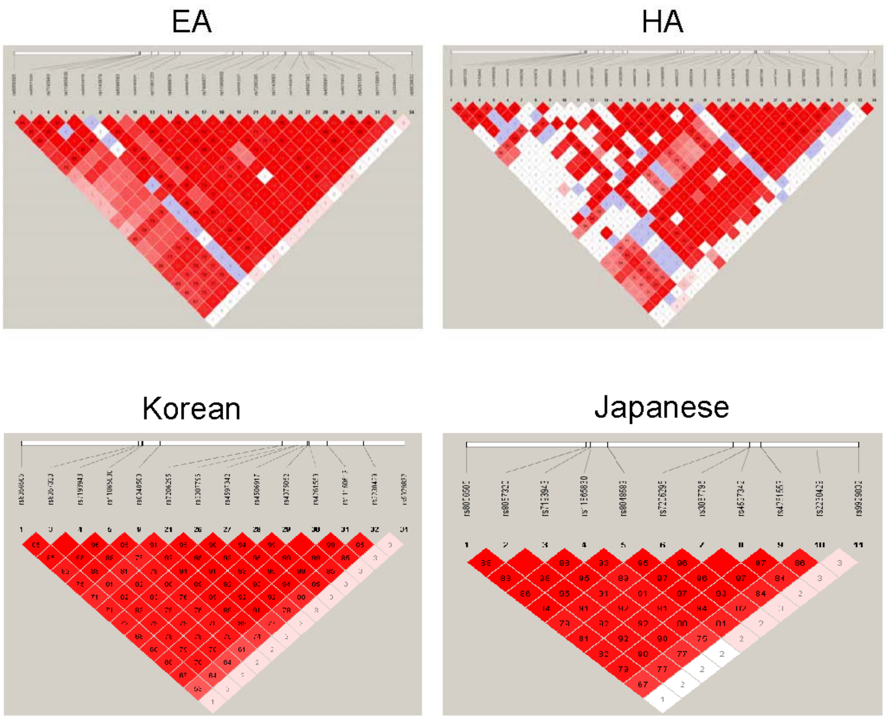
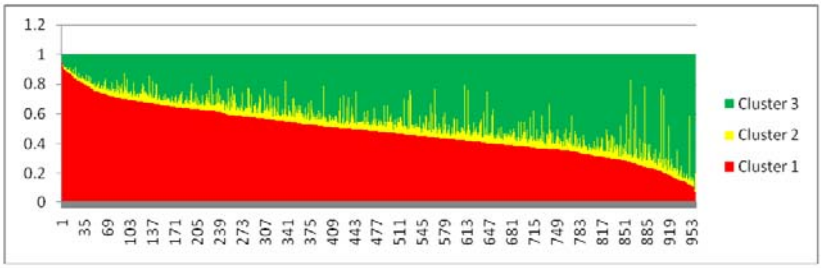
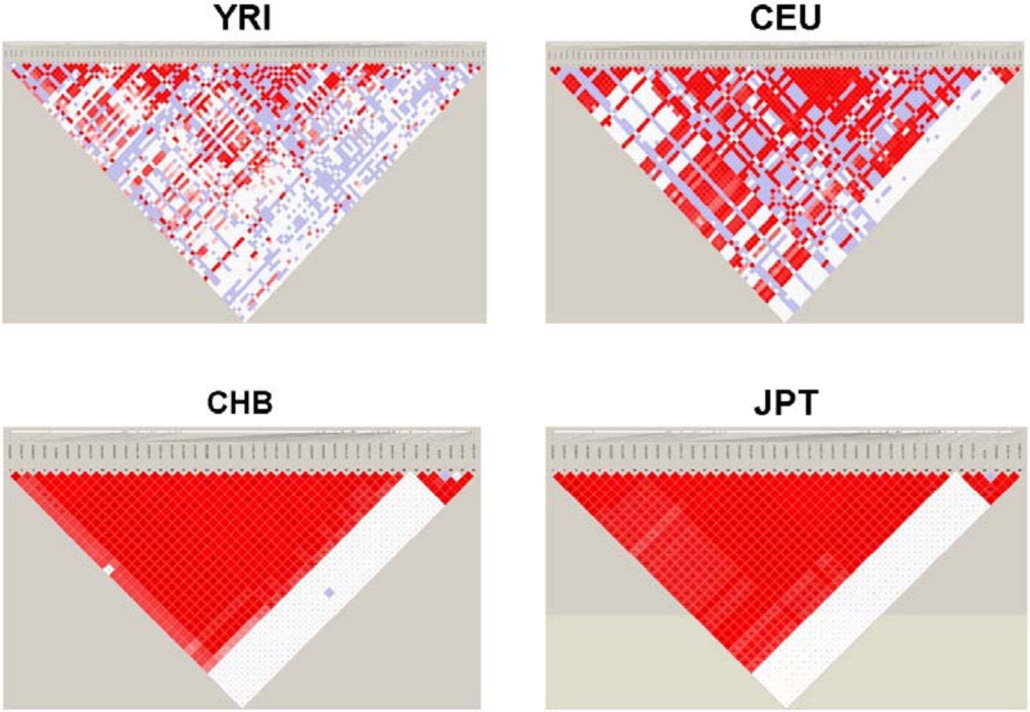


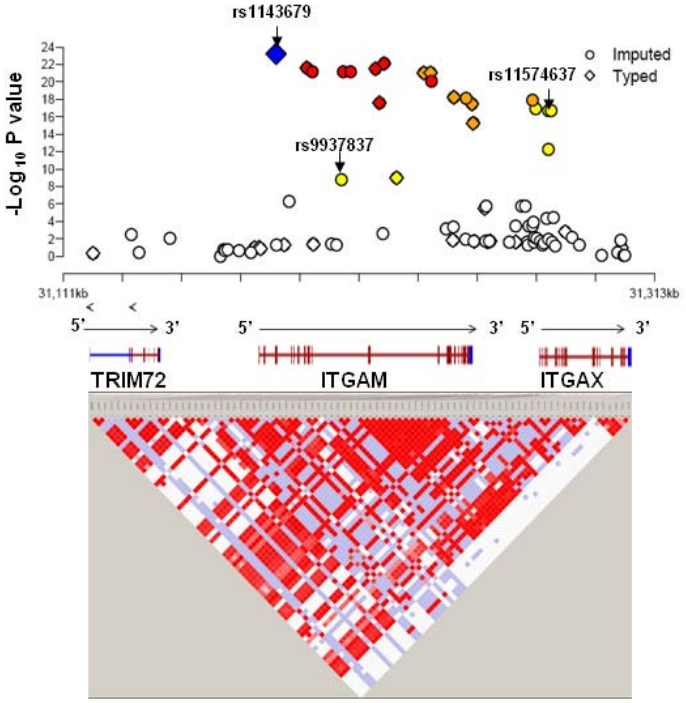
Supplementary Figure 1. LD plot from our genotyped data.



Supplementary Figure 2. Individual admixture proportions for Hispanic cases and controls.



Supplementary Figure 3. LD plot from HapMap data.



Supplementary Figure 4. Bayesian association assessment testing in and around *ITGAM* by IMPUTE/SNPTEST program. All genotyped (diamond) and imputed (circle) SNPs are plotted with their -log $_{10}$ *p-value* along with their physical position (NCBI build 35). The blue diamond is the proposed causal SNP in this study. The colors of white, yellow, orange and red represent the r^2 correlations with rs1143679 (red: $r^2 \geq 0.8$; orange: $0.5 \leq r^2 < 0.8$; yellow: $0.2 \leq r^2 < 0.5$; white: $r^2 < 0.2$). Blocks connecting pairs of SNPs are shaded according to the strength of the linkage disequilibrium between the SNPs, from 0 (white) to 1.0 (bright red), as measured by the disequilibrium coefficient r^2.

Sup Table 1: Genotype Count and HWE for (A) 34 SNPs in European-American, Hispanic-American, Korean, and Japanese Population, and (B) rs 1143679 in UK, Mexican, and Colombian populations

A.

					European-American (742/1054)				**Hispanic-American (731/229)**				**Korean (661/781)**				**Japanese (176/361)**			
GENE	**SNP**	**Position**	**Alleles**	**Function**	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***
TRIM72	rs8056505	31122399	A/G	intron_5	(354/477)	(314/462)	(68/113)	0.944	(239/80)	(369/117)	(123/32)	0.490	(447/507)	(194/244)	(19/30)	0.909	(124/254)	(48/97)	(5/13)	0.620
TRIM72	rs13339393	31123484	A/C	intron_1	(734/1050)	(1/2)	(2/1)	0.003	(720/226)	(8/3)	(1/0)	1	(659/780)	(0/0)	(0/0)	1				
ITGAM	rs8057320	31177052	A/G	5'promoter	(368/495)	(306/452)	(61/104)	0.943	(265/84)	(352/116)	(110/29)	0.403	(435/487)	(201/257)	(25/37)	0.668	(117/224)	(54/105)	(4/16)	0.560
ITGAM	rs7193943	31178564	A/G	5'promoter	(369/504)	(303/447)	(59/101)	0.885	(291/96)	(342/108)	(98/25)	0.661	(435/487)	(201/257)	(25/37)	0.668	(0/0)	(0/0)	(0/0)	1
ITGAM	rs11865830	31179046	A/G	intron_1	(369/500)	(307/449)	(60/102)	1	(284/86)	(347/118)	(100/25)	0.201	(443/496)	(193/248)	(25/37)	0.382	(122/246)	(51/103)	(4/16)	0.470
ITGAM	rs8063978	31179201	A/G	intron_1	(729/1044)	(7/8)	(0/1)	0.021	(700/213)	(31/16)	(0/0)	1	(661/778)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs1549298	31179492	G/A	intron_1	(734/1044)	(4/8)	(0/1)	0.021	(706/214)	(25/15)	(0/0)	1	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	**rs1143679**	**31184312**	**G/A**	**exon_3/nonsyn**	**(494/829)**	**(220/211)**	**(22/11)**	0.752	**(502/189)**	**(210/40)**	**(15/0)**	0.229	**(661/779)**	**(0/0)**	**(0/0)**	1	(0/0)	(0/0)	(0/0)	1
ITGAM	rs8048583	31187037	G/A	intron_5	(355/481)	(311/450)	(71/121)	0.361	(244/74)	(361/120)	(126/35)	0.345	(429/468)	(202/273)	(30/40)	1	(119/242)	(52/106)	(5/17)	0.480
ITGAM	rs9929801	31190973	A/G	intron_7	(705/1037)	(13/12)	(0/2)	0.001	(676/207)	(49/22)	(4/0)	1	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs9936831	31194649	A/T	intron_9	(483/809)	(230/222)	(23/19)	0.390	(477/177)	(223/50)	(30/2)	0.751	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs3087444	31195512	C	exon_10	(738/1052)	(0/0)	(0/0)	1	(731/229)	(0/0)	(0/0)	1	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs11861251	31196897	A/G	exon_12/nonsyn	(544/771)	(174/254)	(16/28)	0.270	(629/196)	(100/32)	(2/1)	1	(661/780)	(0/1)	(0/0)	1	.	.	.	.
ITGAM	rs9888879	31217873	A/G	intron_14	(474/804)	(238/227)	(25/21)	0.267	(451/164)	(241/61)	(39/4)	0.615	(661/780)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs12928810	31219216	G/A	intron_14	(532/828)	(136/190)	(24/20)	0.055	(538/180)	(107/46)	(31/2)	0.747	(659/776)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs9888739	31220754	G/A	intron_14	(464/802)	(240/227)	(25/21)	0.267	(451/164)	(240/61)	(39/4)	0.615	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs7499077	31225006	G/A	intron_14	(331/567)	(318/393)	(89/92)	0.052	(374/137)	(289/80)	(66/12)	1	(661/780)	(0/1)	(0/0)	1	.	.	.	.
ITGAM	rs11860650	31234207	G/A	intron_14	(488/814)	(221/219)	(24/17)	0.561	(498/183)	(206/46)	(24/0)	0.142	(653/767)	(1/4)	(0/0)	1	.	.	.	.
ITGAM	rs6565227	31236492	A/T	intron_14	(475/803)	(238/226)	(25/22)	0.211	(451/164)	(241/61)	(38/4)	0.615	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs8056264	31240156	G/A	exon_15/syn	(730/1044)	(6/9)	(0/0)	1	(705/218)	(26/11)	(0/0)	1	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs7206295	31244020	G/A	intron_19	(360/490)	(298/451)	(61/108)	0.830	(260/80)	(357/119)	(114/30)	0.213	(430/471)	(205/268)	(26/42)	0.609	(119/246)	(53/103)	(3/16)	0.470
ITGAM	rs1143683	31244389	G/A	exon_21/nonsyn	(439/749)	(265/273)	(33/30)	0.352	(474/174)	(222/54)	(34/1)	0.217	(659/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs9930690	31249753	-	intron_28	(0/0)	(0/0)	(0/0)	NA	(0/0)	(0/0)	(0/0)	NA	(0/0)	(0/0)	(0/0)	NA	.	.	.	.
ITGAM	rs1143678	31250506	G/A	exon30/nonsyn	(439/747)	(265/270)	(32/33)	0.203	(472/169)	(223/57)	(35/1)	0.141	(659/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs9933520	31250887	A/G	3'utr	(412/738)	(159/234)	(45/36)	0.003	(463/170)	(114/55)	(50/1)	0.140	(659/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAM	rs3087796	31251154	G/A	3'utr	(421/532)	(203/351)	(65/110)	3.6E-05	(373/87)	(168/93)	(113/30)	0.551	(399/451)	(201/264)	(28/43)	0.608	(120/245)	(53/103)	(4/17)	0.363
ITGAM	rs4597342	31251270	G/A	3'utr	(366/493)	(307/448)	(64/110)	0.568	(260/78)	(357/121)	(114/30)	0.166	(425/464)	(208/274)	(28/43)	0.762	(117/245)	(53/102)	(4/17)	0.330
.	rs4506917	31254851	C/A	.	(154/285)	(384/513)	(189/252)	0.536	(300/80)	(335/103)	(95/46)	0.224	(411/454)	(221/283)	(29/44)	1	.	.	.	.
.	rs4075052	31255734	C/A	.	(361/493)	(305/445)	(63/111)	0.432	(255/76)	(359/122)	(116/31)	0.132	(413/454)	(219/283)	(29/44)	1	.	.	.	.
.	rs4261553	31256665	G/A	.	(362/493)	(280/428)	(65/111)	0.247	(257/76)	(310/118)	(113/31)	0.212	(413/454)	(219/283)	(29/44)	1	(118/243)	(53/104)	(6/18)	0.300
.	rs11150613	31265311	A/G	.	(359/489)	(309/445)	(68/115)	0.394	(255/75)	(359/123)	(116/31)	0.130	(413/454)	(218/283)	(30/43)	1	.	.	.	.
ITGAX	rs2230429	31282036	G/C	missense	(342/458)	(320/459)	(73/136)	0.246	(381/103)	(288/91)	(62/35)	0.059	(412/463)*	(210/274)	(29/36)	0.678	(122/2247)	(52/101)	(3/17)	0.290
ITGAX	rs2230427	31298621	A/G	exon_25	(735/1042)	(3/11)	(0/0)	1	(702/217)	(28/12)	(1/0)	1	(661/781)	(0/0)	(0/0)	1	.	.	.	.
ITGAX	rs9929832	31301045	A/G	3'utr	(194/310)	(345/491)	(195/251)	0.047	(209/57)	(340/118)	(180/54)	0.599	(388/491)	(242/244)	(31/46)	0.044	(123/249)	(50/106)	(4/9)	0.850

*minor allele flipped

B.

					UK (445/528)				**Mexican (389/284)**				**Colombian (205/381)**			
GENE	**SNP**	**Position**	**Alleles**	**Function**	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***	**(1,1)**	**(1,2)**	**(2,2)**	**HWE***
ITGAM	rs1143679	31184312	G/A	exon_3/nonsyn	(294/431)	(109/84)	(19/5)	0.040	(280/277)	(101/52)	(11/2)	0.737	(122/122)	(74/33)	(9/9)	0.596

*** HWE=HWE based on controls**

Sup Table 2: Information on 76 AIMS used to estimate Hispanic population structure and structured association analysis

chrom.	SNP	position	A1	A2	African (Hapmap)*	Seldin EUR*	Seldin AMI*	σ(AF-EUR)	σ(AF-AMI)	σ(EUR-AMI)
chr1	rs3013047	13703164	A	G	0.467	0.19	0.85	0.343	0.317	0.66
chr1	rs7417447	30510596	A	G	0.418	0.89	0.25	0.308	0.332	0.64
chr1	rs10754436	116570421	A	G	0.89	0.86	0.45	0.75	0.34	0.41
chr1	rs6695103	231699287	A	G	0.534	0.14	0.76	0.326	0.294	0.62
chr1	rs6672147	243355116	A	G	0.559	0.79	0.12	0.349	0.321	0.67
chr1	rs10802514	245704372	T	G	0.558	0.82	0.11	0.378	0.332	0.71
chr1	rs9439458	1441243	C	T	0.127	0.14	0.55	0.733	0.323	0.41
chr1	rs1341249	204026499	C	T	0.552	0.82	0.14	0.372	0.308	0.68
chr2	rs6432531	159973766	A	G	0.5	0.86	0.2	0.36	0.3	0.66
chr2	rs6758494	172488332	C	T	0.55	0.12	0.75	0.33	0.3	0.63
chr2	rs4538161	181437273	C	T	0.567	0.11	0.78	0.323	0.347	0.67
chr3	rs709641	10357638	A	G	0.108	0.6	0.13	0.292	0.762	0.47
chr3	rs2033704	41599118	A	G	0.217	0.14	0.47	0.643	0.313	0.33
chr3	rs4687805	52098353	A	G	0.441	0.85	0.24	0.291	0.319	0.61
chr3	rs9830096	124013259	A	G	0.475	0.21	0.82	0.315	0.295	0.61
chr3	rs6441308	101725048	T	C	0.567	0.8	0.11	0.367	0.323	0.69
chr3	rs6810132	13389864	A	G	0.144	0.56	0.11	0.296	0.746	0.45
chr3	rs10433406	125675364	A	C	0.568	0.11	0.73	0.322	0.298	0.62
chr4	rs4272045	61346511	A	G	0.567	0.14	0.84	0.293	0.407	0.7
chr4	rs2288961	101541124	A	G	0.433	0.87	0.2	0.303	0.367	0.67
chr4	rs6824854	182302276	C	T	0.467	0.24	0.85	0.293	0.317	0.61
chr4	rs1377859	178986081	A	G	0.892	0.87	0.51	0.762	0.402	0.36
chr4	rs13113121	22571570	C	T	0.475	0.18	0.83	0.345	0.305	0.65
chr5	rs1816235	5200032	A	G	0.558	0.76	0.13	0.318	0.312	0.63
chr5	rs2289854	53580894	T	G	0.45	0.24	0.88	0.31	0.33	0.64
chr5	rs7734243	109700718	T	C	0.825	0.89	0.57	0.715	0.395	0.32
chr5	rs703727	173134334	T	C	0.483	0.87	0.18	0.353	0.337	0.69
chr6	rs1119220	97558632	A	G	0.417	0.88	0.25	0.297	0.333	0.63
chr6	rs1737324	163718256	A	G	0.442	0.86	0.24	0.302	0.318	0.62
chr6	rs1076929	36456778	A	G	0.417	0.29	0.89	0.293	0.307	0.6
chr6	rs9442831	73417354	A	G	0.525	0.14	0.82	0.335	0.345	0.68
chr6	rs626755	149812757	C	T	0.551	0.14	0.74	0.309	0.291	0.6
chr7	rs1263542	157113869	A	G	0.527	0.79	0.13	0.317	0.343	0.66
chr7	rs2242480	99199402	C	T	0.892	0.89	0.43	0.782	0.322	0.46
chr7	rs4723034	30961436	T	G	0.792	0.87	0.5	0.662	0.292	0.37
chr7	rs801524	18673443	A	G	0.102	0.17	0.54	0.728	0.358	0.37
chr7	rs1859569	139195073	A	G	0.517	0.16	0.84	0.323	0.357	0.68
chr8	rs4237080	34900051	A	G	0.836	0.86	0.46	0.696	0.296	0.4
chr8	rs7006402	10220757	T	C	0.425	0.87	0.21	0.295	0.365	0.66
chr8	rs10106280	13396485	T	A	0.414	0.88	0.17	0.294	0.416	0.71
chr8	rs16895886	122785230	A	G	0.461	0.22	0.83	0.319	0.291	0.61
chr9	rs791656	12481250	A	G	0.567	0.13	0.87	0.303	0.437	0.74
chr10	rs1769236	724229	A	C	0.875	0.89	0.51	0.765	0.385	0.38
chr10	rs7906881	76271373	A	T	0.11	0.11	0.53	0.78	0.36	0.42
chr10	rs2242258	75277174	C	T	0.417	0.21	0.88	0.373	0.297	0.67
chr11	rs7118743	99123810	C	T	0.482	0.22	0.83	0.298	0.312	0.61
chr11	rs11605105	44670504	G	T	0.455	0.87	0.15	0.325	0.395	0.72
chr12	rs584878	48610834	A	C	0.55	0.15	0.75	0.3	0.3	0.6
chr12	rs1486405	114535056	A	G	0.517	0.82	0.12	0.337	0.363	0.7
chr12	rs7961135	7697306	C	T	0.509	0.18	0.8	0.311	0.309	0.62
chr12	rs3809254	3811527	T	C	0.442	0.86	0.26	0.302	0.298	0.6
chr12	rs3111342	17320410	T	G	0.517	0.78	0.12	0.297	0.363	0.66
chr13	rs11164137	113223874	A	G	0.433	0.87	0.21	0.303	0.357	0.66
chr13	rs4769414	24686586	T	C	0.458	0.24	0.85	0.302	0.308	0.61
chr13	rs1158807	33292716	A	G	0.558	0.13	0.74	0.312	0.298	0.61
chr14	rs17116374	81668270	T	A	0.108	0.15	0.58	0.742	0.312	0.43
chr14	rs1191554	29068585	A	C	0.867	0.43	0.87	0.297	0.737	0.44
chr14	rs6575700	98419370	A	G	0.517	0.13	0.84	0.353	0.357	0.71
chr15	rs11073161	34321848	A	C	0.475	0.22	0.88	0.305	0.355	0.66
chr15	rs11070883	50270857	A	G	0.441	0.26	0.89	0.299	0.331	0.63
chr15	rs1077834	56510771	A	G	0.56	0.8	0.14	0.36	0.3	0.66
chr15	rs2898685	37733172	G	A	0.542	0.12	0.83	0.338	0.372	0.71
chr15	rs2068982	72702941	A	G	0.525	0.15	0.79	0.325	0.315	0.64
chr15	rs8036731	91827831	A	G	0.457	0.2	0.85	0.343	0.307	0.65
chr15	rs1532750	80174831	C	T	0.483	0.19	0.81	0.327	0.293	0.62
chr16	rs6564869	79930226	A	C	0.508	0.85	0.19	0.358	0.302	0.66
chr16	rs12596707	8182147	A	G	0.175	0.14	0.49	0.685	0.335	0.35
chr18	rs939233	75962647	A	G	0.5	0.88	0.19	0.38	0.31	0.69
chr18	rs12957402	17885012	T	C	0.417	0.89	0.29	0.307	0.293	0.6
chr18	rs4891724	64961189	A	G	0.867	0.87	0.46	0.737	0.327	0.41
chr18	rs500899	41676278	C	T	0.492	0.14	0.85	0.368	0.342	0.71
chr19	rs3746319	49304071	T	C	0.508	0.18	0.81	0.312	0.318	0.63
chr20	rs4812817	42367435	A	G	0.517	0.78	0.18	0.297	0.303	0.6
chr20	rs6133125	4407954	A	G	0.883	0.41	0.87	0.293	0.753	0.46
chr21	rs12386284	25811939	G	T	0.575	0.79	0.11	0.365	0.315	0.68
chr22	rs2540620	16994874	A	C	0.542	0.86	0.13	0.402	0.328	0.73

σ: the allele frequency difference between 2 populations

AMI: American-Indian

EUR: European

*:the allele2 frequency

Sup Table 3: Genetic Model for rs1143679

European Americans						
Model	**Genotype**	**Control**	**Case**	OR (95% CI)	**P-value**	**AIC**
Codominant	G/G	830 (78.8%)	496 (67.2%)	1	<0.0001	2400.6
	A/G	211 (20%)	220 (29.8%)	1.74 (1.40-2.17)		
	A/A	12 (1.1%)	22 (3%)	3.07 (1.51-6.25)		
Dominant	G/G	830 (78.8%)	496 (67.2%)	1	<0.0001	2401
	A/G-A/A	223 (21.2%)	242 (32.8%)	1.82 (1.47-2.25)		
Recessive	G/G-A/G	1041 (98.9%)	716 (97%)	1	0.0053	2423.4
	A/A	12 (1.1%)	22 (3%)	2.67 (1.31-5.42)		
Multiplicative	---	---	---	1.75 (1.44-2.12)	<0.0001	2398.6

Hispanics Americans						
Model	**Genotype**	**Control**	**Case**	OR (95% CI)	**P-value**	**AIC**
Codominant	G/G	189 (82.5%)	503 (68.8%)	1	<0.0001	1038
	A/G	40 (17.5%)	212 (29%)	1.99 (1.37-2.90)		
	A/A	0 (0%)	16 (2.2%)	NA (0.00-NA)		
Dominant	G/G	189 (82.5%)	503 (68.8%)	1	<0.0001	1041.4
	A/G-A/A	40 (17.5%)	228 (31.2%)	2.14 (1.47-3.12)		
Recessive	G/G-A/G	229 (100%)	715 (97.8%)	1	0.003	1050
	A/A	0 (0%)	16 (2.2%)	NA (0.00-NA)		
Multiplicative	---	---	---	2.16 (1.51-3.10)	<0.0001	1038.7

UK						
Model	**Genotype**	**Control**	**Case**	OR (95% CI)	**P-value**	**AIC**
Codominant	G/G	436 (82.7%)	306 (69.5%)	1	<0.0001	1310.7
	A/G	86 (16.3%)	115 (26.1%)	1.91 (1.39-2.61)		
	A/A	5 (1%)	19 (4.3%)	5.41 (2.00-14.66)		
Dominant	G/G	436 (82.7%)	306 (69.5%)	1	<0.0001	1313.4
	A/G-A/A	91 (17.3%)	134 (30.4%)	2.10 (1.55-2.84)		
Recessive	G/G-A/G	522 (99%)	421 (95.7%)	1	6.00E-04	1325
	A/A	5 (1%)	19 (4.3%)	4.71 (1.74-12.72)		
Multiplicative	---	---	---	2.02 (1.54-2.64)	<0.0001	1309.2

Mexican						
Model	**Genotype**	**Control**	**Case**	OR (95% CI)	**P-value**	**AIC**
Codominant	G/G	227 (80.8%)	280 (71.4%)	1	0.0068	910.6
	A/G	52 (18.5%)	101 (25.8%)	1.57 (1.08-2.30)		
	A/A	2 (0.7%)	11 (2.8%)	4.46 (0.98-20.32)		
Dominant	G/G	227 (80.8%)	280 (71.4%)	1	0.0051	910.7
	A/G-A/A	54 (19.2%)	112 (28.6%)	1.68 (1.16-2.43)		
Recessive	G/G-A/G	279 (99.3%)	381 (97.2%)	1	0.038	914.3
	A/A	2 (0.7%)	11 (2.8%)	4.03 (0.89-18.31)		
Multiplicative	---	---	---	1.68 (1.20-2.35)	0.0021	909.1

Colombian						
Model	**Genotype**	**Control**	**Case**	OR (95% CI)	**P-value**	**AIC**
Codominant	G/G	298 (78.8%)	122 (59.5%)	1	<0.0001	737
	A/G	75 (19.8%)	74 (36.1%)	2.41 (1.64-3.54)		
	A/A	5 (1.3%)	9 (4.4%)	4.40 (1.44-13.39)		
Dominant	G/G	298 (78.8%)	122 (59.5%)	1	<0.0001	736.1
	A/G-A/A	80 (21.2%)	83 (40.5%)	2.53 (1.75-3.68)		
Recessive	G/G-A/G	373 (98.7%)	196 (95.6%)	1	0.025	755.1
	A/A	5 (1.3%)	9 (4.4%)	3.43 (1.13-10.36)		
Multiplicative	---	---	---	2.31 (1.66-3.23)	<0.0001	735.1

Sup Table 4: Comparisons of BIMBAM and IMPUTE/SNPTEST programs for imputation-based association test results.

SNP	POS	TYPE	RSQR	BIMBAM_log10(BF) i=10000	BIMBAM_log10(BF) i=1	IMPUTE/SNPTEST P value
rs8056505	31122399	typed	0.007	-0.434	-0.434	0.448457
rs2288005	31135409	imputed	0.091	1.47	1.704	0.00344042
rs7186832	31137964	imputed	0.006	-0.152	0.007	0.41728
rs12926702	31148472	imputed	0.004	0.433	1.186	0.0093972
rs11639689	31165419	imputed	0.002	0.061	0.238	0.984864
rs1808430	31166494	imputed	0.012	-0.043	0.185	0.163985
rs4561481	31167054	imputed	0.139	-0.231	0.064	0.221376
rs889551	31167923	imputed	0.007	-0.049	0.155	0.159941
rs4889640	31171768	imputed	0.003	-0.181	0.077	0.207168
rs11645526	31175740	imputed	0.003	0.053	0.141	0.338242
rs8057320	31177052	typed	0.004	-0.053	-0.052	0.103761
rs7193943	31178564	typed	0.004	-0.031	-0.032	0.0943874
rs11865830	31179046	typed	0.004	-0.129	-0.129	0.13464
rs1143679	**31184312**	**typed**	**1**	**20.088**	**20.208**	**6.17E-24**
rs3815801	31184438	imputed	0.004	0.124	0.143	0.0454723
rs8048583	31187037	typed	0.012	0.129	0.129	0.0491059
rs2359661	31188648	imputed	0.148	4.485	4.655	5.02E-07
rs9936831	31194649	typed	0.908	18.822	18.911	2.48E-22
rs7184677	31196567	imputed	0.831	18.671	18.55	7.67E-22
rs11861251	31196897	typed	0.018	0.231	0.231	0.0425852
rs11861258	31203045	imputed	0.002	0.461	1.383	0.0373923
rs8060163	31204647	imputed	0.017	0.214	0.217	0.0442214
rs9937837	31206440	imputed	0.303	6.509	6.472	1.76E-09
rs13338069	31206975	imputed	0.831	18.53	18.537	6.40E-22
rs7190807	31209411	imputed	0.831	18.532	18.554	6.60E-22
rs9888879	31217873	typed	0.831	18.418	18.502	3.09E-22
rs12928810	31219216	typed	0.831	18.538	18.483	2.47E-18
rs11645653	31220356	imputed	0.042	1.666	1.526	0.00220925
rs9888739	31220754	typed	0.831	18.635	18.719	7.97E-23
rs7499077	31225006	typed	0.303	6.696	6.732	9.96E-10
rs11860650	31234207	typed	0.764	18.157	18.25	9.46E-22
rs6565227	31236492	typed	0.764	18.066	18.15	8.95E-22
rs6565228	31236781	imputed	0.808	18.506	18.033	7.73E-21
rs11150610	31241737	imputed	0.083	2.289	1.719	0.000810029
rs7206295	31244020	typed	0.04	0.464	0.453	0.0144024
rs1143682	31244220	imputed	0.071	2.931	1.681	0.000392338
rs1143683	31244389	typed	0.656	15.266	15.261	5.82E-19
rs4077810	31248410	imputed	0.034	0.431	0.381	0.0121463
rs7193268	31248498	imputed	0.563	15.353	15.329	7.98E-19
rs1143678	31250506	typed	0.656	15.019	15.02	3.38E-18
rs9933520	31250887	typed	0.656	15.414	15.363	5.61E-16
rs3087796	31251154	imputed	0.04	0.419	0.397	0.020311
rs4597342	31251270	typed	0.04	0.381	0.381	0.0195458
rs4506917	31254851	typed	0.141	3.845	3.827	3.18E-06
rs9673519	31255058	imputed	0.008	0.44	0.388	0.0195657
rs3925075	31255249	imputed	0.141	3.694	1.572	1.88E-06
rs4075052	31255734	typed	0.04	0.396	0.396	0.0214537

rs4608351	31256349	imputed	0.04	0.397	0.411	0.0197694
rs4261553	31256665	typed	0.04	0.362	0.362	0.0181169
rs11150611	31263158	imputed	0.04	0.422	0.396	0.0210941
rs11150612	31265261	imputed	0.065	2.835	-0.165	0.000337938
rs11150613	31265311	typed	0.042	0.342	0.342	0.022834
rs11645917	31267327	imputed	0.134	3.572	1.311	1.85E-06
rs12923297	31268445	imputed	0.144	4.883	1.581	1.84E-06
rs4459557	31269144	imputed	0.04	0.383	0.373	0.0222107
rs4522435	31269424	imputed	0.002	0.266	1.833	0.0537049
rs4889649	31269764	imputed	0.074	4.286	2.168	0.000302291
rs4632147	31270882	imputed	0.665	14.883	11.372	1.28E-18
rs10782004	31270918	imputed	0.059	2.888	1.964	0.000335108
rs11574630	31271289	imputed	0.062	2.828	2.109	0.000120691
rs11574631	31271478	imputed	0.038	0.325	0.354	0.022239
rs11574632	31271554	imputed	0.02	1.877	-0.113	0.00744528
rs4548893	31271994	imputed	0.404	14.344	11.436	1.21E-17
rs11863903	31272410	imputed	0.021	1.896	-0.149	0.00767088
rs11150614	31273517	imputed	0.038	-0.346	0.313	0.0204552
rs9938765	31274259	imputed	0.002	0.277	0.275	0.056404
rs11574633	31274819	imputed	0.013	1.211	1.377	0.0311263
rs7190997	31275679	imputed	0.114	1.354	1.335	4.06E-05
rs11574635	31276317	imputed	0.022	1.948	-0.2	0.0104375
rs11574636	31276336	imputed	0.395	13.019	13.674	4.94E-13
rs11574637	31276375	imputed	0.483	13.014	13.648	1.86E-17
rs11150615	31277304	imputed	0.483	13.015	13.648	2.06E-17
rs11150616	31277591	imputed	0.04	-0.235	0.863	0.0210541
rs1106398	31277953	imputed	0.085	1.915	3.253	3.73E-05
rs4264407	31278694	imputed	0.002	0.228	0.174	0.0569965
rs2230429	31282036	typed	0.077	1.284	1.275	0.00154901
rs11150619	31284350	imputed	0.07	2.931	2.258	0.0060768
rs8046381	31286856	imputed	0.001	0.278	0.108	0.0525204
rs8052139	31294363	imputed	0.037	0.274	0.697	0.783686
rs11150620	31299690	imputed	0.034	0.381	0.41	0.400606
rs2929	31300809	imputed	0.06	0.066	0.152	0.0151748
rs9929832	31301045	typed	0.115	0.131	0.133	0.106695
rs1140195	31301680	imputed	0.04	0.258	0.679	0.822937
rs11574647	31302223	imputed	0.04	0.258	0.679	0.802476

RSQR: the r-squire between each SNP with rs1143679