Supplementary Material to "Positive selection of a *CD36* nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes." Fry *et al.*

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Table S1. Global survey of *CD36* T1264G allele frequencies.

Region	Population	Geographic origin	G allele	Total 2n	Freq	Climate	Prevalence
Sub-Saharan Africa	Yoruba	Nigeria	13	25	0.26	99.4%	48.0%
Sub-Saharan Africa	San	Namibia	0	6	0	7.6%	6.1%
Sub-Saharan Africa	Mbuti Pygmies	Democratic Republic of Congo	0	7	0	99.9%	55.3%
Sub-Saharan Africa	Mandenka	Senegal	0	21	0	96.9%	37.4%
Sub-Saharan Africa	Biaka Pygmies	Central African Republic	3	26	0.058	99.9%	41.7%
Sub-Saharan Africa	Bantu S.W. (Herero)	South Africa	0	2	0	14.8%	-
Sub-Saharan Africa	Bantu S.E. (Zulu)	South Africa	0	1	0	" "	-
Sub-Saharan Africa	Bantu S.E. (Tswana)	South Africa	0	2	0	" "	-
Sub-Saharan Africa	Bantu S.E. (S.Sotho)	South Africa	0	1	0	" "	-
Sub-Saharan Africa	Bantu S.E. (Pedi)	South Africa	0	1	0	" "	-
Sub-Saharan Africa	Kasem	Ghana	140	474	0.148	98.3%	48.6%
Sub-Saharan Africa	Nankan	Ghana	63	249	0.127	" "	" "
Sub-Saharan Africa	Buli	Ghana	3	14	0.107	" "	" "
Sub-Saharan Africa	Fula	Gambia	4	136	0.015	100.0%	36.0%
Sub-Saharan Africa	Jola	Gambia	2	89	0.011	" "	" "
Sub-Saharan Africa	Mandinka	Gambia	5	173	0.014	" "	" "
Sub-Saharan Africa	Manjago	Gambia	2	19	0.053	" "	" "
Sub-Saharan Africa	Serehuli	Gambia	5	52	0.048	" "	" "
Sub-Saharan Africa	Serere	Gambia	1	19	0.026	" "	" "
Sub-Saharan Africa	Wolloff	Gambia	5	94	0.027	" "	" "
Sub-Saharan Africa	Chonyi	Kenya	37	183	0.101	21.2%	36.3%
Sub-Saharan Africa	Duruma	Kenya	8	79	0.051	" "	" "
Sub-Saharan Africa	Giriama	Kenya	75	405	0.093	" "	" "
Sub-Saharan Africa	Kauma	Kenya	4	55	0.036	" "	" "
Sub-Saharan Africa	Bantu N.E.	Kenya	1	11	0.045	" "	" "
Sub-Saharan Africa	Malawian	Malawi	72	405	0.089	77.0%	58.2%
Oceania	Papuan	New Guinea	0	17	0	-	-
Oceania	NAN Melanesian	Bougainville	0	19	0	-	-
North Africa	Mozabite	Algeria (Mzab)	0	23	0	-	-
Middle East	Palestinian	Israel (Central)	0	50	0	-	-
Middle East	Druze	Israel (Carmel)	0	44	0	-	-
Middle East	Bedouin	Israel (Negev)	0	44	0	-	-
Europe	Tuscan	Italy	0	8	0	-	-
Europe	Sardinian	Italy	0	28	0	-	-
Europe	Russian	Russia	0	25	0	-	-
Europe	Orcadian	Orkney Islands	0	15	0	-	-
Europe	North Italian	Italy (Bergamo)	0	13	0	-	-
Europe	French Basque	France	0	22	0	-	-

Table S1. Global survey of *CD36* T1264G allele frequencies (*continued*).

Region	Population	Geographic origin	G allele	Total 2n	Freq	Climate	Prevalence
Europe	French	France	0	29	0	-	-
Europe	Adygei	Russia Caucasus	0	17	0	-	-
Asia	Yizu	China	0	10	0	-	-
Asia	Yakut	Siberia	0	23	0	-	-
Asia	Xibo	China	0	5	0	-	-
Asia	Uygur	China	0	9	0	-	-
Asia	Tujia	China	0	10	0	-	-
Asia	Tu	China	0	6	0	-	-
Asia	Sindhi	Pakistan	0	23	0	-	-
Asia	She	China	0	9	0	-	-
Asia	Pathan	Pakistan	0	23	0	-	-
Asia	Oroqen	China	0	10	0	-	-
Asia	Naxi	China	0	10	0	-	-
Asia	Mongola	China	0	10	0	-	-
Asia	Miaozu	China	0	10	0	-	-
Asia	Makrani	Pakistan	1	24	0.021	-	-
Asia	Lahu	China	0	9	0	-	-
Asia	Kalash	Pakistan	0	24	0	-	-
Asia	Japanese	Japan	0	26	0	-	-
Asia	Hezhen	China	0	9	0	-	-
Asia	Hazara	Pakistan	0	21	0	-	-
Asia	Han	China	0	41	0	-	-
Asia	Daur	China	0	10	0	-	-
Asia	Dai	China	0	9	0	-	-
Asia	Cambodians	Cambodia	0	11	0	-	-
Asia	Burusho	Pakistan	0	21	0	-	-
Asia	Brahui	Pakistan	0	24	0	-	-
Asia	Balochi	Pakistan	0	22	0	-	-
America	Surui	Brazil	0	21	0	-	-
America	Pima	Mexico	0	25	0	-	-
America	Maya	Mexico	0	25	0	-	-
America	Karitiana	Brazil	0	24	0	-	-
America	Colombians	Colombia	0	13	0	-	-

NOTE.- G allele, number of G alleles found; Total 2n, total number of individuals genotyped; Freq, minor allele frequency; Climate, proportion of countries population living in areas >75% suitable for malaria (i.e. endemic; perennial or seasonal areas); Prevalence, average national prevalence of malaria. Epidemiological statistics based on 1990 data (MARA-Lite Software 3.0.0, http://www.mara.org.za).

Table S2. *CD36* SNP association results ($P < 0.05$), in Gambian family and case-control studies.

Study	Phenotype	Model	SNP	Lower	OR	Upper	*P*-value	Perm.
Family	CM	recessive	rs10216184	0.24	0.49	0.98	0.043	
CC	SA	overdominant	rs10480808	1.06	1.45	1.99	0.022	
CC	Severe	allelic	rs1049654	1.03	1.21	1.43	0.021	0.05
CC	Severe	recessive	rs1049654	1.04	1.43	1.96	0.028	
Family	CM	overdominant	rs10499859	0.55	0.71	0.92	0.0099	
CC	CM	overdominant	rs1537593	0.55	0.73	0.96	0.026	
Family	SA	allelic	rs1572230	0.45	0.65	0.95	0.026	0.038
Family	SA	dominant	rs1572230	0.43	0.64	0.94	0.025	
Family	SA	overdominant	rs1572230	0.44	0.66	0.97	0.034	
CC	SA	overdominant	rs1722501	0.42	0.59	0.83	0.0026	
CC	Severe	overdominant	rs1722501	0.61	0.78	0.98	0.036	
CC	SA	overdominant	rs1924	1.02	1.40	1.93	0.039	
CC	SA	recessive	rs3173798	0.07	0.23	0.77	0.017	
CC	Severe	recessive	rs3211817	0.06	0.24	0.92	0.037	
Family	CM	overdominant	rs3211822	1.01	1.25	1.54	0.038	
Family	CM	recessive	rs3211822	0.50	0.69	0.97	0.034	
Family	Severe	overdominant	rs3211822	1.03	1.18	1.34	0.014	
CC	SA	overdominant	rs3211828	1.02	1.41	1.96	0.037	
CC	SA	recessive	rs3211828	0.15	0.36	0.88	0.025	
CC	Severe	recessive	rs3211842	0.50	0.69	0.96	0.026	
CC	SA	overdominant	rs3211867	1.09	1.51	2.07	0.012	
CC	SA	recessive	rs3211869	0.11	0.33	0.95	0.040	
Family	CM	overdominant	rs3211883	0.60	0.74	0.92	0.0071	
CC	SA	allelic	rs3211899	0.35	0.56	0.89	0.015	0.0077
CC	SA	dominant	rs3211899	0.32	0.53	0.87	0.011	
CC	SA	overdominant	rs3211899	0.32	0.52	0.86	0.010	
Family	CM	recessive	rs3211909	0.11	0.32	0.93	0.036	
Family	Severe	recessive	rs3211928	0.36	0.53	0.77	0.0010	
Family	CM	allelic	rs3211930	0.37	0.58	0.92	0.020	0.02
Family	CM	dominant	rs3211930	0.37	0.59	0.95	0.029	
CC	Severe	allelic	rs3211931	1.01	1.22	1.47	0.036	0.467
CC	Severe	dominant	rs3211931	1.00	1.26	1.59	0.046	
Family	CM	recessive	rs3211942	1.74	15.03	129.80	0.013	
CC	Severe	allelic	rs4728191	0.61	0.76	0.96	0.019	0.034
CC	Severe	dominant	rs4728191	0.58	0.76	0.99	0.041	
Family	SA	allelic	rs4728191	0.50	0.70	0.99	0.042	0.072
Family	SA	dominant	rs4728191	0.48	0.69	0.99	0.043	
CC	CM	recessive	rs6968407	1.06	1.89	3.38	0.031	
CC	Severe	overdominant	rs6968407	0.62	0.79	0.99	0.045	

NOTE.- Study, family or case-control (CC), Phenotype, cerebral malaria (CM), severe malarial anaemia (SA) or all severe malaria cases (Severe); Model, genetic model; Genotype/allele, compared with genotype 1/1 (major allele homozygote) or allele 1 (major allele); OR, odds ratio; Lower/Upper, 95% confidence interval of odds ratio; Perm, permutation *P*-value calculated using HAPLOVIEW (100,000 permutations).

Table S3A. UNPHASED analysis of pooled Gambian family and case-control studies (Severe malaria).

Severe	1/2 vs. 1/1		2/2 vs. 1/1					
Marker	OR	95% CI	OR	95% CI	Allelic	Over	Dom	Rec
def	0.83	0.66 - 1.05	1.59	0.74 - 3.39	0.390	0.091	0.194	0.152
G1439C	0.86	0.64 - 1.15	1.99	0.46 - 8.67	0.463	0.269	0.353	0.291
T1264G	0.93	0.67 - 1.31	0.72	0.08 - 6.48	0.649	0.705	0.672	0.796
rs10215288	0.91	0.81 - 1.03	1.01	0.82 - 1.22	0.457	0.100	0.185	0.536
rs10216184	1.11	0.99 - 1.26	1.11	0.84 - 1.47	0.098	0.108	0.077	0.714
rs10480808	1.12	0.99 - 1.27	1.14	0.97 - 1.34	0.086	0.288	0.057	0.462
rs1049654	1.02	0.9 - 1.15	1.02	0.86 - 1.2	0.814	0.821	0.768	0.959
rs10499857	1.00	0.89 - 1.12	0.91	0.71 - 1.17	0.673	0.824	0.890	0.443
rs1054516	0.99	0.89 - 1.12	0.97	0.77 - 1.21	0.806	0.991	0.876	0.787
rs1194178	0.99	0.87 - 1.11	0.97	0.74 - 1.27	0.762	0.842	0.782	0.864
rs1194180	0.93	0.83 - 1.04	0.92	0.74 - 1.14	0.199	0.260	0.171	0.698
rs11971740	1.00	0.89 - 1.12	0.95	0.78 - 1.16	0.722	0.828	0.909	0.576
rs12706912	0.99	0.88 - 1.11	0.91	0.76 - 1.09	0.381	0.728	0.685	0.277
rs13222488	1.06	0.94 - 1.19	1.20	0.95 - 1.52	0.125	0.602	0.234	0.183
rs13228738	1.12	0.99 - 1.28	1.17	0.82 - 1.67	0.069	0.105	0.068	0.553
rs1334511	0.89	0.79 - 1	0.98	0.81 - 1.19	0.322	0.049	0.092	0.555
rs1358337	1.01	0.9 - 1.14	1.03	0.87 - 1.22	0.731	0.987	0.801	0.767
rs1413659	0.95	0.85 - 1.07	0.95	0.76 - 1.18	0.428	0.454	0.384	0.848
rs1413661	1.03	0.92 - 1.16	0.98	0.8 - 1.19	0.877	0.493	0.652	0.664
rs1527463	1.06	0.93 - 1.22	1.06	0.73 - 1.56	0.397	0.413	0.380	0.859
rs1537593	1.04	0.91 - 1.18	1.12	0.95 - 1.31	0.167	0.694	0.401	0.177
rs1572230	0.89	0.77 - 1.03	0.74	0.45 - 1.2	0.060	0.155	0.084	0.313
rs17154155	1.01	0.89 - 1.14	1.07	0.91 - 1.26	0.429	0.700	0.713	0.362
rs17154246	1.01	0.9 - 1.14	0.98	0.77 - 1.25	0.966	0.817	0.887	0.851
rs1722501	0.93	0.83 - 1.04	0.99	0.8 - 1.21	0.403	0.175	0.222	0.757
rs1722502	1.03	0.91 - 1.15	1.03	0.84 - 1.26	0.688	0.722	0.662	0.906
rs1722505	1.02	0.91 - 1.14	0.98	0.8 - 1.2	0.968	0.651	0.796	0.722
rs17263407	1.13	1 - 1.29	1.26	0.9 - 1.78	0.031	0.088	0.039	0.311
rs17266080	1.14	0.99 - 1.3	0.96	0.65 - 1.43	0.163	0.054	0.081	0.600
rs1761661	1.01	0.9 - 1.13	0.97	0.79 - 1.18	0.892	0.780	0.954	0.697
rs1761662	1.02	0.9 - 1.14	0.92	0.71 - 1.19	0.849	0.668	0.918	0.485
rs1761663	1.02	0.9 - 1.16	1.03	0.88 - 1.21	0.676	0.909	0.696	0.789
rs1924	0.96	0.86 - 1.08	0.85	0.68 - 1.05	0.163	0.901	0.349	0.159
rs2366855	0.99	0.88 - 1.12	0.95	0.76 - 1.19	0.720	0.991	0.831	0.674
rs3173798	0.96	0.85 - 1.08	0.90	0.7 - 1.16	0.328	0.589	0.391	0.523
rs3173800	0.99	0.87 - 1.13	1.19	0.85 - 1.68	0.656	0.787	0.909	0.296

NOTE.- Heterozygotes (1/2) or minor allele homozygotes (2/2) compared with major allele homozygotes (1/1); OR, odds ratio; 95% C(onfidence) I(nterval); def, both CD36 deficiency alleles pooled; *P*-values for 4 genetic models: Rec(essive), Over(dominant), Dom(inant) and Allelic.

Table S3B. UNPHASED analysis of pooled Gambian family- and case-control studies (Severe malaria) - *continued*.

Severe	1/2 vs. 1/1		2/2 vs. 1/1					
Marker	OR	95% CI	OR	95% CI	Allelic	Over	Dom	Rec
rs3211810	1.00	0.88 - 1.14	0.90	0.62 - 1.31	0.804	0.915	0.932	0.580
rs3211817	1.09	0.94 - 1.27	0.94	0.54 - 1.64	0.382	0.252	0.298	0.734
rs3211821	1.04	0.92 - 1.17	0.91	0.73 - 1.14	0.865	0.367	0.721	0.297
rs3211822	1.11	0.98 - 1.25	1.03	0.87 - 1.22	0.417	0.092	0.136	0.643
rs3211828	0.99	0.88 - 1.11	0.83	0.66 - 1.05	0.269	0.837	0.572	0.130
rs3211842	1.03	0.91 - 1.15	0.94	0.78 - 1.12	0.667	0.412	0.881	0.307
rs3211849	1.02	0.9 - 1.15	1.02	0.87 - 1.19	0.821	0.845	0.772	0.952
rs3211850	1.02	0.9 - 1.17	0.96	0.65 - 1.41	0.873	0.711	0.785	0.778
rs3211867	0.95	0.85 - 1.07	0.88	0.73 - 1.05	0.152	0.846	0.284	0.224
rs3211869	0.96	0.86 - 1.08	0.92	0.71 - 1.18	0.411	0.645	0.470	0.592
rs3211870	1.09	0.96 - 1.24	1.07	0.91 - 1.26	0.366	0.323	0.197	0.914
rs3211883	0.97	0.86 - 1.09	1.10	0.93 - 1.32	0.518	0.271	0.877	0.142
rs3211886	1.01	0.88 - 1.16	1.18	0.78 - 1.77	0.638	0.988	0.790	0.448
rs3211888	1.01	0.83 - 1.22	0.82	0.37 - 1.82	0.912	0.893	0.993	0.622
rs3211897	1.05	0.86 - 1.28	-	-	0.919	0.569	0.816	0.033
rs3211899	0.89	0.76 - 1.04	1.19	0.67 - 2.13	0.269	0.114	0.169	0.431
rs3211909	1.03	0.9 - 1.17	0.87	0.6 - 1.25	0.927	0.614	0.842	0.403
rs3211911	0.85	0.69 - 1.06	1.35	0.51 - 3.59	0.232	0.127	0.169	0.467
rs3211913	1.01	0.9 - 1.14	0.88	0.73 - 1.07	0.380	0.432	0.868	0.133
rs3211923	1.02	0.78 - 1.34	0.72	0.08 - 6.12	0.942	0.871	0.906	0.755
rs3211928	1.16	1.03 - 1.3	0.86	0.65 - 1.13	0.327	0.006	0.046	0.078
rs3211930	0.87	0.7 - 1.07	0.21	0.03 - 1.56	0.085	0.232	0.140	0.104
rs3211931	1.11	0.99 - 1.24	1.07	0.84 - 1.37	0.143	0.094	0.083	0.947
rs3211942	1.07	0.9 - 1.26	1.88	0.95 - 3.72	0.190	0.534	0.318	0.076
rs4545029	1.00	0.89 - 1.13	0.94	0.75 - 1.19	0.757	0.875	0.914	0.606
rs4728191	0.88	0.77 - 1.01	0.85	0.56 - 1.28	0.060	0.084	0.058	0.606
rs6960369	0.96	0.85 - 1.07	0.96	0.8 - 1.16	0.522	0.507	0.438	0.914
rs6968407	1.06	0.94 - 1.19	1.31	1.04 - 1.64	0.048	0.770	0.180	0.036
rs6969989	1.13	1 - 1.27	1.02	0.74 - 1.41	0.111	0.041	0.052	0.777
rs6972923	1.01	0.89 - 1.15	1.04	0.88 - 1.21	0.674	0.902	0.801	0.675
rs6973242	1.04	0.93 - 1.18	1.23	0.98 - 1.56	0.120	0.804	0.287	0.102
rs7807607	1.01	0.9 - 1.13	0.98	0.8 - 1.21	0.955	0.850	0.951	0.817
rs819436	1.00	0.89 - 1.12	1.08	0.86 - 1.36	0.707	0.815	0.914	0.490
rs9784998	1.00	0.89 - 1.12	0.84	0.67 - 1.06	0.364	0.649	0.750	0.128
rs997906	1.05	0.92 - 1.21	1.12	0.75 - 1.68	0.399	0.534	0.438	0.641

NOTE.- Heterozygotes (1/2) or minor allele homozygotes (2/2) compared with major allele homozygotes (1/1); OR, odds ratio; 95% C(onfidence) I(nterval); *P*-values for 4 genetic models: Rec(essive), Over(dominant), Dom(inant) and Allelic.

Table S3C. UNPHASED analysis of pooled Gambian family- and case-control studies (CM).

CM	1/2 vs. 1/1		2/2 vs. 1/1					
Marker	OR	95% CI	OR	95% CI	Allelic	Over	Dom	Rec
def	0.85	0.6 - 1.21	1.52	0.5 - 4.63	0.634	0.351	0.472	0.462
G1439C	0.83	0.52 - 1.32	2.52	0.39 - 16.22	0.677	0.380	0.513	0.267
T1264G	1.00	0.62 - 1.62	-	-	0.811	0.901	0.951	0.317
rs10215288	0.93	0.78 - 1.11	1.00	0.74 - 1.35	0.696	0.392	0.487	0.755
rs10216184	1.26	1.05 - 1.51	1.01	0.65 - 1.57	0.069	0.011	0.019	0.612
rs10480808	1.12	0.93 - 1.37	1.13	0.89 - 1.44	0.296	0.447	0.215	0.710
rs1049654	1.00	0.84 - 1.2	1.00	0.78 - 1.29	0.973	0.969	0.964	0.998
rs10499857	0.98	0.82 - 1.17	0.70	0.47 - 1.05	0.235	0.824	0.552	0.087
rs1054516	1.00	0.84 - 1.2	1.02	0.72 - 1.44	0.941	0.994	0.967	0.926
rs1194178	0.91	0.76 - 1.09	1.19	0.8 - 1.79	0.825	0.221	0.457	0.266
rs1194180	0.97	0.82 - 1.16	0.95	0.7 - 1.3	0.707	0.817	0.723	0.842
rs11971740	0.95	0.8 - 1.13	0.94	0.69 - 1.27	0.543	0.630	0.523	0.819
rs12706912	1.00	0.84 - 1.19	1.00	0.77 - 1.3	0.984	0.988	0.983	0.994
rs13222488	1.08	0.9 - 1.3	1.35	0.95 - 1.91	0.119	0.682	0.248	0.139
rs13228738	1.21	1 - 1.48	1.48	0.87 - 2.5	0.025	0.085	0.034	0.246
rs1334511	0.81	0.68 - 0.98	0.80	0.6 - 1.08	0.037	0.080	0.023	0.519
rs1358337	0.99	0.83 - 1.19	1.15	0.9 - 1.46	0.348	0.458	0.797	0.183
rs1413659	0.96	0.81 - 1.15	0.93	0.67 - 1.29	0.600	0.785	0.642	0.747
rs1413661	0.98	0.82 - 1.16	1.09	0.8 - 1.5	0.819	0.648	0.927	0.496
rs1527463	1.13	0.92 - 1.38	1.15	0.68 - 1.93	0.249	0.288	0.239	0.755
rs1537593	0.96	0.79 - 1.16	1.24	0.98 - 1.58	0.076	0.060	0.803	0.009
rs1572230	0.97	0.78 - 1.2	0.87	0.44 - 1.74	0.665	0.799	0.718	0.732
rs17154155	1.03	0.85 - 1.24	1.07	0.84 - 1.36	0.586	0.995	0.682	0.652
rs17154246	1.02	0.86 - 1.22	1.02	0.7 - 1.5	0.830	0.840	0.819	0.957
rs1722501	0.91	0.76 - 1.08	1.01	0.75 - 1.36	0.603	0.243	0.350	0.641
rs1722502	0.97	0.81 - 1.16	1.18	0.86 - 1.62	0.602	0.517	0.995	0.236
rs1722505	0.96	0.81 - 1.14	1.02	0.74 - 1.41	0.856	0.584	0.694	0.760
rs17263407	1.19	0.98 - 1.44	1.32	0.78 - 2.21	0.057	0.103	0.059	0.451
rs17266080	1.14	0.93 - 1.4	1.12	0.58 - 2.15	0.243	0.233	0.215	0.874
rs1761661	0.95	0.8 - 1.13	1.03	0.75 - 1.41	0.833	0.512	0.639	0.713
rs1761662	0.92	0.77 - 1.1	1.19	0.81 - 1.75	0.928	0.262	0.537	0.258
rs1761663	1.07	0.88 - 1.31	1.14	0.9 - 1.45	0.269	0.964	0.371	0.390
rs1924	0.92	0.77 - 1.1	0.83	0.59 - 1.15	0.201	0.558	0.274	0.376
rs2366855	0.94	0.79 - 1.12	1.05	0.74 - 1.49	0.800	0.436	0.584	0.636
rs3173798	0.93	0.78 - 1.11	0.82	0.55 - 1.22	0.263	0.591	0.350	0.409
rs3173800	1.04	0.85 - 1.27	1.24	0.77 - 1.99	0.443	0.835	0.589	0.410

NOTE.- Heterozygotes (1/2) or minor allele homozygotes (2/2) compared with major allele homozygotes (1/1); OR, odds ratio; 95% C(onfidence) I(nterval); def, both CD36 deficiency alleles pooled; *P*-values for 4 genetic models: Rec(essive), Over(dominant), Dom(inant) and Allelic.

Table S3D. UNPHASED analysis of pooled Gambian family- and case-control studies (CM) – *continued*.

CM	1/2 vs. 1/1		2/2 vs. 1/1					
Marker	OR	95% CI	OR	95% CI	Allelic	Over	Dom	Rec
rs3211810	0.99	0.82 - 1.21	0.80	0.45 - 1.42	0.660	0.964	0.823	0.453
rs3211817	1.13	0.9 - 1.43	0.38	0.11 - 1.25	0.791	0.217	0.452	0.082
rs3211821	1.02	0.85 - 1.22	1.09	0.77 - 1.53	0.682	0.958	0.782	0.667
rs3211822	1.12	0.93 - 1.35	1.07	0.83 - 1.38	0.435	0.267	0.246	0.940
rs3211828	0.93	0.78 - 1.1	0.74	0.52 - 1.06	0.111	0.679	0.239	0.148
rs3211842	1.03	0.86 - 1.22	0.85	0.65 - 1.12	0.420	0.392	0.929	0.163
rs3211849	1.01	0.83 - 1.22	1.03	0.81 - 1.31	0.801	0.924	0.891	0.795
rs3211850	1.02	0.84 - 1.25	0.74	0.42 - 1.3	0.700	0.675	0.994	0.268
rs3211867	0.88	0.74 - 1.06	0.79	0.6 - 1.03	0.057	0.485	0.099	0.206
rs3211869	0.93	0.77 - 1.11	0.77	0.52 - 1.16	0.185	0.596	0.294	0.276
rs3211870	1.12	0.92 - 1.36	1.21	0.95 - 1.53	0.118	0.802	0.173	0.277
rs3211883	0.91	0.76 - 1.08	1.16	0.89 - 1.51	0.693	0.098	0.537	0.095
rs3211886	1.04	0.84 - 1.29	1.19	0.67 - 2.1	0.572	0.804	0.662	0.594
rs3211888	1.10	0.83 - 1.47	0.50	0.11 - 2.22	0.813	0.459	0.624	0.331
rs3211897	1.18	0.87 - 1.6	-	-	0.593	0.198	0.356	0.071
rs3211899	0.91	0.72 - 1.16	0.99	0.43 - 2.28	0.506	0.453	0.465	0.949
rs3211909	1.04	0.86 - 1.27	0.60	0.33 - 1.11	0.602	0.485	0.957	0.085
rs3211911	0.89	0.65 - 1.21	3.87	0.95 - 15.73	0.913	0.400	0.636	0.037
rs3211913	1.00	0.84 - 1.2	0.83	0.63 - 1.1	0.339	0.539	0.756	0.157
rs3211923	1.07	0.7 - 1.64	2.01	0.2 - 20.78	0.642	0.762	0.697	0.560
rs3211928	1.17	0.98 - 1.41	1.12	0.75 - 1.67	0.144	0.102	0.088	0.915
rs3211930	0.79	0.57 - 1.09	-	-	0.072	0.188	0.116	0.142
rs3211931	1.11	0.93 - 1.32	1.29	0.9 - 1.85	0.119	0.411	0.174	0.270
rs3211942	1.14	0.89 - 1.47	3.10	1.21 - 7.9	0.067	0.372	0.157	0.018
rs4545029	0.91	0.76 - 1.09	1.15	0.82 - 1.63	0.916	0.213	0.487	0.261
rs4728191	0.94	0.77 - 1.15	0.82	0.46 - 1.45	0.394	0.612	0.469	0.543
rs6960369	0.90	0.76 - 1.07	0.88	0.66 - 1.18	0.249	0.359	0.216	0.679
rs6968407	1.11	0.92 - 1.32	1.48	1.05 - 2.09	0.041	0.622	0.135	0.047
rs6969989	1.18	0.99 - 1.42	1.36	0.86 - 2.13	0.045	0.111	0.049	0.347
rs6972923	1.09	0.89 - 1.32	1.15	0.9 - 1.47	0.252	0.873	0.321	0.410
rs6973242	1.08	0.9 - 1.29	1.41	0.99 - 1.99	0.087	0.759	0.231	0.077
rs7807607	0.94	0.79 - 1.12	1.02	0.74 - 1.4	0.735	0.430	0.538	0.730
rs819436	0.92	0.77 - 1.1	1.18	0.83 - 1.67	0.990	0.228	0.539	0.226
rs9784998	0.95	0.8 - 1.12	0.72	0.5 - 1.03	0.119	0.933	0.321	0.088
rs997906	1.07	0.87 - 1.32	1.38	0.8 - 2.37	0.270	0.648	0.398	0.281

NOTE.- Heterozygotes (1/2) or minor allele homozygotes (2/2) compared with major allele homozygotes (1/1); OR, odds ratio; 95% C(onfidence) I(nterval); *P*-values for 4 genetic models: Rec(essive), Over(dominant), Dom(inant) and Allelic.

Table S3E. UNPHASED analysis of pooled Gambian family- and case-control studies (SA).

SA	1/2 vs. 1/1		2/2 vs. 1/1					
Marker	OR	95% CI	OR	95% CI	Allelic	Over	Dom	Rec
def	1.09	0.73 - 1.62	3.56	0.69 - 18.38	0.385	0.803	0.561	0.114
G1439C	1.19	0.73 - 1.95	-	-	0.529	0.483	0.483	-
T1264G	1.09	0.59 - 2.02	-	-	0.563	0.902	0.718	0.083
rs10215288	0.91	0.73 - 1.14	1.18	0.81 - 1.73	0.893	0.26	0.627	0.244
rs10216184	1.10	0.87 - 1.37	1.44	0.9 - 2.32	0.159	0.658	0.292	0.176
rs10480808	1.19	0.93 - 1.52	1.18	0.88 - 1.59	0.255	0.338	0.15	0.749
rs1049654	0.96	0.76 - 1.2	1.13	0.83 - 1.53	0.564	0.376	0.937	0.26
rs10499857	0.98	0.79 - 1.21	0.89	0.56 - 1.43	0.688	0.951	0.787	0.656
rs1054516	0.89	0.72 - 1.1	0.98	0.64 - 1.5	0.449	0.271	0.311	0.843
rs1194178	0.88	0.7 - 1.1	1.06	0.63 - 1.77	0.495	0.239	0.325	0.647
rs1194180	0.94	0.76 - 1.18	1.32	0.89 - 1.96	0.539	0.347	0.92	0.106
rs11971740	1.08	0.87 - 1.33	1.01	0.7 - 1.46	0.696	0.462	0.524	0.827
rs12706912	0.91	0.74 - 1.13	0.74	0.52 - 1.04	0.093	0.861	0.224	0.134
rs13222488	0.99	0.8 - 1.24	1.27	0.83 - 1.94	0.526	0.71	0.846	0.248
rs13228738	1.14	0.9 - 1.44	1.00	0.51 - 1.96	0.375	0.256	0.286	0.846
rs1334511	0.98	0.79 - 1.23	1.02	0.72 - 1.45	0.991	0.836	0.919	0.86
rs1358337	1.03	0.83 - 1.28	1.02	0.74 - 1.39	0.881	0.822	0.82	0.98
rs1413659	0.92	0.74 - 1.15	1.30	0.87 - 1.95	0.668	0.267	0.764	0.116
rs1413661	0.90	0.73 - 1.11	0.93	0.64 - 1.37	0.443	0.377	0.35	0.958
rs1527463	1.01	0.78 - 1.3	1.51	0.75 - 3.05	0.552	0.902	0.791	0.241
rs1537593	1.11	0.87 - 1.43	1.10	0.81 - 1.48	0.551	0.545	0.396	0.919
rs1572230	0.81	0.62 - 1.07	0.61	0.21 - 1.81	0.091	0.163	0.112	0.453
rs17154155	0.85	0.67 - 1.07	1.00	0.75 - 1.34	0.897	0.1	0.29	0.346
rs17154246	0.99	0.8 - 1.22	0.83	0.54 - 1.28	0.523	0.899	0.747	0.389
rs1722501	0.86	0.69 - 1.07	1.16	0.8 - 1.69	0.827	0.097	0.326	0.206
rs1722502	0.88	0.71 - 1.1	0.96	0.66 - 1.41	0.457	0.267	0.299	0.865
rs1722505	0.89	0.72 - 1.1	0.98	0.67 - 1.43	0.494	0.258	0.313	0.789
rs17263407	1.13	0.89 - 1.43	1.16	0.63 - 2.14	0.313	0.355	0.3	0.767
rs17266080	1.03	0.8 - 1.33	1.41	0.68 - 2.95	0.528	0.901	0.681	0.369
rs1761661	0.88	0.71 - 1.09	1.00	0.69 - 1.45	0.527	0.207	0.294	0.665
rs1761662	0.88	0.71 - 1.1	0.89	0.54 - 1.49	0.297	0.292	0.255	0.847
rs1761663	0.96	0.76 - 1.22	1.12	0.84 - 1.49	0.477	0.365	0.989	0.25
rs1924	1.02	0.83 - 1.26	0.82	0.53 - 1.26	0.657	0.604	0.995	0.304
rs2366855	0.93	0.75 - 1.16	0.99	0.66 - 1.48	0.671	0.518	0.555	0.902
rs3173798	1.02	0.82 - 1.26	0.67	0.4 - 1.12	0.424	0.562	0.854	0.101
rs3173800	1.02	0.8 - 1.3	1.01	0.54 - 1.89	0.871	0.852	0.854	0.997

NOTE.- Heterozygotes (1/2) or minor allele homozygotes (2/2) compared with major allele homozygotes (1/1); OR, odds ratio; 95% C(onfidence) I(nterval); def, both CD36 deficiency alleles pooled; *P*-values for 4 genetic models: Rec(essive), Over(dominant), Dom(inant) and Allelic.

Table S3F. UNPHASED analysis of pooled Gambian family- and case-control studies (SA) – *continued*.

SA	1/2 vs. 1/1		2/2 vs. 1/1					
Marker	OR	95% CI	OR	95% CI	Allelic	Over	Dom	Rec
rs3211810	1.04	0.82 - 1.32	0.93	0.44 - 1.96	0.852	0.716	0.777	0.807
rs3211817	1.20	0.9 - 1.58	0.66	0.22 - 1.96	0.46	0.177	0.285	0.374
rs3211821	0.98	0.79 - 1.22	0.94	0.61 - 1.44	0.763	0.927	0.817	0.793
rs3211822	0.99	0.79 - 1.23	1.06	0.77 - 1.45	0.811	0.77	0.996	0.661
rs3211828	1.04	0.84 - 1.29	0.73	0.46 - 1.15	0.56	0.415	0.95	0.126
rs3211842	1.01	0.81 - 1.25	0.91	0.66 - 1.26	0.653	0.733	0.902	0.505
rs3211849	0.83	0.66 - 1.05	0.97	0.73 - 1.3	0.698	0.079	0.191	0.414
rs3211850	0.98	0.76 - 1.26	1.62	0.82 - 3.2	0.59	0.721	0.905	0.151
rs3211867	1.11	0.89 - 1.39	0.76	0.53 - 1.08	0.427	0.07	0.66	0.033
rs3211869	1.03	0.83 - 1.27	0.78	0.46 - 1.31	0.713	0.636	0.983	0.309
rs3211870	1.17	0.92 - 1.49	1.02	0.75 - 1.39	0.84	0.131	0.289	0.428
rs3211883	0.92	0.74 - 1.15	0.91	0.65 - 1.26	0.454	0.6	0.433	0.75
rs3211886	1.02	0.79 - 1.33	1.03	0.47 - 2.24	0.866	0.877	0.865	0.963
rs3211888	0.99	0.71 - 1.4	0.67	0.19 - 2.37	0.754	0.969	0.883	0.533
rs3211897	1.26	0.87 - 1.83	-	-	0.49	0.231	0.336	0.205
rs3211899	0.63	0.46 - 0.86	1.49	0.51 - 4.35	0.018	0.002	0.006	0.251
rs3211909	0.89	0.69 - 1.14	0.94	0.5 - 1.77	0.41	0.364	0.361	0.969
rs3211911	0.88	0.59 - 1.33	-	-	0.372	0.585	0.467	0.251
rs3211913	1.08	0.87 - 1.33	0.86	0.62 - 1.21	0.712	0.248	0.714	0.213
rs3211923	0.96	0.62 - 1.49	-	-	0.726	0.896	0.807	0.426
rs3211928	0.98	0.78 - 1.23	0.84	0.5 - 1.41	0.614	0.99	0.757	0.52
rs3211930	0.92	0.62 - 1.34	-	-	0.502	0.663	0.575	0.358
rs3211931	1.02	0.82 - 1.27	1.05	0.66 - 1.67	0.803	0.884	0.823	0.87
rs3211942	0.94	0.7 - 1.28	0.53	0.12 - 2.35	0.502	0.76	0.614	0.41
rs4545029	0.83	0.66 - 1.03	0.93	0.6 - 1.46	0.198	0.096	0.107	0.891
rs4728191	0.87	0.67 - 1.11	0.59	0.24 - 1.43	0.13	0.329	0.192	0.291
rs6960369	1.11	0.89 - 1.37	1.11	0.78 - 1.59	0.413	0.454	0.348	0.821
rs6968407	0.97	0.78 - 1.2	1.36	0.89 - 2.07	0.485	0.474	0.953	0.112
rs6969989	1.13	0.91 - 1.41	0.96	0.55 - 1.67	0.477	0.243	0.313	0.668
rs6972923	0.95	0.75 - 1.2	1.09	0.81 - 1.46	0.606	0.356	0.883	0.315
rs6973242	0.99	0.8 - 1.23	1.25	0.82 - 1.91	0.561	0.675	0.889	0.259
rs7807607	0.85	0.69 - 1.05	1.03	0.71 - 1.5	0.467	0.107	0.201	0.511
rs819436	0.81	0.66 - 1.01	1.19	0.77 - 1.84	0.404	0.033	0.119	0.208
rs9784998	1.01	0.82 - 1.25	0.74	0.47 - 1.16	0.459	0.615	0.848	0.164
rs997906	0.94	0.72 - 1.22	0.88	0.42 - 1.84	0.594	0.684	0.617	0.797

NOTE.- Heterozygotes (1/2) or minor allele homozygotes (2/2) compared with major allele homozygotes (1/1) ; OR, odds ratio; 95% C(onfidence) I(nterval); *P*-values for 4 genetic models: Rec(essive), Over(dominant),, Dom(inant) and Allelic.

Table S4. 54 SNPs genotyped and analyzed in the HGDP-CEPH Diversity Panel.

SNP	Coord	Success
rs4731338	79779138	96.9%
rs304753	79820301	97.6%
rs304775	79841610	99.4%
rs1878314	79861553	91.3%
rs568125	79882207	97.8%
rs704871	79903613	95.9%
rs2944398	79924797	97.6%
rs6467192	79945734	95.2%
rs10216027	79968467	96.4%
rs2103134	79997284	88.8%
rs1931694	80009513	97.7%
rs1851937	80028981	97.2%
rs2065668	80058544	99.1%
rs1722505	80078625	94.8%
rs10499859	80096746	96.6%
rs13306227	80114006	98.5%
rs1527463	80114267	99.8%
rs3211810	80114953	99.8%
rs3211828	80117539	99.7%
rs3211842	80120572	95.2%
rs3765187	80123939	99.9%
rs5957	80130272	97.4%
rs3211917	80133237	99.2%
rs3211938	80138385	99.8%
rs3211949	80140136	95.9%
rs1803256	80141286	96.7%
rs7755	80144207	98.9%
rs1405745	80146176	100.0%
rs1527480	80155968	97.6%
rs12534038	80167036	97.4%
rs6958863	80177838	99.8%
rs2366858	80178558	97.3%
rs954409	80189667	98.7%
rs1880957	80192165	98.6%
rs1527467	80197742	99.8%
rs1852538	80202937	90.0%
rs1527470	80208765	90.6%
rs1405743	80216084	95.6%
rs10246081	80228534	97.1%
rs12669309	80238106	94.6%
rs3807103	80249157	96.6%
rs12673477	80268683	94.3%
rs6467405	80274281	97.4%
rs17154508	80289376	95.8%
rs10487878	80298261	99.1%
rs4731861	80309471	96.5%
rs7795137	80328382	97.4%
rs7784762	80334149	99.0%
rs7779029	80370048	95.4%
rs2057880	80387869	87.6%
rs17154598	80404725	96.4%
rs740210	80425673	94.8%
rs2367090	80447883	97.2%
rs701327	80474845	98.8%

NOTE.- SNP, dbSNP reference SNP identifier; Coord, chromosome 7 coordinate values from NCBI build 36/dbSNP 126; Genotyping success rate in the 974 individuals used for our population genetic analysis.

Table S5. Sample sizes and demographics by study design and region of origin.

Study Site	Samples	Size	Male (%)	Mean Age (Months)	Ethnic Groups
Population-based studies					
Gambia	Cases	727	50.8	52.1	106 Fula, 183 Jola, 274 Mandinka, 80 Wolloff, 84 Other
	Controls	623	50.1	0	136 Fula, 89 Jola, 173 Mandinka, 94 Wolloff, 131 Other
Malawi	Cases	718	49.3	42.1	*
	Controls	405	52.2	0	
Kenya	Cases	708	55.1	30.3	108 Chonyi, 320 Giriama, 41 Kauma, 239 other
	Controls	902	51.6	0	183 Chonyi, 405 Giriama, 55 Kauma, 259 other
Ghana	Cases	792	57.4	18.5	435 Kasem, 305 Nankan, 28 Buli, 28 other
	Controls	806	56.3	20.5	508 Kasem, 269 Nankan, 15 Buli, 14 other
Family-based studies					
Gambia	Trios	1288	54.0	47.7	189 Fula, 216 Jola, 526 Mandinka, 174 Wolloff, 183 Other
Malawi	Trios	225	54.7	38.5	*
Kenya	Trios	234	48.1	29.8	51 Chonyi, 134 Giriama, 15 Kauma, 34 other

NOTE.- Apart from the Ghanaians, all controls are cord blood samples are therefore from children age zero. *Malawians in the study region are considered relatively ethnically homogenous; therefore no ethnicity information was gathered. Gender (% male) and mean age of probands are reported.

Table S6A. *CD36* genotyping assay performance (Gambian case-control study).

	Controls					HWE	Cases				
Marker	1/1	1/2	2/2	Freq	Success	*P*	1/1	1/2	2/2	Freq	Success
G1439C	594	22	0	0.018	98.9%	0.493	706	17	1	0.013	99.6%
T1264G	595	24	0	0.019	99.4%	0.579	706	20	0	0.014	99.9%
rs10215288	317	247	56	0.290	99.5%	0.478	371	267	79	0.296	98.6%
rs10216184	383	207	29	0.214	99.4%	0.952	446	243	34	0.215	99.4%
rs10480808	189	284	148	0.467	99.7%	0.049	191	371	161	0.479	99.4%
rs1049654	251	279	88	0.368	99.2%	0.503	255	338	130	0.414	99.4%
rs10499857	376	213	31	0.222	99.5%	0.972	448	243	31	0.211	99.3%
rs1054516	380	209	31	0.219	99.5%	0.818	427	251	45	0.236	99.4%
rs1194178	409	191	21	0.188	99.7%	0.906	482	211	30	0.187	99.4%
rs1194180	353	223	47	0.254	100.0%	0.185	404	260	61	0.263	99.7%
rs11971740	298	267	54	0.303	99.4%	0.647	347	302	73	0.310	99.3%
rs12706912	251	279	90	0.370	99.5%	0.422	306	327	92	0.352	99.7%
rs13222488	343	250	28	0.246	99.7%	0.045	420	256	46	0.241	99.3%
rs13228738	442	163	16	0.157	99.7%	0.932	523	183	19	0.152	99.7%
rs1334511	302	241	62	0.302	97.1%	0.206	353	268	89	0.314	97.7%
rs1358337	212	300	107	0.415	99.4%	0.980	253	344	128	0.414	99.7%
rs1413659	348	215	46	0.252	97.8%	0.138	396	255	59	0.263	97.7%
rs1413661	326	253	41	0.270	99.5%	0.433	378	280	63	0.282	99.2%
rs1527463	474	134	13	0.129	99.7%	0.421	546	158	20	0.137	99.6%
rs1537593	150	309	162	0.510	99.7%	0.956	181	350	191	0.507	99.3%
rs1572230	478	130	13	0.126	99.7%	0.313	585	129	8	0.100	99.3%
rs17154155	171	313	136	0.472	99.5%	0.794	219	354	150	0.452	99.4%
rs17154246	373	204	45	0.236	99.8%	0.029	422	265	38	0.235	99.7%
rs1722501	329	243	48	0.273	99.5%	0.798	396	250	77	0.279	99.4%
rs1722502	320	248	44	0.275	98.2%	0.727	371	274	67	0.287	97.9%
rs1722505	325	253	41	0.271	99.4%	0.424	380	282	62	0.280	99.6%
rs17263407	416	180	20	0.179	98.9%	0.971	494	205	24	0.175	99.4%
rs17266080	466	143	11	0.133	99.5%	0.880	538	172	10	0.133	99.0%
rs1761661	318	260	43	0.279	99.7%	0.338	375	287	64	0.286	99.9%
rs1761662	395	205	22	0.200	99.8%	0.531	454	240	31	0.208	99.7%
rs1761663	156	318	148	0.494	99.8%	0.613	194	345	186	0.494	99.7%
rs1924	337	239	45	0.265	99.7%	0.832	400	277	46	0.255	99.4%
rs2366855	362	214	40	0.239	98.9%	0.317	425	245	50	0.240	99.0%
rs3173798	374	212	35	0.227	99.7%	0.556	454	240	28	0.205	99.3%
rs3173800	456	147	18	0.147	99.7%	0.192	530	174	21	0.149	99.7%
rs3211810	476	129	16	0.130	99.7%	0.068	533	170	21	0.146	99.6%

NOTE.- Genotype counts for major allele homozygotes (1/1), heterozygotes (1/2) and minor allele homozygotes (2/2); Freq, minor allele frequency; Success, percentage genotyping success; HWE, exact test Hardy-Weinberg equilibrium *P*-value (controls only).

Table S6B. *CD36* genotyping assay performance (Gambian case-control study) – *continued.*

	Controls					HWE	Cases				
Marker	1/1	1/2	2/2	Freq	Success	*P*	1/1	1/2	2/2	Freq	Success
rs3211817	512	96	11	0.095	99.4%	0.022	596	125	3	0.090	99.6%
rs3211821	359	226	32	0.235	99.0%	0.708	409	258	45	0.244	97.9%
rs3211822	219	285	108	0.409	98.2%	0.395	258	324	135	0.414	98.6%
rs3211828	358	217	41	0.243	98.9%	0.345	429	260	31	0.224	99.0%
rs3211842	258	262	101	0.374	99.7%	0.017	302	338	85	0.350	99.7%
rs3211849	179	305	135	0.464	99.4%	0.859	197	355	170	0.481	99.3%
rs3211850	492	115	14	0.115	99.7%	0.036	541	166	17	0.138	99.6%
rs3211867	278	261	81	0.341	99.5%	0.130	307	329	79	0.341	98.3%
rs3211869	379	208	34	0.222	99.7%	0.497	456	239	28	0.204	99.4%
rs3211870	159	303	156	0.498	99.2%	0.673	184	363	175	0.494	99.3%
rs3211883	276	270	76	0.339	99.8%	0.470	326	303	95	0.340	99.6%
rs3211886	477	134	12	0.127	100.0%	0.577	563	143	16	0.121	99.3%
rs3211888	557	56	6	0.055	99.4%	0.005	667	55	3	0.042	99.7%
rs3211897	569	50	2	0.043	99.7%	0.733	656	69	0	0.048	99.7%
rs3211899	508	110	3	0.093	99.7%	0.353	607	110	8	0.087	99.7%
rs3211909	454	145	22	0.152	99.7%	0.025	524	180	18	0.150	99.3%
rs3211911	552	62	3	0.055	99.0%	0.612	664	57	3	0.044	99.6%
rs3211913	268	262	91	0.357	99.7%	0.049	296	345	83	0.353	99.6%
rs3211923	582	35	2	0.032	99.4%	0.234	691	32	0	0.022	99.4%
rs3211928	344	236	37	0.251	99.0%	0.742	364	288	41	0.267	95.3%
rs3211930	559	61	1	0.051	99.7%	0.905	674	51	1	0.037	99.9%
rs3211931	348	236	39	0.252	100.0%	0.966	378	296	51	0.274	99.7%
rs3211942	528	82	8	0.079	99.2%	0.044	595	118	7	0.092	99.0%
rs4545029	367	222	31	0.229	99.5%	0.799	446	233	44	0.222	99.4%
rs4728191	453	143	24	0.154	99.5%	0.006	564	148	13	0.120	99.7%
rs6960369	277	286	60	0.326	100.0%	0.294	321	314	85	0.336	99.0%
rs6968407	343	249	30	0.248	99.8%	0.087	420	255	52	0.247	100.0%
rs6969989	361	230	17	0.217	97.6%	0.007	433	252	19	0.206	96.8%
rs6972923	154	313	147	0.494	98.6%	0.669	193	338	183	0.493	98.2%
rs6973242	343	248	30	0.248	99.7%	0.094	422	257	48	0.243	100.0%
rs7807607	322	248	42	0.271	98.2%	0.591	386	269	62	0.274	98.6%
rs819436	389	205	28	0.210	99.8%	0.955	451	229	41	0.216	99.2%
rs9784998	370	213	37	0.231	99.5%	0.446	429	264	30	0.224	99.4%
rs997906	454	151	13	0.143	99.2%	0.959	535	164	19	0.141	98.8%

NOTE.- Genotype counts for major allele homozygotes (1/1), heterozygotes (1/2) and minor allele homozygotes (2/2); Freq, minor allele frequency; Success, percentage genotyping success; HWE, exact test Hardy-Weinberg equilibrium *P*-value (controls only).

Table S6C. *CD36* genotyping assay performance (Gambian family study).

	Parents					Cases				
Marker	1/1	1/2	2/2	Freq	Success	1/1	1/2	2/2	Freq	Success
G1439C	2454	110	7	0.024	99.8%	1220	65	2	0.027	99.9%
T1264G	2496	77	1	0.015	99.9%	1248	36	1	0.015	99.8%
rs10215288	1249	1031	213	0.292	96.8%	643	507	110	0.288	97.8%
rs10216184	1714	766	87	0.183	99.7%	858	382	41	0.181	99.5%
rs10480808	751	1262	539	0.458	99.1%	371	629	284	0.466	99.7%
rs1049654	869	1248	435	0.415	99.1%	442	620	218	0.413	99.4%
rs10499857	1520	907	143	0.232	99.8%	744	475	67	0.237	99.8%
rs1054516	1462	969	143	0.244	99.9%	748	454	85	0.242	99.9%
rs1194178	1638	835	86	0.197	99.3%	830	392	56	0.197	99.2%
rs1194180	1390	993	182	0.265	99.6%	717	483	87	0.255	99.9%
rs11971740	1216	1087	248	0.310	99.0%	615	547	121	0.307	99.6%
rs12706912	1066	1162	342	0.359	99.8%	540	580	167	0.355	99.9%
rs13222488	1560	881	126	0.221	99.7%	780	430	75	0.226	99.8%
rs13228738	1942	591	41	0.131	99.9%	967	293	27	0.135	99.9%
rs1334511	1210	969	363	0.333	98.7%	610	482	190	0.336	99.5%
rs1358337	901	1246	424	0.407	99.8%	450	623	212	0.407	99.8%
rs1413659	1386	960	181	0.262	98.1%	713	479	86	0.255	99.2%
rs1413661	1295	1105	173	0.282	99.9%	669	511	108	0.282	100.0%
rs1527463	1993	529	46	0.121	99.7%	992	271	20	0.121	99.6%
rs1537593	692	1267	611	0.484	99.8%	346	628	313	0.487	99.9%
rs1572230	2038	489	36	0.109	99.5%	1034	234	16	0.104	99.7%
rs17154155	778	1254	541	0.454	99.9%	388	606	293	0.463	99.9%
rs17154246	1543	897	123	0.223	99.5%	785	432	70	0.222	99.9%
rs1722501	1349	1008	217	0.280	99.9%	673	520	94	0.275	99.9%
rs1722502	1265	1061	174	0.282	97.0%	661	499	107	0.281	98.4%
rs1722505	1303	1097	173	0.280	99.9%	673	504	106	0.279	99.6%
rs17263407	1851	636	49	0.145	98.4%	925	312	28	0.145	98.2%
rs17266080	1934	552	66	0.134	99.1%	942	301	36	0.146	99.3%
rs1761661	1285	1101	183	0.286	99.7%	664	511	111	0.285	99.8%
rs1761662	1595	872	100	0.209	99.7%	813	415	59	0.207	99.9%
rs1761663	683	1327	559	0.476	99.7%	350	653	283	0.474	99.8%
rs1924	1364	997	197	0.272	99.3%	693	493	98	0.268	99.7%
rs2366855	1416	981	141	0.249	98.5%	725	464	83	0.248	98.8%
rs3173798	1543	879	131	0.223	99.1%	771	438	74	0.228	99.6%
rs3173800	1922	598	47	0.135	99.7%	977	280	30	0.132	99.9%
rs3211810	1854	669	50	0.149	99.9%	919	348	19	0.150	99.8%

NOTE.- Genotype counts for major allele homozygotes (1/1), heterozygotes (1/2) and minor allele homozygotes (2/2); Freq, minor allele frequency; Success, percentage genotyping success; HWE, exact test Hardy-Weinberg equilibrium *P*-value (controls only).

Table S6D. ***CD36*** **genotyping assay performance (Gambian family study) –** ***continued.***

	Parents					Cases				
Marker	1/1	1/2	2/2	Freq	Success	1/1	1/2	2/2	Freq	Success
rs3211817	2159	394	17	0.083	99.8%	1076	198	14	0.088	100.0%
rs3211821	1427	947	171	0.253	98.8%	719	478	84	0.252	99.5%
rs3211822	959	1217	381	0.387	99.3%	464	630	180	0.389	98.9%
rs3211828	1456	961	154	0.247	99.8%	728	474	83	0.249	99.8%
rs3211842	1054	1170	330	0.358	99.1%	535	576	176	0.361	99.9%
rs3211849	702	1286	584	0.477	99.8%	356	631	296	0.477	99.6%
rs3211850	1929	596	50	0.135	100.0%	955	307	22	0.137	99.7%
rs3211867	1042	1157	325	0.358	98.0%	542	559	176	0.357	99.1%
rs3211869	1547	873	128	0.222	98.9%	775	434	71	0.225	99.4%
rs3211870	683	1276	606	0.485	99.6%	334	640	310	0.491	99.7%
rs3211883	1136	1137	294	0.336	99.7%	588	519	171	0.337	99.2%
rs3211886	2033	497	29	0.108	99.3%	1027	237	18	0.106	99.5%
rs3211888	2315	255	5	0.051	100.0%	1149	133	5	0.056	99.9%
rs3211897	2358	204	13	0.045	100.0%	1175	110	0	0.043	99.8%
rs3211899	2173	382	19	0.082	99.9%	1102	175	10	0.076	99.9%
rs3211909	1869	617	51	0.142	98.5%	930	323	23	0.145	99.1%
rs3211911	2338	189	9	0.041	98.4%	1181	92	3	0.038	99.1%
rs3211913	1104	1136	290	0.339	98.2%	570	573	138	0.331	99.5%
rs3211923	2440	112	2	0.023	99.1%	1225	61	1	0.024	99.9%
rs3211928	1384	833	119	0.229	90.7%	686	450	42	0.227	91.5%
rs3211930	2370	201	2	0.040	99.9%	1189	97	0	0.038	99.8%
rs3211931	1502	901	151	0.236	99.1%	744	480	56	0.231	99.4%
rs3211942	2240	309	7	0.063	99.2%	1137	141	6	0.060	99.7%
rs4545029	1528	913	131	0.228	99.8%	773	443	71	0.227	99.9%
rs4728191	1946	571	51	0.131	99.7%	982	284	20	0.126	99.8%
rs6960369	1102	1119	307	0.343	98.1%	560	563	153	0.341	99.1%
rs6968407	1562	874	126	0.220	99.5%	781	427	77	0.226	99.8%
rs6969989	1638	814	72	0.190	98.0%	819	405	43	0.194	98.4%
rs6972923	681	1309	554	0.475	98.8%	347	643	283	0.475	98.8%
rs6973242	1555	880	128	0.222	99.5%	779	431	76	0.227	99.8%
rs7807607	1288	1057	168	0.277	97.6%	661	497	106	0.280	98.1%
rs819436	1524	935	104	0.223	99.5%	774	436	76	0.229	99.8%
rs9784998	1448	974	150	0.248	99.8%	724	480	82	0.250	99.8%
rs997906	1953	518	36	0.118	97.3%	1001	258	17	0.114	99.1%

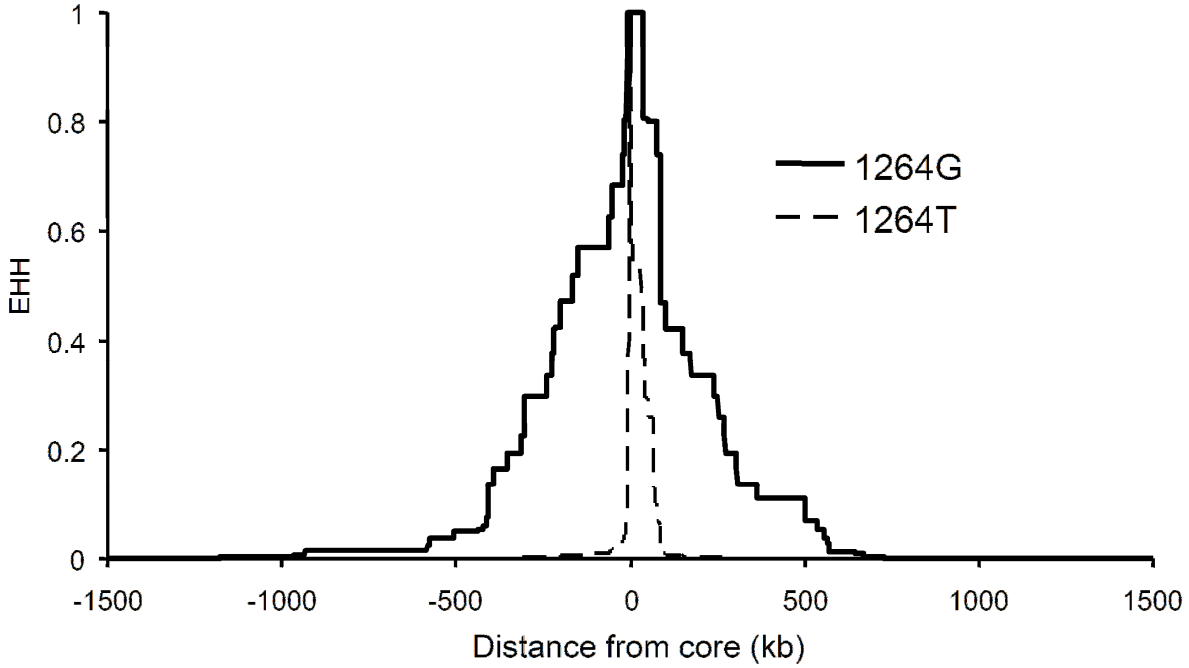
NOTE.- Genotype counts for major allele homozygotes (1/1), heterozygotes (1/2) and minor allele homozygotes (2/2); Freq, minor allele frequency; Success, percentage genotyping success; HWE, exact test Hardy-Weinberg equilibrium *P*-value (controls only).

Table S6E. *CD36* genotyping assay performance (Malawian, Kenyan & Ghanaian studies).

Marker		1/1	1/2	2/2	Freq	Success	HWE
T1264G							
Family-based studies							
Malawi	Parents	375	84	3	0.097	98.7%	-
	Cases	188	31	8	0.104	97.0%	-
Kenya	Parents	371	67	8	0.093	99.1%	-
	Cases	182	42	0	0.094	99.6%	-
Population-based studies							
Malawi	Controls	334	64	4	0.090	99.3%	0.544
	Cases	603	111	4	0.083	100.0%	-
Kenya	Controls	754	140	4	0.082	99.6%	0.506
	Cases	568	126	4	0.096	98.6%	-
Ghana	Controls	553	183	15	0.142	93.2%	1.0
	Cases	561	174	22	0.144	95.6%	-
G1439C							
Population-based studies							
Ghana	Controls	689	2	0	0.001	85.7%	1.0
	Cases	727	2	0	0.001	92.1%	-

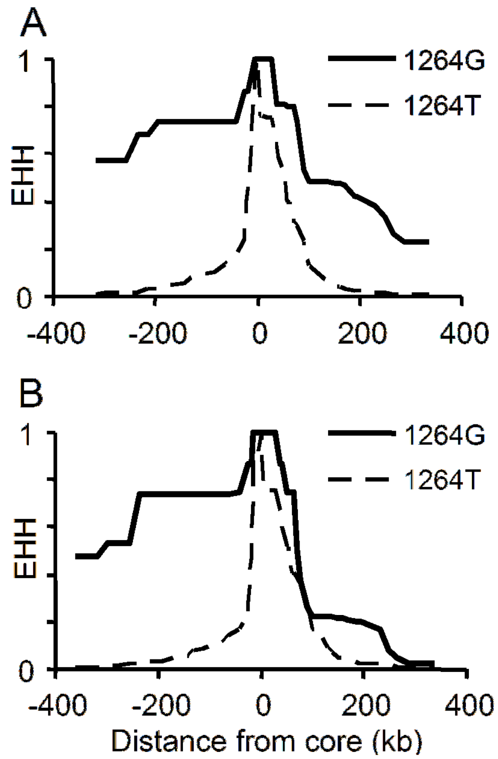
NOTE.- Genotype counts for major allele homozygotes (1/1), heterozygotes (1/2) and minor allele homozygotes (2/2); Freq, minor allele frequency; Success, percentage genotyping success; HWE, exact test Hardy-Weinberg equilibrium *P*-value (controls only).

Figure S1. Distant decay in EHH surrounding T1264G in the HapMap Yoruba.



Breakdown of extended haplotype homozygosity (EHH) with distance on haplotypes partitioned by the alleles of T1264G (rs3211938; the 'core' SNP). Phased haplotype data (comprising 3627 polymorphic markers) from 30 Yoruba parent-offspring trios (120 parental haplotypes) downloaded from the HapMap project (HapMap release 21a, January 2007). Subtle differences between 1264G- and T-haplotypes are detectable over 1.1 Mb upstream and 0.7 Mb downstream of the core SNP.

Figure S2. The effects of using offspring genotypes to resolve phase of parental haplotypes.



EHH decay surrounding T1264G in 30 HapMap Yoruba parent-offspring trios. We compared (A) parental haplotypes phased using offspring genotypes to help resolve phase, and (B) parental haplotypes phased without using offspring genotypes to help resolve phase. Note that the lack of offspring genotypes particularly impacts EHH values 3’ to T1264G.