+00	4.E-02	--	9.E-02	1.E-01	7.E-01	1.E-01	+-	3.E-01	1.E-01	1.E+00	5	147883281	HTR4	intron	a	c	A	A	A
rs12152801	6.E-01	++	5.E-01	5.E-01	7.E-01	9.E-01	+-	8.E-01	7.E-01	8.E-01	7.E-02	++	4.E-01	2.E-02	6.E-01	5	147888538	HTR4	intron	t	g	G	G	G
rs2278392	1.E-01	--	4.E-02	3.E-01	6.E-01	7.E-01	+-	6.E-02	8.E-01	4.E-01	9.E-02	+-	2.E-01	1.E-01	9.E-01	5	147908418	HTR4	intron	a	g	A	A	A
rs1345697	5.E-02	++	7.E-02	1.E-01	1.E+00	7.E-01	+-	9.E-02	8.E-01	3.E-01	1.E-02	++	3.E-01	2.E-04	4.E-01	5	147922431	HTR4	intron	a	g	G	G	A
rs4599527	1.E-01	++	2.E-01	3.E-01	7.E-01	5.E-01	++	2.E-01	8.E-01	3.E-01	3.E-01	++	5.E-01	2.E-01	7.E-01	5	147932732	HTR4	intron	t	c	C	C	C
rs867522	2.E-01	--	1.E-01	3.E-01	9.E-01	7.E-01	+-	4.E-01	4.E-01	4.E-01	4.E-02	+-	8.E-02	3.E-02	4.E-01	5	147946439	HTR4	intron	a	g	A	A	A
rs1833710	8.E-03	++	6.E-02	9.E-02	3.E-01	6.E-03	++	1.E-01	1.E-01	1.E-01	2.E-01	++	2.E-01	5.E-01	1.E+00	5	147947939	HTR4	intron	t	c	C	C	C
rs2964276	6.E-01	+-	2.E-01	5.E-01	3.E-01	7.E-01	+-	5.E-01	1.E-01	5.E-01	5.E-02	--	1.E-01	3.E-01	4.E-01	5	147959171	HTR4	intron	t	c	T	T	T
rs7711800	2.E-01	--	2.E-02	6.E-01	1.E-01	5.E-01	+-	2.E-01	7.E-01	1.E-01	8.E-03	--	3.E-02	1.E-01	4.E-01	5	147963048	HTR4	intron	t	c	T	T	T
rs1011427	1.E-01	++	2.E-01	3.E-01	7.E-01	9.E-01	++	4.E-01	9.E-01	8.E-01	2.E-02	++	1.E-01	1.E-02	9.E-01	5	147968170	HTR4	intron	t	c	T	T	T
rs13182913	7.E-01	++	4.E-01	4.E-01	4.E-01	7.E-01	++	7.E-01	1.E-01	4.E-01	2.E-01	++	4.E-01	4.E-01	6.E-01	5	147975798	HTR4	intron	t	c	C	C	C
rs2068190	2.E-01	++	9.E-01	2.E-01	4.E-01	2.E-01	++	9.E-01	2.E-01	4.E-01	7.E-01	++	8.E-01	4.E-01	5.E-01	5	147987206	HTR4	intron	t	c	T	T	T
rs5028114	4.E-01	++	3.E-01	7.E-01	3.E-01	6.E-01	++	7.E-01	1.E+00	4.E-01	2.E-01	++	3.E-01	6.E-01	4.E-01	5	147991932	HTR4	intron	t	c	T	T	T
rs888961	1.E+00	+-	7.E-01	9.E-01	9.E-01	1.E+00	+-	9.E-01	6.E-01	1.E+00	8.E-01	+-	7.E-01	1.E+00	9.E-01	5	148019090	HTR4	flanking_5UTR	t	g	T	T	T
rs4425495	9.E-01	+-	3.E-01	9.E-01	9.E-01	9.E-01	+-	1.E+00	9.E-01	6.E-01	3.E-01	++	1.E-01	8.E-01	8.E-01	5	148041010	HTR4	flanking_5UTR	t	c	C	C	C
rs9325113	8.E-01	+-	3.E-01	4.E-01	6.E-01	5.E-01	+-	8.E-01	1.E-01	2.E-01	1.E-01	+-	9.E-02	4.E-01	8.E-01	5	148078196	HTR4	flanking_5UTR	t	c	T	T	T
rs6580565	1.E+00	+-	4.E-01	1.E+00	9.E-01	9.E-01	+-	1.E+00	8.E-01	7.E-01	4.E-01	+-	2.E-01	9.E-01	9.E-01	5	148078895	HTR4	flanking_5UTR	t	c	C	C	C
rs2400642	9.E-01	+-	7.E-01	6.E-01	8.E-01	8.E-01	+-	8.E-01	7.E-01	6.E-01	4.E-01	--	7.E-01	8.E-01	5.E-01	5	148094999	HTR4	flanking_5UTR	a	g	G	G	G

SNP	pmeta_FEV1	FEV1_meta_Direction	p_TENOR_FEV1	p_SARP_FEV1	p_CSGA_FEV1	pmeta_FVC	FVC_meta_Direction	p_TENOR_FVC	p_SARP_FVC	p_CSGA_FVC	p_meta_FEV1/FVC	FEV1/FVC_meta_Direction	p_TENOR_FEV1/FVC	p_SARP_FEV1/FVC	p_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs1053924	4.E-02	++	5.E-02	1.E-01	5.E-01	7.E-01	+-	1.E-01	6.E-01	4.E-01	3.E-02	++	3.E-01	1.E-01	2.E-01	6	32228693	PPT2	flanking_5UTR	a	g	A	A	A

rs9267810	8.E-01	++	4.E-01	5.E-01	6.E-01	9.E-01	++	6.E-01	2.E-01	8.E-01	8.E-01	+-	4.E-01	6.E-01	1.E+00	6	32229572	PPT2	intron	t	c	C	C	C
rs2269425	6.E-03	+++	5.E-02	5.E-02	5.E-01	7.E-02	+++	2.E-01	2.E-01	1.E+00	2.E-02	+++	1.E-01	2.E-01	2.E-01	6	32231617	PPT2	intron	t	c	T	T	T
rs3134603	8.E-01	+-	7.E-01	8.E-01	8.E-01	2.E-01	---	1.E+00	5.E-01	4.E-01	3.E-01	+++	7.E-01	2.E-01	1.E+00	6	32233980	PPT2	intron	t	c	T	T	T
rs2269424	8.E-01	+-	3.E-01	5.E-01	6.E-01	9.E-01	+-	6.E-01	2.E-01	8.E-01	8.E-01	+-	4.E-01	7.E-01	1.E+00	6	32240211	PPT2	flanking_3UTR	t	c	T	T	T
rs3096697	7.E-01	+-	5.E-01	7.E-01	7.E-01	4.E-01	+-	7.E-01	4.E-01	6.E-01	5.E-01	---	9.E-01	6.E-01	5.E-01	6	32242488	EGFL8	coding	t	c	T	T	T
rs3130347	7.E-01	+-	5.E-01	7.E-01	8.E-01	4.E-01	+-	7.E-01	4.E-01	6.E-01	4.E-01	+++	9.E-01	6.E-01	5.E-01	6	32242634	EGFL8	intron	t	c	C	C	C
rs3130283	6.E-01	+++	6.E-01	8.E-01	8.E-01	7.E-01	+-	8.E-01	5.E-01	5.E-01	2.E-01	+++	8.E-01	2.E-01	6.E-01	6	32246523	AGPAT1	intron	a	c	A	A	A
rs3130284	7.E-01	+-	5.E-01	7.E-01	7.E-01	4.E-01	+-	6.E-01	4.E-01	6.E-01	5.E-01	+++	9.E-01	6.E-01	5.E-01	6	32248465	AGPAT1	intron	t	c	C	C	C
rs2269423	8.E-02	+++	5.E-03	3.E-01	3.E-01	9.E-01	+-	3.E-02	7.E-01	3.E-01	1.E-02	+++	1.E-01	2.E-01	6.E-02	6	32253685	AGPAT1	intron	t	g	T	T	T
rs3134945	7.E-01	+-	5.E-01	7.E-01	7.E-01	4.E-01	+-	7.E-01	4.E-01	5.E-01	5.E-01	---	9.E-01	6.E-01	5.E-01	6	32254470	RNF5	intron	t	g	T	T	T
rs3130349	7.E-01	+-	8.E-01	7.E-01	9.E-01	8.E-01	+-	9.E-01	4.E-01	6.E-01	4.E-01	---	8.E-01	6.E-01	4.E-01	6	32255674	RNF5	coding	a	g	A	A	A
rs3134943	4.E-01	+++	5.E-01	6.E-01	6.E-01	9.E-01	+-	7.E-01	6.E-01	7.E-01	1.E-01	+++	7.E-01	1.E-01	6.E-01	6	32255739	RNF5	intron	a	g	A	A	A
rs1035798	9.E-01	+-	3.E-01	8.E-01	7.E-01	1.E+00	+-	7.E-01	2.E-01	1.E+00	5.E-01	+-	2.E-01	9.E-01	9.E-01	6	32259200	AGER	intron	t	c	T	T	T
rs2070600	9.E-01	+-	7.E-01	2.E-01	8.E-01	4.E-01	+-	8.E-01	3.E-01	2.E-01	8.E-01	+-	4.E-01	6.E-01	3.E-01	6	32259421	AGER	coding	a	g	A	A	A
rs1800624	9.E-01	+-	3.E-01	8.E-01	8.E-01	1.E+00	+-	7.E-01	2.E-01	1.E+00	5.E-01	+-	2.E-01	9.E-01	9.E-01	6	32260365	PBX2	flanking_3UTR	a	t	A	A	A
rs204995	7.E-02	+++	4.E-01	2.E-01	7.E-01	9.E-01	+-	9.E-01	4.E-02	8.E-01	8.E-02	+++	2.E-01	5.E-01	2.E-01	6	32262263	PBX2	intron	t	c	C	C	C
rs204994	6.E-02	---	4.E-01	2.E-01	6.E-01	1.E-02	+-	9.E-01	3.E-02	5.E-01	1.E-01	---	4.E-01	6.E-01	1.E-01	6	32262976	PBX2	intron	a	g	A	A	A
rs204993	2.E-03	+++	8.E-01	2.E-02	8.E-01	4.E-03	+-	9.E-01	1.E-02	4.E-01	9.E-02	+++	8.E-01	2.E-01	1.E-01	6	32263559	PBX2	intron	t	c	C	C	C
rs176095	7.E-02	+++	6.E-01	2.E-01	7.E-01	8.E-01	+-	9.E-01	3.E-02	6.E-01	2.E-01	+++	5.E-01	6.E-01	2.E-01	6	32266297	GPSM3	flanking_3UTR	t	c	C	C	C
rs204991	5.E-03	+++	3.E-01	3.E-02	9.E-01	9.E-04	+-	4.E-01	4.E-03	4.E-01	2.E-01	+++	8.E-01	3.E-01	4.E-01	6	32269344	GPSM3	intron	a	g	G	G	G
rs204990	4.E-03	---	3.E-01	3.E-02	9.E-01	9.E-04	+-	4.E-01	4.E-03	4.E-01	2.E-01	---	7.E-01	3.E-01	4.E-01	6	32269408	GPSM3	intron	t	g	T	T	T
rs8192575	9.E-03	---	9.E-01	3.E-02	7.E-01	4.E-01	+-	6.E-01	4.E-01	6.E-01	1.E-01	+-	1.E+00	3.E-02	8.E-01	6	32274362	NOTCH4	intron	c	g	C	C	C
rs3134942	1.E-01	+-	5.E-01	1.E-01	4.E-01	2.E-01	+-	7.E-01	1.E-01	2.E-01	2.E-01	---	8.E-01	2.E-01	7.E-01	6	32276749	NOTCH4	coding	a	c	A	A	A
rs2071277	1.E+00	+-	6.E-02	3.E-01	1.E+00	8.E-01	+-	7.E-01	2.E-01	6.E-01	7.E-02	+++	2.E-02	1.E+00	5.E-01	6	32279661	NOTCH4	intron	a	g	A	G	A
rs3131296	1.E-01	+-	5.E-01	1.E-01	4.E-01	2.E-01	+-	7.E-01	1.E-01	2.E-01	2.E-01	---	8.E-01	2.E-01	7.E-01	6	32280971	NOTCH4	intron	a	g	A	A	A
rs3130292	9.E-01	+-	9.E-01	6.E-01	8.E-01	1.E+00	+-	5.E-01	3.E-01	9.E-01	3.E-01	---	7.E-01	4.E-01	6.E-01	6	32284186	NOTCH4	intron	c	g	C	C	C
rs206017	5.E-01	---	2.E-02	6.E-01	8.E-01	8.E-01	+-	3.E-01	9.E-01	4.E-01	1.E-02	---	1.E-02	5.E-01	2.E-01	6	32284189	NOTCH4	intron	a	g	G	G	G
rs3132942	9.E-01	+-	6.E-02	9.E-01	6.E-01	6.E-01	+-	3.E-01	5.E-01	3.E-01	2.E-01	---	1.E-01	6.E-01	7.E-01	6	32284490	NOTCH4	intron	a	g	A	A	A
rs9267833	1.E+00	+++	1.E-02	3.E-01	1.E+00	7.E-01	+-	2.E-01	6.E-02	3.E-01	7.E-02	+-	1.E-02	8.E-01	4.E-01	6	32285878	NOTCH4	intron	t	c	C	C	C
rs2071286	1.E+00	+++	6.E-03	3.E-01	1.E+00	7.E-01	+-	2.E-01	3.E-02	3.E-01	6.E-02	+-	3.E-03	7.E-01	5.E-01	6	32287874	NOTCH4	intron	a	g	A	A	A
rs206019	8.E-04	---	5.E-01	1.E-02	6.E-01	3.E-03	+-	5.E-01	1.E-02	7.E-01	2.E-01	---	6.E-01	3.E-01	4.E-01	6	32288219	NOTCH4	intron	t	c	T	T	T
rs206015	2.E-04	---	6.E-01	7.E-03	5.E-01	9.E-04	+-	4.E-01	4.E-03	6.E-01	2.E-01	+-	9.E-01	3.E-01	1.E-01	6	32290737	NOTCH4	intron	t	c	T	T	T
rs404860	9.E-01	+-	2.E-01	1.E-01	7.E-01	8.E-01	+-	3.E-01	8.E-02	6.E-01	9.E-01	+-	6.E-01	9.E-01	8.E-01	6	32292323	NOTCH4	intron	t	c	C	C	C
rs2854050	9.E-01	+-	8.E-01	4.E-02	7.E-01	5.E-01	+-	8.E-01	4.E-01	6.E-01	2.E-01	+-	7.E-01	4.E-02	8.E-01	6	32293583	NOTCH4	intron	t	c	T	T	T
rs394657	9.E-01	+-	1.E-02	4.E-01	8.E-01	5.E-01	+-	4.E-01	2.E-01	2.E-01	2.E-02	+++	6.E-03	9.E-01	2.E-01	6	32295001	NOTCH4	intron	a	g	G	G	G
rs1109771	5.E-01	+++	2.E-01	9.E-01	3.E-01	6.E-01	+++	8.E-01	8.E-01	7.E-01	2.E-01	+-	7.E-02	7.E-01	3.E-01	6	32295583	NOTCH4	intron	a	g	A	A	A
rs422951	1.E+00	+-	3.E-02	4.E-01	9.E-01	7.E-01	+-	8.E-01	3.E-01	4.E-01	1.E-02	+-	3.E-03	9.E-01	2.E-01	6	32296361	NOTCH4	coding	a	g	G	G	G
rs3132946	6.E-01	+++	2.E-01	9.E-01	5.E-01	9.E-01	+-	5.E-01	2.E-01	8.E-01	3.E-02	+++	3.E-01	6.E-02	6.E-01	6	32298006	NOTCH4	intron	a	g	A	A	A
rs443198	1.E-01	+++	4.E-01	4.E-01	4.E-01	3.E-01	+-	6.E-01	3.E-01	8.E-01	8.E-02	+++	5.E-01	3.E-01	1.E-01	6	32298384	NOTCH4	coding	t	c	C	C	C
rs3134931	7.E-01	+-	5.E-01	6.E-01	6.E-01	4.E-01	---	9.E-01	6.E-01	8.E-01	6.E-01	+-	2.E-01	9.E-01	6.E-01	6	32298598	NOTCH4	intron	a	g	G	G	G
rs434841	7.E-01	+-	2.E-01	4.E-01	4.E-01	9.E-01	+-	8.E-01	5.E-01	8.E-01	9.E-02	---	1.E-01	9.E-01	2.E-01	6	32299019	NOTCH4	intron	a	g	A	A	A
rs3830041	4.E-01	+-	6.E-02	3.E-01	2.E-01	1.E+00	+-	2.E-02	6.E-01	2.E-01	9.E-01	+-	8.E-01	4.E-01	2.E-01	6	32299317	NOTCH4	intron	a	g	A	A	A
rs479536	6.E-02	+-	1.E-01	1.E-01	9.E-01	2.E-02	+-	7.E-02	3.E-02	3.E-01	5.E-01	---	8.E-01	8.E-01	5.E-01	6	32301656	NOTCH4	flanking_5UTR	t	c	T	T	T
rs9267845	8.E-01	+-	3.E-01	8.E-01	3.E-01	7.E-01	+-	7.E-01	1.E+00	4.E-01	5.E-01	+-	3.E-01	8.E-01	7.E-01	6	32301676	NOTCH4	flanking_5UTR	a	t	T	T	T
rs499691	9.E-01	+-	2.E-02	4.E-01	3.E-02	6.E-01	+-	5.E-02	6.E-01	2.E-02	2.E-01	+-	1.E-01	5.E-01	7.E-01	6	32302317	NOTCH4	flanking_5UTR	t	c	T	T	T
rs483574	8.E-01	+-	2.E-01	6.E-01	4.E-01	1.E+00	+-	1.E-01	7.E-01	2.E-01	8.E-01	+-	1.E+00	8.E-01	9.E-01	6	32302934	NOTCH4	flanking_5UTR	t	c	T	T	T
rs482759	7.E-01	+-	2.E-01	5.E-01	4.E-01	1.E+00	+-	1.E-01	6.E-01	2.E-01	7.E-01	+++	9.E-01	8.E-01	9.E-01	6	32302995	NOTCH4	flanking_5UTR	t	c	C	C	C
rs532385	6.E-01	+-	4.E-02	7.E-01	4.E-02	5.E-01	+-	1.E-01	8.E-01	1.E-01	6.E-01	+++	2.E-01	6.E-01	2.E-01	6	32303337	NOTCH4	flanking_5UTR	t	c	T	T	T
rs9378123	6.E-01	+-	2.E-01	7.E-01	3.E-01	6.E-01	+-	3.E-01	5.E-01	3.E-01	7.E-01	+-	5.E-01	7.E-01	2.E-01	6	32304842	NOTCH4	flanking_5UTR	a	g	G	G	G
rs1426713	1.E+00	+-	2.E-01	9.E-01	7.E-01	9.E-01	+-	4.E-01	9.E-01	9.E-01	9.E-01	+-	4.E-01	7.E-01	4.E-01	6	32306027	NOTCH4	flanking_5UTR	a	g	A	A	A
rs404890	3.E-03	---	3.E-03	2.E-02	8.E-01	1.E-02	---	2.E-01	2.E-02	4.E-01	1.E-03	---	1.E-03	2.E-01	4.E-01	6	32306845	NOTCH4	flanking_5UTR	t	g	T	T	T
rs2849015	3.E-03	---	3.E-03	2.E-02	8.E-01	1.E-02	+-	2.E-01	2.E-02	4.E-01	1.E-03	---	1.E-03	2.E-01	4.E-01	6	32306914	NOTCH4	flanking_5UTR	a	g	A	A	A
rs9267873	2.E-03	---	4.E-01	5.E-02	1.E-01	6.E-01	+-	7.E-01	7.E-02	3.E-01	1.E-02	---	1.E-01	9.E-02	3.E-01	6	32307330	NOTCH4	flanking_5UTR	t	c	C	C	C
rs6936346	1.E-01	---	3.E-01	3.E-01	4.E-01	1.E-01	---	8.E-01	3.E-01	5.E-01	3.E-01	+-	6.E-02	8.E-01	7.E-01	6	32308732	NOTCH4	flanking_5UTR	t	c	T	T	T
rs12182351	5.E-02	+++	2.E-02	2.E-01	6.E-01	4.E-02	+-	2.E-01	8.E-02	8.E-01	6.E-02	+-	5.E-03	9.E-01	7.E-01	6	32309685	NOTCH4	flanking_5UTR	t	c	C	C	C
rs9501398	1.E+00	+-	3.E-01	9.E-01	7.E-01	9.E-01	+-	4.E-01	9.E-01	9.E-01	8.E-01	+-	5.E-01	7.E-01	4.E-01	6	32310575	NOTCH4	flanking_5UTR	t	g	T	T	T

rs3130299	4.E-02	+++	2.E-02	2.E-01	6.E-01	3.E-02	+-	2.E-01	8.E-02	8.E-01	6.E-02	++	5.E-03	9.E-01	7.E-01	6	32311515	NOTCH4	flanking_5UTR	a	g	G	G	G
rs693797	2.E-02	+++	1.E-02	6.E-02	9.E-01	3.E-02	+-	3.E-01	5.E-02	4.E-01	7.E-03	+++	3.E-03	3.E-01	6.E-01	6	32312411	NOTCH4	flanking_5UTR	a	g	G	G	G
rs6906128	2.E-01	+++	3.E-01	4.E-01	7.E-01	8.E-02	+-	6.E-01	1.E-01	7.E-01	5.E-01	++	1.E-01	5.E-01	9.E-01	6	32314282	NOTCH4	flanking_5UTR	a	c	C	C	C
rs511027	7.E-01	+-	6.E-01	8.E-01	4.E-01	6.E-01	+-	3.E-01	5.E-01	7.E-01	6.E-01	+-	8.E-01	3.E-01	6.E-01	6	32314665	NOTCH4	flanking_5UTR	a	t	A	A	A

SNP	pmeta_FEV1	FEV1_meta_Direction	p_TENOR_FEV1	p_SARP_FEV1	p_CSGA_FEV1	pmeta_FVC	FVC_meta_Direction	p_TENOR_FVC	p_SARP_FVC	p_CSGA_FVC	p_meta_FEV1/FVC	FEV1/FVC_meta_Direction	p_TENOR_FEV1/FVC	p_SARP_FEV1/FVC	p_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs6494904	7.E-01	+-	6.E-01	4.E-02	5.E-01	7.E-01	++	8.E-02	4.E-01	4.E-01	9.E-02	+-	1.E-01	3.E-02	2.E-01	15	69396576	THSD4	flanking_5UTR	a	g	G	G	G
rs11855237	9.E-01	+-	3.E-01	8.E-01	8.E-01	9.E-01	++	6.E-02	8.E-01	8.E-01	9.E-01	+-	6.E-01	6.E-01	7.E-01	15	69404788	THSD4	flanking_5UTR	a	g	A	A	A
rs11856837	8.E-01	++	7.E-01	4.E-01	7.E-01	6.E-01	+++	8.E-01	9.E-01	3.E-01	9.E-01	+-	3.E-01	1.E-01	8.E-01	15	69408616	THSD4	flanking_5UTR	t	c	C	C	C
rs11637373	6.E-01	++	7.E-01	1.E+00	2.E-01	5.E-02	+++	8.E-01	2.E-01	6.E-01	4.E-01	+-	1.E+00	1.E-01	8.E-01	15	69418080	THSD4	flanking_5UTR	a	g	G	G	G
rs1441356	1.E+00	++	9.E-01	1.E-01	1.E+00	9.E-01	+-	6.E-01	8.E-01	8.E-01	2.E-02	+-	5.E-01	5.E-03	9.E-01	15	69418227	THSD4	flanking_5UTR	t	c	T	T	T
rs2028467	8.E-01	++	6.E-01	6.E-02	6.E-01	8.E-01	++	3.E-01	2.E-01	6.E-01	9.E-02	+-	6.E-01	2.E-02	8.E-01	15	69424902	THSD4	flanking_5UTR	t	c	T	T	T
rs4777372	9.E-01	+-	7.E-01	5.E-02	8.E-01	8.E-01	+-	5.E-01	6.E-01	5.E-01	9.E-02	+-	9.E-01	3.E-03	6.E-01	15	69430841	THSD4	flanking_5UTR	t	c	C	C	C
rs1913768	4.E-01	++	8.E-01	4.E-01	6.E-01	1.E+00	++	2.E-01	7.E-01	9.E-01	7.E-02	++	9.E-03	5.E-01	5.E-01	15	69436598	THSD4	flanking_5UTR	a	g	A	A	A
rs1866920	7.E-01	++	6.E-01	7.E-01	3.E-01	9.E-01	+-	5.E-01	2.E-01	8.E-01	9.E-01	++	7.E-01	9.E-01	4.E-01	15	69443763	THSD4	flanking_5UTR	a	g	G	G	G
rs2028465	6.E-01	++	6.E-01	6.E-01	3.E-01	9.E-01	++	6.E-01	4.E-01	8.E-01	7.E-01	++	7.E-01	5.E-01	5.E-01	15	69446412	THSD4	flanking_5UTR	a	c	C	C	C
rs1561711	7.E-01	+-	9.E-01	4.E-01	4.E-01	9.E-01	++	5.E-01	5.E-01	7.E-01	8.E-01	+-	3.E-01	3.E-02	4.E-01	15	69453220	THSD4	flanking_5UTR	t	c	C	C	C
rs1568010	1.E-01	++	9.E-01	1.E-01	6.E-01	8.E-01	++	5.E-01	9.E-01	6.E-01	5.E-02	++	1.E-01	4.E-02	7.E-01	15	69455566	THSD4	flanking_5UTR	a	c	C	C	C
rs4777376	7.E-01	+-	7.E-01	9.E-01	4.E-01	1.E+00	++	7.E-01	3.E-01	1.E+00	9.E-01	++	7.E-01	9.E-01	6.E-01	15	69459899	THSD4	flanking_5UTR	t	c	T	T	T
rs1441355	9.E-01	++	8.E-01	4.E-02	8.E-01	7.E-01	++	6.E-01	4.E-01	4.E-01	1.E-01	++	8.E-01	1.E-02	8.E-01	15	69465232	THSD4	flanking_5UTR	t	c	T	T	T
rs10518959	2.E-01	+-	9.E-01	1.E-01	1.E-01	7.E-01	+++	8.E-01	8.E-01	9.E-01	2.E-01	+-	5.E-01	2.E-02	3.E-01	15	69477995	THSD4	flanking_5UTR	t	c	T	T	T
rs7165378	6.E-01	++	3.E-01	9.E-02	3.E-01	9.E-01	++	9.E-01	5.E-01	8.E-01	7.E-01	++	1.E-01	1.E-02	6.E-01	15	69478558	THSD4	flanking_5UTR	t	c	T	T	T
rs1837763	5.E-01	++	7.E-01	9.E-01	7.E-02	1.E+00	++	1.E+00	7.E-01	1.E+00	1.E+00	++	4.E-01	6.E-01	7.E-02	15	69494429	THSD4	flanking_5UTR	a	g	G	G	G
rs920547	6.E-01	+-	6.E-02	6.E-01	3.E-01	9.E-01	++	4.E-01	8.E-01	8.E-01	1.E+00	+-	3.E-02	5.E-01	5.E-02	15	69505833	THSD4	flanking_5UTR	t	c	T	T	T
rs8027920	9.E-01	++	4.E-01	2.E-01	7.E-01	9.E-01	++	3.E-01	7.E-01	9.E-01	1.E-01	++	1.E+00	5.E-02	4.E-01	15	69515583	THSD4	flanking_5UTR	a	g	A	A	A
rs751998	9.E-01	+-	9.E-01	6.E-02	9.E-01	6.E-01	++	6.E-01	5.E-01	2.E-01	2.E-01	++	8.E-01	1.E-02	4.E-01	15	69524430	THSD4	flanking_5UTR	t	c	T	T	T
rs4777391	8.E-01	++	6.E-01	6.E-01	6.E-01	7.E-01	++	7.E-01	6.E-01	4.E-01	9.E-01	++	3.E-01	2.E-01	9.E-01	15	69529460	THSD4	flanking_5UTR	a	c	A	A	A
rs4332701	9.E-01	++	9.E-02	8.E-01	9.E-01	2.E-01	+++	5.E-01	6.E-01	2.E-01	8.E-01	+-	4.E-02	3.E-01	4.E-01	15	69539513	THSD4	flanking_5UTR	a	g	G	G	G
rs12907251	7.E-01	+-	6.E-02	3.E-01	4.E-01	4.E-01	--	4.E-01	1.E+00	1.E-01	8.E-01	++	2.E-02	1.E-01	8.E-01	15	69546460	THSD4	flanking_5UTR	a	g	A	A	A
rs4414447	3.E-01	+++	6.E-01	9.E-01	4.E-02	6.E-01	+++	9.E-01	9.E-01	6.E-01	1.E-01	++	3.E-01	9.E-01	3.E-02	15	69564568	THSD4	flanking_5UTR	t	c	T	T	T
rs7164165	7.E-01	+-	7.E-01	6.E-02	4.E-01	8.E-01	++	3.E-01	3.E-02	6.E-01	7.E-02	--	4.E-01	5.E-01	5.E-02	15	69571590	THSD4	flanking_5UTR	t	g	G	G	G
rs4132884	5.E-01	--	6.E-01	8.E-01	3.E-01	8.E-01	+-	8.E-01	7.E-01	6.E-01	4.E-01	+-	6.E-01	5.E-01	1.E+00	15	69588095	THSD4	flanking_5UTR	t	c	T	C	T
rs6494940	4.E-01	+-	6.E-02	1.E+00	6.E-02	6.E-01	+-	2.E-01	1.E+00	2.E-01	3.E-01	+-	2.E-01	8.E-01	4.E-01	15	69592172	THSD4	flanking_5UTR	a	g	G	G	G
rs4357892	9.E-01	++	7.E-01	2.E-01	7.E-01	1.E+00	+-	6.E-01	3.E-01	9.E-01	6.E-01	++	9.E-01	5.E-01	7.E-01	15	69609351	THSD4	flanking_5UTR	a	c	A	A	A
rs4482234	7.E-01	+++	4.E-01	1.E+00	4.E-01	2.E-01	+++	3.E-01	5.E-01	2.E-01	7.E-01	--	1.E+00	6.E-01	9.E-01	15	69610822	THSD4	flanking_5UTR	a	g	A	A	A
rs4777408	2.E-01	+-	7.E-01	1.E+00	8.E-03	4.E-01	+-	1.E+00	6.E-01	6.E-02	9.E-01	+-	3.E-01	5.E-01	4.E-01	15	69621046	THSD4	flanking_5UTR	a	g	A	A	A
rs4777409	8.E-01	+-	8.E-01	4.E-01	6.E-01	9.E-01	+-	8.E-01	3.E-01	8.E-01	9.E-01	+-	7.E-01	7.E-01	7.E-01	15	69623478	THSD4	flanking_5UTR	t	g	G	T	G
rs6494947	9.E-01	+-	1.E-01	1.E+00	7.E-01	1.E+00	+-	4.E-01	6.E-01	2.E-01	4.E-01	+-	2.E-01	2.E-01	1.E-01	15	69630134	THSD4	flanking_5UTR	t	c	C	C	C
rs4447378	1.E-01	++	3.E-01	1.E-01	3.E-01	4.E-02	++	6.E-01	4.E-02	2.E-01	3.E-01	--	2.E-01	8.E-01	8.E-01	15	69634381	THSD4	flanking_5UTR	a	g	A	A	A
rs8040598	9.E-01	+-	6.E-01	5.E-01	7.E-01	6.E-01	+-	3.E-01	5.E-01	3.E-01	5.E-01	+++	9.E-01	9.E-01	4.E-01	15	69644422	THSD4	flanking_5UTR	a	g	G	G	G
rs8042355	8.E-01	+-	7.E-01	9.E-01	7.E-01	8.E-01	++	6.E-01	6.E-01	5.E-01	9.E-01	++	9.E-01	5.E-01	2.E-01	15	69647900	THSD4	flanking_5UTR	a	g	G	G	G
rs3923493	8.E-01	++	5.E-01	7.E-01	5.E-01	6.E-01	++	7.E-01	7.E-01	3.E-01	8.E-01	+-	1.E-01	1.E-01	6.E-01	15	69653686	THSD4	flanking_5UTR	a	g	A	A	A
rs3923492	9.E-01	+-	7.E-01	8.E-02	8.E-01	3.E-02	--	1.E+00	2.E-01	2.E-01	1.E+00	++	3.E-01	1.E-01	4.E-01	15	69653762	THSD4	flanking_5UTR	t	c	C	C	C
rs4321149	4.E-01	+-	6.E-01	3.E-01	4.E-01	1.E-01	--	9.E-01	3.E-01	7.E-01	8.E-01	+-	5.E-01	7.E-01	2.E-01	15	69656526	THSD4	flanking_5UTR	a	g	A	A	A
rs4459504	7.E-01	+-	8.E-01	8.E-01	3.E-01	6.E-01	+-	4.E-01	8.E-01	2.E-01	7.E-01	++	1.E-01	2.E-01	7.E-01	15	69670984	THSD4	flanking_5UTR	a	g	G	G	G
rs4777414	7.E-01	++	3.E-01	3.E-01	4.E-01	8.E-01	+-	6.E-01	5.E-01	7.E-01	8.E-01	++	2.E-01	4.E-01	8.E-01	15	69675927	THSD4	flanking_5UTR	t	c	C	C	C
rs4398066	7.E-01	++	5.E-01	7.E-01	3.E-01	8.E-01	++	9.E-01	1.E+00	6.E-01	1.E+00	++	2.E-01	3.E-01	6.E-01	15	69679269	THSD4	flanking_5UTR	a	g	G	G	G
rs4349100	1.E-01	+++	1.E+00	2.E-01	9.E-01	3.E-01	+++	9.E-01	5.E-01	7.E-01	8.E-01	++	7.E-01	4.E-01	1.E+00	15	69684923	THSD4	flanking_5UTR	a	g	A	A	A
rs4430697	9.E-01	++	7.E-01	5.E-01	8.E-01	7.E-01	++	6.E-01	2.E-01	5.E-01	7.E-01	+++	1.E+00	7.E-01	9.E-01	15	69685390	THSD4	flanking_5UTR	a	g	G	G	G

rs4354882	1.E+00	++	7.E-02	9.E-01	6.E-01	9.E-01	+++	6.E-01	9.E-01	9.E-01	2.E-01	++	2.E-02	9.E-01	9.E-01	15	69688282	THSD4	flanking_5UTR	a	g	G	G	G
rs13379548	7.E-01	++	2.E-01	8.E-01	4.E-01	9.E-01	++	5.E-01	4.E-01	8.E-01	8.E-02	+++	1.E-01	7.E-01	2.E-01	15	69689719	THSD4	flanking_5UTR	t	c	C	C	C
rs11858418	7.E-01	+-	9.E-01	2.E-01	3.E-01	9.E-01	++	9.E-01	2.E-01	8.E-01	4.E-01	+-	8.E-01	3.E-01	4.E-01	15	69691889	THSD4	flanking_5UTR	a	g	G	G	G
rs1501429	9.E-01	+-	3.E-02	5.E-01	7.E-01	9.E-01	++	6.E-01	9.E-01	8.E-01	2.E-01	+-	6.E-04	2.E-01	9.E-01	15	69692566	THSD4	flanking_5UTR	a	g	A	A	A
rs1983033	3.E-01	--	9.E-02	4.E-01	1.E+00	2.E-01	--	6.E-01	3.E-01	1.E+00	2.E-01	+-	4.E-02	8.E-01	5.E-01	15	69696544	THSD4	flanking_5UTR	t	g	T	T	T
rs7182578	9.E-01	++	5.E-01	1.E+00	7.E-01	1.E+00	++	9.E-01	5.E-01	9.E-01	2.E-01	+++	2.E-01	5.E-01	7.E-01	15	69699005	THSD4	flanking_5UTR	t	c	C	C	C
rs985868	6.E-01	+-	5.E-01	7.E-01	9.E-01	6.E-01	+-	1.E+00	4.E-01	3.E-01	3.E-01	+-	3.E-01	1.E-01	3.E-01	15	69702332	THSD4	flanking_5UTR	t	c	C	C	C
rs7167646	7.E-01	++	6.E-01	1.E+00	4.E-01	5.E-01	++	6.E-01	4.E-01	1.E-01	8.E-01	++	6.E-01	4.E-01	1.E-02	15	69707213	THSD4	flanking_5UTR	a	c	C	C	C
rs950667	2.E-01	--	4.E-01	3.E-01	9.E-01	5.E-01	+-	8.E-01	4.E-01	3.E-01	9.E-02	--	2.E-01	7.E-01	2.E-01	15	69708689	THSD4	flanking_5UTR	t	c	C	C	C
rs1392989	9.E-01	++	3.E-01	1.E-01	8.E-01	6.E-01	++	2.E-01	3.E-01	3.E-01	4.E-01	--	9.E-01	3.E-01	7.E-01	15	69708797	THSD4	flanking_5UTR	a	c	C	C	C
rs950668	9.E-01	++	6.E-01	9.E-01	8.E-01	8.E-01	+++	3.E-01	9.E-01	8.E-01	1.E+00	+-	9.E-01	5.E-01	2.E-01	15	69708893	THSD4	flanking_5UTR	a	g	A	A	A
rs2279787	5.E-01	+-	1.E-01	5.E-01	1.E-01	3.E-01	--	7.E-01	5.E-01	6.E-01	6.E-01	+-	6.E-02	4.E-02	2.E-01	15	69714177	THSD4	flanking_5UTR	a	c	C	C	C
rs1995336	7.E-01	+-	6.E-01	5.E-01	4.E-01	7.E-01	+-	5.E-01	2.E-01	3.E-03	4.E-01	++	9.E-01	8.E-01	2.E-02	15	69736380	THSD4	flanking_5UTR	a	g	G	G	G
rs8036118	3.E-01	++	9.E-01	2.E-01	1.E-01	7.E-01	++	5.E-01	3.E-01	4.E-04	1.E-01	++	5.E-01	1.E-01	4.E-02	15	69747631	THSD4	flanking_5UTR	a	g	A	A	A
rs931728	6.E-01	+-	9.E-01	3.E-01	1.E-01	5.E-01	+-	6.E-01	5.E-01	3.E-04	2.E-01	++	5.E-01	2.E-01	4.E-02	15	69754600	THSD4	flanking_5UTR	t	c	C	C	C
rs8026748	3.E-01	+-	6.E-01	1.E-01	3.E-02	1.E-01	+-	1.E+00	5.E-02	2.E-03	8.E-01	++	4.E-01	4.E-01	5.E-01	15	69757818	THSD4	flanking_5UTR	a	g	A	A	A
rs8033100	8.E-01	+-	9.E-01	3.E-01	7.E-01	6.E-01	+-	7.E-01	5.E-01	3.E-01	3.E-01	+-	6.E-01	1.E-02	6.E-01	15	69764500	THSD4	flanking_5UTR	t	c	C	C	C
rs8027960	6.E-01	++	9.E-01	8.E-01	2.E-01	5.E-01	++	8.E-01	5.E-02	2.E-01	5.E-01	++	9.E-01	1.E-01	3.E-01	15	69780809	THSD4	flanking_5UTR	t	c	C	C	C
rs872471	6.E-01	++	7.E-02	2.E-01	3.E-01	7.E-01	++	2.E-01	1.E-01	4.E-01	4.E-01	++	1.E-01	6.E-01	7.E-01	15	69785119	THSD4	flanking_5UTR	a	g	G	G	G
rs12591953	9.E-01	+-	8.E-01	5.E-01	8.E-01	8.E-01	+-	6.E-01	1.E-01	5.E-01	6.E-01	++	9.E-01	4.E-01	1.E+00	15	69787332	THSD4	flanking_5UTR	a	g	A	A	A
rs8033309	8.E-01	+-	2.E-01	5.E-01	6.E-01	8.E-01	+-	5.E-01	5.E-01	6.E-01	6.E-01	++	2.E-01	9.E-01	5.E-01	15	69797752	THSD4	flanking_5UTR	a	g	A	A	A
rs8041918	8.E-01	+-	4.E-01	4.E-01	6.E-01	9.E-01	+-	7.E-01	9.E-01	1.E+00	9.E-01	+-	3.E-01	1.E-01	6.E-01	15	69806558	THSD4	flanking_5UTR	t	c	C	C	C
rs4777451	4.E-02	+++	1.E+00	2.E-01	4.E-01	8.E-01	++	1.E+00	8.E-01	6.E-01	1.E-01	+++	9.E-01	3.E-02	9.E-01	15	69812229	THSD4	intron	t	c	C	C	C
rs11072323	9.E-02	--	3.E-01	4.E-01	2.E-01	2.E-01	--	7.E-01	4.E-01	7.E-01	3.E-01	--	2.E-01	7.E-01	8.E-01	15	69813033	THSD4	intron	t	c	T	T	T
rs1472587	6.E-01	+-	8.E-02	1.E+00	3.E-01	4.E-01	+-	5.E-01	4.E-01	6.E-01	9.E-01	+-	6.E-02	2.E-01	5.E-01	15	69828335	THSD4	intron	a	g	A	A	A
rs1564693	7.E-01	+-	3.E-01	5.E-01	4.E-01	5.E-01	+-	2.E-01	2.E-01	2.E-01	1.E+00	++	7.E-01	1.E+00	7.E-01	15	69847103	THSD4	intron	t	c	C	C	C
rs3825804	9.E-01	+-	7.E-01	5.E-01	7.E-01	9.E-01	+-	4.E-01	5.E-01	8.E-01	8.E-01	++	8.E-01	5.E-01	9.E-01	15	69857059	THSD4	3UTR	a	g	A	A	A
rs3743052	1.E+00	+-	7.E-01	6.E-01	1.E+00	2.E-01	+++	9.E-01	3.E-01	9.E-01	5.E-01	+-	3.E-01	8.E-01	7.E-01	15	69862918	THSD4	flanking_3UTR	a	g	A	A	A
rs11639050	4.E-01	--	4.E-01	7.E-01	5.E-01	1.E-01	+-	7.E-01	1.E-01	4.E-01	7.E-01	+-	4.E-01	2.E-01	1.E-01	15	69868334	THSD4	flanking_3UTR	t	g	T	T	T
rs900542	9.E-01	++	7.E-01	3.E-01	8.E-01	5.E-02	+++	8.E-01	2.E-01	8.E-01	6.E-01	++	3.E-01	8.E-01	9.E-01	15	69869678	THSD4	flanking_3UTR	a	g	A	A	A
rs11634405	1.E-01	++	5.E-01	1.E-01	6.E-01	6.E-03	+++	4.E-01	4.E-02	7.E-01	9.E-01	+-	9.E-01	7.E-01	6.E-01	15	69871747	THSD4	flanking_3UTR	a	g	A	A	A

SNP	p _{meta} _FEV1	FEV1 _{_meta} _Direction	p _{TENOR} _FEV1	p _{SARP} _FEV1	p _{CSGA} _FEV1	p _{meta} _FVC	FVC _{_meta} _Direction	p _{TENOR} _FVC	p _{SARP} _FVC	p _{CSGA} _FVC	p _{meta} _FEV1/FVC	FEV1/FVC _{_meta} _Direction	p _{TENOR} _FEV1/FVC	p _{SARP} _FEV1/FVC	p _{CSGA} _FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs1953319	1.E-01	++	3.E-01	9.E-02	2.E-01	5.E-01	++	5.E-02	8.E-01	1.E-01	2.E-01	++	3.E-01	8.E-03	6.E-01	6	142625119	GPR126	flanking_5UTR	t	c	C	C	C
rs1931989	9.E-01	++	5.E-01	1.E+00	7.E-01	5.E-01	++	5.E-02	5.E-01	5.E-01	1.E-01	++	1.E-01	3.E-01	8.E-01	6	142628271	GPR126	flanking_5UTR	a	g	G	G	G
rs9321861	1.E+00	++	6.E-01	8.E-01	9.E-01	2.E-01	++	3.E-01	3.E-01	8.E-01	1.E-01	+++	8.E-01	1.E-01	8.E-01	6	142629017	GPR126	flanking_5UTR	a	c	C	C	C
rs2782535	7.E-01	++	9.E-01	4.E-01	1.E-01	2.E-01	++	1.E-01	9.E-01	2.E-03	1.E+00	++	3.E-02	3.E-01	1.E-01	6	142631783	GPR126	flanking_5UTR	t	c	T	T	T
rs1931991	1.E-01	+-	3.E-01	2.E-01	9.E-01	1.E+00	+-	4.E-01	7.E-01	9.E-01	9.E-02	--	6.E-01	4.E-02	9.E-01	6	142639061	GPR126	flanking_5UTR	a	c	C	C	C
rs6903707	8.E-01	+-	2.E-01	5.E-01	2.E-01	7.E-01	++	3.E-03	1.E+00	3.E-01	5.E-01	++	2.E-01	6.E-01	7.E-01	6	142653680	GPR126	flanking_5UTR	a	g	A	A	A
rs9376685	3.E-01	+-	8.E-01	2.E-01	3.E-02	4.E-01	+-	1.E+00	1.E+00	4.E-02	7.E-01	+-	4.E-01	1.E-01	8.E-01	6	142671524	GPR126	intron	t	c	T	T	T
rs9389983	7.E-01	++	5.E-02	3.E-01	5.E-01	8.E-01	++	6.E-03	9.E-01	5.E-01	3.E-01	++	8.E-01	3.E-02	7.E-01	6	142675437	GPR126	intron	t	c	C	T	T
rs12189801	3.E-01	+-	7.E-01	3.E-01	5.E-01	9.E-01	++	8.E-01	5.E-01	8.E-01	3.E-01	++	4.E-01	4.E-01	8.E-01	6	142683299	GPR126	intron	t	c	C	C	C
rs6570507	4.E-01	+-	6.E-01	4.E-02	9.E-02	6.E-01	+-	5.E-01	2.E-01	2.E-01	3.E-01	+-	6.E-01	2.E-02	8.E-01	6	142721265	GPR126	intron	a	g	A	A	A
rs11155242	2.E-01	+-	7.E-01	1.E-01	3.E-01	8.E-01	++	9.E-01	4.E-01	5.E-01	2.E-01	+-	5.E-01	1.E-01	7.E-01	6	142733242	GPR126	coding	a	c	C	C	C
rs9403384	5.E-01	+-	4.E-01	4.E-01	1.E-01	4.E-01	+-	7.E-01	9.E-01	7.E-02	8.E-01	++	1.E-01	1.E-01	7.E-01	6	142751294	GPR126	intron	a	c	A	A	A
rs3748069	5.E-01	++	5.E-01	2.E-02	1.E-01	5.E-01	++	6.E-01	2.E-01	2.E-01	3.E-01	++	4.E-01	8.E-03	9.E-01	6	142809326	GPR126	flanking_3UTR	a	g	G	G	G
rs7776356	7.E-01	++	1.E+00	6.E-02	4.E-01	9.E-01	++	7.E-01	2.E-01	8.E-01	3.E-01	+-	7.E-01	1.E-01	5.E-01	6	142818722	GPR126	flanking_3UTR	a	g	G	G	G
rs9321871	2.E-01	+++	6.E-01	8.E-01	6.E-02	6.E-02	+++	1.E+00	5.E-01	3.E-02	9.E-01	+-	2.E-01	3.E-01	8.E-01	6	142853625	GPR126	flanking_3UTR	t	c	C	C	C
rs171891	2.E-02	++	9.E-01	2.E-02	2.E-01	9.E-01	+-	9.E-01	2.E-01	9.E-01	4.E-01	++	8.E-01	2.E-02	1.E-01	6	142892305	GPR126	flanking_3UTR	a	g	A	A	A

rs263174	9.E-01	++	5.E-01	8.E-01	7.E-01	2.E-01	++	7.E-01	4.E-01	6.E-01	6.E-01	+-	6.E-01	1.E+00	8.E-02	6	142910792	GPR126	flanking_3UTR	t	c	T	T	T
rs839556	7.E-01	+-	5.E-01	6.E-01	6.E-01	2.E-01	-	7.E-01	3.E-01	7.E-01	7.E-01	+-	6.E-01	8.E-01	7.E-02	6	142913571	GPR126	flanking_3UTR	a	c	C	C	C
rs263114	9.E-01	+-	9.E-01	1.E-01	9.E-01	9.E-01	++	9.E-01	8.E-02	7.E-01	8.E-01	++	9.E-01	2.E-01	3.E-01	6	142924648	GPR126	flanking_3UTR	t	g	A	A	A
rs263164	7.E-01	++	2.E-01	1.E-01	4.E-01	4.E-01	++	3.E-01	5.E-02	8.E-02	4.E-01	+-	3.E-01	5.E-01	3.E-01	6	142938348	GPR126	flanking_3UTR	a	g	A	A	A
rs263156	7.E-01	++	5.E-01	6.E-01	7.E-01	9.E-02	+++	8.E-01	2.E-01	6.E-01	7.E-01	++	5.E-01	1.E+00	8.E-02	6	142949208	GPR126	flanking_3UTR	t	g	T	T	T

SNP	p _{meta} _FEV1	FEV1 _{_meta} _Direction	p _{TENOR} _FEV1	p _{SARP} _FEV1	p _{CSGA} _FEV1	p _{meta} _FVC	FVC _{_meta} _Direction	p _{TENOR} _FVC	p _{SARP} _FVC	p _{CSGA} _FVC	p _{meta} _FEV1/FVC	FEV1/FVC _{_meta} _Direction	p _{TENOR} _FEV1/FVC	p _{SARP} _FEV1/FVC	p _{CSGA} _FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs2161396	1.E+00	+-	6.E-01	9.E-01	7.E-01	9.E-01	+-	1.E-01	8.E-01	3.E-01	8.E-01	+-	4.E-01	9.E-01	7.E-01	5	156800802	ADAM19	flanking_3UTR	t	g	G	G	G
rs7714353	1.E+00	+-	8.E-01	4.E-01	1.E+00	8.E-01	++	5.E-01	8.E-01	6.E-01	8.E-01	++	7.E-01	6.E-01	5.E-01	5	156803112	ADAM19	flanking_3UTR	t	c	T	T	T
rs11750519	7.E-01	+-	2.E-01	6.E-01	4.E-01	3.E-01	+-	5.E-02	4.E-01	8.E-01	4.E-01	+++	8.E-01	6.E-01	6.E-01	5	156804994	ADAM19	flanking_3UTR	t	c	T	T	T
rs11951889	9.E-01	++	3.E-01	6.E-01	2.E-01	4.E-01	+-	2.E-01	3.E-01	3.E-01	1.E+00	++	9.E-01	8.E-01	6.E-01	5	156809362	ADAM19	flanking_3UTR	t	c	T	T	T
rs1559144	8.E-01	+-	9.E-01	5.E-01	5.E-01	7.E-01	+-	6.E-01	8.E-01	3.E-01	8.E-01	+-	8.E-01	8.E-01	9.E-01	5	156814431	ADAM19	flanking_3UTR	a	g	G	G	G
rs951958	7.E-01	++	2.E-01	5.E-01	4.E-01	4.E-01	+-	1.E-01	3.E-01	4.E-01	9.E-01	+-	9.E-01	7.E-01	8.E-01	5	156821675	ADAM19	flanking_3UTR	a	c	A	A	A
rs4704742	9.E-01	++	7.E-01	1.E+00	8.E-01	6.E-01	+++	8.E-01	1.E+00	3.E-01	8.E-01	+-	7.E-01	7.E-01	6.E-01	5	156823931	ADAM19	flanking_3UTR	t	c	T	T	C
rs6860507	9.E-01	++	6.E-01	9.E-01	9.E-01	6.E-01	+++	7.E-01	9.E-01	4.E-01	6.E-01	+-	9.E-01	6.E-01	5.E-01	5	156831268	ADAM19	flanking_3UTR	a	g	A	A	G
rs11134766	6.E-01	+-	3.E-01	7.E-01	1.E+00	2.E-01	-	7.E-01	5.E-01	3.E-01	6.E-01	+-	2.E-01	7.E-01	2.E-01	5	156840895	ADAM19	intron	a	g	A	A	A
rs10067096	6.E-01	+-	1.E-01	6.E-01	6.E-01	2.E-01	+++	5.E-02	4.E-01	6.E-01	8.E-01	++	7.E-01	1.E+00	3.E-01	5	156849918	ADAM19	coding	a	c	C	C	C
rs2287749	9.E-01	+-	2.E-01	7.E-01	5.E-01	5.E-01	+-	3.E-02	6.E-01	9.E-01	4.E-01	+++	5.E-01	6.E-01	7.E-01	5	156851428	ADAM19	coding	t	c	T	T	T
rs1990950	9.E-01	++	8.E-01	8.E-01	7.E-01	8.E-01	+-	9.E-01	7.E-01	5.E-01	4.E-01	+++	6.E-01	5.E-01	1.E+00	5	156853334	ADAM19	intron	t	g	T	T	T
rs1990951	9.E-01	+-	8.E-01	1.E+00	9.E-01	6.E-01	+-	8.E-01	9.E-01	3.E-01	6.E-01	++	9.E-01	7.E-01	5.E-01	5	156853489	ADAM19	intron	t	c	C	T	T
rs2277027	5.E-01	++	1.E+00	5.E-01	8.E-01	8.E-01	+-	9.E-01	1.E+00	6.E-01	6.E-01	+-	1.E+00	3.E-01	7.E-01	5	156864954	ADAM19	intron	a	c	C	C	C
rs1422795	5.E-01	++	1.E+00	5.E-01	8.E-01	8.E-01	+-	9.E-01	1.E+00	6.E-01	6.E-01	+-	1.E+00	3.E-01	7.E-01	5	156868942	ADAM19	coding	a	g	G	G	G
rs1422794	8.E-01	+-	2.E-01	9.E-01	7.E-01	9.E-01	+-	8.E-02	7.E-01	2.E-01	8.E-01	++	8.E-01	7.E-01	6.E-01	5	156869127	ADAM19	intron	a	c	C	C	C
rs3734031	7.E-01	++	1.E-01	2.E-01	4.E-01	1.E+00	+-	9.E-02	7.E-01	1.E+00	4.E-01	++	6.E-01	2.E-01	4.E-01	5	156873338	ADAM19	intron	a	g	G	G	G
rs3822696	2.E-01	+-	9.E-01	3.E-01	9.E-01	2.E-01	+-	5.E-01	5.E-01	5.E-01	8.E-01	++	6.E-01	5.E-01	5.E-01	5	156890319	ADAM19	intron	t	c	T	C	C
rs11746606	2.E-01	-	5.E-01	4.E-01	8.E-01	3.E-01	+-	1.E-01	4.E-01	9.E-01	1.E+00	+-	6.E-01	1.E+00	4.E-01	5	156895077	ADAM19	intron	t	c	T	T	T
rs6875485	8.E-01	+-	6.E-01	1.E+00	6.E-01	7.E-01	++	8.E-01	1.E+00	5.E-01	8.E-01	++	5.E-01	9.E-01	2.E-01	5	156899173	ADAM19	intron	a	c	C	C	C
rs4461616	9.E-01	++	6.E-01	6.E-01	8.E-01	7.E-01	+-	9.E-01	9.E-01	4.E-01	8.E-01	+-	4.E-01	9.E-01	4.E-01	5	156914491	ADAM19	intron	t	g	G	G	G
rs11749965	1.E-01	+++	6.E-01	3.E-01	7.E-01	7.E-01	+-	1.E+00	5.E-01	4.E-01	6.E-01	+-	4.E-01	6.E-01	4.E-01	5	156929992	ADAM19	intron	t	c	C	C	C
rs7719224	1.E-01	-	7.E-01	2.E-01	1.E+00	4.E-01	+-	8.E-01	4.E-01	6.E-01	7.E-01	+-	7.E-01	8.E-01	9.E-01	5	156931918	ADAM19	intron	t	c	T	T	T
rs6890282	2.E-01	+++	6.E-01	4.E-01	6.E-01	7.E-01	++	1.E+00	4.E-01	4.E-01	6.E-01	+-	4.E-01	6.E-01	5.E-01	5	156934313	ADAM19	intron	t	g	G	G	G
rs10476093	9.E-01	-	8.E-01	1.E+00	8.E-01	6.E-01	+-	9.E-01	8.E-01	2.E-01	9.E-01	+-	6.E-01	7.E-01	4.E-01	5	156939579	ADAM19	flanking_5UTR	a	c	A	A	A

SNP	p _{meta} _FEV1	FEV1 _{_meta} _Direction	p _{TENOR} _FEV1	p _{SARP} _FEV1	p _{CSGA} _FEV1	p _{meta} _FVC	FVC _{_meta} _Direction	p _{TENOR} _FVC	p _{SARP} _FVC	p _{CSGA} _FVC	p _{meta} _FEV1/FVC	FEV1/FVC _{_meta} _Direction	p _{TENOR} _FEV1/FVC	p _{SARP} _FEV1/FVC	p _{CSGA} _FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs2924936	9.E-01	++	7.E-01	5.E-01	2.E-01	1.E+00	++	8.E-01	7.E-01	4.E-01	7.E-01	++	8.E-01	4.E-01	5.E-01	4	89860537	FAM13A1	flanking_3UTR	a	g	A	A	A
rs13130	9.E-01	+-	6.E-01	6.E-01	2.E-01	1.E+00	+-	7.E-01	8.E-01	5.E-01	7.E-01	+-	7.E-01	4.E-01	4.E-01	4	89867868	FAM13A1	3UTR	t	c	C	C	C
rs3017895	9.E-01	+-	6.E-01	5.E-01	2.E-01	9.E-01	+-	7.E-01	7.E-01	5.E-01	8.E-01	+-	7.E-01	5.E-01	4.E-01	4	89868514	FAM13A1	3UTR	t	c	C	C	C
rs2972028	4.E-01	+-	2.E-01	2.E-01	5.E-02	2.E-01	-	4.E-01	4.E-01	9.E-01	4.E-01	+-	1.E-01	1.E-01	8.E-03	4	89874214	FAM13A1	intron	a	g	A	A	A
rs3775391	8.E-01	+-	6.E-01	5.E-01	2.E-01	9.E-01	+-	6.E-01	7.E-01	5.E-01	8.E-01	+-	9.E-01	4.E-01	4.E-01	4	89884216	FAM13A1	intron	t	c	C	C	C
rs6855961	2.E-01	-	5.E-01	5.E-01	3.E-01	9.E-01	+-	5.E-01	8.E-01	3.E-01	3.E-02	+-	5.E-02	1.E-01	8.E-01	4	89886877	FAM13A1	intron	a	c	C	C	C
rs7657817	9.E-02	+-	3.E-02	2.E-02	5.E-03	5.E-02	+-	2.E-01	9.E-02	8.E-01	6.E-02	+-	1.E-02	7.E-03	2.E-03	4	89887882	FAM13A1	coding	t	c	T	T	T

rs7662156	8.E-02	--	4.E-02	2.E-02	6.E-03	3.E-02	--	2.E-01	6.E-02	8.E-01	7.E-02	--	1.E-02	8.E-03	2.E-03	4	89891828	FAM13A1	intron	t	c	T	T	T
rs1965869	6.E-01	--	1.E-01	1.E-01	8.E-04	8.E-01	--	8.E-02	5.E-01	2.E-01	5.E-01	--	4.E-01	2.E-02	2.E-03	4	89896560	FAM13A1	intron	t	c	T	T	T
rs1947379	3.E-01	--	4.E-02	1.E-01	1.E-01	2.E-01	--	3.E-01	3.E-01	9.E-01	3.E-02	--	5.E-03	6.E-02	7.E-02	4	89908809	FAM13A1	intron	t	c	T	T	T
rs2290782	9.E-01	--	5.E-01	6.E-01	3.E-01	3.E-01	--	3.E-01	3.E-01	6.E-01	7.E-01	+++	9.E-01	7.E-01	9.E-01	4	89930872	FAM13A1	intron	a	g	G	G	G
rs9991328	9.E-01	++	4.E-01	6.E-01	3.E-01	3.E-01	++	3.E-01	3.E-01	6.E-01	7.E-01	--	1.E+00	7.E-01	7.E-01	4	89932144	FAM13A1	intron	t	c	T	T	T
rs7680994	7.E-02	--	4.E-01	4.E-01	8.E-02	6.E-01	--	7.E-01	1.E+00	2.E-01	9.E-02	--	2.E-01	1.E-01	9.E-01	4	89937013	FAM13A1	intron	a	g	A	A	A
rs10516821	2.E-01	--	3.E-01	6.E-01	2.E-01	7.E-01	+-	7.E-01	1.E-01	4.E-01	9.E-02	+-	8.E-03	7.E-01	6.E-01	4	89947002	FAM13A1	intron	t	c	C	C	C
rs2869950	4.E-01	++	3.E-01	4.E-01	8.E-01	1.E-01	++	1.E-01	2.E-01	9.E-01	1.E+00	++	9.E-01	6.E-01	7.E-01	4	89961787	FAM13A1	intron	t	c	T	T	T
rs2305934	2.E-02	+++	1.E-01	3.E-01	2.E-02	2.E-01	+++	5.E-01	6.E-01	2.E-01	4.E-03	+++	4.E-02	4.E-01	3.E-02	4	89963265	FAM13A1	5UTR	t	c	C	C	C
rs10021465	3.E-01	++	4.E-02	3.E-01	5.E-01	5.E-02	+++	6.E-01	2.E-01	7.E-01	1.E-01	++	2.E-03	9.E-01	4.E-01	4	89969384	FAM13A1	intron	a	g	G	G	G
rs1379935	6.E-01	++	5.E-01	1.E+00	2.E-01	7.E-01	++	1.E+00	8.E-01	5.E-01	1.E+00	++	2.E-01	7.E-01	2.E-01	4	89970314	FAM13A1	intron	t	c	T	T	T
rs7660000	7.E-01	++	2.E-02	6.E-01	5.E-01	2.E-01	+++	5.E-01	4.E-01	6.E-01	3.E-01	+-	2.E-03	7.E-01	1.E-01	4	89970881	FAM13A1	intron	t	c	T	T	T
rs11735482	7.E-01	++	8.E-01	4.E-01	5.E-01	7.E-01	++	7.E-01	3.E-01	5.E-01	4.E-01	--	6.E-01	5.E-01	8.E-01	4	89995269	FAM13A1	intron	t	c	C	C	C
rs6830970	2.E-01	++	1.E-01	1.E-01	3.E-01	7.E-03	+++	1.E+00	4.E-02	8.E-01	1.E-01	++	3.E-03	8.E-01	3.E-01	4	89996104	FAM13A1	intron	a	g	G	G	G
rs1979290	7.E-01	++	7.E-01	9.E-01	4.E-01	7.E-01	++	6.E-01	9.E-01	5.E-01	8.E-01	++	2.E-01	6.E-01	6.E-01	4	90008501	FAM13A1	intron	t	g	T	T	T
rs10049947	9.E-01	+-	7.E-01	3.E-01	8.E-01	2.E-01	--	8.E-01	3.E-01	9.E-01	5.E-01	+-	5.E-01	4.E-01	3.E-01	4	90009616	FAM13A1	intron	t	c	T	T	T
rs10516823	4.E-01	+++	8.E-01	8.E-01	2.E-01	5.E-01	++	5.E-01	7.E-01	1.E-01	5.E-01	++	8.E-01	3.E-01	7.E-01	4	90016661	FAM13A1	intron	t	c	T	T	T
rs17816002	7.E-01	++	9.E-01	1.E+00	3.E-01	7.E-01	++	4.E-01	9.E-01	4.E-01	9.E-01	++	8.E-01	9.E-01	6.E-01	4	90017977	FAM13A1	intron	a	c	A	A	A
rs1458562	5.E-01	--	8.E-02	4.E-01	3.E-01	4.E-02	--	6.E-01	1.E-01	1.E+00	3.E-01	++	2.E-02	1.E+00	4.E-01	4	90072621	FAM13A1	intron	a	g	G	G	G
rs1903009	6.E-01	+-	3.E-01	2.E-01	2.E-01	4.E-01	+-	2.E-01	2.E-01	7.E-02	4.E-01	++	8.E-01	2.E-01	7.E-01	4	90075300	FAM13A1	intron	a	g	A	A	A
rs2446309	6.E-01	++	3.E-01	2.E-01	2.E-01	4.E-01	++	2.E-01	2.E-01	7.E-02	4.E-01	+-	8.E-01	2.E-01	7.E-01	4	90076175	FAM13A1	intron	t	c	C	C	C
rs987314	8.E-01	+-	1.E+00	1.E-01	5.E-01	6.E-01	+-	9.E-01	1.E-01	2.E-01	2.E-01	+++	7.E-01	2.E-01	7.E-01	4	90081192	FAM13A1	intron	t	c	T	T	T
rs2869967	2.E-01	++	1.E-02	2.E-01	5.E-01	5.E-03	+++	2.E-01	3.E-02	9.E-01	9.E-02	+-	2.E-03	1.E+00	5.E-01	4	90088355	FAM13A1	intron	t	c	C	C	C
rs1903003	1.E-01	--	6.E-03	1.E-01	4.E-01	3.E-02	--	2.E-01	7.E-02	7.E-01	3.E-02	+-	7.E-04	1.E+00	9.E-01	4	90105320	FAM13A1	intron	t	c	C	C	C
rs1921679	3.E-01	--	2.E-02	3.E-01	9.E-01	8.E-03	--	2.E-01	8.E-02	3.E-01	1.E-01	++	4.E-03	7.E-01	9.E-01	4	90109807	FAM13A1	intron	t	c	T	T	T
rs11737182	2.E-01	--	2.E-02	4.E-01	9.E-01	9.E-03	--	2.E-01	9.E-02	3.E-01	1.E-01	+-	5.E-03	6.E-01	9.E-01	4	90117499	FAM13A1	intron	t	c	T	T	T
rs1921681	8.E-01	--	2.E-02	1.E+00	8.E-01	5.E-01	--	4.E-02	1.E+00	1.E-01	5.E-01	++	7.E-02	7.E-01	5.E-01	4	90123147	FAM13A1	intron	t	c	T	T	T
rs7697075	2.E-01	++	2.E-02	3.E-01	8.E-01	7.E-03	--	2.E-01	8.E-02	3.E-01	1.E-01	++	5.E-03	7.E-01	9.E-01	4	90127331	FAM13A1	intron	a	g	A	A	A
rs10516827	7.E-01	+-	5.E-01	7.E-01	5.E-01	6.E-01	+-	6.E-01	9.E-01	3.E-01	1.E+00	+-	5.E-01	3.E-01	6.E-01	4	90137926	FAM13A1	intron	a	g	A	A	A
rs10516826	9.E-01	--	3.E-01	8.E-01	6.E-01	6.E-01	--	9.E-01	8.E-01	7.E-02	2.E-01	--	1.E-01	1.E+00	5.E-01	4	90137991	FAM13A1	intron	a	g	A	A	A
rs10516825	8.E-01	++	4.E-01	5.E-01	5.E-01	6.E-01	+-	6.E-01	7.E-01	3.E-01	9.E-01	+-	5.E-01	2.E-01	7.E-01	4	90139105	FAM13A1	intron	t	g	T	T	T
rs6849143	3.E-01	--	4.E-03	3.E-01	5.E-01	1.E-01	--	1.E-01	1.E-01	5.E-01	2.E-02	--	7.E-04	9.E-01	8.E-01	4	90147512	FAM13A1	intron	t	c	T	T	T
rs2670620	7.E-01	+-	8.E-01	1.E-01	4.E-01	4.E-01	+-	3.E-01	7.E-02	9.E-02	1.E-01	+++	4.E-01	5.E-01	2.E-01	4	90153229	FAM13A1	intron	t	c	T	T	T
rs1708661	8.E-01	++	3.E-01	5.E-01	5.E-01	1.E+00	++	3.E-01	2.E-01	9.E-01	9.E-01	+-	5.E-01	4.E-01	6.E-01	4	90157587	FAM13A1	intron	a	g	A	A	A
rs1795722	2.E-01	++	2.E-02	3.E-01	7.E-01	2.E-02	+++	2.E-01	9.E-02	6.E-01	4.E-02	++	2.E-03	7.E-01	9.E-01	4	90161886	FAM13A1	intron	a	g	G	G	G
rs1343921	9.E-01	+-	2.E-01	8.E-01	8.E-01	5.E-01	--	4.E-01	9.E-01	2.E-01	6.E-01	++	1.E-01	7.E-01	5.E-01	4	90166485	FAM13A1	intron	t	c	T	T	T
rs1533291	4.E-01	++	2.E-01	4.E-01	7.E-01	5.E-02	+++	9.E-01	1.E-01	8.E-01	1.E-01	+++	3.E-02	8.E-01	1.E+00	4	90183479	FAM13A1	intron	a	g	G	G	G
rs2670626	6.E-01	++	2.E-01	6.E-01	7.E-01	1.E-01	+++	9.E-01	3.E-01	8.E-01	1.E-01	+++	3.E-02	9.E-01	1.E+00	4	90186315	FAM13A1	intron	t	c	C	C	C
rs6826407	1.E+00	+-	2.E-02	7.E-01	1.E+00	5.E-01	--	1.E-01	7.E-01	7.E-01	3.E-01	++	6.E-03	3.E-01	8.E-01	4	90194056	FAM13A1	intron	t	c	C	C	C
rs756175	8.E-01	+-	2.E-01	2.E-01	6.E-01	9.E-01	+-	1.E-01	3.E-01	8.E-01	6.E-01	++	6.E-01	3.E-01	7.E-01	4	90218064	FAM13A1	flanking_5UTR	a	g	A	A	A

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_TENOR_FEV1	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_TENOR_FVC	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_TENOR_FEV1/FVC	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs357542	9.E-01	+-	2.E-01	3.E-01	7.E-01	7.E-01	++	3.E-01	2.E-01	5.E-01	6.E-01	+-	3.E-01	4.E-01	2.E-01	9	97183463	PTCH	flanking_3UTR	a	g	A	A	A
rs7860361	7.E-01	+-	1.E-01	4.E-01	5.E-01	6.E-01	+-	4.E-01	4.E-01	3.E-01	8.E-01	+-	1.E-01	2.E-01	9.E-01	9	97187625	PTCH	flanking_3UTR	t	c	T	T	T
rs357536	1.E+00	++	2.E-01	1.E+00	8.E-01	7.E-01	+-	4.E-01	1.E+00	4.E-01	5.E-01	+-	2.E-01	6.E-01	7.E-01	9	97193095	PTCH	flanking_3UTR	a	g	G	G	G
rs357528	8.E-01	++	8.E-01	7.E-01	4.E-01	4.E-01	++	9.E-01	5.E-01	9.E-01	6.E-01	++	7.E-01	4.E-01	6.E-01	9	97207403	PTCH	flanking_3UTR	a	c	A	A	A
rs357527	7.E-01	+-	2.E-01	8.E-01	4.E-01	7.E-01	++	5.E-01	5.E-01	5.E-01	5.E-01	+-	1.E-01	6.E-01	2.E-01	9	97207632	PTCH	flanking_3UTR	t	c	T	T	T
rs7388704	1.E+00	+-	3.E-01	9.E-01	9.E-01	9.E-01	+-	2.E-01	8.E-01	7.E-01	8.E-01	+-	8.E-01	7.E-01	6.E-01	9	97211238	PTCH	flanking_3UTR	a	g	G	G	G
rs7389278	6.E-01	+++	7.E-01	9.E-01	4.E-01	6.E-01	+++	3.E-01	1.E+00	3.E-01	1.E+00	++	8.E-01	8.E-01	9.E-01	9	97211906	PTCH	flanking_3UTR	t	c	T	T	T

rs357522	8.E-01	+-	6.E-01	9.E-01	6.E-01	8.E-01	++	2.E-01	5.E-01	6.E-01	9.E-01	+-	9.E-01	1.E+00	1.E+00	9	97229279	PTCH	flanking_3UTR	t	c	C	C	C
rs10512249	9.E-01	+-	5.E-01	9.E-01	8.E-01	2.E-01	+++	6.E-01	8.E-01	8.E-02	8.E-01	++	4.E-01	1.E+00	7.E-02	9	97296130	PTCH	intron	t	c	T	T	T
rs4448343	9.E-01	+-	5.E-01	6.E-01	8.E-01	4.E-01	---	5.E-01	7.E-01	4.E-01	3.E-01	++	7.E-01	2.E-01	3.E-01	9	97306191	PTCH	intron	a	g	G	G	G
rs28536742	1.E+00	+-	3.E-01	9.E-01	1.E+00	1.E-01	+++	2.E-01	4.E-01	2.E-01	2.E-01	+-	5.E-01	2.E-01	7.E-02	9	97322914	PTCH	flanking_5UTR	t	c	T	T	T
rs576594	7.E-07	---	2.E-01	5.E-04	2.E-01	2.E-05	---	3.E-01	7.E-03	6.E-02	1.E-03	---	1.E-01	8.E-04	6.E-01	9	97359032	PTCH	flanking_5UTR	t	c	T	T	T
rs7040739	6.E-01	+-	7.E-01	8.E-02	3.E-01	2.E-02	---	5.E-01	1.E-01	4.E-01	6.E-01	+-	1.E-01	5.E-02	4.E-01	9	97388706	PTCH	flanking_5UTR	t	g	G	G	G
rs1889616	7.E-01	++	9.E-01	4.E-01	4.E-01	6.E-01	+++	3.E-01	1.E+00	3.E-01	9.E-01	+-	9.E-02	8.E-02	9.E-01	9	97399009	PTCH	flanking_5UTR	t	c	T	T	T
rs1932075	4.E-01	++	4.E-01	5.E-01	9.E-01	2.E-01	+++	3.E-01	5.E-01	3.E-01	8.E-01	+-	1.E+00	4.E-01	1.E-01	9	97399937	PTCH	flanking_5UTR	a	g	A	A	A
rs10818991	6.E-03	+++	2.E-02	3.E-02	1.E+00	6.E-02	+++	1.E-02	3.E-01	3.E-01	1.E-02	++	2.E-01	4.E-03	8.E-01	9	97407538	PTCH	flanking_5UTR	t	c	T	T	T
rs1984119	7.E-01	++	4.E-02	9.E-01	4.E-01	5.E-01	++	4.E-01	4.E-01	1.E-01	5.E-03	---	5.E-03	4.E-01	3.E-01	9	97408582	PTCH	flanking_5UTR	a	g	G	G	G
rs3824491	5.E-01	++	2.E-01	4.E-01	2.E-01	8.E-01	+++	8.E-01	9.E-01	8.E-01	1.E+00	+-	3.E-03	1.E-01	3.E-02	9	97408698	PTCH	flanking_5UTR	a	c	A	A	A
rs6478154	3.E-02	+++	8.E-01	2.E-01	3.E-01	2.E-01	+++	9.E-01	6.E-01	1.E-01	3.E-02	+++	7.E-01	8.E-03	5.E-01	9	97411347	PTCH	flanking_5UTR	a	c	A	A	A
rs10988802	5.E-01	++	7.E-01	4.E-01	2.E-01	5.E-01	++	8.E-01	3.E-01	1.E-01	9.E-01	+-	6.E-01	3.E-01	8.E-01	9	97416520	PTCH	flanking_5UTR	a	g	A	A	A
rs6478302	3.E-02	+-	2.E-01	4.E-02	4.E-01	7.E-01	+-	7.E-01	6.E-01	5.E-01	5.E-04	+++	1.E-01	9.E-04	4.E-01	9	97432161	PTCH	flanking_5UTR	t	g	T	T	T
rs7854581	3.E-02	+-	1.E-01	5.E-02	5.E-01	5.E-01	+-	6.E-01	5.E-01	7.E-01	4.E-04	---	5.E-02	3.E-03	4.E-01	9	97433100	PTCH	flanking_5UTR	t	c	C	C	C
rs10989496	5.E-02	+-	4.E-01	1.E-01	8.E-01	5.E-02	+++	7.E-01	2.E-01	6.E-01	3.E-01	++	3.E-01	2.E-01	4.E-01	9	97436827	PTCH	flanking_5UTR	a	g	A	A	A
rs10819953	2.E-02	---	1.E+00	2.E-01	9.E-02	6.E-04	---	8.E-01	4.E-02	5.E-02	1.E+00	++	8.E-01	6.E-01	7.E-01	9	97438777	PTCH	flanking_5UTR	a	g	G	G	G
rs4743125	5.E-01	+-	8.E-01	1.E-01	1.E-01	2.E-03	---	1.E+00	8.E-02	4.E-02	7.E-01	++	6.E-01	2.E-01	8.E-01	9	97444324	PTCH	flanking_5UTR	t	c	C	C	C
rs9695781	6.E-01	+-	9.E-01	4.E-01	2.E-01	3.E-02	---	1.E+00	2.E-01	1.E-01	9.E-01	++	8.E-01	5.E-01	8.E-01	9	97447347	PTCH	flanking_5UTR	a	c	C	C	C
rs10990303	1.E-02	+++	6.E-01	9.E-02	4.E-01	3.E-03	+++	7.E-01	8.E-02	1.E-01	4.E-01	+-	6.E-01	1.E-01	4.E-01	9	97450226	PTCH	flanking_5UTR	t	c	T	T	T
rs10990568	9.E-01	++	8.E-01	6.E-01	9.E-01	6.E-01	+-	6.E-01	9.E-01	2.E-01	3.E-01	++	9.E-01	4.E-01	2.E-01	9	97453958	PTCH	flanking_5UTR	a	g	G	G	G
rs10761011	7.E-01	++	8.E-01	9.E-01	4.E-01	8.E-01	+-	5.E-01	7.E-01	6.E-01	5.E-01	++	9.E-01	7.E-01	1.E-01	9	97463497	PTCH	flanking_5UTR	a	g	A	A	A
rs10991145	1.E-03	---	8.E-01	4.E-02	1.E-01	9.E-03	---	6.E-01	2.E-01	5.E-02	7.E-01	+-	4.E-01	1.E-01	1.E+00	9	97464363	PTCH	flanking_5UTR	a	g	A	A	A
rs4743148	7.E-01	++	2.E-01	2.E-01	3.E-01	1.E+00	+-	7.E-01	1.E-01	9.E-01	4.E-01	+-	4.E-02	7.E-01	1.E-01	9	97470395	PTCH	flanking_5UTR	a	g	G	G	G
rs700998	8.E-01	++	1.E-01	8.E-01	7.E-01	7.E-01	+-	1.E-01	3.E-01	5.E-01	5.E-01	+-	3.E-01	5.E-01	3.E-01	9	97475094	PTCH	flanking_5UTR	t	g	T	T	T
rs10978343	7.E-01	+-	7.E-01	9.E-02	3.E-01	9.E-01	+-	9.E-01	2.E-02	7.E-01	7.E-01	++	3.E-01	6.E-01	2.E-01	9	97481707	PTCH	flanking_5UTR	t	c	T	T	T
rs915228	6.E-01	+-	7.E-01	8.E-01	2.E-01	6.E-02	+++	5.E-01	3.E-01	2.E-01	2.E-01	++	8.E-01	2.E-02	8.E-01	9	97484124	PTCH	flanking_5UTR	a	g	G	G	G
rs817184	9.E-01	++	2.E-01	9.E-01	9.E-01	7.E-01	+-	2.E-01	5.E-01	5.E-01	4.E-01	+-	3.E-01	5.E-01	5.E-01	9	97486993	PTCH	flanking_5UTR	a	c	A	A	A
rs4743181	6.E-01	++	5.E-01	4.E-01	3.E-01	1.E+00	++	8.E-01	9.E-01	9.E-01	2.E-01	++	3.E-01	1.E-01	4.E-01	9	97492614	PTCH	flanking_5UTR	a	g	G	G	G
rs10739231	6.E-01	+-	7.E-01	1.E+00	2.E-01	1.E-01	---	9.E-01	3.E-01	4.E-01	5.E-01	+-	7.E-01	8.E-02	7.E-01	9	97493501	PTCH	flanking_5UTR	t	g	T	T	T

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_TENOR_FEV1	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_TENOR_FVC	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_TENOR_FEV1/FVC	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	TENOR_A1	SARP_A1	CSGA_A1
rs10498231	6.E-01	+-	4.E-01	9.E-01	2.E-01	7.E-01	+-	4.E-01	9.E-01	3.E-01	5.E-01	++	6.E-01	6.E-01	8.E-01	2	229212309	PID1	flanking_3UTR	a	c	A	A	A
rs3943747	2.E-01	++	4.E-01	2.E-01	8.E-01	2.E-02	++	8.E-01	9.E-02	8.E-01	3.E-01	++	5.E-01	4.E-01	9.E-01	2	229218732	PID1	flanking_3UTR	a	c	C	C	C
rs1435862	2.E-01	+-	4.E-01	3.E-01	9.E-01	2.E-02	---	9.E-01	8.E-02	8.E-01	2.E-01	---	3.E-01	4.E-01	7.E-01	2	229227453	PID1	flanking_3UTR	a	g	A	A	A
rs11890478	3.E-02	+++	6.E-01	2.E-01	4.E-01	7.E-01	+-	8.E-01	1.E-01	4.E-01	2.E-01	+++	3.E-01	4.E-01	9.E-01	2	229228232	PID1	flanking_3UTR	a	g	G	G	G
rs6737010	3.E-02	---	6.E-01	2.E-01	4.E-01	6.E-01	+-	8.E-01	1.E-01	3.E-01	2.E-01	---	3.E-01	4.E-01	9.E-01	2	229237357	PID1	flanking_3UTR	t	c	T	T	T
rs6752171	5.E-02	---	5.E-01	3.E-01	3.E-01	5.E-01	+-	9.E-01	2.E-01	2.E-01	2.E-01	---	3.E-01	5.E-01	9.E-01	2	229246373	PID1	flanking_3UTR	t	g	T	T	T
rs1358443	4.E-01	+-	5.E-01	3.E-01	3.E-01	2.E-01	++	5.E-01	2.E-01	4.E-01	4.E-01	+++	8.E-01	4.E-01	6.E-01	2	229290648	PID1	flanking_3UTR	t	c	C	C	C
rs1534458	7.E-01	++	7.E-01	6.E-01	5.E-01	7.E-01	+-	1.E+00	9.E-01	4.E-01	8.E-01	+-	6.E-01	7.E-01	7.E-01	2	229308807	PID1	flanking_3UTR	t	c	T	C	T
rs6722400	7.E-01	+-	7.E-01	6.E-01	4.E-01	7.E-01	+-	1.E+00	9.E-01	3.E-01	8.E-01	++	6.E-01	7.E-01	7.E-01	2	229316515	PID1	flanking_3UTR	a	g	G	A	G
rs7603424	6.E-01	++	9.E-01	5.E-01	4.E-01	6.E-01	+-	8.E-01	4.E-01	3.E-01	9.E-01	+-	8.E-01	9.E-01	1.E+00	2	229317612	PID1	flanking_3UTR	a	g	A	A	A
rs6719964	4.E-01	++	6.E-01	9.E-01	3.E-02	9.E-01	+-	7.E-01	6.E-01	5.E-02	8.E-01	+-	6.E-01	1.E+00	8.E-01	2	229324480	PID1	flanking_3UTR	t	c	C	C	C
rs10451593	5.E-01	+-	4.E-01	2.E-01	3.E-02	2.E-01	++	8.E-01	1.E-01	2.E-01	4.E-01	++	2.E-01	3.E-01	2.E-01	2	229325779	PID1	flanking_3UTR	t	c	C	C	C
rs1405837	8.E-01	+-	7.E-01	5.E-01	5.E-01	7.E-01	+-	9.E-01	9.E-01	4.E-01	9.E-01	+-	6.E-01	6.E-01	7.E-01	2	229348479	PID1	flanking_3UTR	t	g	G	T	G
rs1881025	8.E-01	+-	9.E-01	4.E-01	6.E-01	1.E+00	++	5.E-01	7.E-01	3.E-01	8.E-01	+-	5.E-01	1.E-01	8.E-01	2	229352180	PID1	flanking_3UTR	a	g	A	A	A
rs6756903	3.E-01	+++	9.E-01	6.E-01	5.E-01	7.E-01	++	8.E-01	9.E-01	4.E-01	8.E-01	+-	1.E+00	6.E-01	7.E-01	2	229354345	PID1	flanking_3UTR	t	c	T	C	T
rs1527669	8.E-01	+-	9.E-01	6.E-01	5.E-01	6.E-01	+-	9.E-01	5.E-01	6.E-01	6.E-01	+-	9.E-01	4.E-01	1.E+00	2	229360707	PID1	flanking_3UTR	a	g	A	A	A
rs3920427	7.E-01	+-	9.E-01	4.E-01	5.E-01	9.E-01	++	5.E-01	7.E-01	2.E-01	8.E-01	+-	5.E-01	2.E-01	8.E-01	2	229366708	PID1	flanking_3UTR	t	c	T	T	T

rs6712405	7.E-01	+-	9.E-01	4.E-01	5.E-01	1.E+00	++	5.E-01	7.E-01	2.E-01	7.E-01	+-	5.E-01	1.E-01	8.E-01	2	229366897	PID1	flanking_3UTR	a	g	A	A	A
rs776975	2.E-01	+++	9.E-01	3.E-01	9.E-01	4.E-01	+++	7.E-01	6.E-01	7.E-01	5.E-01	++	8.E-01	2.E-01	7.E-01	2	2293772213	PID1	flanking_3UTR	t	c	T	T	T
rs12471368	6.E-01	+-	6.E-01	2.E-01	2.E-01	8.E-01	++	9.E-01	2.E-01	5.E-01	5.E-01	+++	6.E-01	1.E+00	6.E-01	2	229389331	PID1	flanking_3UTR	t	c	T	T	T
rs1527671	1.E+00	+-	1.E+00	3.E-01	9.E-01	4.E-01	---	8.E-01	6.E-01	8.E-01	6.E-01	+-	1.E+00	2.E-01	6.E-01	2	229392944	PID1	flanking_3UTR	a	g	G	G	G
rs11899696	4.E-02	+++	4.E-01	2.E-01	4.E-01	1.E-01	+++	7.E-01	4.E-01	1.E-01	1.E-01	++	2.E-01	1.E-01	7.E-01	2	229403044	PID1	flanking_3UTR	t	c	T	T	T
rs4487082	1.E+00	++	8.E-01	5.E-01	9.E-01	1.E+00	+-	6.E-01	9.E-01	1.E+00	9.E-01	++	9.E-01	5.E-01	8.E-01	2	229432205	PID1	flanking_3UTR	a	g	G	G	G
rs800736	7.E-01	++	7.E-01	6.E-01	4.E-01	6.E-01	++	7.E-01	7.E-01	2.E-01	8.E-01	+-	5.E-01	1.E-01	7.E-01	2	229438161	PID1	flanking_3UTR	a	g	A	A	A
rs7578485	8.E-01	+-	5.E-01	1.E+00	6.E-01	4.E-01	+++	8.E-01	5.E-01	9.E-01	4.E-01	+-	7.E-01	2.E-01	5.E-01	2	229451253	PID1	flanking_3UTR	a	g	A	A	A
rs13428414	7.E-01	++	6.E-01	5.E-01	3.E-01	8.E-01	++	3.E-01	1.E+00	6.E-01	3.E-01	++	7.E-02	4.E-01	3.E-01	2	229456612	PID1	flanking_3UTR	t	c	C	C	C
rs800746	9.E-01	+-	5.E-01	8.E-01	9.E-01	6.E-01	+-	2.E-01	7.E-01	2.E-01	3.E-01	+++	7.E-01	7.E-01	3.E-01	2	229457475	PID1	flanking_3UTR	a	g	A	A	A
rs9288639	5.E-01	+-	8.E-01	7.E-02	1.E-01	7.E-01	+-	6.E-01	7.E-02	4.E-01	8.E-01	++	1.E+00	3.E-01	3.E-01	2	229462042	PID1	flanking_3UTR	t	c	C	C	C
rs800729	1.E-01	+++	6.E-01	2.E-01	1.E+00	5.E-01	+++	3.E-01	7.E-01	7.E-01	6.E-01	+-	1.E+00	2.E-01	5.E-01	2	229467572	PID1	flanking_3UTR	t	c	T	C	T
rs800742	3.E-02	+++	4.E-01	2.E-01	3.E-01	4.E-02	+++	6.E-01	3.E-01	7.E-02	1.E-01	++	3.E-01	1.E-01	7.E-01	2	229471910	PID1	flanking_3UTR	a	g	A	A	A
rs809616	3.E-01	++	4.E-01	8.E-01	4.E-02	3.E-01	++	7.E-01	5.E-01	3.E-02	3.E-01	+++	3.E-01	8.E-01	6.E-01	2	229472163	PID1	flanking_3UTR	t	c	T	T	T
rs2396595	8.E-01	+-	6.E-02	3.E-01	6.E-01	9.E-01	+-	3.E-01	6.E-01	7.E-01	7.E-01	++	1.E-01	3.E-01	8.E-01	2	229489214	PID1	flanking_3UTR	t	c	T	T	T
rs10205926	1.E+00	+-	7.E-01	3.E-01	1.E+00	6.E-01	++	8.E-01	3.E-01	2.E-01	7.E-01	++	8.E-01	8.E-01	4.E-01	2	229491242	PID1	flanking_3UTR	t	c	C	C	T
rs11901307	9.E-01	++	1.E+00	7.E-02	9.E-01	1.E-02	+++	9.E-01	9.E-02	4.E-01	6.E-01	++	9.E-01	3.E-01	6.E-01	2	229494524	PID1	flanking_3UTR	t	g	T	T	T
rs7558980	1.E-01	+++	5.E-01	3.E-01	6.E-01	3.E-01	++	7.E-01	4.E-01	7.E-01	6.E-02	+++	3.E-01	2.E-01	3.E-01	2	229513328	PID1	flanking_3UTR	a	g	G	G	G
rs9808412	1.E-02	+++	9.E-01	5.E-02	9.E-01	7.E-01	++	9.E-01	6.E-02	4.E-01	4.E-01	++	5.E-01	3.E-01	6.E-01	2	229522013	PID1	flanking_3UTR	t	c	T	T	T
rs7593561	2.E-01	+++	5.E-01	3.E-01	8.E-01	3.E-01	++	7.E-01	2.E-01	4.E-01	1.E-01	+++	3.E-01	4.E-01	3.E-01	2	229536702	PID1	flanking_3UTR	t	g	G	G	G
rs995159	7.E-01	+-	1.E-01	7.E-01	5.E-01	6.E-01	+++	4.E-01	1.E+00	3.E-01	8.E-01	+-	2.E-01	4.E-01	3.E-01	2	229536991	PID1	flanking_3UTR	t	c	C	C	C
rs10490036	2.E-01	---	2.E-02	3.E-01	1.E+00	7.E-01	---	2.E-02	8.E-01	8.E-01	2.E-01	+-	3.E-01	3.E-01	9.E-01	2	229549846	PID1	flanking_3UTR	a	g	G	G	G
rs10180529	8.E-01	++	6.E-01	8.E-01	7.E-01	6.E-01	+-	7.E-01	8.E-01	3.E-01	3.E-01	+++	7.E-01	8.E-01	2.E-01	2	229556970	PID1	flanking_3UTR	t	c	C	C	C
rs11894050	9.E-01	+-	7.E-01	7.E-01	9.E-01	6.E-01	++	8.E-01	8.E-01	2.E-01	4.E-01	---	7.E-01	9.E-01	3.E-01	2	229568683	PID1	flanking_3UTR	a	c	A	A	A
rs1072282	1.E+00	---	7.E-01	7.E-01	9.E-01	6.E-01	++	8.E-01	8.E-01	2.E-01	5.E-01	---	7.E-01	1.E+00	3.E-01	2	229571469	PID1	flanking_3UTR	a	g	A	A	A
rs7559725	5.E-02	---	6.E-01	2.E-01	6.E-01	4.E-01	---	7.E-01	6.E-01	9.E-01	1.E-01	---	5.E-01	8.E-02	9.E-01	2	229575991	PID1	flanking_3UTR	t	c	C	C	C
rs1544688	7.E-01	+-	5.E-03	4.E-01	3.E-01	9.E-01	++	1.E-01	6.E-01	7.E-01	6.E-01	+-	1.E-02	3.E-01	4.E-01	2	229582523	PID1	flanking_3UTR	t	c	C	C	C
rs2072556	8.E-02	+++	1.E-01	2.E-01	7.E-01	3.E-01	++	3.E-01	4.E-01	9.E-01	2.E-02	+++	5.E-02	4.E-01	3.E-01	2	229584972	PID1	flanking_3UTR	t	c	C	C	C
rs10211472	7.E-01	++	9.E-03	6.E-01	5.E-01	9.E-01	+-	5.E-02	1.E+00	7.E-01	7.E-01	++	3.E-02	3.E-01	4.E-01	2	229591666	PID1	flanking_3UTR	t	c	T	T	T
rs10490035	3.E-01	---	7.E-01	5.E-01	7.E-01	4.E-01	+-	6.E-01	4.E-01	7.E-01	5.E-01	---	6.E-01	7.E-01	8.E-01	2	229593322	PID1	flanking_3UTR	a	c	C	C	C
rs3771286	3.E-01	++	2.E-02	3.E-01	5.E-01	8.E-02	+++	7.E-02	2.E-01	9.E-01	2.E-01	++	4.E-02	8.E-01	6.E-01	2	229597727	PID1	3UTR	t	c	C	C	C
rs6436823	9.E-01	+-	6.E-01	6.E-04	7.E-01	9.E-01	+-	8.E-01	7.E-03	9.E-01	1.E-01	+-	6.E-01	5.E-03	5.E-01	2	229601027	PID1	intron	a	g	A	A	A
rs2536214	7.E-02	++	1.E-01	1.E-01	6.E-01	3.E-03	+++	3.E-01	3.E-02	6.E-01	5.E-01	+-	2.E-01	1.E+00	7.E-01	2	229602126	PID1	intron	t	c	T	T	T
rs3845823	1.E-02	++	2.E-01	4.E-02	7.E-01	1.E-03	+++	3.E-01	2.E-02	5.E-01	6.E-01	++	4.E-01	7.E-01	6.E-01	2	229611365	PID1	intron	t	g	T	T	T
rs2109818	9.E-01	+-	1.E-01	4.E-01	8.E-01	9.E-01	+-	6.E-01	5.E-01	8.E-01	2.E-01	++	2.E-02	6.E-01	9.E-01	2	229614496	PID1	intron	a	g	G	G	G
rs2215598	6.E-01	++	7.E-01	2.E-02	3.E-01	1.E+00	++	3.E-01	2.E-01	1.E+00	2.E-01	+-	5.E-01	2.E-02	1.E-01	2	229616489	PID1	intron	t	c	T	T	T
rs724395	9.E-01	+-	6.E-01	3.E-01	8.E-01	6.E-01	+-	1.E-01	4.E-01	3.E-01	7.E-01	+-	3.E-01	6.E-01	2.E-01	2	229619810	PID1	intron	t	c	T	T	T
rs31276	4.E-02	+-	6.E-01	5.E-02	4.E-01	4.E-01	+-	1.E-01	2.E-01	5.E-02	6.E-01	+-	2.E-01	1.E-01	5.E-01	2	229628764	PID1	intron	t	c	C	C	C
rs31278	7.E-01	+-	5.E-02	1.E-01	4.E-01	1.E+00	+-	3.E-01	5.E-01	9.E-01	8.E-01	+-	3.E-02	6.E-03	2.E-01	2	229630498	PID1	intron	t	c	T	T	T
rs4608504	8.E-01	+-	4.E-01	1.E-01	7.E-01	9.E-01	+-	6.E-01	2.E-01	7.E-01	8.E-01	+-	3.E-01	4.E-02	5.E-01	2	229640616	PID1	intron	t	c	T	T	T
rs1860761	8.E-01	++	9.E-01	5.E-02	5.E-01	2.E-01	+++	5.E-01	3.E-01	7.E-01	4.E-01	+-	3.E-01	9.E-03	8.E-01	2	229645080	PID1	intron	a	g	A	A	A
rs1860762	3.E-02	---	5.E-01	1.E-01	7.E-01	4.E-01	---	3.E-01	6.E-01	6.E-01	5.E-01	++	7.E-01	7.E-02	5.E-01	2	229648879	PID1	intron	t	c	C	C	C
rs2014401	7.E-01	+-	4.E-01	3.E-02	5.E-01	9.E-01	++	1.E+00	2.E-01	8.E-01	5.E-01	+-	1.E-01	1.E-03	5.E-01	2	229659963	PID1	intron	a	g	A	A	A
rs1014174	7.E-01	+-	1.E+00	1.E-01	5.E-01	1.E-01	+++	6.E-01	2.E-01	9.E-01	9.E-01	+-	6.E-01	1.E-01	3.E-01	2	229660208	PID1	intron	a	g	G	G	G
rs2109820	3.E-03	+++	5.E-01	7.E-02	1.E-01	8.E-01	++	4.E-01	9.E-01	6.E-01	2.E-02	++	8.E-01	2.E-03	1.E-01	2	229665247	PID1	intron	t	g	G	G	G
rs7589888	4.E-01	+-	3.E-01	9.E-01	9.E-02	9.E-01	+-	5.E-01	3.E-01	8.E-01	2.E-01	---	4.E-01	9.E-01	1.E-01	2	229670668	PID1	intron	t	c	T	T	T
rs10200706	8.E-01	+-	1.E+00	9.E-01	6.E-01	6.E-01	---	8.E-01	9.E-01	5.E-01	4.E-01	+++	5.E-01	7.E-01	8.E-01	2	229673882	PID1	intron	t	c	T	T	C
rs6436839	4.E-01	---	8.E-01	6.E-01	8.E-01	9.E-01	+-	7.E-01	9.E-01	8.E-01	5.E-01	+-	9.E-01	2.E-01	1.E+00	2	229678042	PID1	intron	a	g	G	G	G
rs6759815	7.E-01	+-	5.E-01	3.E-01	5.E-01	8.E-01	+-	6.E-01	8.E-01	7.E-01	5.E-01	+-	7.E-01	8.E-02	6.E-01	2	229680665	PID1	intron	t	c	C	C	C
rs2765936	1.E+00	+-	4.E-01	1.E+00	1.E+00	2.E-01	---	9.E-01	6.E-01	2.E-01	8.E-01	++	2.E-01	4.E-01	2.E-01	2	229683166	PID1	intron	t	c	T	T	T
rs10490031	4.E-01	++	1.E-01	5.E-01	1.E+00	7.E-01	---	2.E-01	8.E-01	9.E-01	2.E-01	+-	3.E-01	2.E-01	9.E-01	2	229689857	PID1	intron	a	g	A	A	A
rs1319273	9.E-01	+-	2.E-01	5.E-01	8.E-01	7.E-01	+-	1.E-01	5.E-01	4.E-01	7.E-01	++	1.E+00	9.E-01	4.E-01	2	229697273	PID1	intron	t	c	C	C	C
rs9755583	9.E-01	++	3.E-01	8.E-01	8.E-01	9.E-01	+-	1.E-01	7.E-01	4.E-01	5.E-01	++	8.E-01	5.E-01	9.E-01	2	229698937	PID1	intron	a	g	A	A	A
rs12467995	8.E-01	+-	2.E-01	6.E-01	6.E-01	9.E-01	+-	7.E-01	5.E-01	8.E-01	3.E-01	++	1.E-01	9.E-01	9.E-01	2	229702613	PID1	intron	t	c	C	C	C
rs12329005	9.E-01	+-	3.E-01	3.E-01	8.E-01	5.E-01	+-	2.E-01	4.E-01	1.E-01	7.E-01	+-	9.E-01	7.E-01	9.E-02	2	229708818	PID1	intron	t	c	C	C	C
rs4973160	7.E-01	+-	3.E-02	4.E-01	4.E-01	3.E-01	+-	2.E-02	4.E-01	4.E-02	2.E-01	+++	5.E-01	9.E-01	9.E-02	2	229710850	PID1	intron	t	g	T	T	T

rs2023499	9.E-01	+-	1.E+00	3.E-01	7.E-01	2.E-02	---	9.E-01	1.E-01	3.E-01	4.E-01	+++	8.E-01	8.E-01	3.E-01	2	229715103	PID1	intron	t	c	C	C	C
rs7561470	3.E-01	++	4.E-01	3.E-01	8.E-01	1.E-01	+++	8.E-01	3.E-01	7.E-01	1.E+00	+-	2.E-01	1.E+00	1.E-01	2	229721264	PID1	intron	a	g	A	A	A
rs17476328	1.E+00	+++	2.E-01	8.E-01	1.E+00	9.E-01	--	2.E-01	8.E-01	3.E-01	9.E-01	-+	9.E-01	6.E-01	4.E-01	2	229724395	PID1	intron	a	g	A	A	A
rs985891	5.E-01	++	4.E-02	6.E-01	2.E-01	4.E-01	--	5.E-02	1.E+00	7.E-02	9.E-01	++	5.E-01	7.E-01	9.E-01	2	229727592	PID1	intron	a	g	A	A	A
rs2396616	9.E-01	+-	7.E-01	8.E-01	7.E-01	9.E-01	+-	7.E-01	1.E+00	7.E-01	6.E-01	+-	9.E-01	6.E-01	5.E-01	2	229729646	PID1	intron	a	g	A	A	A
rs4973166	6.E-01	++	1.E-02	7.E-01	2.E-01	5.E-01	++	2.E-02	6.E-01	1.E-01	2.E-01	---	4.E-01	6.E-01	6.E-01	2	229733854	PID1	intron	a	g	G	G	G
rs4973171	3.E-01	+-	3.E-03	9.E-01	3.E-02	4.E-01	+-	9.E-04	6.E-01	5.E-02	7.E-01	+-	5.E-01	8.E-01	6.E-01	2	229738649	PID1	intron	a	g	A	A	A
rs1419958	7.E-01	++	2.E-01	7.E-01	1.E-01	7.E-01	+-	9.E-02	9.E-01	3.E-01	8.E-01	++	8.E-01	1.E+00	3.E-01	2	229741804	PID1	intron	t	g	G	G	G
rs12477036	5.E-01	+-	1.E-01	3.E-01	2.E-01	7.E-01	+-	1.E-01	2.E-01	3.E-01	7.E-01	+-	4.E-01	8.E-01	6.E-01	2	229742326	PID1	intron	a	g	G	G	G
rs12694800	8.E-01	++	4.E-02	7.E-01	1.E-01	8.E-01	++	2.E-02	8.E-01	2.E-01	1.E+00	+-	9.E-01	9.E-01	8.E-01	2	229743258	PID1	intron	t	c	C	C	C
rs1362256	1.E+00	--	3.E-01	8.E-01	4.E-01	6.E-01	--	1.E-01	1.E+00	2.E-01	9.E-01	+-	7.E-01	1.E+00	4.E-01	2	229747285	PID1	intron	t	c	T	T	T
rs2159723	6.E-01	++	5.E-01	5.E-01	6.E-01	6.E-01	+++	1.E-01	8.E-01	8.E-01	2.E-01	---	5.E-01	8.E-01	2.E-01	2	229753516	PID1	intron	t	c	T	T	T
rs1419936	7.E-01	+-	5.E-01	1.E-01	5.E-01	1.E+00	++	8.E-01	4.E-01	1.E+00	5.E-01	+-	3.E-01	2.E-01	2.E-01	2	229762039	PID1	intron	a	g	G	G	G
rs1362238	3.E-01	++	9.E-01	4.E-01	9.E-01	1.E+00	++	9.E-01	7.E-01	3.E-01	1.E-01	+++	1.E+00	2.E-01	1.E-01	2	229767104	PID1	intron	t	c	T	T	T
rs988889	9.E-01	+-	9.E-01	3.E-01	7.E-01	8.E-01	++	9.E-01	9.E-01	5.E-01	7.E-02	+-	8.E-01	6.E-02	6.E-02	2	229769945	PID1	intron	a	g	G	G	G
rs6736122	2.E-01	+++	9.E-01	4.E-01	7.E-01	8.E-01	-+	9.E-01	9.E-01	7.E-01	8.E-02	+-	9.E-01	8.E-02	1.E-01	2	229773255	PID1	intron	a	g	A	A	A
rs12478812	6.E-01	+-	1.E-01	3.E-01	3.E-01	6.E-01	+-	9.E-02	3.E-01	3.E-01	1.E+00	+-	5.E-01	7.E-01	8.E-01	2	229777030	PID1	intron	t	c	C	C	C
rs1362240	8.E-01	++	9.E-01	8.E-01	1.E+00	9.E-01	+-	5.E-01	9.E-01	7.E-01	1.E+00	++	9.E-01	9.E-01	1.E+00	2	229784591	PID1	intron	a	c	A	A	A
rs883731	3.E-01	+++	8.E-01	6.E-01	5.E-01	6.E-01	++	9.E-01	2.E-02	3.E-01	4.E-01	+-	1.E+00	1.E-01	8.E-01	2	229789287	PID1	intron	a	g	A	A	A
rs1946124	5.E-01	-+	2.E-01	7.E-01	1.E-01	9.E-01	+-	8.E-01	7.E-01	2.E-01	5.E-02	---	2.E-02	8.E-01	5.E-01	2	229802147	PID1	intron	a	g	G	G	G
rs1226984	8.E-01	-+	3.E-01	5.E-01	5.E-01	3.E-01	---	8.E-01	7.E-01	3.E-01	9.E-01	-+	2.E-01	2.E-01	7.E-01	2	229806982	PID1	intron	t	c	C	C	C
rs6747101	6.E-01	---	2.E-01	9.E-01	4.E-01	9.E-01	---	3.E-01	1.E+00	8.E-01	2.E-01	---	5.E-01	6.E-01	4.E-01	2	229811615	PID1	intron	t	c	C	T	T
rs1226998	8.E-01	-+	2.E-01	7.E-01	6.E-01	5.E-01	---	8.E-02	7.E-01	8.E-01	7.E-01	+-	9.E-01	5.E-01	6.E-01	2	229817917	PID1	intron	t	c	C	C	C
rs10498235	9.E-01	---	9.E-01	1.E+00	9.E-01	2.E-01	+++	4.E-01	3.E-01	7.E-01	8.E-02	---	2.E-01	2.E-01	7.E-01	2	229824279	PID1	intron	a	g	G	G	G
rs1227003	3.E-01	-+	2.E-01	2.E-02	2.E-02	3.E-01	-+	3.E-01	2.E-01	1.E-02	4.E-01	-+	4.E-01	2.E-02	9.E-01	2	229827522	PID1	intron	t	c	C	C	C
rs6724020	9.E-01	-+	1.E-01	2.E-01	8.E-01	9.E-01	++	2.E-01	1.E-01	7.E-01	3.E-01	---	3.E-01	1.E+00	6.E-01	2	229830491	PID1	intron	a	g	A	A	A
rs1227005	8.E-01	++	1.E+00	4.E-01	6.E-01	4.E-01	--	5.E-01	3.E-01	4.E-01	1.E+00	+-	3.E-01	6.E-01	5.E-01	2	229830629	PID1	intron	a	g	G	G	G
rs4321351	9.E-01	++	5.E-01	3.E-01	9.E-01	1.E-02	+++	8.E-01	8.E-02	7.E-01	2.E-01	-+	9.E-02	7.E-01	9.E-01	2	229837737	PID1	intron	a	g	G	G	G
rs1227009	9.E-01	++	7.E-01	1.E+00	8.E-01	4.E-01	+++	6.E-01	7.E-01	5.E-01	8.E-01	---	9.E-01	8.E-01	9.E-01	2	229839896	PID1	intron	a	g	A	A	A
rs10498237	1.E-01	+++	7.E-01	2.E-01	9.E-01	2.E-01	+++	3.E-01	4.E-01	7.E-01	6.E-01	-+	8.E-01	2.E-01	8.E-01	2	229850093	PID1	flanking_5UTR	a	g	G	G	G
rs12988652	1.E+00	-+	6.E-01	4.E-01	1.E+00	8.E-01	++	9.E-01	3.E-01	6.E-01	5.E-01	---	6.E-01	8.E-01	7.E-01	2	229850323	PID1	flanking_5UTR	a	g	A	A	A
rs10498238	7.E-01	+-	7.E-02	5.E-01	4.E-01	5.E-01	+-	3.E-01	2.E-01	1.E-01	7.E-02	+++	4.E-02	6.E-01	6.E-01	2	229874808	PID1	flanking_5UTR	t	c	T	T	T
rs4973184	9.E-01	++	6.E-01	1.E+00	8.E-01	6.E-01	+-	2.E-01	7.E-01	1.E+00	4.E-01	---	6.E-01	6.E-01	7.E-01	2	229874891	PID1	flanking_5UTR	t	c	T	T	T
rs1226950	8.E-01	++	5.E-02	2.E-01	7.E-01	6.E-01	++	9.E-02	1.E-01	2.E-01	8.E-01	+-	2.E-01	5.E-01	1.E-01	2	229882408	PID1	flanking_5UTR	t	c	C	C	C
rs12621639	4.E-01	+-	6.E-01	5.E-01	8.E-01	2.E-01	+-	2.E-01	3.E-01	6.E-01	5.E-01	-+	4.E-01	7.E-01	9.E-01	2	229884058	PID1	flanking_5UTR	a	c	C	A	C
rs6715968	5.E-01	++	7.E-01	3.E-01	2.E-01	1.E-01	--	7.E-01	7.E-02	1.E-01	2.E-01	+-	1.E-01	3.E-01	7.E-01	2	229884476	PID1	flanking_5UTR	t	g	T	T	T

Table E6. Meta-analysis results of 10 candidate genes in two African American asthmatic populations.

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs2373078	1.E-01	++	3.E-01	3.E-01	3.E-01	++	4.E-01	6.E-01	5.E-01	++	6.E-01	7.E-01	2	218100800	TNS1	flanking_3UTR	t	c	T	T
rs1002353	8.E-02	++	2.E-01	3.E-01	1.E-01	++	5.E-01	1.E-01	1.E-01	++	2.E-01	4.E-01	2	218103390	TNS1	flanking_3UTR	t	c	C	C
rs2373079	4.E-01	+	3.E-01	1.E+00	2.E-01	+	3.E-01	3.E-01	6.E-01	++	8.E-01	2.E-01	2	218106382	TNS1	flanking_3UTR	a	g	A	A
rs3796025	5.E-01	+-	9.E-01	2.E-01	5.E-02	+	3.E-01	5.E-02	4.E-01	+	2.E-01	9.E-01	2	218112318	TNS1	flanking_3UTR	t	c	T	T
rs17203333	1.E+00	+	9.E-01	8.E-01	7.E-01	+	3.E-01	4.E-01	8.E-01	+	6.E-01	2.E-01	2	218112453	TNS1	flanking_3UTR	t	c	C	C
rs4672833	5.E-01	+	9.E-01	2.E-01	6.E-02	++	3.E-01	7.E-02	4.E-01	+	2.E-01	1.E+00	2	218118260	TNS1	flanking_3UTR	t	c	C	C
rs4674189	6.E-01	+	3.E-01	6.E-01	3.E-01	+	4.E-01	6.E-01	7.E-01	+	6.E-01	2.E-01	2	218122227	TNS1	flanking_3UTR	t	c	T	T
rs6714500	7.E-01	+	4.E-01	6.E-01	7.E-01	+	9.E-01	5.E-01	1.E+00	+	4.E-01	3.E-01	2	218147088	TNS1	flanking_3UTR	t	c	T	T
rs6719545	3.E-02	++	1.E-01	1.E-01	3.E-02	++	1.E-01	1.E-01	3.E-01	++	5.E-01	4.E-01	2	218160079	TNS1	flanking_3UTR	t	g	T	T
rs2565686	2.E-01	+	2.E-01	8.E-01	2.E-02	+	4.E-02	2.E-01	7.E-01	++	9.E-01	6.E-01	2	218168866	TNS1	flanking_3UTR	t	c	C	C
rs2568177	1.E+00	+	6.E-01	5.E-01	7.E-01	+	7.E-01	9.E-01	9.E-01	+	8.E-01	6.E-01	2	218172299	TNS1	flanking_3UTR	t	c	C	C
rs1549733	9.E-01	+-	7.E-01	5.E-01	8.E-01	+-	7.E-01	1.E+00	8.E-01	+	8.E-01	6.E-01	2	218180417	TNS1	flanking_3UTR	t	c	T	T
rs7563651	7.E-01	+	8.E-01	4.E-01	8.E-01	+	6.E-01	2.E-01	7.E-01	++	8.E-01	9.E-01	2	218192012	TNS1	flanking_3UTR	a	g	A	A
rs6733585	5.E-01	+	3.E-01	9.E-01	8.E-01	+	3.E-01	3.E-01	6.E-01	+	9.E-01	4.E-01	2	218220843	TNS1	flanking_3UTR	a	g	A	A
rs6759238	2.E-01	++	7.E-01	1.E-01	3.E-01	++	8.E-01	2.E-01	8.E-01	+	9.E-01	6.E-01	2	218244694	TNS1	flanking_3UTR	a	g	A	A
rs6761086	2.E-01	++	1.E-01	9.E-01	3.E-01	+	2.E-01	9.E-01	3.E-01	++	4.E-01	5.E-01	2	218251675	TNS1	flanking_3UTR	t	c	T	T
rs4674200	1.E+00	+	7.E-01	5.E-01	1.E+00	+	7.E-01	6.E-01	1.E+00	+	6.E-01	5.E-01	2	218264996	TNS1	flanking_3UTR	a	c	C	C
rs10932725	5.E-01	+-	3.E-01	1.E+00	7.E-01	+	2.E-01	3.E-01	2.E-01	+	5.E-01	2.E-01	2	218270341	TNS1	flanking_3UTR	t	c	C	C
rs934241	3.E-01	++	5.E-01	5.E-01	6.E-01	+	5.E-01	1.E+00	2.E-01	++	5.E-01	3.E-01	2	218271711	TNS1	flanking_3UTR	t	c	T	T
rs11688171	5.E-01	++	5.E-01	7.E-01	5.E-01	+	1.E+00	2.E-01	6.E-01	+	3.E-01	6.E-01	2	218282177	TNS1	flanking_3UTR	a	c	A	A
rs10168801	6.E-01	+	6.E-01	8.E-01	9.E-01	+	6.E-01	5.E-01	4.E-01	+	7.E-01	4.E-01	2	218288795	TNS1	flanking_3UTR	a	g	A	A
rs10932727	2.E-01	++	1.E-01	8.E-01	4.E-01	++	2.E-01	7.E-01	3.E-01	++	3.E-01	7.E-01	2	218313957	TNS1	flanking_3UTR	a	g	A	A
rs2052928	8.E-01	+-	7.E-01	4.E-01	5.E-01	++	5.E-01	7.E-01	4.E-01	+	1.E-01	5.E-01	2	218328797	TNS1	flanking_3UTR	t	c	C	C
rs11677547	8.E-01	+-	2.E-01	3.E-01	6.E-01	+	4.E-01	9.E-01	7.E-01	+	4.E-01	9.E-02	2	218331734	TNS1	flanking_3UTR	t	c	C	C
rs7560625	4.E-01	+	3.E-01	9.E-01	6.E-01	+	5.E-01	1.E-01	1.E-01	+	1.E-01	5.E-01	2	218334032	TNS1	flanking_3UTR	a	g	G	G
rs1835338	6.E-01	+-	3.E-01	6.E-01	6.E-01	+	6.E-01	1.E-01	1.E-01	++	2.E-01	5.E-01	2	218338844	TNS1	flanking_3UTR	a	g	A	A
rs1583109	3.E-01	+	5.E-01	4.E-01	9.E-01	+	7.E-01	5.E-01	1.E-01	+	5.E-01	1.E-01	2	218342264	TNS1	flanking_3UTR	a	g	G	G
rs10197943	9.E-01	+-	2.E-01	8.E-02	6.E-01	+	9.E-01	6.E-01	1.E+00	+	6.E-02	2.E-02	2	218344279	TNS1	flanking_3UTR	t	c	T	T
rs2373146	7.E-01	+	5.E-01	1.E-01	6.E-01	+	8.E-01	2.E-01	7.E-01	+	6.E-01	2.E-01	2	218346421	TNS1	flanking_3UTR	t	c	C	C
rs7577167	5.E-01	+-	3.E-01	9.E-01	4.E-01	++	4.E-01	9.E-01	6.E-01	+	5.E-01	9.E-01	2	218357732	TNS1	flanking_3UTR	t	g	G	G
rs11677208	7.E-01	+-	6.E-01	3.E-01	9.E-01	+-	4.E-01	4.E-01	8.E-01	+	9.E-01	8.E-01	2	218361192	TNS1	flanking_3UTR	t	c	C	C
rs2571460	5.E-01	+-	1.E-01	4.E-01	7.E-01	+	2.E-01	4.E-01	7.E-01	+	2.E-01	4.E-01	2	218362333	TNS1	flanking_3UTR	a	g	A	A
rs2571457	7.E-01	+	6.E-01	9.E-01	8.E-01	+	5.E-01	6.E-01	9.E-01	+	7.E-01	7.E-01	2	218367229	TNS1	flanking_3UTR	t	c	C	C
rs3747	9.E-02	++	8.E-02	6.E-01	3.E-01	++	2.E-01	1.E+00	3.E-01	++	4.E-01	5.E-01	2	218372878	TNS1	flanking_3UTR	t	g	T	T
rs918949	5.E-01	+-	9.E-02	3.E-01	2.E-01	++	1.E-01	9.E-01	7.E-01	+	4.E-01	7.E-02	2	218382942	TNS1	coding	t	c	C	C
rs1035672	5.E-01	+-	2.E-01	5.E-01	1.E-01	++	1.E-01	7.E-01	5.E-01	+	8.E-01	2.E-01	2	218383444	TNS1	intron	a	g	G	G
rs2059408	9.E-01	+	4.E-01	3.E-01	8.E-01	+	8.E-01	5.E-01	1.E+00	+	4.E-01	3.E-01	2	218387844	TNS1	intron	t	c	C	C
rs2161969	8.E-02	++	7.E-01	2.E-02	2.E-01	++	5.E-01	2.E-01	3.E-01	+	9.E-01	8.E-02	2	218388815	TNS1	intron	a	g	A	A
rs2571445	8.E-02	+	9.E-02	5.E-01	5.E-02	+	2.E-02	8.E-01	8.E-01	+	1.E+00	7.E-01	2	218391399	TNS1	coding	t	c	T	T
rs2552527	4.E-01	+-	2.E-01	8.E-01	1.E-01	+	1.E-01	7.E-01	9.E-01	+	9.E-01	1.E+00	2	218396841	TNS1	intron	t	g	T	T
rs2571435	1.E+00	+	8.E-01	7.E-01	6.E-01	++	6.E-01	8.E-01	7.E-01	+	7.E-01	8.E-01	2	218400004	TNS1	intron	t	c	T	T
rs1008835	6.E-01	+	6.E-01	1.E-01	8.E-01	+	6.E-01	7.E-01	4.E-01	+	1.E+00	1.E-01	2	218412483	TNS1	intron	t	c	C	C
rs929937	2.E-01	++	6.E-01	2.E-01	2.E-02	++	1.E-01	7.E-02	8.E-01	+	6.E-01	3.E-01	2	218417460	TNS1	intron	t	c	T	T

rs3796033	4.E-02	-	3.E-02	5.E-01	2.E-03	-	6.E-03	1.E-01	6.E-01	-	8.E-01	7.E-01	2	218421527	TNS1	coding	a	g	G	A
rs3791978	4.E-01	+	1.E-01	6.E-01	1.E-01	+	4.E-03	3.E-01	8.E-01	+	1.E+00	7.E-01	2	218422931	TNS1	intron	t	g	T	T
rs1035674	9.E-01	+	9.E-01	8.E-01	8.E-02	++	1.E-01	4.E-01	2.E-01	-	4.E-01	3.E-01	2	218441371	TNS1	intron	a	g	A	A
rs2042542	8.E-02	-	3.E-01	1.E-01	2.E-01	-	5.E-01	2.E-01	4.E-01	-	5.E-01	7.E-01	2	218444537	TNS1	intron	a	g	G	G
rs1424916	9.E-01	+	3.E-01	3.E-01	9.E-02	++	4.E-02	9.E-01	6.E-01	-	8.E-01	6.E-01	2	218447545	TNS1	intron	t	c	T	T
rs4674220	8.E-01	+	1.E-01	2.E-01	6.E-02	+	5.E-03	6.E-01	7.E-01	++	7.E-01	8.E-01	2	218450247	TNS1	intron	a	g	G	G
rs890049	1.E-01	++	5.E-02	1.E+00	1.E-02	++	1.E-02	4.E-01	6.E-01	++	5.E-01	1.E+00	2	218453131	TNS1	intron	t	c	T	T
rs3791940	3.E-01	+	3.E-02	3.E-01	2.E-01	+	4.E-02	7.E-01	5.E-01	+	3.E-01	8.E-01	2	218457624	TNS1	intron	t	c	T	T
rs3791936	1.E+00	+	6.E-01	6.E-01	2.E-01	++	3.E-01	5.E-01	3.E-01	-	7.E-01	2.E-01	2	218476667	TNS1	intron	a	c	A	A
rs6755375	7.E-02	+	2.E-02	9.E-01	3.E-02	-	1.E-02	7.E-01	3.E-01	-	3.E-01	8.E-01	2	218484617	TNS1	intron	t	c	T	T
rs3791913	6.E-02	++	4.E-02	6.E-01	8.E-03	++	6.E-03	5.E-01	3.E-01	++	5.E-01	4.E-01	2	218495921	TNS1	intron	t	c	T	T
rs3791911	5.E-01	++	5.E-01	9.E-01	9.E-01	+	1.E+00	7.E-01	8.E-01	+	6.E-01	8.E-01	2	218502228	TNS1	intron	t	c	T	T
rs3791906	7.E-01	+	5.E-01	8.E-01	2.E-01	++	4.E-01	4.E-01	8.E-01	+	4.E-01	5.E-01	2	218511574	TNS1	intron	a	g	A	A
rs1549589	7.E-01	+	6.E-01	9.E-01	5.E-01	+	9.E-01	2.E-01	2.E-01	++	5.E-01	2.E-01	2	218519380	TNS1	flanking_5UTR	t	c	C	C
rs744753	4.E-02	-	6.E-02	4.E-01	5.E-02	-	1.E-01	3.E-01	5.E-01	+	2.E-01	6.E-01	2	218524323	TNS1	flanking_5UTR	a	g	A	A
rs3791890	2.E-01	++	3.E-01	5.E-01	3.E-01	++	6.E-01	3.E-01	4.E-01	+	1.E-01	7.E-01	2	218529831	TNS1	flanking_5UTR	t	c	C	C
rs3791884	9.E-02	-	4.E-02	9.E-01	1.E-01	-	1.E-01	6.E-01	2.E-01	+	3.E-02	5.E-01	2	218534627	TNS1	flanking_5UTR	a	g	G	G
rs11694996	7.E-02	++	2.E-01	2.E-01	2.E-02	++	3.E-01	1.E-02	9.E-01	+	5.E-01	3.E-01	2	218536158	TNS1	flanking_5UTR	t	c	T	T
rs12619872	4.E-01	-	9.E-01	2.E-01	5.E-01	-	6.E-01	7.E-01	5.E-01	+	7.E-01	9.E-02	2	218541196	TNS1	flanking_5UTR	t	c	T	T
rs11674313	5.E-01	-	9.E-01	4.E-01	6.E-01	-	6.E-01	1.E+00	6.E-01	+	7.E-01	2.E-01	2	218546592	TNS1	flanking_5UTR	t	c	T	T
rs750132	1.E+00	+	9.E-01	9.E-01	1.E-01	-	5.E-01	1.E-01	8.E-02	++	4.E-01	8.E-02	2	218548607	TNS1	flanking_5UTR	a	g	G	A
rs934039	3.E-01	-	3.E-01	8.E-01	2.E-01	-	2.E-01	5.E-01	8.E-01	+	6.E-01	8.E-01	2	218561636	TNS1	flanking_5UTR	t	c	T	T

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs9307305	3.E-01	-	4.E-01	6.E-01	6.E-01	++	1.E+00	4.E-01	3.E-01	-	4.E-01	5.E-01	4	106661967	FLJ20184	flanking_5UTR	t	c	C	C
rs4082504	6.E-01	+	1.E+00	3.E-01	3.E-01	+	9.E-01	8.E-02	9.E-01	+	1.E+00	8.E-01	4	106668349	FLJ20184	flanking_5UTR	a	c	C	C
rs12499086	4.E-01	-	3.E-01	1.E+00	9.E-01	++	6.E-01	4.E-01	2.E-01	-	2.E-01	7.E-01	4	106670760	FLJ20184	flanking_5UTR	a	g	A	A
rs3960769	4.E-01	++	4.E-01	8.E-01	3.E-01	-	7.E-01	2.E-01	5.E-02	++	5.E-02	5.E-01	4	106671248	FLJ20184	flanking_5UTR	a	c	A	A
rs730850	7.E-01	+	5.E-01	9.E-01	7.E-01	-	9.E-01	6.E-01	2.E-01	++	1.E-01	8.E-01	4	106686037	FLJ20184	flanking_5UTR	t	g	T	T
rs2189228	3.E-01	++	4.E-01	6.E-01	6.E-01	+	9.E-01	3.E-01	3.E-01	++	4.E-01	4.E-01	4	106692026	FLJ20184	flanking_5UTR	a	c	A	A
rs17584487	8.E-02	++	3.E-01	1.E-01	6.E-01	+	2.E-01	3.E-01	2.E-01	++	9.E-01	5.E-02	4	106703347	FLJ20184	intron	a	g	G	G
rs7684945	6.E-01	++	9.E-01	6.E-01	6.E-01	++	5.E-01	1.E+00	9.E-01	+	4.E-01	2.E-01	4	106706033	FLJ20184	intron	a	c	C	C
rs2593305	4.E-01	++	8.E-01	3.E-01	9.E-01	+	7.E-01	7.E-01	6.E-01	++	9.E-01	6.E-01	4	106723939	FLJ20184	intron	a	g	G	G
rs199330	6.E-01	+	5.E-01	9.E-01	8.E-02	++	1.E-01	5.E-01	2.E-01	-	6.E-01	2.E-01	4	106724392	FLJ20184	intron	t	c	C	C
rs199332	3.E-01	+	2.E-01	9.E-01	3.E-01	+	1.E-01	7.E-01	2.E-01	++	6.E-01	1.E-01	4	106727975	FLJ20184	intron	a	g	A	A
rs715706	6.E-01	++	7.E-01	7.E-01	7.E-01	-	9.E-01	7.E-01	6.E-01	++	6.E-01	7.E-01	4	106735477	FLJ20184	intron	t	c	T	T
rs1374530	3.E-01	-	3.E-01	7.E-01	7.E-01	+	6.E-01	1.E+00	1.E+00	+	8.E-01	6.E-01	4	106743426	FLJ20184	intron	a	g	G	G
rs7687176	9.E-01	+	8.E-01	6.E-01	8.E-01	+	6.E-01	7.E-01	6.E-01	-	9.E-01	5.E-01	4	106746555	FLJ20184	intron	t	c	T	T
rs4326019	8.E-01	+	6.E-01	9.E-01	9.E-01	+	6.E-01	7.E-01	8.E-01	-	7.E-01	1.E+00	4	106746830	FLJ20184	intron	a	g	G	G
rs17035960	9.E-01	+	9.E-01	7.E-01	8.E-01	-	9.E-01	9.E-01	5.E-01	++	7.E-01	5.E-01	4	106751295	FLJ20184	intron	t	c	T	T
rs1447096	9.E-01	+	6.E-01	4.E-01	9.E-01	+	6.E-01	4.E-01	5.E-01	-	7.E-01	6.E-01	4	106778827	FLJ20184	flanking_3UTR	t	g	G	G
rs1447098	1.E+00	+	3.E-01	2.E-01	9.E-01	+	6.E-01	4.E-01	7.E-01	++	6.E-01	1.E+00	4	106783049	FLJ20184	flanking_3UTR	t	c	T	T
rs1374534	1.E-01	++	1.E-01	4.E-01	6.E-01	+	5.E-02	1.E-01	2.E-02	++	5.E-01	4.E-03	4	106791905	FLJ20184	flanking_3UTR	a	g	A	A
rs4235415	8.E-01	+	4.E-01	2.E-01	5.E-01	+	7.E-01	8.E-02	7.E-01	+	4.E-01	7.E-01	4	106813299	PHF22	flanking_3UTR	a	g	A	A
rs6820671	7.E-01	+	7.E-01	3.E-01	1.E+00	+	9.E-01	9.E-01	9.E-01	+	5.E-01	3.E-01	4	106833270	PHF22	intron	a	g	G	G
rs11727735	6.E-01	++	7.E-01	7.E-01	7.E-01	++	7.E-01	9.E-01	5.E-01	-	7.E-01	5.E-01	4	106851319	FLJ13273	intron	a	g	G	G
rs4698951	2.E-01	+	3.E-02	6.E-01	3.E-01	+	4.E-02	3.E-01	4.E-01	++	3.E-01	9.E-01	4	106891647	FLJ13273	intron	t	c	T	T
rs10516526	7.E-01	++	1.E+00	6.E-01	2.E-01	++	6.E-01	2.E-01	7.E-01	+	1.E+00	5.E-01	4	106908353	FLJ13273	intron	a	g	G	G
rs2553449	7.E-01	+	9.E-01	4.E-01	3.E-01	++	5.E-01	4.E-01	6.E-01	+	5.E-01	9.E-01	4	106918341	FLJ13273	intron	t	c	C	C

rs2553463	9.E-02	-	6.E-02	7.E-01	1.E-01	+	3.E-02	8.E-01	7.E-01	+	6.E-01	1.E+00	4	106950112	FLJ13273	intron	t	c	C	C
rs2553435	8.E-01	+	9.E-01	9.E-01	5.E-01	-	5.E-01	8.E-01	8.E-01	+	6.E-01	8.E-01	4	107016314	NPNT	flanking_5UTR	t	c	C	C
rs2544408	9.E-01	+	9.E-02	2.E-02	8.E-01	+	3.E-01	8.E-02	9.E-01	+	7.E-02	4.E-02	4	107027489	NPNT	flanking_5UTR	a	g	G	A
rs2553453	3.E-01	+	2.E-02	2.E-01	3.E-01	-	2.E-01	8.E-01	3.E-01	+	2.E-02	1.E-01	4	107027621	NPNT	flanking_5UTR	a	g	A	A
rs11933466	1.E+00	+	5.E-01	4.E-01	5.E-01	++	9.E-01	3.E-01	3.E-01	+	2.E-01	8.E-01	4	107032181	NPNT	flanking_5UTR	a	g	G	G
rs10470990	4.E-03	++	2.E-02	7.E-02	4.E-02	++	2.E-01	9.E-02	3.E-02	++	4.E-02	4.E-01	4	107041027	NPNT	intron	t	c	T	T
rs4600917	6.E-01	+	9.E-01	3.E-01	3.E-01	-	7.E-01	2.E-01	7.E-01	+	6.E-01	9.E-01	4	107049094	NPNT	intron	t	c	T	T
rs4340795	4.E-01	+	1.E-01	5.E-01	3.E-01	++	2.E-01	8.E-01	8.E-01	+	2.E-01	2.E-01	4	107081179	NPNT	coding	a	g	A	A
rs4074127	3.E-01	+	1.E-01	7.E-01	2.E-01	++	2.E-01	7.E-01	6.E-01	+	2.E-01	3.E-01	4	107086429	NPNT	intron	a	g	A	A
rs6817700	4.E-01	+	1.E+00	2.E-01	5.E-01	++	5.E-01	7.E-01	5.E-01	+	5.E-01	7.E-02	4	107110980	NPNT	3UTR	a	g	G	G
rs7691244	3.E-01	++	8.E-01	2.E-01	4.E-01	++	8.E-01	3.E-01	5.E-01	++	1.E+00	3.E-01	4	107120677	NPNT	flanking_3UTR	a	g	G	G
rs13125117	3.E-01	-	5.E-01	4.E-01	3.E-01	-	5.E-01	4.E-01	7.E-01	+	1.E+00	6.E-01	4	107129147	NPNT	flanking_3UTR	t	c	T	T
rs2156507	1.E-01	++	5.E-01	1.E-01	7.E-01	+	3.E-01	6.E-01	2.E-01	+	1.E+00	2.E-02	4	107133446	NPNT	flanking_3UTR	a	g	G	G
rs11730681	1.E-01	++	4.E-01	2.E-01	5.E-02	++	5.E-02	5.E-01	1.E+00	+	4.E-01	3.E-01	4	107142409	NPNT	flanking_3UTR	a	g	G	G

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
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rs3995090	5.E-01	+	3.E-01	9.E-01	1.E+00	+	7.E-01	6.E-01	2.E-01	+	1.E-01	9.E-01	5	147826008	HTR4	intron	a	c	C	C
rs7723153	9.E-01	+	5.E-01	5.E-01	8.E-01	+	7.E-01	8.E-01	7.E-01	++	8.E-01	8.E-01	5	147857917	HTR4	intron	a	g	G	G
rs1368384	6.E-01	+	4.E-01	8.E-01	1.E-01	-	5.E-01	9.E-02	2.E-01	+	1.E-01	8.E-01	5	147875141	HTR4	intron	t	c	C	C
rs1368386	8.E-01	+	5.E-01	2.E-01	9.E-01	+	8.E-01	6.E-01	7.E-01	++	7.E-01	1.E+00	5	147875331	HTR4	intron	t	g	G	G
rs2277049	1.E+00	+	4.E-01	3.E-01	1.E+00	+	9.E-01	8.E-01	5.E-01	+	2.E-01	6.E-01	5	147883281	HTR4	intron	a	c	A	A
rs12152801	6.E-01	-	8.E-01	5.E-01	4.E-01	-	4.E-01	9.E-01	9.E-01	+	5.E-01	3.E-01	5	147888538	HTR4	intron	t	g	G	G
rs2278392	5.E-01	+	5.E-01	5.E-01	9.E-01	++	9.E-01	8.E-01	7.E-01	+	3.E-01	4.E-01	5	147908418	HTR4	intron	a	g	A	A
rs1345697	5.E-01	++	6.E-01	6.E-01	9.E-02	++	3.E-01	2.E-01	7.E-01	-	9.E-01	7.E-01	5	147922431	HTR4	intron	a	g	A	A
rs4599527	5.E-01	++	1.E+00	3.E-01	7.E-01	++	6.E-01	2.E-01	3.E-01	++	2.E-01	9.E-01	5	147932732	HTR4	intron	t	c	C	C
rs867522	6.E-01	-	7.E-01	8.E-01	4.E-01	-	6.E-01	5.E-01	8.E-01	++	8.E-01	8.E-01	5	147946439	HTR4	intron	a	g	A	A
rs1833710	6.E-01	+	5.E-01	1.E+00	1.E+00	+	9.E-01	9.E-01	2.E-01	-	2.E-01	8.E-01	5	147947939	HTR4	intron	t	c	C	C
rs2964276	6.E-01	+	3.E-01	7.E-01	5.E-01	+	3.E-01	8.E-01	8.E-01	+	4.E-01	5.E-01	5	147959171	HTR4	intron	t	c	T	T
rs7711800	6.E-01	++	1.E+00	4.E-01	9.E-01	+	7.E-01	7.E-01	4.E-01	++	8.E-01	3.E-01	5	147963048	HTR4	intron	t	c	C	C
rs1011427	2.E-01	-	9.E-01	9.E-02	2.E-01	-	6.E-01	2.E-01	6.E-01	+	8.E-01	2.E-01	5	147968170	HTR4	intron	t	c	T	T
rs13182913	9.E-01	+	8.E-01	6.E-01	6.E-01	+	4.E-01	7.E-01	7.E-01	-	7.E-01	8.E-01	5	147975798	HTR4	intron	t	c	C	C
rs2068190	6.E-01	+	4.E-01	1.E+00	3.E-01	-	3.E-01	6.E-01	2.E-01	+	2.E-02	4.E-01	5	147987206	HTR4	intron	t	c	C	C
rs5028114	6.E-01	+	7.E-01	2.E-01	3.E-01	++	4.E-01	6.E-01	7.E-01	+	4.E-01	8.E-02	5	147991932	HTR4	intron	t	c	T	T
rs888961	6.E-01	+	3.E-01	7.E-01	5.E-01	-	4.E-01	1.E+00	9.E-01	+	8.E-01	6.E-01	5	148019090	HTR4	flanking_5UTR	t	g	T	T
rs4425495	8.E-01	++	1.E+00	8.E-01	7.E-02	++	2.E-01	2.E-01	4.E-01	+	3.E-01	1.E+00	5	148041010	HTR4	flanking_5UTR	t	c	T	T
rs9325113	7.E-01	+	6.E-02	8.E-02	9.E-01	+	3.E-01	2.E-01	1.E+00	+	4.E-01	3.E-01	5	148078196	HTR4	flanking_5UTR	t	c	T	T
rs6580565	6.E-01	++	1.E+00	4.E-01	1.E-01	++	1.E-01	6.E-01	6.E-01	+	2.E-01	4.E-01	5	148078895	HTR4	flanking_5UTR	t	c	T	T
rs2400642	7.E-01	+	1.E+00	5.E-01	8.E-01	+	7.E-01	3.E-01	7.E-01	-	7.E-01	8.E-01	5	148094999	HTR4	flanking_5UTR	a	g	G	G

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
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rs1053924	6.E-01	+	2.E-01	5.E-01	5.E-01	-	5.E-01	8.E-01	5.E-01	+	2.E-01	6.E-01	6	32228693	PPT2	flanking_5UTR	a	g	A	A
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rs9267810	5.E-01	++	6.E-01	7.E-01	3.E-01	++	1.E+00	1.E-01	6.E-01	+-	4.E-01	7.E-02	6	32229572	PPT2	intron	t	c	C	C
rs2269425	6.E-01	+-	2.E-01	4.E-01	7.E-01	+-	3.E-01	5.E-01	3.E-01	--	3.E-01	7.E-01	6	32231617	PPT2	intron	t	c	T	T
rs13134603	9.E-01	+-	2.E-01	2.E-01	8.E-01	--	8.E-01	9.E-01	8.E-01	+-	2.E-01	2.E-01	6	32233980	PPT2	intron	t	c	T	T
rs2269424	8.E-01	--	9.E-01	8.E-01	6.E-01	+-	9.E-01	3.E-01	6.E-01	+-	8.E-01	2.E-01	6	32240211	PPT2	flanking_3UTR	t	c	T	T
rs3096697	5.E-01	++	5.E-01	8.E-01	8.E-01	+-	7.E-01	9.E-01	7.E-01	+-	6.E-01	1.E+00	6	32242488	EGFL8	coding	t	c	T	T
rs13130347	4.E-01	--	5.E-01	6.E-01	9.E-01	+-	6.E-01	7.E-01	7.E-01	--	8.E-01	8.E-01	6	32242634	EGFL8	intron	t	c	C	C
rs13130283	5.E-01	+-	2.E-01	7.E-01	6.E-01	--	9.E-01	6.E-01	4.E-01	+-	2.E-01	6.E-01	6	32246523	AGPAT1	intron	a	c	A	A
rs13130284	6.E-01	--	6.E-01	8.E-01	8.E-01	+-	7.E-01	9.E-01	8.E-01	+-	7.E-01	1.E+00	6	32248465	AGPAT1	intron	t	c	C	C
rs2269423	9.E-01	+-	7.E-01	4.E-01	1.E+00	++	1.E+00	1.E+00	3.E-01	+-	2.E-01	9.E-01	6	32253685	AGPAT1	intron	t	g	T	T
rs13134945	6.E-01	++	6.E-01	8.E-01	8.E-01	+-	7.E-01	9.E-01	8.E-01	+-	7.E-01	1.E+00	6	32254470	RNF5	intron	t	g	T	T
rs13130349	8.E-01	--	9.E-01	8.E-01	6.E-01	+-	3.E-01	7.E-01	8.E-01	+-	4.E-01	5.E-01	6	32255674	RNF5	coding	a	g	A	A
rs13134943	6.E-01	+-	7.E-01	2.E-01	9.E-01	+-	9.E-01	1.E+00	5.E-01	+-	7.E-01	1.E-01	6	32255739	RNF5	intron	a	g	A	A
rs1035798	8.E-01	--	9.E-01	8.E-01	6.E-01	+-	9.E-01	3.E-01	6.E-01	+-	8.E-01	2.E-01	6	32259200	AGER	intron	t	c	T	T
rs2070600	7.E-02	++	1.E-01	4.E-01	5.E-01	+-	3.E-01	8.E-01	2.E-02	++	2.E-01	3.E-02	6	32259421	AGER	coding	a	g	A	A
rs1800624	9.E-01	--	9.E-01	9.E-01	6.E-01	+-	8.E-01	2.E-01	5.E-01	+-	7.E-01	1.E-01	6	32260365	PBX2	flanking_3UTR	a	t	A	A
rs204995	9.E-01	+-	8.E-01	5.E-01	7.E-01	+-	7.E-01	3.E-01	7.E-01	+-	3.E-01	5.E-01	6	32262263	PBX2	intron	t	c	C	C
rs204994	9.E-01	+-	2.E-01	2.E-01	9.E-01	+-	8.E-01	7.E-01	4.E-01	+-	9.E-02	4.E-01	6	32262976	PBX2	intron	a	g	A	A
rs204993	9.E-01	+-	2.E-01	2.E-01	1.E+00	+-	7.E-01	5.E-01	3.E-01	+-	5.E-02	5.E-01	6	32263559	PBX2	intron	t	c	C	C
rs176095	9.E-01	+-	3.E-01	2.E-01	8.E-01	0+	1.E+00	7.E-01	5.E-01	+-	8.E-02	3.E-01	6	32266297	GPSM3	flanking_3UTR	t	c	C	C
rs204991	9.E-01	+-	4.E-01	2.E-01	7.E-01	+-	8.E-01	3.E-01	6.E-01	+-	4.E-01	7.E-01	6	32269344	GPSM3	intron	a	g	G	G
rs204990	9.E-01	+-	2.E-01	2.E-01	8.E-01	+-	7.E-01	3.E-01	5.E-01	+-	3.E-01	7.E-01	6	32269408	GPSM3	intron	t	g	T	T
rs8192575	5.E-01	++	8.E-01	4.E-01	8.E-01	++	9.E-01	8.E-01	2.E-01	++	7.E-01	1.E-01	6	32274362	NOTCH4	intron	c	g	C	C
rs13134942	8.E-01	+-	6.E-01	3.E-01	6.E-01	--	6.E-01	9.E-01	1.E+00	+-	3.E-01	2.E-01	6	32276749	NOTCH4	coding	a	c	A	A
rs2071277	7.E-01	+-	5.E-01	1.E-01	6.E-01	+-	4.E-01	6.E-02	8.E-01	+-	8.E-01	5.E-01	6	32279661	NOTCH4	intron	a	g	G	G
rs13131296	8.E-01	+-	6.E-01	3.E-01	6.E-01	--	6.E-01	9.E-01	1.E+00	+-	3.E-01	2.E-01	6	32280971	NOTCH4	intron	a	g	A	A
rs13130292	5.E-01	--	6.E-01	7.E-01	2.E-01	--	3.E-01	4.E-01	8.E-01	+-	7.E-01	9.E-01	6	32284186	NOTCH4	intron	c	g	C	C
rs206017	1.E+00	+-	1.E-01	6.E-02	8.E-01	+-	1.E-01	2.E-02	8.E-01	+-	5.E-01	7.E-01	6	32284189	NOTCH4	intron	a	g	G	G
rs13132942	9.E-01	+-	1.E-01	4.E-02	8.E-01	+-	2.E-01	4.E-02	9.E-01	+-	5.E-01	2.E-01	6	32284490	NOTCH4	intron	a	g	A	A
rs9267833	9.E-01	+-	3.E-01	3.E-01	7.E-01	+-	1.E-01	2.E-01	1.E+00	+-	8.E-01	7.E-01	6	32285878	NOTCH4	intron	t	c	C	C
rs2071286	6.E-01	+-	9.E-01	4.E-01	8.E-01	+-	6.E-01	2.E-01	9.E-01	+-	8.E-01	6.E-01	6	32287874	NOTCH4	intron	a	g	A	A
rs206019	7.E-01	+-	3.E-01	5.E-01	6.E-01	+-	2.E-01	4.E-01	6.E-01	++	7.E-01	7.E-01	6	32288219	NOTCH4	intron	t	c	T	T
rs206015	5.E-01	+-	2.E-01	5.E-01	6.E-01	+-	1.E-01	2.E-01	5.E-01	++	6.E-01	6.E-01	6	32290737	NOTCH4	intron	t	c	T	T
rs404860	4.E-01	+-	7.E-02	4.E-01	6.E-01	+-	2.E-01	3.E-01	5.E-01	--	4.E-01	9.E-01	6	32292323	NOTCH4	intron	t	c	C	C
rs2854050	5.E-01	++	8.E-01	4.E-01	8.E-01	++	9.E-01	8.E-01	2.E-01	++	7.E-01	1.E-01	6	32293583	NOTCH4	intron	t	c	T	T
rs394657	4.E-01	+-	9.E-01	1.E-01	5.E-01	+-	6.E-01	7.E-02	7.E-01	+-	8.E-01	4.E-01	6	32295001	NOTCH4	intron	a	g	G	G
rs1109771	7.E-01	+-	3.E-01	6.E-02	4.E-02	++	1.E+00	1.E-03	2.E-01	--	2.E-01	7.E-01	6	32295583	NOTCH4	intron	a	g	G	G
rs422951	9.E-01	+-	4.E-01	2.E-01	7.E-01	+-	5.E-01	1.E-01	7.E-01	+-	3.E-01	5.E-01	6	32296361	NOTCH4	coding	a	g	G	G
rs13132946	9.E-01	+-	9.E-01	7.E-01	1.E+00	+-	9.E-01	9.E-01	7.E-01	+-	6.E-01	9.E-01	6	32298006	NOTCH4	intron	a	g	A	A
rs443198	5.E-01	+-	3.E-01	2.E-02	8.E-01	+-	5.E-01	3.E-01	1.E+00	+-	2.E-01	1.E-01	6	32298384	NOTCH4	coding	t	c	C	C
rs13134931	2.E-01	+-	2.E-02	4.E-01	3.E-01	--	3.E-01	8.E-01	1.E-01	+-	2.E-02	6.E-01	6	32298598	NOTCH4	intron	a	g	G	G
rs434841	2.E-01	--	3.E-01	3.E-01	3.E-02	--	3.E-01	3.E-02	8.E-01	+-	5.E-01	8.E-01	6	32299019	NOTCH4	intron	a	g	A	A
rs3830041	6.E-01	--	8.E-01	7.E-01	1.E+00	+-	7.E-01	6.E-01	3.E-01	--	4.E-01	7.E-01	6	32299317	NOTCH4	intron	a	g	A	A
rs479536	1.E-01	++	1.E-01	7.E-01	5.E-02	++	4.E-02	6.E-01	3.E-01	++	5.E-01	5.E-01	6	32301656	NOTCH4	flanking_5UTR	t	c	T	T
rs9267845	9.E-01	+-	8.E-01	9.E-01	9.E-01	+-	8.E-01	1.E+00	1.E+00	+-	8.E-01	9.E-01	6	32301676	NOTCH4	flanking_5UTR	a	t	A	A
rs499691	9.E-01	--	9.E-01	9.E-01	8.E-01	--	8.E-01	9.E-01	8.E-01	--	9.E-01	8.E-01	6	32302317	NOTCH4	flanking_5UTR	t	c	T	T
rs483574	6.E-01	+-	5.E-01	9.E-01	4.E-01	++	4.E-01	8.E-01	6.E-01	++	6.E-01	1.E+00	6	32302934	NOTCH4	flanking_5UTR	t	c	T	T
rs482759	7.E-01	+-	5.E-01	9.E-01	5.E-01	--	4.E-01	9.E-01	7.E-01	+-	6.E-01	1.E+00	6	32302995	NOTCH4	flanking_5UTR	t	c	C	C
rs532385	7.E-01	+-	6.E-01	9.E-01	1.E+00	+-	7.E-01	7.E-01	6.E-01	--	8.E-01	6.E-01	6	32303337	NOTCH4	flanking_5UTR	t	c	T	T
rs9378123	4.E-01	+-	2.E-01	7.E-01	6.E-01	+-	2.E-01	4.E-01	6.E-01	++	9.E-01	5.E-01	6	32304842	NOTCH4	flanking_5UTR	a	g	G	G
rs1426713	4.E-01	+-	4.E-01	2.E-02	8.E-01	+-	1.E-01	1.E-01	2.E-01	++	5.E-01	3.E-01	6	32306027	NOTCH4	flanking_5UTR	a	g	A	A
rs404890	6.E-01	+-	4.E-01	1.E+00	9.E-01	+-	9.E-01	7.E-01	4.E-01	++	3.E-01	9.E-01	6	32306845	NOTCH4	flanking_5UTR	t	g	T	T
rs2849015	2.E-01	+-	1.E-01	9.E-01	7.E-01	+-	3.E-01	4.E-01	4.E-01	++	3.E-01	8.E-01	6	32306914	NOTCH4	flanking_5UTR	a	g	A	A
rs9267873	8.E-01	+-	8.E-01	4.E-01	6.E-01	++	9.E-01	6.E-01	9.E-02	+-	1.E+00	6.E-03	6	32307330	NOTCH4	flanking_5UTR	t	c	C	C
rs6926346	3.E-01	++	3.E-01	7.E-01	5.E-01	+-	3.E-01	8.E-01	5.E-01	+-	9.E-01	4.E-01	6	32308732	NOTCH4	flanking_5UTR	t	c	T	T
rs12182351	5.E-01	--	8.E-01	4.E-01	7.E-01	--	7.E-01	9.E-01	3.E-01	--	9.E-01	2.E-01	6	32309685	NOTCH4	flanking_5UTR	t	c	C	C
rs9501398	9.E-01	+-	2.E-01	2.E-01	4.E-01	+-	6.E-02	3.E-01	6.E-01	++	6.E-01	8.E-01	6	32310575	NOTCH4	flanking_5UTR	t	g	T	T

rs3130299	5.E-01	-	8.E-01	4.E-01	7.E-01	-	7.E-01	9.E-01	3.E-01	-	9.E-01	2.E-01	6	32311515	NOTCH4	flanking_5UTR	a	g	G	G
rs693797	4.E-01	+	2.E-01	9.E-01	9.E-01	++	8.E-01	5.E-01	3.E-01	-	2.E-01	1.E+00	6	32312411	NOTCH4	flanking_5UTR	a	g	G	G
rs6906128	7.E-01	-	8.E-01	7.E-01	7.E-01	++	9.E-01	4.E-01	3.E-01	-	9.E-01	1.E-01	6	32314282	NOTCH4	flanking_5UTR	a	c	C	C
rs511027	1.E+00	+	8.E-01	7.E-01	6.E-01	-	9.E-01	6.E-01	4.E-01	++	9.E-01	3.E-01	6	32314665	NOTCH4	flanking_5UTR	a	t	A	A

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs6494904	2.E-02	++	2.E-02	4.E-01	1.E-01	++	1.E-01	6.E-01	7.E-02	++	1.E-01	4.E-01	15	69396576	THSD4	flanking_5UTR	a	g	A	A
rs11855237	5.E-01	+	4.E-01	1.E+00	6.E-01	-	5.E-01	9.E-01	9.E-01	+	8.E-01	9.E-01	15	69404788	THSD4	flanking_5UTR	a	g	A	A
rs11856837	4.E-03	++	2.E-02	9.E-02	9.E-03	++	2.E-02	2.E-01	2.E-01	++	4.E-01	3.E-01	15	69408616	THSD4	flanking_5UTR	t	c	C	C
rs11637373	6.E-01	+	2.E-01	6.E-01	3.E-01	++	8.E-01	2.E-01	5.E-02	-	4.E-02	6.E-01	15	69418080	THSD4	flanking_5UTR	a	g	G	G
rs1441356	8.E-01	+	9.E-01	5.E-01	5.E-01	+	2.E-01	6.E-01	2.E-01	-	5.E-01	2.E-01	15	69418227	THSD4	flanking_5UTR	t	c	T	T
rs2028467	7.E-01	+	6.E-01	2.E-01	6.E-01	+	2.E-01	4.E-01	1.E-01	++	4.E-01	2.E-01	15	69424902	THSD4	flanking_5UTR	t	c	T	T
rs4777372	5.E-01	+	5.E-01	5.E-02	5.E-01	+	8.E-01	2.E-01	9.E-01	+	4.E-01	4.E-01	15	69430841	THSD4	flanking_5UTR	t	c	C	C
rs1913768	6.E-01	+	3.E-01	8.E-01	4.E-01	-	4.E-01	7.E-01	4.E-01	-	5.E-01	6.E-01	15	69436598	THSD4	flanking_5UTR	a	g	A	A
rs1866920	2.E-01	-	3.E-01	4.E-01	7.E-01	++	8.E-01	8.E-01	2.E-02	-	7.E-02	2.E-01	15	69443763	THSD4	flanking_5UTR	a	g	G	G
rs2028465	2.E-01	-	2.E-01	9.E-01	6.E-01	-	5.E-01	9.E-01	2.E-01	-	2.E-01	5.E-01	15	69446412	THSD4	flanking_5UTR	a	c	C	C
rs1561711	2.E-01	++	3.E-01	3.E-01	8.E-01	-	1.E+00	7.E-01	6.E-02	++	2.E-01	2.E-01	15	69453220	THSD4	flanking_5UTR	t	c	T	C
rs1568010	5.E-01	++	8.E-01	5.E-01	4.E-01	-	3.E-01	9.E-01	1.E-02	++	9.E-02	5.E-02	15	69455566	THSD4	flanking_5UTR	a	c	C	C
rs4777376	3.E-01	+	1.E-01	7.E-01	8.E-01	+	4.E-01	5.E-01	2.E-01	++	1.E-01	7.E-01	15	69459899	THSD4	flanking_5UTR	t	c	T	T
rs1441355	7.E-01	+	2.E-01	3.E-01	2.E-01	-	1.E-01	1.E+00	7.E-01	++	9.E-01	4.E-01	15	69465232	THSD4	flanking_5UTR	t	c	T	T
rs10518959	8.E-01	+	8.E-02	7.E-02	8.E-01	+	3.E-02	2.E-02	6.E-01	+	8.E-01	3.E-01	15	69477995	THSD4	flanking_5UTR	t	c	T	T
rs7165378	3.E-01	++	3.E-01	7.E-01	4.E-01	+	2.E-01	7.E-01	4.E-01	++	5.E-01	7.E-01	15	69478558	THSD4	flanking_5UTR	t	c	T	T
rs1837763	9.E-01	+	7.E-01	5.E-01	9.E-01	+	6.E-01	7.E-01	5.E-01	+	2.E-01	7.E-01	15	69494429	THSD4	flanking_5UTR	a	g	G	G
rs920547	4.E-01	+	1.E+00	2.E-01	3.E-01	-	7.E-01	2.E-01	9.E-01	+	9.E-01	7.E-01	15	69505833	THSD4	flanking_5UTR	t	c	T	T
rs8027920	7.E-01	+	8.E-01	3.E-01	7.E-01	+	9.E-01	4.E-01	7.E-01	+	9.E-01	4.E-01	15	69515583	THSD4	flanking_5UTR	a	g	A	A
rs751998	9.E-01	+	1.E-01	1.E-01	4.E-01	+	6.E-02	3.E-01	7.E-01	+	1.E+00	5.E-01	15	69524430	THSD4	flanking_5UTR	t	c	T	T
rs4777391	6.E-02	++	4.E-01	4.E-02	1.E-01	++	2.E-01	3.E-01	4.E-01	+	9.E-01	1.E-01	15	69529460	THSD4	flanking_5UTR	a	c	A	A
rs4332701	8.E-01	++	8.E-01	9.E-01	1.E+00	+-	9.E-01	9.E-01	5.E-01	++	5.E-01	8.E-01	15	69539513	THSD4	flanking_5UTR	a	g	G	G
rs12907251	8.E-01	-	1.E+00	7.E-01	1.E+00	+-	9.E-01	9.E-01	7.E-01	-	7.E-01	9.E-01	15	69546460	THSD4	flanking_5UTR	a	g	A	A
rs4414447	6.E-01	+	9.E-01	3.E-01	1.E+00	++	7.E-01	6.E-01	1.E-01	++	6.E-01	6.E-02	15	69564568	THSD4	flanking_5UTR	t	c	T	T
rs7164165	9.E-01	+	1.E+00	9.E-01	9.E-01	+-	5.E-01	5.E-01	9.E-01	+	4.E-01	4.E-01	15	69571590	THSD4	flanking_5UTR	t	g	G	G
rs4132884	8.E-01	+	7.E-01	4.E-01	1.E+00	+-	9.E-01	8.E-01	8.E-01	+-	3.E-01	3.E-01	15	69588095	THSD4	flanking_5UTR	t	c	T	T
rs6494940	1.E-02	-	7.E-02	9.E-02	3.E-01	-	7.E-01	3.E-01	1.E-03	-	4.E-02	7.E-03	15	69592172	THSD4	flanking_5UTR	a	g	G	G
rs4357892	1.E+00	+	5.E-01	5.E-01	8.E-01	-	1.E+00	7.E-01	9.E-01	+	3.E-01	2.E-01	15	69609351	THSD4	flanking_5UTR	a	c	A	A
rs4482234	4.E-01	+	9.E-01	2.E-01	8.E-01	+-	6.E-01	3.E-01	8.E-01	+	1.E+00	7.E-01	15	69610822	THSD4	flanking_5UTR	a	g	A	A
rs4777408	8.E-01	+	1.E+00	6.E-01	1.E+00	-	1.E+00	1.E+00	7.E-01	+	7.E-01	2.E-01	15	69621046	THSD4	flanking_5UTR	a	g	A	A
rs4777409	1.E+00	+	9.E-01	9.E-01	6.E-01	+-	6.E-01	1.E-01	3.E-01	+-	8.E-01	6.E-02	15	69623478	THSD4	flanking_5UTR	t	g	T	T
rs6494947	5.E-01	+	2.E-01	4.E-01	8.E-01	+-	3.E-01	4.E-01	6.E-01	++	4.E-01	8.E-01	15	69630134	THSD4	flanking_5UTR	t	c	T	T
rs4447378	2.E-01	++	3.E-01	4.E-01	9.E-01	+-	1.E+00	8.E-01	2.E-01	++	4.E-01	4.E-01	15	69634381	THSD4	flanking_5UTR	a	g	A	A
rs8040598	9.E-01	+	7.E-01	5.E-01	8.E-01	+-	9.E-01	6.E-01	9.E-01	+-	6.E-01	7.E-01	15	69644422	THSD4	flanking_5UTR	a	g	G	G
rs8042355	5.E-01	-	9.E-01	3.E-01	8.E-01	+-	6.E-01	3.E-01	3.E-01	+	2.E-01	1.E+00	15	69647900	THSD4	flanking_5UTR	a	g	G	G
rs3923493	6.E-01	+	5.E-01	1.E-01	9.E-01	+-	3.E-01	1.E-01	1.E+00	+-	1.E+00	9.E-01	15	69653686	THSD4	flanking_5UTR	a	g	A	A
rs3923492	9.E-01	+	2.E-01	7.E-02	1.E+00	+-	1.E-01	4.E-02	9.E-01	-	1.E+00	9.E-01	15	69653762	THSD4	flanking_5UTR	t	c	C	C
rs4321149	7.E-01	+	8.E-01	3.E-01	6.E-01	+-	7.E-01	1.E-01	5.E-01	++	5.E-01	1.E+00	15	69656526	THSD4	flanking_5UTR	a	g	A	A
rs4459504	6.E-01	+	7.E-01	2.E-01	7.E-01	+-	8.E-01	3.E-01	8.E-01	-	9.E-01	8.E-01	15	69670984	THSD4	flanking_5UTR	a	g	G	G
rs4777414	6.E-01	++	8.E-01	8.E-01	8.E-01	+-	9.E-01	5.E-01	2.E-01	++	4.E-01	5.E-01	15	69675927	THSD4	flanking_5UTR	t	c	C	C
rs4398066	3.E-01	+-	6.E-02	5.E-01	6.E-01	++	5.E-01	9.E-01	1.E-01	+	2.E-02	7.E-01	15	69679269	THSD4	flanking_5UTR	a	g	G	G
rs4349100	1.E+00	+	6.E-01	5.E-01	7.E-01	+-	8.E-01	3.E-01	6.E-01	+-	5.E-01	9.E-01	15	69684923	THSD4	flanking_5UTR	a	g	A	G
rs4430697	6.E-01	+-	4.E-01	8.E-01	1.E+00	+-	8.E-01	8.E-01	4.E-01	+-	2.E-01	8.E-01	15	69685390	THSD4	flanking_5UTR	a	g	G	G

rs4354882	8.E-01	+	8.E-01	6.E-01	8.E-01	+	5.E-01	2.E-01	6.E-01	++	1.E+00	4.E-01	15	69688282	THSD4	flanking_5UTR	a	g	G	G
rs13379548	6.E-01	+	8.E-01	3.E-01	7.E-01	+	1.E+00	6.E-01	7.E-02	++	7.E-01	2.E-02	15	69689719	THSD4	flanking_5UTR	t	c	C	C
rs11858418	8.E-04	-	3.E-02	5.E-02	-	-	8.E-02	3.E-01	2.E-02	++	3.E-01	2.E-02	15	69691889	THSD4	flanking_5UTR	a	g	G	G
rs1501429	4.E-01	-	3.E-01	9.E-01	3.E-01	-	6.E-01	3.E-01	5.E-01	+	3.E-01	7.E-01	15	69692566	THSD4	flanking_5UTR	a	g	A	A
rs1983033	1.E+00	+	7.E-01	7.E-01	9.E-01	+	6.E-01	5.E-01	5.E-01	+	6.E-01	6.E-02	15	69696544	THSD4	flanking_5UTR	t	g	T	T
rs7182578	7.E-01	+	8.E-01	3.E-01	8.E-01	+	4.E-01	6.E-01	6.E-01	++	7.E-01	8.E-01	15	69699005	THSD4	flanking_5UTR	t	c	C	C
rs985868	1.E+00	+	8.E-01	7.E-01	7.E-01	+	4.E-01	8.E-02	5.E-01	+	7.E-01	1.E-01	15	69702332	THSD4	flanking_5UTR	t	c	C	C
rs7167646	7.E-01	+	9.E-01	5.E-01	4.E-01	+	5.E-01	2.E-02	8.E-01	+	6.E-01	3.E-01	15	69707213	THSD4	flanking_5UTR	a	c	C	C
rs950667	3.E-01	++	6.E-01	3.E-01	8.E-01	+	7.E-01	1.E+00	7.E-02	++	3.E-01	1.E-01	15	69708689	THSD4	flanking_5UTR	t	c	T	T
rs1392989	4.E-01	++	6.E-01	4.E-01	2.E-01	++	6.E-01	2.E-01	1.E+00	+	8.E-01	7.E-01	15	69708797	THSD4	flanking_5UTR	a	c	C	C
rs950668	5.E-01	+	9.E-01	2.E-01	6.E-01	+	9.E-01	3.E-01	1.E+00	+	1.E+00	9.E-01	15	69708893	THSD4	flanking_5UTR	a	g	A	A
rs2279787	9.E-02	-	6.E-01	4.E-02	3.E-01	-	8.E-01	2.E-01	3.E-02	+	4.E-01	2.E-02	15	69714177	THSD4	flanking_5UTR	a	c	C	C
rs1995336	4.E-01	-	5.E-01	6.E-01	2.E-02	-	3.E-01	2.E-02	4.E-01	++	8.E-01	3.E-01	15	69736380	THSD4	flanking_5UTR	a	g	G	G
rs8036118	1.E+00	++	1.E+00	1.E+00	7.E-02	++	3.E-01	1.E-01	7.E-02	-	4.E-01	6.E-02	15	69747631	THSD4	flanking_5UTR	a	g	A	A
rs931728	9.E-01	+	8.E-01	8.E-01	2.E-01	-	8.E-01	5.E-02	1.E-01	++	4.E-01	1.E-01	15	69754600	THSD4	flanking_5UTR	t	c	C	C
rs8026748	9.E-01	++	9.E-01	1.E+00	1.E-01	++	5.E-01	1.E-01	1.E-01	+	6.E-01	4.E-02	15	69757818	THSD4	flanking_5UTR	a	g	A	A
rs8033100	6.E-01	-	9.E-01	4.E-01	2.E-01	-	6.E-01	1.E-01	8.E-01	+	5.E-01	2.E-01	15	69764500	THSD4	flanking_5UTR	t	c	C	C
rs8027960	4.E-01	-	8.E-01	3.E-01	2.E-02	-	4.E-01	8.E-03	5.E-01	++	5.E-01	8.E-01	15	69780809	THSD4	flanking_5UTR	t	c	T	T
rs872471	8.E-01	+	8.E-01	5.E-01	2.E-01	-	2.E-01	7.E-01	7.E-02	++	3.E-01	1.E-01	15	69785119	THSD4	flanking_5UTR	a	g	G	G
rs12591953	9.E-01	+	7.E-01	6.E-01	4.E-01	++	6.E-01	5.E-01	3.E-01	-	2.E-01	9.E-01	15	69787332	THSD4	flanking_5UTR	a	g	G	G
rs8033309	5.E-01	+	8.E-01	1.E-01	6.E-01	+	2.E-01	4.E-01	9.E-02	-	4.E-01	1.E-01	15	69797752	THSD4	flanking_5UTR	a	g	A	A
rs8041918	7.E-01	+	8.E-01	4.E-01	9.E-01	+	5.E-01	5.E-01	3.E-01	-	7.E-01	3.E-01	15	69806558	THSD4	flanking_5UTR	t	c	C	C
rs4777451	9.E-01	+	7.E-01	8.E-01	3.E-01	-	3.E-01	6.E-01	4.E-01	++	4.E-01	7.E-01	15	69812229	THSD4	intron	t	c	T	T
rs11072323	5.E-01	+	9.E-01	2.E-01	9.E-01	+	6.E-01	7.E-01	7.E-01	+	8.E-01	7.E-01	15	69813033	THSD4	intron	t	c	T	T
rs1472587	9.E-01	+	4.E-01	3.E-01	1.E+00	++	9.E-01	1.E+00	7.E-01	+	3.E-01	3.E-02	15	69828335	THSD4	intron	a	g	A	A
rs1564693	2.E-01	-	2.E-01	7.E-01	9.E-01	++	5.E-01	3.E-01	1.E-01	+	3.E-01	3.E-01	15	69847103	THSD4	intron	t	c	C	C
rs3825804	3.E-01	++	4.E-01	6.E-01	9.E-01	+	6.E-01	6.E-01	6.E-02	++	2.E-01	1.E-01	15	69857059	THSD4	3UTR	a	g	A	G
rs3743052	8.E-01	+	4.E-01	2.E-01	3.E-01	+	2.E-01	1.E+00	5.E-01	++	7.E-01	5.E-01	15	69862918	THSD4	flanking_3UTR	a	g	A	A
rs11639050	7.E-01	+	8.E-01	4.E-01	7.E-01	++	1.E+00	5.E-01	8.E-01	+	6.E-01	3.E-01	15	69868334	THSD4	flanking_3UTR	t	g	T	T
rs900542	1.E+00	+	8.E-01	8.E-01	2.E-01	-	5.E-01	3.E-01	7.E-01	++	8.E-01	8.E-01	15	69869678	THSD4	flanking_3UTR	a	g	A	A
rs11634405	5.E-01	+	3.E-01	8.E-01	6.E-01	+	3.E-01	5.E-01	4.E-01	+	5.E-01	6.E-01	15	69871747	THSD4	flanking_3UTR	a	g	G	G

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs1953319	1.E-01	+	9.E-01	1.E-02	2.E-01	+	6.E-01	5.E-03	4.E-01	+	4.E-01	7.E-01	6	142625119	GPR126	flanking_5UTR	t	c	C	C
rs1931989	3.E-01	+	7.E-02	5.E-01	5.E-02	+	4.E-03	6.E-01	5.E-01	+	6.E-01	6.E-01	6	142628271	GPR126	flanking_5UTR	a	g	G	G
rs9321861	6.E-02	+	8.E-03	8.E-01	4.E-02	++	3.E-02	6.E-01	2.E-01	+	6.E-02	6.E-01	6	142629017	GPR126	flanking_5UTR	a	c	C	C
rs2782535	4.E-01	+	3.E-01	2.E-02	8.E-01	+	1.E-01	2.E-02	4.E-01	++	5.E-01	6.E-01	6	142631783	GPR126	flanking_5UTR	t	c	T	T
rs1931991	3.E-01	-	3.E-01	6.E-01	1.E-01	-	3.E-01	2.E-01	1.E+00	+	8.E-01	7.E-01	6	142639061	GPR126	flanking_5UTR	a	c	C	C
rs6903707	7.E-01	+	7.E-01	3.E-01	3.E-01	-	8.E-01	2.E-01	7.E-01	+	3.E-01	6.E-01	6	142653680	GPR126	flanking_5UTR	a	g	A	A
rs9376685	1.E+00	+	8.E-01	7.E-01	1.E+00	+	7.E-01	6.E-01	9.E-01	+	7.E-01	7.E-01	6	142671524	GPR126	intron	t	c	T	T
rs9389983	5.E-01	+	1.E-01	4.E-01	2.E-01	-	1.E-01	9.E-01	5.E-01	+	2.E-01	6.E-01	6	142675437	GPR126	intron	t	c	T	T
rs12189801	2.E-01	+	8.E-01	1.E-01	4.E-01	-	7.E-01	4.E-01	5.E-01	-	1.E+00	3.E-01	6	142683299	GPR126	intron	t	c	C	C
rs6570507	9.E-01	+	7.E-01	4.E-01	8.E-01	+	6.E-01	7.E-01	9.E-01	+	7.E-01	6.E-01	6	142721265	GPR126	intron	a	g	G	G
rs11155242	7.E-01	+	1.E+00	5.E-01	7.E-01	+	9.E-01	4.E-01	9.E-01	-	1.E+00	8.E-01	6	142733242	GPR126	coding	a	c	C	C
rs9403384	3.E-01	++	8.E-01	1.E-01	6.E-01	+	8.E-01	3.E-01	4.E-01	++	1.E+00	2.E-01	6	142751294	GPR126	intron	a	c	A	A
rs3748069	3.E-01	-	8.E-01	2.E-01	4.E-02	-	3.E-01	7.E-02	4.E-01	++	4.E-01	9.E-01	6	142809326	GPR126	flanking_3UTR	a	g	A	A
rs7776356	4.E-01	-	4.E-01	8.E-01	5.E-01	-	6.E-01	7.E-01	9.E-01	+	8.E-01	7.E-01	6	142818722	GPR126	flanking_3UTR	a	g	G	G
rs9321871	3.E-01	-	9.E-01	1.E-01	2.E-01	-	4.E-01	2.E-01	1.E+00	+	8.E-01	7.E-01	6	142853625	GPR126	flanking_3UTR	t	c	C	C
rs171891	6.E-01	++	7.E-01	7.E-01	9.E-01	++	1.E+00	9.E-01	8.E-01	++	9.E-01	8.E-01	6	142892305	GPR126	flanking_3UTR	a	g	A	A

rs263174	4.E-01	+	5.E-01	6.E-01	5.E-01	+	8.E-01	4.E-01	5.E-01	+	4.E-01	9.E-01	6	142910792	GPR126	flanking_3UTR	t	c	C	C
rs839556	6.E-01	+	4.E-01	7.E-01	9.E-01	+	7.E-01	5.E-01	5.E-01	+	2.E-01	6.E-01	6	142913571	GPR126	flanking_3UTR	t	c	T	T
rs263114	3.E-01	+	1.E-01	7.E-01	7.E-01	+	6.E-01	1.E+00	2.E-01	+	5.E-02	8.E-01	6	142924648	GPR126	flanking_3UTR	a	g	G	A
rs263164	4.E-01	+	3.E-01	8.E-01	7.E-01	+	8.E-01	8.E-01	2.E-01	+	2.E-01	5.E-01	6	142938348	GPR126	flanking_3UTR	a	g	A	A
rs263156	4.E-01	+	5.E-01	6.E-01	6.E-01	+	8.E-01	5.E-01	5.E-01	+	4.E-01	1.E+00	6	142949208	GPR126	flanking_3UTR	t	g	G	G

SNP	Pmeta_FEVI	FEVI_meta_Direction	P_SARP_FEVI	P_CSGA_FEVI	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEVI/FVC	FEVI/FVC_meta_Direction	P_SARP_FEVI/FVC	P_CSGA_FEVI/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs2161396	8.E-01	+	7.E-01	9.E-01	2.E-01	+	3.E-01	4.E-01	9.E-01	+	7.E-01	9.E-01	5	156800802	ADAM19	flanking_3UTR	t	g	G	G
rs7714353	9.E-01	+	3.E-01	2.E-01	1.E+00	+	3.E-01	2.E-01	6.E-01	+	4.E-01	8.E-01	5	156803112	ADAM19	flanking_3UTR	t	c	T	T
rs11750519	6.E-01	+	1.E-01	3.E-01	4.E-01	+	7.E-01	7.E-02	1.E-01	+	4.E-02	7.E-01	5	156804994	ADAM19	flanking_3UTR	t	c	T	T
rs11951889	9.E-01	+	8.E-01	9.E-01	1.E-01	++	4.E-01	2.E-01	5.E-01	+	7.E-01	6.E-01	5	156809362	ADAM19	flanking_3UTR	t	c	T	T
rs1559144	8.E-01	+	2.E-01	3.E-01	9.E-01	+	3.E-01	2.E-01	4.E-01	+	2.E-01	7.E-01	5	156814431	ADAM19	flanking_3UTR	a	g	A	A
rs951958	6.E-01	+	9.E-01	4.E-01	6.E-01	++	6.E-01	9.E-01	5.E-01	+	8.E-01	5.E-01	5	156821675	ADAM19	flanking_3UTR	a	c	A	A
rs4704742	4.E-01	+	4.E-01	9.E-02	7.E-01	++	2.E-01	4.E-01	7.E-01	+	8.E-01	3.E-01	5	156823931	ADAM19	flanking_3UTR	t	c	C	C
rs6860507	6.E-01	+	4.E-01	9.E-02	7.E-01	++	2.E-01	4.E-01	7.E-01	+	8.E-01	3.E-01	5	156831268	ADAM19	flanking_3UTR	a	g	G	G
rs11134766	7.E-01	+	5.E-01	9.E-01	6.E-01	++	8.E-01	6.E-01	2.E-01	++	3.E-01	4.E-01	5	156840895	ADAM19	intron	a	g	A	A
rs10067096	1.E+00	+	2.E-01	1.E-01	8.E-01	++	9.E-02	9.E-03	8.E-01	+	7.E-01	1.E+00	5	156849918	ADAM19	coding	a	c	C	C
rs2287749	8.E-01	+	1.E+00	8.E-01	8.E-01	+	6.E-01	7.E-01	8.E-01	+	1.E+00	7.E-01	5	156851428	ADAM19	coding	t	c	T	T
rs1990950	8.E-01	+	8.E-01	9.E-01	2.E-01	++	3.E-01	3.E-01	3.E-01	+	3.E-01	5.E-01	5	156853334	ADAM19	intron	t	g	T	T
rs1990951	9.E-01	+	5.E-01	3.E-01	6.E-01	+	3.E-01	5.E-01	8.E-01	+	7.E-01	4.E-01	5	156853489	ADAM19	intron	t	c	T	T
rs2277027	8.E-01	+	7.E-01	1.E+00	4.E-01	++	6.E-01	5.E-01	4.E-01	+	5.E-01	5.E-01	5	156864954	ADAM19	intron	a	c	A	A
rs1422795	8.E-01	+	7.E-01	1.E+00	4.E-01	++	7.E-01	5.E-01	3.E-01	+	4.E-01	5.E-01	5	156868942	ADAM19	coding	a	g	A	A
rs1422794	1.E+00	+	9.E-01	8.E-01	7.E-01	++	8.E-01	3.E-01	1.E+00	+	1.E+00	9.E-01	5	156869127	ADAM19	intron	a	c	C	C
rs3734031	3.E-01	+	5.E-01	4.E-01	9.E-01	+	9.E-01	7.E-01	1.E-01	+	2.E-01	4.E-01	5	156873338	ADAM19	intron	a	g	G	G
rs3822696	8.E-01	+	9.E-01	9.E-01	5.E-01	+	8.E-01	4.E-01	7.E-01	++	1.E+00	6.E-01	5	156890319	ADAM19	intron	t	c	C	C
rs11746606	6.E-01	+	1.E+00	4.E-01	3.E-01	+	8.E-01	1.E-01	6.E-01	++	4.E-01	7.E-01	5	156895077	ADAM19	intron	t	c	T	T
rs6875485	3.E-01	++	6.E-01	4.E-01	4.E-01	+	7.E-01	5.E-01	2.E-01	++	3.E-01	3.E-01	5	156899173	ADAM19	intron	a	c	C	C
rs4461616	6.E-01	+	2.E-01	5.E-01	6.E-01	+	4.E-01	8.E-01	7.E-01	+	6.E-01	9.E-01	5	156914491	ADAM19	intron	t	g	G	G
rs11749965	1.E-01	++	2.E-01	2.E-01	8.E-01	+	7.E-01	4.E-01	8.E-02	++	2.E-01	2.E-01	5	156929992	ADAM19	intron	t	c	T	T
rs7719224	1.E-01	++	4.E-02	8.E-01	2.E-01	++	4.E-02	5.E-01	3.E-01	+	4.E-01	5.E-01	5	156931918	ADAM19	intron	t	c	T	T
rs6890282	5.E-02	++	2.E-01	2.E-01	9.E-01	+	7.E-01	8.E-01	6.E-02	++	2.E-01	2.E-01	5	156934313	ADAM19	intron	t	g	T	T
rs10476093	5.E-01	+	9.E-01	2.E-01	5.E-01	+	3.E-01	8.E-01	3.E-01	+	5.E-01	4.E-01	5	156939579	ADAM19	flanking_5UTR	a	c	A	A

SNP	Pmeta_FEVI	FEVI_meta_Direction	P_SARP_FEVI	P_CSGA_FEVI	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEVI/FVC	FEVI/FVC_meta_Direction	P_SARP_FEVI/FVC	P_CSGA_FEVI/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs2924936	9.E-01	+	4.E-01	4.E-01	8.E-01	+	8.E-01	9.E-01	7.E-01	+	1.E-01	2.E-01	4	89860537	FAM13A1	flanking_3UTR	a	g	A	A
rs13130	4.E-01	+	9.E-01	2.E-01	1.E+00	++	1.E+00	1.E+00	2.E-01	+	7.E-01	1.E-02	4	89867868	FAM13A1	3UTR	t	c	C	C
rs3017895	7.E-01	+	3.E-01	5.E-01	5.E-01	++	3.E-01	5.E-01	8.E-01	+	5.E-01	1.E-01	4	89868514	FAM13A1	3UTR	t	c	C	C
rs2972028	5.E-01	+	4.E-01	1.E+00	3.E-01	+	2.E-01	9.E-01	4.E-01	+	9.E-01	1.E-01	4	89874214	FAM13A1	intron	a	g	G	G
rs3775391	1.E+00	+	6.E-01	6.E-01	5.E-01	++	1.E+00	4.E-01	8.E-01	++	2.E-01	2.E-01	4	89884216	FAM13A1	intron	t	c	C	C
rs6855961	7.E-01	+	9.E-01	4.E-01	4.E-01	+	6.E-01	5.E-01	2.E-01	++	3.E-01	6.E-01	4	89886877	FAM13A1	intron	a	c	C	C
rs7657817	3.E-01	+	5.E-01	5.E-01	5.E-01	+	2.E-01	6.E-01	4.E-01	++	5.E-01	6.E-01	4	89887882	FAM13A1	coding	t	c	T	T

rs7662156	3.E-01	--	6.E-01	4.E-01	4.E-01	+-	2.E-01	8.E-01	4.E-01	++	4.E-01	7.E-01	4	89891828	FAM13A1	intron	t	c	T	T
rs1965869	6.E-01	+-	2.E-01	5.E-01	4.E-01	+-	9.E-02	4.E-01	3.E-01	++	6.E-01	3.E-01	4	89896560	FAM13A1	intron	t	c	T	T
rs1947379	9.E-01	+-	8.E-01	9.E-01	4.E-01	--	4.E-01	8.E-01	1.E-01	++	6.E-01	6.E-02	4	89908809	FAM13A1	intron	t	c	C	C
rs2290782	1.E+00	+-	8.E-01	7.E-01	8.E-01	+-	7.E-01	4.E-01	5.E-01	++	1.E+00	3.E-01	4	89930872	FAM13A1	intron	a	g	A	A
rs9991328	7.E-01	+-	5.E-01	8.E-01	8.E-01	+-	7.E-01	4.E-01	9.E-01	+-	6.E-01	3.E-01	4	89932144	FAM13A1	intron	t	c	C	C
rs7680994	8.E-01	+-	2.E-01	2.E-01	3.E-01	+-	2.E-01	8.E-01	1.E+00	+-	8.E-01	6.E-01	4	89937013	FAM13A1	intron	a	g	A	A
rs10516821	9.E-01	+-	8.E-01	9.E-01	2.E-01	--	3.E-01	6.E-01	4.E-02	++	5.E-02	4.E-01	4	89947002	FAM13A1	intron	t	c	C	C
rs2869950	5.E-01	+-	3.E-01	8.E-01	6.E-01	+-	5.E-01	9.E-01	1.E+00	+-	3.E-01	2.E-01	4	89961787	FAM13A1	intron	t	c	T	T
rs2305934	7.E-01	++	7.E-01	8.E-01	3.E-01	++	3.E-01	7.E-01	8.E-01	+-	6.E-01	8.E-01	4	89963265	FAM13A1	5UTR	t	c	C	C
rs10021465	2.E-01	++	5.E-01	2.E-01	1.E-02	++	7.E-02	7.E-02	3.E-01	--	2.E-01	9.E-01	4	89969384	FAM13A1	intron	a	g	G	G
rs1379935	2.E-02	--	2.E-02	4.E-01	4.E-01	--	5.E-01	6.E-01	1.E-01	+-	2.E-03	2.E-01	4	89970314	FAM13A1	intron	t	c	T	T
rs7660000	8.E-01	+-	4.E-01	5.E-01	3.E-01	+-	1.E-01	8.E-01	7.E-01	+-	1.E+00	5.E-01	4	89970881	FAM13A1	intron	t	c	T	T
rs11735482	4.E-02	--	5.E-01	2.E-02	1.E-01	+-	1.E+00	1.E-02	6.E-01	--	6.E-01	1.E+00	4	89995269	FAM13A1	intron	t	c	C	C
rs6830970	4.E-01	++	6.E-01	5.E-01	9.E-02	++	3.E-01	1.E-01	3.E-01	--	6.E-01	4.E-01	4	89996104	FAM13A1	intron	a	g	G	G
rs1979290	6.E-01	--	8.E-01	6.E-01	4.E-01	--	5.E-01	7.E-01	1.E-01	++	4.E-01	1.E-01	4	90008501	FAM13A1	intron	t	g	T	T
rs10049947	3.E-01	--	5.E-01	3.E-01	2.E-01	--	4.E-01	3.E-01	4.E-01	--	7.E-01	4.E-01	4	90009616	FAM13A1	intron	t	c	C	C
rs10516823	5.E-01	--	5.E-01	8.E-01	8.E-01	+-	6.E-01	2.E-01	1.E+00	+-	9.E-01	8.E-01	4	90016661	FAM13A1	intron	t	c	T	T
rs17816002	4.E-01	++	8.E-01	3.E-01	2.E-01	++	8.E-01	1.E-01	4.E-01	+-	9.E-01	2.E-01	4	90017977	FAM13A1	intron	a	c	A	A
rs1458562	2.E-01	+-	7.E-02	7.E-01	6.E-01	+-	6.E-01	1.E-01	2.E-01	++	2.E-01	7.E-01	4	90072621	FAM13A1	intron	a	g	G	G
rs1903009	9.E-01	+-	5.E-01	5.E-01	1.E-01	++	8.E-01	4.E-02	4.E-01	+-	2.E-01	1.E+00	4	90075300	FAM13A1	intron	a	g	A	A
rs2446309	1.E+00	+-	3.E-01	2.E-01	1.E-01	--	8.E-01	5.E-02	4.E-01	+-	2.E-01	7.E-01	4	90076175	FAM13A1	intron	t	c	C	C
rs987314	7.E-01	+-	4.E-01	1.E-01	5.E-02	++	7.E-01	8.E-03	5.E-01	+-	1.E-01	5.E-01	4	90081192	FAM13A1	intron	t	c	T	T
rs2869967	9.E-01	+-	2.E-01	2.E-01	3.E-01	+-	6.E-01	2.E-02	7.E-01	+-	4.E-01	6.E-01	4	90088355	FAM13A1	intron	t	c	T	T
rs1903003	8.E-01	+-	2.E-01	3.E-01	8.E-01	+-	8.E-01	5.E-01	8.E-01	+-	2.E-01	2.E-01	4	90105320	FAM13A1	intron	t	c	C	C
rs1921679	4.E-01	++	6.E-01	4.E-01	5.E-01	++	6.E-01	7.E-01	6.E-01	+-	6.E-01	9.E-01	4	90109807	FAM13A1	intron	t	c	T	T
rs11737182	5.E-01	++	8.E-01	4.E-01	4.E-01	++	5.E-01	6.E-01	3.E-01	--	3.E-01	8.E-01	4	90117499	FAM13A1	intron	t	c	T	T
rs1921681	5.E-01	+-	3.E-01	7.E-01	5.E-01	--	4.E-01	9.E-01	6.E-01	+-	4.E-01	8.E-01	4	90123147	FAM13A1	intron	t	c	C	C
rs7697075	6.E-01	++	6.E-01	8.E-01	6.E-01	++	6.E-01	9.E-01	9.E-01	+-	1.E+00	9.E-01	4	90127331	FAM13A1	intron	a	g	A	A
rs10516827	6.E-01	+-	4.E-01	8.E-01	9.E-01	+-	5.E-01	3.E-01	3.E-01	--	6.E-01	3.E-01	4	90137926	FAM13A1	intron	a	g	A	A
rs10516826	5.E-01	++	5.E-01	8.E-01	3.E-01	+-	1.E-01	6.E-01	2.E-01	+-	8.E-01	2.E-02	4	90137991	FAM13A1	intron	a	g	A	A
rs10516825	9.E-01	+-	8.E-01	1.E+00	4.E-01	++	9.E-01	2.E-01	2.E-01	--	9.E-01	9.E-02	4	90139105	FAM13A1	intron	t	g	T	T
rs6849143	4.E-01	--	8.E-01	4.E-01	4.E-01	--	8.E-01	2.E-01	6.E-01	--	7.E-01	6.E-01	4	90147512	FAM13A1	intron	t	c	C	C
rs2670620	2.E-01	--	1.E-01	1.E+00	4.E-01	+-	1.E-01	6.E-01	6.E-01	+-	5.E-01	9.E-01	4	90153229	FAM13A1	intron	t	c	T	T
rs1708661	3.E-01	--	2.E-01	1.E+00	6.E-01	+-	3.E-01	5.E-01	5.E-01	--	5.E-01	8.E-01	4	90157587	FAM13A1	intron	a	g	G	G
rs1795722	6.E-01	+-	4.E-01	7.E-01	4.E-01	++	4.E-01	9.E-01	4.E-01	++	6.E-01	5.E-01	4	90161886	FAM13A1	intron	a	g	G	G
rs1343921	6.E-01	+-	3.E-01	6.E-01	1.E-01	--	1.E-01	6.E-01	7.E-01	++	8.E-01	7.E-01	4	90166485	FAM13A1	intron	t	c	C	C
rs1533291	9.E-01	+-	9.E-01	7.E-01	2.E-01	++	5.E-01	3.E-01	5.E-01	--	5.E-01	9.E-01	4	90183479	FAM13A1	intron	a	g	G	G
rs2670626	8.E-01	+-	9.E-01	5.E-01	3.E-01	++	6.E-01	4.E-01	5.E-01	--	6.E-01	7.E-01	4	90186315	FAM13A1	intron	t	c	C	C
rs6826407	6.E-01	+-	2.E-01	5.E-01	6.E-02	--	1.E-01	3.E-01	4.E-01	++	1.E+00	2.E-01	4	90194056	FAM13A1	intron	t	c	C	C
rs756175	4.E-01	+-	2.E-01	6.E-01	9.E-01	+-	7.E-01	8.E-01	8.E-01	+-	2.E-01	2.E-01	4	90218064	FAM13A1	flanking_5UTR	a	g	A	A

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs357542	8.E-01	+-	8.E-01	4.E-01	5.E-01	++	5.E-01	7.E-01	3.E-01	++	1.E+00	8.E-02	9	97183463	PTCH	flanking_3UTR	a	g	A	A
rs7860361	3.E-01	+-	8.E-01	7.E-02	7.E-02	++	3.E-01	1.E-01	8.E-01	+-	5.E-02	4.E-02	9	97187625	PTCH	flanking_3UTR	t	c	T	T
rs357536	4.E-01	--	3.E-01	8.E-01	4.E-01	+-	7.E-01	6.E-02	5.E-02	--	8.E-02	3.E-01	9	97193095	PTCH	flanking_3UTR	a	g	A	G
rs357528	3.E-01	--	9.E-01	2.E-01	7.E-01	++	4.E-01	6.E-01	3.E-01	+-	9.E-01	5.E-02	9	97207403	PTCH	flanking_3UTR	a	c	A	A
rs357527	4.E-01	+-	9.E-01	1.E-01	9.E-01	+-	9.E-01	7.E-01	9.E-01	+-	6.E-01	4.E-01	9	97207632	PTCH	flanking_3UTR	t	c	T	T
rs7388704	4.E-01	--	8.E-01	4.E-01	1.E+00	+-	9.E-01	9.E-01	6.E-01	--	7.E-01	8.E-01	9	97211238	PTCH	flanking_3UTR	a	g	G	G
rs7389278	6.E-01	--	6.E-01	9.E-01	7.E-01	++	2.E-01	3.E-01	8.E-01	+-	6.E-01	3.E-01	9	97211906	PTCH	flanking_3UTR	t	c	T	C

rs357522	2.E-01	--	7.E-01	2.E-01	7.E-01	--	1.E+00	5.E-01	9.E-01	+	8.E-01	9.E-01	9	97229279	PTCH	flanking_3UTR	t	c	C	C
rs10512249	6.E-01	++	3.E-01	6.E-01	7.E-01	++	8.E-01	3.E-01	4.E-01	--	5.E-01	6.E-01	9	97296130	PTCH	intron	t	c	T	T
rs4448343	1.E-01	--	4.E-01	2.E-01	2.E-01	--	2.E-01	5.E-01	3.E-01	--	9.E-01	2.E-01	9	97306191	PTCH	intron	a	g	G	G
rs28536742	5.E-01	++	5.E-01	9.E-01	4.E-01	++	3.E-01	9.E-01	6.E-01	++	5.E-01	1.E+00	9	97322914	PTCH	flanking_5UTR	t	c	T	T
rs576594	4.E-02	++	7.E-02	3.E-01	3.E-02	++	2.E-01	7.E-02	9.E-01	+	7.E-01	7.E-01	9	97359032	PTCH	flanking_5UTR	t	c	T	T
rs7040739	2.E-01	++	2.E-01	5.E-01	2.E-01	++	4.E-01	3.E-01	1.E+00	+	7.E-01	7.E-01	9	97388706	PTCH	flanking_5UTR	t	g	G	G
rs1889616	4.E-01	--	7.E-01	4.E-01	6.E-01	+-	3.E-01	5.E-02	9.E-01	+-	3.E-01	2.E-01	9	97399009	PTCH	flanking_5UTR	t	c	C	C
rs1932075	4.E-01	--	4.E-01	7.E-01	2.E-01	--	6.E-01	1.E-01	7.E-01	+-	8.E-01	3.E-01	9	97399937	PTCH	flanking_5UTR	a	g	A	G
rs10818991	3.E-01	+-	2.E-01	1.E+00	4.E-02	--	2.E-02	7.E-01	2.E-01	++	2.E-01	7.E-01	9	97407538	PTCH	flanking_5UTR	t	c	C	C
rs1984119	3.E-01	--	7.E-01	2.E-01	4.E-01	--	7.E-01	4.E-01	6.E-01	+-	7.E-01	2.E-01	9	97408582	PTCH	flanking_5UTR	a	g	G	G
rs3824491	3.E-02	--	8.E-02	2.E-01	2.E-02	--	2.E-02	5.E-01	2.E-01	--	8.E-01	1.E-01	9	97408698	PTCH	flanking_5UTR	a	c	A	A
rs6478154	7.E-01	+-	3.E-01	6.E-01	1.E+00	+-	3.E-01	2.E-01	8.E-01	++	9.E-01	9.E-01	9	97411347	PTCH	flanking_5UTR	a	c	A	A
rs10988802	5.E-01	++	8.E-01	4.E-01	5.E-01	++	5.E-01	8.E-01	1.E+00	++	5.E-01	4.E-01	9	97416520	PTCH	flanking_5UTR	a	g	A	A
rs6478302	7.E-01	--	7.E-01	9.E-01	8.E-01	--	8.E-01	1.E+00	8.E-01	--	7.E-01	1.E+00	9	97432161	PTCH	flanking_5UTR	t	g	T	T
rs7854581	8.E-01	+-	6.E-01	8.E-01	1.E+00	+-	6.E-01	5.E-01	6.E-01	++	7.E-01	7.E-01	9	97433100	PTCH	flanking_5UTR	t	c	C	C
rs10989496	5.E-01	--	9.E-01	3.E-01	4.E-01	--	8.E-01	3.E-01	1.E+00	+-	9.E-01	8.E-01	9	97436827	PTCH	flanking_5UTR	a	g	A	A
rs10819953	3.E-01	+-	1.E-01	8.E-01	4.E-01	+-	7.E-02	3.E-01	4.E-01	++	5.E-01	6.E-01	9	97438777	PTCH	flanking_5UTR	a	g	G	G
rs4743125	4.E-02	++	6.E-02	3.E-01	2.E-02	+-	2.E-03	1.E+00	9.E-01	+-	7.E-01	4.E-01	9	97444324	PTCH	flanking_5UTR	t	c	C	C
rs9695781	7.E-01	+-	2.E-01	4.E-01	1.E+00	+-	3.E-01	1.E-01	8.E-01	++	9.E-01	9.E-01	9	97447347	PTCH	flanking_5UTR	a	c	C	C
rs10990303	3.E-01	--	2.E-01	8.E-01	6.E-01	+-	2.E-01	5.E-01	5.E-01	+-	9.E-01	3.E-01	9	97450226	PTCH	flanking_5UTR	t	c	T	T
rs10990568	9.E-01	+-	5.E-01	5.E-01	2.E-01	++	8.E-01	1.E-01	4.E-01	+-	6.E-01	3.E-02	9	97453958	PTCH	flanking_5UTR	a	g	A	A
rs10761011	7.E-01	+-	6.E-01	9.E-01	2.E-01	++	7.E-01	8.E-02	4.E-01	+	8.E-01	8.E-02	9	97463497	PTCH	flanking_5UTR	a	g	A	A
rs10991145	1.E+00	+-	1.E+00	9.E-01	5.E-01	++	6.E-01	7.E-01	3.E-01	--	6.E-01	3.E-01	9	97464363	PTCH	flanking_5UTR	a	g	A	A
rs4743148	5.E-02	++	9.E-02	3.E-01	3.E-02	++	6.E-02	3.E-01	1.E+00	+	7.E-01	7.E-01	9	97470395	PTCH	flanking_5UTR	a	g	G	G
rs700998	5.E-01	++	6.E-01	7.E-01	4.E-01	++	1.E+00	2.E-01	1.E+00	+	6.E-01	5.E-01	9	97475094	PTCH	flanking_5UTR	t	g	T	T
rs10978343	1.E-01	--	2.E-01	4.E-01	2.E-01	--	3.E-01	3.E-01	7.E-01	+-	4.E-01	7.E-01	9	97481707	PTCH	flanking_5UTR	t	c	T	T
rs915228	1.E-01	--	4.E-01	1.E-01	2.E-01	--	3.E-01	4.E-01	7.E-01	+-	8.E-01	3.E-01	9	97484124	PTCH	flanking_5UTR	a	g	G	G
rs817184	8.E-02	++	2.E-01	2.E-01	9.E-02	++	6.E-01	4.E-02	6.E-01	+-	5.E-01	9.E-01	9	97486993	PTCH	flanking_5UTR	a	c	A	A
rs4743181	1.E-02	--	9.E-02	6.E-02	3.E-01	--	4.E-01	5.E-01	8.E-02	--	2.E-01	3.E-01	9	97492614	PTCH	flanking_5UTR	a	g	G	G
rs10739231	9.E-01	+-	5.E-01	5.E-01	9.E-01	+-	8.E-01	1.E+00	9.E-01	+-	7.E-01	4.E-01	9	97493501	PTCH	flanking_5UTR	t	g	G	G

SNP	Pmeta_FEV1	FEV1_meta_Direction	P_SARP_FEV1	P_CSGA_FEV1	Pmeta_FVC	FVC_meta_Direction	P_SARP_FVC	P_CSGA_FVC	Pmeta_FEV1/FVC	FEV1/FVC_meta_Direction	P_SARP_FEV1/FVC	P_CSGA_FEV1/FVC	Chromosome	Coordinate	GeneSymbol	Location	meta_Allele1	meta_Allele2	SARP_A1	CSGA_A1
rs10498231	6.E-01	--	5.E-01	1.E+00	4.E-01	--	4.E-01	7.E-01	5.E-01	++	7.E-01	6.E-01	2	229212309	PID1	flanking_3UTR	a	c	A	A
rs3943747	3.E-01	++	2.E-01	9.E-01	8.E-01	++	1.E+00	7.E-01	2.E-01	+-	9.E-02	8.E-01	2	229218732	PID1	flanking_3UTR	a	c	C	A
rs1435862	6.E-01	--	5.E-01	9.E-01	6.E-02	++	6.E-02	5.E-01	1.E-02	--	3.E-02	2.E-01	2	229227453	PID1	flanking_3UTR	a	g	G	G
rs11890478	8.E-01	++	9.E-01	8.E-01	9.E-01	++	5.E-01	6.E-01	9.E-01	+-	6.E-01	7.E-01	2	229228232	PID1	flanking_3UTR	a	g	G	G
rs6737010	9.E-01	++	1.E+00	9.E-01	3.E-01	++	3.E-01	8.E-01	7.E-01	+-	5.E-01	8.E-01	2	229237357	PID1	flanking_3UTR	t	c	T	T
rs6752171	7.E-01	++	7.E-01	9.E-01	3.E-01	++	2.E-01	8.E-01	8.E-01	--	9.E-01	9.E-01	2	229246373	PID1	flanking_3UTR	t	g	T	T
rs1358443	2.E-01	++	9.E-02	9.E-01	8.E-01	+-	1.E+00	7.E-01	1.E-02	++	6.E-03	5.E-01	2	229290648	PID1	flanking_3UTR	t	c	C	C
rs1534458	7.E-01	+-	3.E-01	5.E-01	2.E-01	++	1.E-01	9.E-01	1.E+00	+-	6.E-01	5.E-01	2	229308807	PID1	flanking_3UTR	t	c	C	C
rs6722400	8.E-01	+-	3.E-01	4.E-01	2.E-01	+-	1.E-01	1.E+00	9.E-01	+-	6.E-01	4.E-01	2	229316515	PID1	flanking_3UTR	a	g	A	A
rs7603424	7.E-01	+-	3.E-01	5.E-01	7.E-01	+-	4.E-01	6.E-01	8.E-01	+-	8.E-01	5.E-01	2	229317612	PID1	flanking_3UTR	a	g	A	A
rs6719964	1.E-01	--	4.E-01	1.E-01	1.E-02	--	1.E-01	4.E-02	1.E+00	+-	1.E+00	1.E+00	2	229324480	PID1	flanking_3UTR	t	c	C	C
rs10451593	7.E-01	++	7.E-01	8.E-01	4.E-01	--	7.E-01	3.E-01	3.E-01	++	5.E-01	4.E-01	2	229325779	PID1	flanking_3UTR	t	c	C	C
rs1405837	7.E-01	+-	3.E-01	5.E-01	2.E-01	--	1.E-01	9.E-01	1.E+00	+-	6.E-01	5.E-01	2	229348479	PID1	flanking_3UTR	t	g	T	T
rs1881025	1.E-01	+-	3.E-02	8.E-01	4.E-02	--	1.E-02	9.E-01	9.E-01	+-	1.E+00	8.E-01	2	229352180	PID1	flanking_3UTR	a	g	A	A
rs6756903	1.E+00	+-	8.E-01	8.E-01	7.E-01	++	9.E-01	6.E-01	4.E-01	--	7.E-01	3.E-01	2	229354345	PID1	flanking_3UTR	t	c	C	C
rs1527669	8.E-01	+-	5.E-01	6.E-01	3.E-01	++	3.E-01	6.E-01	3.E-01	--	8.E-01	1.E-01	2	229360707	PID1	flanking_3UTR	a	g	A	A
rs3920427	1.E-01	+-	3.E-02	8.E-01	4.E-02	--	1.E-02	9.E-01	9.E-01	+-	1.E+00	8.E-01	2	229366708	PID1	flanking_3UTR	t	c	T	T

rs6712405	1.E-01	+	3.E-02	1.E+00	3.E-02	--	1.E-02	8.E-01	9.E-01	+	1.E+00	8.E-01	2	229366897	PID1	flanking_3UTR	a	g	A	A
rs776975	8.E-01	+	3.E-01	5.E-01	4.E-01	--	4.E-01	9.E-01	1.E+00	+	9.E-01	8.E-01	2	229372213	PID1	flanking_3UTR	t	c	T	T
rs12471368	3.E-01	--	7.E-01	3.E-01	9.E-01	0	8.E-01	1.E+00	8.E-01	0	7.E-01	1.E+00	2	229389331	PID1	flanking_3UTR	t	c	T	T
rs1527671	8.E-01	+	4.E-01	6.E-01	4.E-01	++	4.E-01	8.E-01	8.E-01	--	8.E-01	9.E-01	2	229392944	PID1	flanking_3UTR	a	g	G	G
rs11899696	3.E-02	++	2.E-01	5.E-02	4.E-01	++	5.E-01	6.E-01	4.E-02	++	2.E-01	1.E-01	2	229403044	PID1	flanking_3UTR	t	c	T	T
rs4487082	9.E-01	+	6.E-01	6.E-01	1.E+00	+	8.E-01	8.E-01	5.E-01	+	4.E-01	1.E+00	2	229432205	PID1	flanking_3UTR	a	g	G	G
rs800736	1.E+00	+	7.E-01	7.E-01	8.E-01	+	8.E-01	5.E-01	9.E-01	+	7.E-01	5.E-01	2	229438161	PID1	flanking_3UTR	a	g	G	G
rs7578485	4.E-01	++	7.E-01	4.E-01	2.E-01	++	6.E-01	2.E-01	5.E-01	++	1.E+00	2.E-01	2	229451253	PID1	flanking_3UTR	a	g	A	A
rs13428414	8.E-01	+	5.E-01	7.E-01	7.E-01	+	5.E-01	9.E-01	1.E+00	+	8.E-01	7.E-01	2	229456612	PID1	flanking_3UTR	t	c	C	C
rs800746	1.E-01	--	1.E-01	5.E-01	2.E-01	--	2.E-01	7.E-01	5.E-01	--	7.E-01	5.E-01	2	229457475	PID1	flanking_3UTR	a	g	A	A
rs9288639	6.E-01	--	5.E-01	1.E+00	2.E-01	--	3.E-01	4.E-01	4.E-01	++	8.E-01	3.E-01	2	229462042	PID1	flanking_3UTR	t	c	C	C
rs800729	6.E-01	+	2.E-01	6.E-01	6.E-01	+	1.E-01	3.E-01	6.E-01	++	8.E-01	6.E-01	2	229467572	PID1	flanking_3UTR	t	c	C	C
rs800742	2.E-01	--	7.E-01	2.E-01	7.E-03	--	4.E-01	8.E-04	5.E-01	++	9.E-01	4.E-01	2	229471910	PID1	flanking_3UTR	a	g	A	A
rs809616	4.E-02	--	4.E-01	2.E-02	2.E-03	--	2.E-01	3.E-04	9.E-01	--	9.E-01	1.E+00	2	229472163	PID1	flanking_3UTR	t	c	T	T
rs2396595	4.E-01	++	4.E-01	8.E-01	6.E-01	++	9.E-01	4.E-01	3.E-01	++	3.E-01	6.E-01	2	229489214	PID1	flanking_3UTR	t	c	T	T
rs10205926	8.E-01	--	7.E-01	1.E+00	7.E-01	+	4.E-01	6.E-01	8.E-01	+	6.E-01	8.E-01	2	229491242	PID1	flanking_3UTR	t	c	C	C
rs11901307	8.E-01	+	5.E-01	7.E-01	5.E-01	+	1.E-01	4.E-01	3.E-01	--	5.E-01	5.E-01	2	229494524	PID1	flanking_3UTR	t	g	T	T
rs7558980	1.E-01	++	2.E-01	4.E-01	6.E-02	++	3.E-01	8.E-02	3.E-01	++	3.E-01	9.E-01	2	229513328	PID1	flanking_3UTR	a	g	G	G
rs9808412	4.E-01	+	2.E-01	8.E-01	5.E-01	+	9.E-02	3.E-01	6.E-01	++	8.E-01	7.E-01	2	229522013	PID1	flanking_3UTR	t	c	T	T
rs7593561	5.E-01	++	5.E-01	7.E-01	6.E-01	++	8.E-01	5.E-01	2.E-01	++	2.E-01	6.E-01	2	229536702	PID1	flanking_3UTR	t	g	G	G
rs995159	4.E-01	++	4.E-01	8.E-01	5.E-01	++	5.E-01	9.E-01	7.E-01	++	9.E-01	6.E-01	2	229536991	PID1	flanking_3UTR	t	c	C	C
rs10490036	8.E-01	+	9.E-01	5.E-01	6.E-01	--	9.E-01	5.E-01	9.E-01	+	4.E-01	4.E-01	2	229549846	PID1	flanking_3UTR	a	g	G	G
rs10180529	2.E-01	++	3.E-01	6.E-01	2.E-01	++	6.E-01	1.E-01	4.E-01	+	3.E-01	9.E-01	2	229556970	PID1	flanking_3UTR	t	c	C	C
rs11894050	9.E-01	--	9.E-01	1.E+00	1.E+00	+	6.E-01	5.E-01	5.E-01	+	3.E-01	9.E-01	2	229568683	PID1	flanking_3UTR	a	c	A	A
rs1072282	9.E-01	--	9.E-01	9.E-01	9.E-01	+	6.E-01	4.E-01	4.E-01	--	3.E-01	1.E+00	2	229571469	PID1	flanking_3UTR	a	g	A	A
rs7559725	1.E-01	++	5.E-01	2.E-01	4.E-01	+	7.E-01	5.E-02	1.E-01	++	8.E-02	7.E-01	2	229575991	PID1	flanking_3UTR	t	c	C	C
rs1544688	2.E-01	++	3.E-01	6.E-01	1.E-01	++	8.E-02	7.E-01	7.E-01	+	3.E-01	5.E-01	2	229582523	PID1	flanking_3UTR	t	c	T	T
rs2072556	7.E-03	++	8.E-03	3.E-01	2.E-04	++	9.E-04	8.E-02	4.E-01	++	5.E-01	7.E-01	2	229584972	PID1	flanking_3UTR	t	c	C	C
rs10211472	7.E-01	+	1.E+00	5.E-01	5.E-01	+	9.E-01	2.E-01	7.E-01	++	6.E-01	9.E-01	2	229591666	PID1	flanking_3UTR	t	c	T	T
rs10490035	6.E-01	+	4.E-01	8.E-01	7.E-01	+	3.E-01	6.E-02	2.E-01	--	6.E-01	3.E-01	2	229593322	PID1	flanking_3UTR	a	c	C	C
rs3771286	8.E-01	+	7.E-01	1.E+00	8.E-01	+	6.E-01	3.E-01	6.E-01	+	7.E-01	2.E-01	2	229597727	PID1	3UTR	t	c	C	C
rs6436823	8.E-02	++	2.E-01	2.E-01	2.E-01	++	5.E-01	3.E-01	2.E-01	++	3.E-01	4.E-01	2	229601027	PID1	intron	a	g	A	A
rs2536214	7.E-01	++	7.E-01	9.E-01	2.E-01	++	2.E-01	7.E-01	1.E+00	+	3.E-01	3.E-01	2	229602126	PID1	intron	t	c	T	T
rs3845823	8.E-01	+	1.E+00	7.E-01	2.E-01	++	3.E-01	4.E-01	5.E-01	+	1.E-01	5.E-01	2	229611365	PID1	intron	t	g	T	T
rs2109818	4.E-01	--	6.E-01	5.E-01	5.E-02	--	1.E-01	2.E-01	3.E-01	++	4.E-01	6.E-01	2	229614496	PID1	intron	a	g	G	G
rs2215598	1.E-01	++	2.E-01	3.E-01	8.E-01	+	9.E-01	6.E-01	3.E-02	++	4.E-02	4.E-01	2	229616489	PID1	intron	t	c	T	T
rs724395	6.E-01	+	5.E-01	1.E+00	4.E-01	--	6.E-01	5.E-01	1.E-01	++	1.E-01	7.E-01	2	229619810	PID1	intron	t	c	C	C
rs31276	9.E-01	+	9.E-01	1.E+00	1.E+00	+	9.E-01	8.E-01	9.E-01	+	7.E-01	7.E-01	2	229628764	PID1	intron	t	c	C	C
rs31278	1.E-01	+	1.E+00	8.E-03	1.E+00	+	8.E-01	7.E-01	7.E-02	+	7.E-01	7.E-04	2	229630498	PID1	intron	t	c	T	T
rs4608504	6.E-02	++	3.E-01	1.E-01	7.E-01	+	3.E-01	5.E-01	2.E-02	++	3.E-01	1.E-02	2	229640616	PID1	intron	t	c	T	T
rs1860761	5.E-01	--	5.E-01	1.E+00	4.E-01	--	6.E-01	4.E-01	6.E-01	++	1.E+00	5.E-01	2	229645080	PID1	intron	a	g	A	A
rs1860762	6.E-02	++	2.E-01	1.E-01	9.E-01	+	9.E-01	1.E+00	1.E-02	++	9.E-02	5.E-02	2	229648879	PID1	intron	t	c	C	C
rs2014401	7.E-01	+	5.E-01	8.E-01	8.E-01	+	4.E-01	4.E-01	5.E-01	++	9.E-01	4.E-01	2	229659963	PID1	intron	a	g	A	A
rs1014174	9.E-01	+	1.E+00	9.E-01	4.E-01	++	9.E-01	2.E-01	1.E+00	+	8.E-01	7.E-01	2	229660208	PID1	intron	a	g	G	G
rs2109820	3.E-01	++	3.E-01	7.E-01	6.E-01	+	1.E-01	4.E-01	8.E-01	+	8.E-01	4.E-01	2	229665247	PID1	intron	t	g	G	G
rs7589888	8.E-01	+	1.E+00	7.E-01	8.E-01	+	7.E-01	1.E+00	7.E-01	++	8.E-01	7.E-01	2	229670668	PID1	intron	t	c	C	C
rs10200706	1.E+00	+	7.E-01	6.E-01	5.E-01	+	3.E-01	8.E-01	7.E-01	++	8.E-01	6.E-01	2	229673882	PID1	intron	t	c	C	C
rs6436839	5.E-01	+	8.E-01	5.E-01	5.E-01	+	7.E-01	1.E-01	8.E-01	+	1.E+00	7.E-01	2	229678042	PID1	intron	a	g	G	G
rs6759815	1.E+00	+	5.E-01	4.E-01	8.E-01	+	2.E-01	3.E-01	9.E-01	+	9.E-01	8.E-01	2	229680665	PID1	intron	t	c	C	C
rs2765936	4.E-01	+	5.E-01	3.E-02	6.E-01	+	9.E-01	3.E-01	4.E-01	+	8.E-01	1.E-01	2	229683166	PID1	intron	t	c	T	T
rs10490031	4.E-01	--	5.E-01	7.E-01	5.E-01	+	4.E-01	9.E-01	4.E-01	--	5.E-01	6.E-01	2	229689857	PID1	intron	a	g	A	A
rs1319273	6.E-01	+	1.E+00	3.E-01	8.E-01	+	6.E-01	8.E-01	1.E+00	+	1.E-01	4.E-02	2	229697273	PID1	intron	t	c	T	T
rs975583	5.E-01	+	3.E-01	9.E-01	8.E-01	+	3.E-01	8.E-02	1.E+00	+	6.E-01	5.E-01	2	229698937	PID1	intron	a	g	A	A
rs12467995	7.E-01	--	8.E-01	7.E-01	9.E-01	+	9.E-01	7.E-01	5.E-01	--	9.E-01	3.E-01	2	229702613	PID1	intron	t	c	C	C
rs12329005	2.E-01	++	2.E-01	5.E-01	7.E-02	++	6.E-01	2.E-02	6.E-01	+	2.E-01	3.E-01	2	229708818	PID1	intron	t	c	C	C
rs4973160	1.E-01	++	2.E-01	4.E-01	2.E-02	++	2.E-01	3.E-02	5.E-01	+	2.E-01	5.E-01	2	229710850	PID1	intron	t	g	G	G

rs2023499	9.E-01	+-	4.E-01	4.E-01	4.E-01	++	4.E-01	8.E-01	8.E-01	+-	2.E-01	5.E-02	2	229715103	PID1	intron	t	c	C	C
rs7561470	1.E-01	--	1.E-01	6.E-01	1.E-01	--	2.E-01	5.E-01	4.E-01	+-	1.E-01	5.E-01	2	229721264	PID1	intron	a	g	A	A
rs17476328	6.E-01	+-	8.E-01	2.E-01	1.E-01	+-	5.E-01	1.E-03	6.E-01	+-	5.E-01	9.E-01	2	229724395	PID1	intron	a	g	A	A
rs985891	3.E-01	+-	1.E+00	6.E-02	9.E-02	--	9.E-01	7.E-03	9.E-01	+-	6.E-01	6.E-01	2	229727592	PID1	intron	a	g	A	A
rs2396616	9.E-01	+-	1.E-01	7.E-02	5.E-01	+-	6.E-01	9.E-02	5.E-02	+-	1.E-03	4.E-01	2	229729646	PID1	intron	a	g	A	A
rs4973166	4.E-01	+-	1.E-01	6.E-01	4.E-01	--	5.E-01	8.E-01	2.E-01	+-	4.E-02	7.E-01	2	229733854	PID1	intron	a	g	G	G
rs4973171	7.E-01	+-	1.E+00	4.E-01	1.E-01	++	9.E-01	2.E-02	7.E-01	--	7.E-01	8.E-01	2	229738649	PID1	intron	a	g	G	G
rs1419958	9.E-01	++	9.E-01	9.E-01	8.E-01	+-	9.E-01	6.E-01	4.E-01	++	4.E-01	8.E-01	2	229741804	PID1	intron	t	g	G	G
rs12477036	9.E-01	+-	8.E-01	9.E-01	6.E-01	++	9.E-01	5.E-01	4.E-01	--	4.E-01	7.E-01	2	229742326	PID1	intron	a	g	G	G
rs12694800	4.E-01	+-	1.E+00	2.E-01	2.E-01	+-	8.E-01	2.E-02	8.E-01	+-	1.E+00	7.E-01	2	229743258	PID1	intron	t	c	C	C
rs1362256	6.E-01	--	6.E-01	8.E-01	6.E-01	+-	9.E-01	3.E-01	7.E-01	+-	6.E-01	9.E-01	2	229747285	PID1	intron	t	c	T	T
rs2159723	3.E-02	++	4.E-01	2.E-02	2.E-02	++	3.E-01	1.E-02	9.E-01	+-	4.E-01	4.E-01	2	229753516	PID1	intron	t	c	T	T
rs1419936	1.E-01	+-	1.E+00	7.E-03	3.E-02	--	8.E-01	1.E-03	7.E-01	+-	2.E-01	3.E-01	2	229762039	PID1	intron	a	g	G	G
rs1362238	4.E-01	+-	9.E-01	1.E-01	5.E-01	++	9.E-01	3.E-01	7.E-01	+-	6.E-01	2.E-01	2	229767104	PID1	intron	t	c	T	T
rs988889	4.E-01	+-	7.E-01	9.E-02	6.E-01	+-	9.E-01	3.E-01	7.E-01	+-	6.E-01	2.E-01	2	229769945	PID1	intron	a	g	G	G
rs6736122	2.E-01	++	5.E-01	2.E-01	6.E-01	++	8.E-01	5.E-01	3.E-01	++	7.E-01	2.E-01	2	229773255	PID1	intron	a	g	A	A
rs12478812	8.E-01	+-	9.E-01	6.E-01	3.E-01	++	8.E-01	2.E-01	4.E-01	--	4.E-01	8.E-01	2	229777030	PID1	intron	t	c	C	C
rs1362240	8.E-01	+-	9.E-01	6.E-01	4.E-01	+-	2.E-01	8.E-01	8.E-01	+-	5.E-01	7.E-01	2	229784591	PID1	intron	a	c	A	A
rs883731	1.E-02	++	2.E-02	2.E-01	5.E-03	++	2.E-03	5.E-01	5.E-01	++	9.E-01	3.E-01	2	229789287	PID1	intron	a	g	A	A
rs1946124	3.E-01	--	2.E-01	1.E+00	6.E-02	--	2.E-02	9.E-01	7.E-01	++	8.E-01	8.E-01	2	229802147	PID1	intron	a	g	G	G
rs1226984	5.E-02	--	1.E-01	3.E-01	9.E-03	--	1.E-02	3.E-01	8.E-01	+-	9.E-01	5.E-01	2	229806982	PID1	intron	t	c	C	C
rs6747101	3.E-01	--	6.E-01	4.E-01	4.E-01	--	3.E-01	1.E+00	6.E-01	+-	9.E-01	4.E-01	2	229811615	PID1	intron	t	c	T	T
rs1226998	3.E-01	--	4.E-01	6.E-01	2.E-01	--	5.E-01	2.E-01	9.E-01	+-	6.E-01	6.E-01	2	229817917	PID1	intron	t	c	C	C
rs10498235	8.E-01	--	9.E-01	9.E-01	3.E-01	++	7.E-01	2.E-01	2.E-01	--	5.E-01	2.E-01	2	229824279	PID1	intron	a	g	G	G
rs1227003	4.E-01	+-	1.E+00	2.E-01	4.E-02	--	5.E-02	5.E-01	6.E-01	+-	1.E-01	3.E-01	2	229827522	PID1	intron	t	c	C	C
rs6724020	3.E-01	--	4.E-01	6.E-01	7.E-01	+-	4.E-01	7.E-01	4.E-01	--	8.E-01	3.E-01	2	229830491	PID1	intron	a	g	A	A
rs1227005	1.E-01	--	1.E-01	5.E-01	2.E-01	--	3.E-01	5.E-01	3.E-01	--	4.E-01	7.E-01	2	229830629	PID1	intron	a	g	G	G
rs4321351	4.E-01	--	3.E-01	9.E-01	5.E-01	++	9.E-01	3.E-01	1.E-01	--	2.E-01	5.E-01	2	229837737	PID1	intron	a	g	G	G
rs1227009	2.E-02	++	5.E-02	2.E-01	1.E-01	++	1.E-01	4.E-01	2.E-01	++	4.E-01	4.E-01	2	229839896	PID1	intron	a	g	A	A
rs10498237	2.E-01	+-	1.E-01	1.E+00	5.E-01	+-	3.E-01	7.E-01	2.E-01	++	1.E-01	9.E-01	2	229850093	PID1	flanking_5UTR	a	g	G	G
rs12988652	4.E-02	++	3.E-01	5.E-02	2.E-01	++	7.E-01	2.E-01	3.E-02	++	1.E-01	1.E-01	2	229850323	PID1	flanking_5UTR	a	g	A	A
rs10498238	2.E-01	--	6.E-01	1.E-01	3.E-02	--	2.E-01	4.E-02	6.E-01	+-	3.E-01	6.E-01	2	229874808	PID1	flanking_5UTR	t	c	T	T
rs4973184	1.E-01	++	2.E-01	5.E-01	5.E-01	+-	3.E-01	9.E-01	2.E-01	++	2.E-01	6.E-01	2	229874891	PID1	flanking_5UTR	t	c	T	T
rs1226950	5.E-01	++	5.E-01	8.E-01	8.E-01	++	8.E-01	9.E-01	8.E-01	+-	4.E-01	5.E-01	2	229882408	PID1	flanking_5UTR	t	c	C	C
rs12621639	4.E-02	++	3.E-02	5.E-01	2.E-01	+-	6.E-02	6.E-01	1.E-01	++	1.E-01	6.E-01	2	229884058	PID1	flanking_5UTR	a	c	A	A
rs6715968	1.E-01	++	1.E-01	6.E-01	3.E-01	++	3.E-01	7.E-01	5.E-01	++	6.E-01	6.E-01	2	229884476	PID1	flanking_5UTR	t	g	T	T

Table E7. Meta-analysis results of gene-gene interaction of ppFEV₁ between rs1512288 of *HHIP* and 14 SNPs of *PTCH1*.

SNP	Coordinate	P _{meta} [*]	Direction [†]	P _{meta_C} [*]	P _{TENOR} [‡]	P _{SARP_C} [‡]	P _{CSGA_C} [‡]	P _{meta_A} [*]	P _{SARP_A} [§]	P _{CSGA_A} [§]
rs357527	97207632	0.491	++--+	0.579	0.363	0.726	0.603	0.675	0.513	0.142
rs7389278	97211906	0.791	+----	0.872	0.089	0.649	0.171	0.405	0.796	0.317
rs357522	97229279	0.740	+--+--	0.933	0.345	0.187	0.491	0.406	0.666	0.431
rs10512249	97296130	0.574	-+---	0.851	0.737	0.328	0.198	0.414	0.881	0.266
rs28536742	97322914	0.877	-+-++	0.740	0.516	0.709	0.735	0.361	0.776	0.272
rs576594	97359032	0.088	-++++	0.216	0.544	0.088	0.227	0.199	0.748	0.101
rs10818991	97407538	0.324	--+--	0.929	0.399	0.733	0.151	0.062	0.105	0.337
rs1984119	97408582	0.836	+--+--	0.900	0.936	0.918	0.807	0.842	0.854	0.588
rs3824491	97408698	0.076	-----	0.571	0.757	0.564	0.982	8.5E-03	0.071	0.051
rs6478154	97411347	0.905	--+++	0.501	0.979	0.031	0.128	0.337	0.840	0.203
rs7854581	97433100	0.839	++-+-	0.907	0.433	0.812	0.249	0.837	0.480	0.588
rs10989496	97436827	0.576	++--+	0.749	0.231	0.578	0.086	0.565	0.994	0.356
rs10990303	97450226	0.106	+---+	0.462	0.066	0.855	0.497	0.046	0.121	0.207
rs915228	97484124	0.689	++---	0.139	0.012	0.901	0.683	0.067	0.687	0.016

* P_{meta}, P_{meta_C}, and P_{meta_A} represent the meta-analysis P value for all five, three non-Hispanic White, or two African American asthmatic populations, respectively.

† Direction is the meta-analysis effect size direction of TENOR, non-Hispanic Whites of SARP and CSGA, and African Americans of SARP and CSGA.

‡ P_{TENOR}, P_{SARP_C}, and P_{CSGA_C} represent the P value for TENOR, non-Hispanic Whites of SARP and CSGA, respectively.

§ P_{SARP_A} and P_{CSGA_A} represent the P value for African Americans of SARP and CSGA, respectively.

Table E8. Joint analysis of 5 SNPs in *HHIP*, *PTCH1*, *FAM13A*, *PID1*, and *NOTCH4*.

	SARP non-Hispanic whites							
Number of risk SNPs*	0	1	2	3	4	5	P value	R²
N	18	91	144	138	33	4		
ppFEV₁	85 ± 19	81 ± 24	79 ± 20	75 ± 21	63 ± 26	60 ± 17	9.8E-06	0.045
ppFVC	93 ± 16	91 ± 19	88 ± 18	86 ± 17	75 ± 21	75 ± 7	1.1E-05	0.045
FEV₁/FVC	0.76 ± 0.1	0.72 ± 0.1	0.73 ± 0.1	0.70 ± 0.1	0.67 ± 0.2	0.66 ± 0.1	0.004	0.019
	TENOR non-Hispanic whites							
Number of risk SNPs*	0	1	2	3	4	5	P value	R²
N	26	90	162	118	36	3		
ppFEV₁	87 ± 25	78 ± 21	79 ± 20	77 ± 21	74 ± 19	44 ± 15	0.011	0.015
ppFVC	91 ± 19	90 ± 19	89 ± 17	89 ± 18	85 ± 18	70 ± 24	0.097	0.006
FEV₁/FVC	0.78 ± 0.1	0.72 ± 0.1	0.73 ± 0.1	0.71 ± 0.1	0.72 ± 0.1	0.51 ± 0.1	0.045	0.009

*Number of risk SNPs is the sum of risk SNPs in *HHIP* (rs1512288), *PTCH1* (rs576594), *FAM13A* (rs2869967), *PID1* (rs3845823), and *NOTCH4* (rs206015).

Table E9. Association results of SNPs of *HHIP* region in TENOR case-control study.

SNP	P value	Coordinate	Location
rs4362772	0.9074	145549252	flanking_5UTR
rs749316	0.6768	145590796	flanking_5UTR
rs7684769	0.7781	145638960	flanking_5UTR
rs12641251	0.7099	145644293	flanking_5UTR
rs6827794	0.3567	145649747	flanking_5UTR
rs1512282	0.804	145650947	flanking_5UTR
rs6845536	0.8451	145672233	flanking_5UTR
rs720485	0.3633	145682038	flanking_5UTR
rs1828591	0.3043	145700230	flanking_5UTR
rs1512288	0.2599	145710731	flanking_5UTR
rs2175586	0.7793	145716391	flanking_5UTR
rs6852830	0.5251	145726008	flanking_5UTR
rs1996020	0.3487	145730644	flanking_5UTR
rs7670758	0.5408	145731325	flanking_5UTR
rs7677662	0.988	145732503	flanking_5UTR
rs4835180	0.5494	145740058	flanking_5UTR
rs2035901	0.9799	145741317	flanking_5UTR
rs11947381	0.7495	145757300	flanking_5UTR
rs2575570	0.781	145768383	flanking_5UTR
rs1398244	0.4952	145781907	flanking_5UTR
rs6845999	0.8977	145785276	flanking_5UTR
rs1812175	0.3989	145794294	intron
rs2220514	0.7351	145796008	intron
rs2306924	0.9688	145801986	intron
rs6537307	0.3568	145821313	intron
rs2575580	0.4509	145824475	intron
rs6537310	0.1516	145856182	intron
rs6854783	0.1784	145862529	intron
rs11944404	0.5185	145890321	flanking_3UTR
rs4835186	0.8686	145906597	flanking_3UTR
rs2353934	0.4015	145916490	flanking_3UTR
rs12647866	0.276	145928136	flanking_3UTR
rs12651029	0.5748	145989617	flanking_3UTR
rs13102609	0.5209	145990671	flanking_3UTR