

SUPPLEMENTAL MATERIAL

Appendix

Computation of IBD probabilities based on observed genotype and individual ancestry proportion.

We assume that each SNP has exactly 2 alleles and that the admixed population derived from intermating between exactly 2 ancestral populations. We also assume that the individual ancestry proportions are known (without error) or have been estimated.

Let P_{ik} be the reference allele frequency of the i^{th} marker in the k^{th} ancestral population. Following this notation, P_{11} would be the frequency of the reference allele in ancestral population A and P_{21} would be the frequency of the reference allele in ancestral population B. We also have $P_{12} = 1 - P_{11}$, $P_{22} = 1 - P_{21}$ and $\delta = \text{abs}(P_{11} - P_{21})$. This quantity is known as the delta-value, a well-known measure of ancestry informativeness content. Note the delta-value almost never equal to 1 since there are very few perfectly informative markers.

Also, let $G_{ij} = (g_1, g_2)$ be the observed genotype of the i^{th} individual at the j^{th} marker. Therefore, we have $G_{ij} \in \{(1,1), (1,2), (2,1), (2,2)\}$. Let θ_i denote the probability that the i^{th} person comes from ancestral population "A". We need to determine the ancestry at a marker given the observed genotype. This ancestry can only be known probabilistically given the limited number of perfectly informative markers.

Let π_1 (and π_2) denote the probability that the first allele (and second allele respectively) is inherited for came from ancestral population "A". Finally we will use the notation $Anc_{ij} = A$ to denote the event that the i^{th} individual inherited the j^{th} marker from ancestral population A. The ancestry at given marker can be computed by applied Bayes' theorem.

$$P(Anc_{ij} = A | g_s = t) = \frac{P(Anc_{ij} = A, g_s = t)}{P(g_s = t)} \quad (1)$$

$$P(Anc_{ij} = A | g_s = t) = \frac{P(Anc_{ij} = A)P(g_s = t | Anc_{ij} = A)}{P(Anc_{ij} = A)P(g_s = t | Anc_{ij} = A) + P(Anc_{ij} = B)P(g_s = t | Anc_{ij} = B)} \quad (2)$$

For $s \in \{1, 2\}$ and $t \in \{1, 2\}$, we have:

$$\pi_1 = P(Anc_{ij} = A | g_1 = 1) = \frac{\theta_i p_{11}}{\theta_i p_{11} + (1 - \theta_i) p_{21}} \quad (4)$$

$$\pi_1 = P(Anc_{ij} = A | g_1 = 2) = \frac{\theta_i p_{21}}{\theta_i p_{21} + (1 - \theta_i) p_{22}} \quad (5)$$

$$\pi_2 = P(Anc_{ij} = A | g_2 = 1) = \frac{\theta_i p_{11}}{\theta_i p_{11} + (1 - \theta_i) p_{12}} \quad (6)$$

$$\pi_2 = P(Anc_{ij} = A | g_2 = 2) = \frac{\theta_i p_{21}}{\theta_i p_{21} + (1 - \theta_i) p_{22}} \quad (7)$$

Therefore, the probability the i^{th} individual inherits 0 allele from ancestral population A is.

$$P\{I_i(j=0)\} = (1 - \pi_1)(1 - \pi_2) \quad (8)$$

The probability the i^{th} individual inherits 1 allele from ancestral population A is.

$$P\{I_i(j=1)\} = (1 - \pi_1)\pi_2 + \pi_1(1 - \pi_2) \quad (9)$$

Finally, the probability the i^{th} individual inherits 2 alleles from ancestral population A is.

$$P\{I_i(j=2)\} = \pi_1\pi_2 \quad (10)$$

We can also code for typical mode of inheritances by noting the recessive model corresponds to $P\{I_i(j=2)\}$, the dominant model is equivalent to $P\{I_i(j=1)\} + P\{I_i(j=2)\}$ and the additive model can be written as $P\{I_i(j=1)\} + 2P\{I_i(j=2)\}$.

Supplemental Table 1: Characteristics of the combined cohort of participants

Variable	AA-DHS (N=635)			FHS (N=103)			MESA (N=302)			ALL (N=1040)			P-value ¹
	Mean	SD	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD	Median	
Age (years)	56.11	9.56	56	58.43	10.55	58	64.48	9.08	65.5	58.77	10.22	59	<.0001
Diabetes duration (years)	10.28	8.05	8	11.78	9.06	10	10.13	9.32	7	10.4	8.46	8	0.1476
Hemoglobin A1c (%)	8.16	2.06	7.7	NA	NA	NA	7.43	1.78	7	7.94	2.02	7.5	<.0001
High sensitivity CRP (mg/dl)	0.97	1.51	0.46	0.86	1.12	0.48	0.53	0.67	0.29	0.82	1.28	0.36	<.0001
Glucose, fasting (mg/dl)	150.26	65.8	134	156.83	66.73	139.00	155.98	53.98	146	152.57	62.68	138	0.0289
HDL-cholesterol (mg/dl)	47.7	13.28	45	51.67	15.29	50.50	47.76	12.83	45	48.11	13.4	48.11	0.1351
LDL-cholesterol (mg/dl)	108.37	36.42	103	105.55	35.00	101.00	114.12	34.22	114	109.77	35.73	107	0.0064
Triglycerides (mg/dl)	128.93	124.47	104	122.66	80.70	98.50	130.92	114.27	106	128.89	117.8	104	0.7721
BMI (kg/m ²)	35.06	8.53	33.56	33.68	7.27	32.60	31.47	5.64	30.74	33.88	7.84	32.64	<.0001
CAC (original scale)	294.12	654.19	16	393.17	820.18	35.75	199.26	475.98	9.87	276.0	628.7	16.5	0.0009
CAC (log ₁₀ scale)	1.29	1.2	1.23	1.48	1.23	1.56	1.16	1.16	1.03	1.27	1.19	1.24	0.0009
ACE inhibitor use (%)	40.6%			44.0%			42.1			41.4%			0.1817
Current smoker (%)	24.3%			40.8%			16.6%			23.7%			0.00016
Past Smoker (%)	37.2%			17.5%			38.1%			35.6%			0.00044
Hypertension (%)	81.1%			91.3%			78.2%			82.3%			0.0193
Lipid-lowering medication (%)	47.9%			36.9%			29.5%			44.8%			<.0001
CAC > 10 (%)	52.1%			59.2%			49.7%			53.1%			0.0573

ACE – angiotensin converting enzyme inhibitor; BMI - body mass index; LDL - low density lipoprotein; HDL - high density lipoprotein; CAC – coronary artery calcified plaque; SD – standard deviation.

1: P-value of the Mann-Whitney test comparing the distribution of each variable in the 3 studies.

Supplemental Table 2: Summary of LOD scores observed with coronary artery calcified plaque in African Americans with type 2 diabetes stratified by study.

SNP	Chromosomal region	Nearest gene	Outcome	Study			Meta-analysis LOD score
				AA-DHS	MESA	FHS	
rs6663966	1p32.3	GLIS1	CAC < 10 vs. \geq 10	3.9	0.0	0.0	2.6
			Log(CAC+1)	5.0	0.1	0.1	4.0
rs7530895	1q32.1	61.9 kb from CHIT1	CAC <10 vs. \geq 10	3.0	0.3	0.8	3.7
			Log(CAC+1)	2.2	0.2	0.8	2.9
rs9309717	2p25.3	6.611 kb from ADI1	CAC <10 vs. \geq 10	1.0	1.1	0.4	2.4
			Log(CAC+1)	0.6	1.0	0.3	1.8
rs1712373	4q21.2	29.1 KB from PRKG2	CAC <10 vs. \geq 10	3.1	0.1	0.3	2.9
			Log(CAC+1)	3.3	0.1	0.8	3.6
rs1872861	4q31.1	78.4 kb from TBC1D9	CAC <10 vs. \geq 10	1.5	0.4	0.1	1.9
			Log(CAC+1)	0.6	0.7	0.1	1.4
rs6994682	8q22.2	26.7 kb from MIR4471	CAC <10 vs. \geq 10	1.8	1.1	0.2	2.2
			Log(CAC+1)	2.4	1.1	0.4	2.4
rs439314	9p21.2	261.4 kb from LOC100506422	CAC <10 vs. \geq 10	1.6	0.1	0.2	1.0
			Log(CAC+1)	2.2	0.6	0.0	2.6
rs7933164	11p15.4	STIM1	CAC <10 vs. \geq 10	0.1	2.2	0.5	1.4
			Log(CAC+1)	0.2	1.9	1.3	2.1
rs6590705	11q25	OPCML	CAC <10 vs. \geq 10	1.9	0.9	0.9	3.6
			Log(CAC+1)	1.5	0.5	0.8	2.7
rs7492028	13q32.1	77.3 kb from HS6ST3	CAC <10 vs. \geq 10	3.7	0.0	0.0	2.5
			Log(CAC+1)	3.9	0.0	0.0	2.9

Supplemental Table 3. Admixture mapping of coronary artery calcified plaque treated as a binary outcome (cases CAC ≥ 10 ; controls CAC < 10), largest LOD per chromosome.

Chromosome	Position	SNP	LOD	Model	Beta	Std Error	P-value
1	199992413	rs7530895	2.9	Recessive	-2.661	0.729	2.6E-04
2	5033361	rs9309717	2.5	Dominant	0.794	0.2348	7.2E-04
3	30007534	rs2197896	1.8	Recessive	-1.579	0.5466	3.9E-03
4	142113495	rs1872861	2.6	Dominant	-1.471	0.4411	4.2E-04
5	39207788	rs12657366	1.4	Recessive	-2.179	0.8574	1.1E-02
6	105717639	rs1190286	1.6	Recessive	-1.634	0.5983	6.3E-03
7	84793614	rs7807771	2.2	Recessive	-2.696	0.8548	1.6E-03
8	101490974	rs6994682	2.5	Recessive	-2.215	0.6529	6.9E-04
9	26369840	rs439314	2.3	Recessive	-2.193	0.6739	1.1E-03
10	131538677	rs7100028	2.2	Additive	-0.674	0.2136	1.6E-03
11	132839732	rs6590705	3.4	Recessive	-2.263	0.5717	7.6E-05
12	115433412	rs7969190	2.2	Recessive	-2.159	0.6862	1.7E-03
13	56527759	rs790325	2.9	Recessive	-2.444	0.6649	2.4E-04
14	44385429	rs17115651	1.8	Additive	-0.657	0.2288	4.1E-03
15	85301162	rs2859553	1.7	Recessive	-1.776	0.6293	4.8E-03
16	56672535	rs7191378	1.6	Recessive	-2.302	0.8484	6.7E-03
17	60833655	rs2904210	2.3	Dominant	0.777	0.2375	1.1E-03
18	73185272	rs874299	1.2	Dominant	0.501	0.2151	2.0E-02
19	37779881	rs10553	2.4	Recessive	2.051	0.6217	9.7E-04
20	61629948	rs310644	1.9	Recessive	-1.482	0.505	3.3E-03
21	32634146	rs2833775	0.7	Recessive	-1.042	0.5612	6.3E-02
22	47082281	rs742022	2.0	Recessive	-2.421	0.8018	2.5E-03

Supplemental Table 4. Admixture mapping of coronary artery calcified plaque treated as continuous outcome after logarithm transformation, largest LOD per chromosome.

Chromosome	Position	SNP	LOD	Model	Beta	Std Error	P-value
1	53782034	rs6663966	3.7	Dominant	1.3614	0.3286	3.7E-05
2	5033361	rs9309717	2.3	Dominant	0.8535	0.2641	1.3E-03
3	9092788	rs9825026	1.9	Recessive	-2.1800	0.7306	2.9E-03
4	82512488	rs1712373	3.0	Recessive	-1.8449	0.4939	2.0E-04
5	38254937	rs4869577	1.8	Additive	0.5982	0.2093	4.4E-03
6	143457111	rs4489173	1.6	Dominant	0.8206	0.3034	7.0E-03
7	3716791	rs6977305	1.8	Additive	-0.5694	0.1952	3.6E-03
8	101490974	rs6994682	2.7	Recessive	-2.6140	0.7351	4.0E-04
9	26369840	rs439314	2.7	Recessive	-2.6844	0.7558	4.0E-04
10	1401286	rs10794743	1.7	Recessive	-2.4276	0.8540	4.6E-03
11	4050526	rs7933164	2.5	Recessive	-2.0256	0.5914	6.4E-04
12	74600665	rs7967984	2.0	Recessive	-1.9360	0.6404	2.6E-03
13	96367097	rs7492028	2.8	Dominant	-1.0026	0.2801	3.6E-04
14	66596315	rs2144061	1.9	Additive	-0.8626	0.2911	3.1E-03
15	85301162	rs2859553	2.0	Recessive	-2.1625	0.7143	2.5E-03
16	56672535	rs7191378	2.1	Recessive	-3.0064	0.9585	1.8E-03
17	60833655	rs2904210	2.3	Dominant	0.8836	0.2689	1.1E-03
18	9690456	rs1869735	1.2	Dominant	0.8479	0.3611	1.9E-02
19	37779881	rs10553	1.7	Recessive	1.7471	0.6200	4.9E-03
20	61629948	rs310644	1.2	Recessive	-1.3337	0.5660	1.9E-02
21	15607469	rs722098	0.9	Additive	-0.4889	0.2353	3.8E-02
22	47082281	rs742022	1.8	Recessive	-2.65706	0.90864	3.5E-03

Table 5a: Coarse fine mapping of coronary artery calcified plaque on chromosome 1 (nearest gene, GLIS1)

SNP	Position (hg18)	Alleles	Frequency		Delta	Dominant model			Same model conditioning on sentinel SNP		
			YRI	CEU		Estimate	Std Error	P-Value	Estimate	Std Error	P-Value
rs1288373	53579402	T/C	0.58	0.04	0.53	0.56	0.46	0.225E-01	0.18	0.47	0.7006
rs1288509	53755911	C/G	0.17	0.85	0.68	0.27	0.33	4.18E-01	-0.12	0.35	0.7241
rs6663966^{*†}	53782034	C/A	0.26	1.00	0.74	1.48	0.33	1.11E-05	NA	NA	NA
rs10788957	54035689	T/C	0.21	0.92	0.70	0.69	0.33	3.71E-02	0.35	0.34	0.3046
rs12079966	54408585	G/C	0.18	0.91	0.73	0.70	0.30	2.17E-02	0.43	0.31	0.1664
rs1556528	54796767	A/G	0.29	0.93	0.64	0.81	0.39	3.67E-02	0.49	0.40	0.2227
rs6656290	54943752	T/C	0.55	0.02	0.53	0.98	0.43	2.29E-02	0.61	0.44	0.1676
rs299872	55014160	C/T	0.16	0.69	0.53	0.10	0.39	7.90E-01	-0.14	0.39	0.7202
rs449484	55030530	G/A	0.30	0.86	0.57	-0.01	0.45	9.84E-01	-0.49	0.46	0.2841
rs1702003	55060362	G/A	0.56	0.02	0.54	0.50	0.44	2.53E-01	0.02	0.45	0.9680
rs683880	55546895	T/C	0.19	0.78	0.59	0.57	0.38	1.31E-01	0.26	0.38	0.4907
rs7534516	55979412	G/A	0.06	0.58	0.53	0.48	0.34	1.56E-01	0.14	0.35	0.6774
rs4926690	56056400	G/A	0.04	0.63	0.59	0.04	0.30	9.01E-01	-0.24	0.30	0.4181
rs9436516	56123166	G/A	0.26	0.95	0.69	0.27	0.35	4.34E-01	-0.15	0.36	0.6718
rs7553801	56427400	A/G	0.23	0.96	0.73	0.47	0.31	1.35E-01	0.10	0.33	0.7634
rs12025982	56564716	A/G	0.05	0.56	0.51	0.40	0.39	3.16E-01	0.08	0.40	0.8334
rs778406	56476093	T/G	0.32	0.96	0.64	0.48	0.38	2.05E-01	0.11	0.38	0.7794

* Sentinel SNP for which the initial result was observed.

Supplementary Table 5b: Coarse fine mapping of coronary artery calcified plaque on chromosome 9

SNP	Position (hg18)	Alleles	Frequency	Delta	Recessive model			Same model conditioning on sentinel SNP			
			YRI	CEU		Estimate	Std Error	P-Value	Estimate	Std Error	P-Value
rs12340520	25587291	A/G	0.33	0.93	0.76	-2.12	0.91	1.96E-02	-1.18	0.9469	0.21
rs1937939	25700869	T/G	0.25	0.86	0.61	-2.01	0.88	2.29E-02	-1.29	0.9085	0.16
rs4978012	25721796	C/G	0.18	0.75	0.58	-1.72	0.87	4.87E-02	-0.81	0.9113	0.37
rs1231375	25755952	T/C	0.15	0.87	0.70	-1.16	0.71	1.02E-01	-0.45	0.7361	0.54
rs1220081	25792486	C/A	0.26	0.8	0.52	-2.91	1.11	8.70E-03	-2.52	1.1104	0.02
rs10738735	25882559	C/T	0.23	0.96	0.67	-1.25	0.76	1.02E-01	-0.49	0.7945	0.54
rs637039	25941211	C/T	0.16	0.88	0.73	-0.71	0.78	3.62E-01	0.05	0.8049	0.95
rs564225	25970121	G/C	0.36	0.93	0.57	-2.07	0.91	2.39E-02	-1.39	0.9783	0.16
rs7033724	26167022	T/A	0.18	0.93	0.75	-1.58	0.66	1.60E-02	-0.61	0.7411	0.41
rs1529827	26203626	C/A	0.32	0.88	0.56	-2.71	1.01	7.62E-03	-1.34	1.1518	0.24
rs2618024	26276392	C/T	0.16	0.73	0.58	-3.13	1.01	2.13E-03	-2.16	1.0714	0.04
rs439314*	26369840	A/C	0.31	0.99	0.68	-3.06	0.77	7.70E-05	NA	NA	NA
rs959697	26607589	G/A	0.26	0.76	0.50	-1.51	1.14	1.83E-01	-0.04	1.2213	0.97
rs10812461	26776862	C/T	0.26	0.58	0.43	-2.40	1.54	1.19E-01	-1.20	1.5950	0.45
rs12338945	27260176	G/A	0.32	0.83	0.51	-4.99	1.72	3.75E-03	-3.88	1.7657	0.03
rs7044345	27296595	G/C	0.6	0.01	0.58	-1.30	0.85	1.25E-01	-0.61	0.8660	0.48
rs10118453	27336663	T/C	0.56	0.03	0.53	-2.22	0.92	1.59E-02	-1.67	0.9336	0.07
rs4879540	27527479	A/T	0.08	0.59	0.51	-1.94	1.08	7.30E-02	-1.02	1.1118	0.36
rs10732349	27725305	A/G	0.58	0.05	0.52	-2.44	0.95	1.00E-02	-1.79	0.9649	0.06
rs4879740	27750375	G/A	0.69	0.03	0.67	-1.37	0.71	5.43E-02	-0.88	0.7228	0.23

* Sentinel SNP for which the initial result was observed.

Supplementary Table 5c: Coarse fine mapping of coronary artery calcified plaque on chromosome 11

SNP	Position (hg18)	Alleles	Frequency		Delta	Recessive model			Same model conditioning on sentinel SNP		
			YRI	CEU		Estimate	Std Error	P-Value	Estimate	Std Error	P-Value
rs11022922	2479195	T/C	0.19	0.82	0.63	-2.02	0.89	2.29E-02	-1.34	0.92	0.1440
rs10832134	2502486	C/T	0.17	0.62	0.52	0.04	1.08	9.71E-01	0.65	1.09	0.5546
rs11023094	2527361	A/G	0.37	0.79	0.50	0.27	1.28	8.31E-01	1.29	1.33	0.3319
rs4930137	2630594	C/T	0.24	0.83	0.61	-2.12	0.93	2.25E-02	-1.33	0.96	0.1662
rs231887	2739180	C/T	0.6	0.1	0.51	-1.93	0.99	5.26E-02	-1.21	1.01	0.2326
rs3852527	2826603	G/A	0.4	0.87	0.45	-1.59	1.13	1.58E-01	-0.40	1.18	0.7333
rs438384	3045651	T/C	0.01	0.43	0.46	-1.83	0.84	3.06E-02	-1.15	0.87	0.1839
rs2100087	3106604	T/C	0.46	0.01	0.45	-1.92	1.05	6.69E-02	-1.09	1.07	0.3113
rs10742077	3641703	G/C	0.21	0.86	0.65	-0.76	0.74	3.10E-01	0.07	0.78	0.9325
rs4910581	3643964	G/T	0.24	0.86	0.62	-1.10	0.81	1.73E-01	-0.17	0.86	0.8414
rs7120836	3841463	G/A	0.14	0.77	0.64	-0.76	0.77	3.20E-01	0.22	0.81	0.7910
rs7933164*	4050526	C/A	0.11	0.88	0.79	-2.36	0.60	8.90E-05	NA	NA	NA
rs12276850	4401360	G/A	0.29	0.9	0.61	-1.55	0.90	8.64E-02	-0.37	0.98	0.7028
rs7130283	4463048	C/G	0.59	0.01	0.58	0.80	0.84	3.41E-01	1.20	0.85	0.1590
rs331537	4471276	A/G	0.23	0.97	0.74	-1.23	0.67	6.70E-02	-0.24	0.74	0.7500
rs7110328	4500876	A/G	0.29	0.98	0.72	0.55	0.67	4.18E-01	1.29	0.70	0.0674
rs10768113	4629210	T/C	0.21	0.94	0.74	-0.52	0.65	4.20E-01	0.27	0.68	0.6948
rs4625457	4659187	A/C	0.2	0.74	0.54	0.03	0.92	9.70E-01	1.24	0.97	0.2019
rs2124447	4995989	G/A	0.34	0.87	0.59	-1.93	1.03	6.08E-02	-0.62	1.10	0.5713

* Sentinel SNP for which the initial result was observed.

Supplementary Table 6a: Summary of results in other samples for coronary artery calcified plaque treated as continuous outcome after logarithm transformation

Initial result		MESA AA Non-diabetic		MESA EA Diabetic		MESA EA Non-Diabetic		DHS EA Diabetic	
SNP	Region	SNP	P-value	SNP	P-value	SNP	P-value	SNP	P-value
rs6663966	1p32.3	rs1181183	2.9E-04	rs10888802	1.8E-03	rs2948047	1.5E-02	rs17392743	1.0E-03
rs7530895	1q32.1	rs495886	8.9E-04	rs2271763	2.0E-04	rs16849691	2.0E-04	rs7534078	6.8E-03
rs9309717	2p25.3	rs17019832	2.4E-04	rs12464169	2.3E-03	rs11123565	3.2E-03	rs17509530	4.0E-04
rs1712373	4q21.2	rs4565072	6.4E-04	rs13353802	8.8E-03	rs7696473	7.3E-03	rs9998218	5.0E-03
rs1872861	4q31.1	rs17354582	8.7E-03	rs11726692	2.5E-04	rs17007294	4.7E-03	Not available	
rs6994682	8q22.2	rs7002825	2.3E-05	rs7842985	4.7E-03	rs7016579	1.9E-03	rs1125111	3.5E-03
rs439314	9p21.2	rs1843467	1.1E-04	rs7874407	1.9E-02	rs1999461	1.8E-03	rs16910448	5.8E-03
rs7933164	11p15.4	rs7126968	6.0E-04	rs7119248	1.9E-05	rs276888	6.5E-04	rs12277512	5.6E-03
rs6590705	11q25	rs4936204	6.1E-04	rs7130004	8.9E-03	rs713278	3.8E-03	rs7936936	1.3E-02
rs790325	13q21.1	rs12869811	1.5E-03	rs213280	4.0E-04	rs17054168	3.7E-03	rs8000204	1.1E-02
rs7492028	13q32.1	rs1336099	3.3E-03	rs7324153	3.6424	rs9300366	2.1E-03	rs16953068	5.1E-03

Supplementary Table 6b: Summary of results in other samples for coronary artery calcified plaque treated as a binary outcome (cases CAC \geq 10; controls CAC <10)

Initial result		MESA AA Non-diabetic		MESA EA Diabetic		MESA EA Non-Diabetic		DHS EA Diabetic	
SNP	Region	SNP	P-value	SNP	P-value	SNP	P-value	SNP	P-value
rs6663966	1p32.3	rs12069945	2.2E-04	rs17387330	3.6E-03	rs12731127	8.1E-03	rs17392743	8.0E-04
rs7530895	1q32.1	rs12044612	1.9E-03	rs1022361	1.5E-03	rs1736450	1.9E-03	rs2993655	5.8E-03
rs9309717	2p25.3	rs11688192	8.7E-04	rs12464169	1.8E-03	rs12464169	8.2E-03	rs17509530	1.6E-03
rs1712373	4q21.2	rs4565072	9.8E-04	rs10213073	1.2E-02	rs9992933	4.7E-03	rs17004865	1.1E-03
rs1872861	4q31.1	rs17006636	6.1E-03	rs10222880	1.5E-03	rs6537004	4.2E-03	Not available	
rs6994682	8q22.2	rs7002825	8.7E-04	rs4734457	1.3E-02	rs879390	8.1E-03	rs1460930	1.8E-02
rs439314	9p21.2	rs17692968	5.6E-05	rs10967250	1.9E-02	rs1336466	4.7E-04	rs16910448	1.6E-02
rs7933164	11p15.4	rs7119863	2.1E-04	rs276885	1.5E-05	rs276888	2.4E-04	rs16907254	2.2E-03
rs6590705	11q25	rs1453833	1.7E-03	rs12791420	1.5E-02	rs11223506	8.7E-04	rs3758927	9.9E-03
rs790325	13q21.1	rs12869811	4.0E-03	rs213280	2.1E-03	rs17054168	1.7E-03	rs8000204	4.5E-03
rs7492028	13q32.1	rs7321303	7.6E-03	rs7324153	2.5E-04	rs7335011	9.7E-03	rs16953622	2.0E-02