

Table S1. Characteristics of thirty-one ancestry informative markers (AIMs)

Marker	dbSNP accession	Location	Allele frequency in three different ancestral populations			δ^b			HWE test ^c
			Eu ^a	Af ^a	NA ^a	Eu/Af	Af/NA	Eu/NA	
Rs3188519	rs3188519	1p34.1	0.37	0.76	0.32	0.39	0.44	0.05	0.34
FY	rs2814778	1q23.2	0.99	0	0.99	0.99	0.99	0	0.52
Rs6003	rs6003	1q31.3	0.08	0.7	0.03	0.62	0.67	0.05	0.73
TSC1102055	rs2065160	1q32.1	0.92	0.5	0.17	0.42	0.32	0.75	0.18
Rs723632	rs723632	1q32.3	0.92	0.1	0.67	0.82	0.57	0.25	0.36
WI16857	rs3287	2p16.1	0.2	0.73	0.21	0.53	0.53	0.01	0.21
WI11153	rs17203	3p12.3	0.15	0.81	0.76	0.66	0.05	0.61	0.71
Rs584059	rs584059	3q22.3	0.14	0.49	0.47	0.36	0.03	0.33	0.65
GC1	rs7041	4q13.3	0.41	0.93	0.45	0.52	0.48	0.04	0.05
Rs930072	rs930072	5p13.2	0.1	0.96	0.45	0.87	0.51	0.35	0.31
SGC30055	rs3317	5q23.1	0.59	0.05	0.73	0.53	0.68	0.15	0.66
Rs1985080	rs1985080	7p14.3	0.64	0.1	0.97	0.54	0.87	0.32	0.72
LPL	rs285	8p21.3	0.52	0.97	0.45	0.45	0.52	0.07	0.5
Rs518116	rs518116	9q33.3	0.67	0.13	0.58	0.54	0.45	0.09	0.36
Rs7349	rs7349	10p11.22	0.87	0.04	0.96	0.83	0.92	0.08	1
Rs994174	rs994174	10q23.1	0.25	0.76	0.26	0.51	0.49	0.02	0.33
L192	rs594689	11q11	0.47	0.09	0.13	0.37	0.04	0.34	0.08
TYR192	rs1042602	11q21	0.47	0	0.05	0.46	0.05	0.41	1
DRD2 Taq_D	rs1800498	11q23.1	0.65	0.14	0.09	0.51	0.05	0.56	0.64
Rs326946	rs326946	11q23.1	0.17	0.61	0.07	0.44	0.54	0.1	0.13
Rs146026	rs146026	13q13.1	0.92	0.26	0.83	0.66	0.57	0.09	0.55
OCA2	rs1800404	15q13.1	0.72	0.14	0.48	0.58	0.34	0.23	0.75
Rs2228478	rs2228478	16q24.3	0.14	0.51	0.04	0.37	0.47	0.09	0.13
WI7423	rs2816	17p12	0.49	0	0.08	0.49	0.07	0.42	0.01*
WI14867	rs2891	17p13.2	0.51	0.02	0.43	0.49	0.41	0.08	0.81
Rs2077863	rs2077863	18p11	0.93	0.51	0.93	0.41	0.42	0	0.81
Rs1989486	rs1989486	19q13.42	0.58	0.04	0.4	0.53	0.36	0.17	0.13
Rs3188520	rs3188520	20q11.22	0.35	0.83	0.44	0.48	0.39	0.09	0.68
Rs722098	rs722098	21q21.1	0.18	0.9	0.72	0.73	0.19	0.54	0.53
Rs235936	rs235936	21q21.3	0.49	0.18	0.37	0.31	0.2	0.11	0.22
MID93	rs16383	22q13.2	0.8	0.27	0.11	0.52	0.17	0.69	0.73

^a Eu: European subjects; Af: African subjects; NA: Native American subjects^b δ : difference of allele frequencies between two ancestral populations (Eu/Af: Europeans and Africans; Af/NA: Africans and Native Americans; Eu/NA: Europeans and Native Americans)^c P-value

* Marker out of Hardy-Weinberg equilibrium in SAGE subjects (N = 352)

Table S2. Association of asthma disease status with 30 AIMs in a subset (N = 200) of 352 SAGE subjects ^a.

Independent predictor	Count of positives ^b (P value < 0.05) ^c		
	No adjustment	w/covariates adjustment, but w/o IAEs adjustment ^d	w/covariates and IAEs adjustment ^e
AIMs (N = 30)	21	14	1

NOTE:

- ^a Cases in the subset are the subjects with top 100 African proportions; controls in the subset are the subjects with bottom 100 African proportions.
- ^b Under 5% type I error rate ($P = 0.05$), counts of expected false positives are 1.5 markers.
- ^c Analyses were carried out by using multiple regression analysis.
- ^d Covariates included in the analyses are age, gender and SES.
- ^e Counts of positives are the same by including IAEs computed by either ADMIXMAP or Structure2.1.