MATERIALS AND METHODS

FSGS cohort and analysis

All focal segmental glomerulosclerosis (FSGS) cases were biopsy proven. Among these cases, 53 were recruited through the Brigham and Women's Hospital (BWH) from medical centers in the northeastern United States, and 152 were recruited in the US National Institutes of Health (NIH) FSGS Genetic Study from 22 academic medical centers in the United States (S*1, S2*). As controls, we used DNA from 180 individuals from the NIH Blood Bank and the National Cancer Institute-Frederick normal donor programs.

We selected variants for our initial FSGS genotype study from the 1000 Genomes Project (http://www.1000genomes.org/) data using the Integrative Genomics Viewer (http://www.broadinstitute.org/igv). We selected variants in the region 34,930kb-35,060kb (NCBI 36) with large frequency differences between Africans and Europeans, together with some additional single nucleotide polymorphisms (SNPs) with biological relevance, and genotyped these SNPs using Sequenom technology (http://www.sequenom.com/). We performed association analysis with plink (http://pngu.mgh.harvard.edu/~purcell/plink/)(S*3*) using Fisher's exact test and logistic regression.

This study was approved by the relevant Institutional Review Boards. Investigators obtained written informed consent from all participants in the study.

Hypertension-attributed ESKD cohort and analysis

Selection criteria for controls and hypertension-attributed end-stage kidney disease (H-ESKD) cases are described in detail in Freedman et al (S*4*). Briefly, self-reported African Americans from North Carolina, South Carolina, Georgia, Virginia, or Tennessee were recruited. Hypertension-attributed ESKD cases were diagnosed with hypertension prior to initiation of renal replacement therapy, and demonstrated hypertensive target end-organ damage (retinopathy or left ventricular hypertrophy) and low grade or absence of proteinuria. Only a minority of cases had quantified urinary protein excretion. Patients with diabetic (type 1 and 2) ESKD were excluded, as were known cases of cystic kidney disease, hereditary nephritis, and urologic causes of ESKD.

Geographically similar controls all denied a history of kidney disease and diabetes, or first-degree relatives with these diseases. Most controls did not have direct measurements of arterial blood pressure or renal function indices. Consequently, some controls may have had occult kidney disease, which would underestimate the effect size between cases and controls.

The ESKD study was approved by the Wake Forest University School of Medicine Institutional Review Board and conformed with research guidelines in the Declaration of Helsinki Principles. Investigators obtained written informed consent from all participants in the study.

In this cohort, we selected SNPs for association testing based on strong integrated haplotype scores (iHS) scores (http://hgdp.uchicago.edu)(S*5*), composite of multiple signals analysis(S*6*), and nearby common coding mutations likely to alter protein function.

Expression of ApoL1 proteins and trypanolytic assays

We used two independent systems for expression of recombinant ApoL1: Escherichia coli and in 293T cells. The various ApoL1 mutants were generated by site-directed mutagenesis and expressed in E. coli as described in Lecordier et al. (S*7*), except that we used the pStaby1.2 plasmid (Delphi Genetics). For production of ApoL1 protein in 293T cells with and without the G1 and G2 risk mutations, an I.M.A.G.E. clone containing the ApoL1 cDNA lacking the G1 and G2 mutations was purchased from Open Biosystems (reference sequence BC141823). This cDNA is cloned into the pCMV-SPORT6 expression vector. The G1 and G2 mutations were introduced by synthesis of cDNA minigene fragments (Integrated DNA Technologies) containing the corresponding mutations flanked with 5' AleI and 3' XbaI restriction sequences. The minigene fragments were then cloned into the parental vector replacing the sequence between the AleI and XbaI restrictions sites. The resulting constructs were transfected into 293T cells using Fugene (Promega). The transfection media was replaced with OPTI-MEM reduced serum media without phenol red (Invitrogen) at 12 hours post transfection. At 72 hours post transfection, the supernatants were harvested and concentrated 100-fold using an Amicon Ultracel-10K centrifugal filter unit (Millipore). The media was exchanged by centrifugation within the Ultracel filters with fresh Iscove's Modified Dulbecco's Medium for compatibility with the trypanosome killing assay. The evaluation of trypanolytic activity of the various ApoL1 mutants was performed as described in Lecordier et al (S*7*). The trypanosome clones used in these experiments were ETat 1.2: Edinburgh

Trypanozoon antigenic type 1, clone 2.

Natural selection analyses

To perform the haplotype computations for natural selection we used all 167 Yoruba samples (YRI) and the 165 European samples (CEU) genotyped from Hapmap (http://hapmap.ncbi.nlm.nih.gov/) genotyped on a panel of 1,440,616 SNPs. Data was phased using Beagle (S*8*) and analyzed using Matlab (http://www.mathworks.com/).

To test for statistically significant differentiation of allele frequency between CEU and YRI, we modeled random genetic drift as described in Ayodo et al (S*9*). We assumed that the difference in frequencies for a given polymorphism has mean 0 and variance cp(1-p), where p is the ancestral frequency and c=2xF_{ST}. We modeled sampling noise as having variance p(1-p)(1/N_1+N_2), where N_1 and N_2 are the total count for the alleles for the two populations. Therefore, to test for differentiation of frequency at a given allele, we model the difference as a normal random variable with mean 0 and variance p(1-p)(c+1/N_1+1/N_2) and we compute for each allele a χ^2 statistic with 1 degree of freedom.

We computed iHS and ΔiHH as in Voight et al.(S*5*) and Grossman et al (S*6*). We determined the derived allele using data from the Haplotter website (http://haplotter.uchicago.edu/selection/). For every SNP with minor allele frequency above 5% we computed extended haplotype homozygosity (EHH) values for haplotypes carrying the ancestral and the derived allele. As performed in Sabeti et al.(S*10*), we integrated the quantity (EHH-0.05+1/N), with N equal to the number of haplotypes containing the ancestral allele, over the genetic distance measured in centimorgans (cM) provided from the Hapmap website (http://hapmap.ncbi.nlm.nih.gov/downloads/recombination/) to obtain iHH_A. The value for iHH_D was computed in the same way using the EHH for the derived allele. We then computed $\Delta iHH=iHH_D-iHH_A$ and the unstandardized integrated haplotype score $iHS=\ln(iHH_A/iHH_D)$ and we computed this value for every SNP in the Yoruba dataset. For SNPs with the same number of haplotypes containing the derived allele we normalized the score by removing the mean and dividing by the standard deviation of that particular group. The normalized scores define the iHS. Results for the whole region from 34,900kb-35,100kb

(NCBI 36) are reported in Table S4. We omitted the Cross Population Extended Haplotype Homozygosity test (XP-EHH) as this test is devised to detect selective sweeps in which the selected allele has approached or achieved fixation in one population but remains polymorphic in the human population as a whole(S*10*).

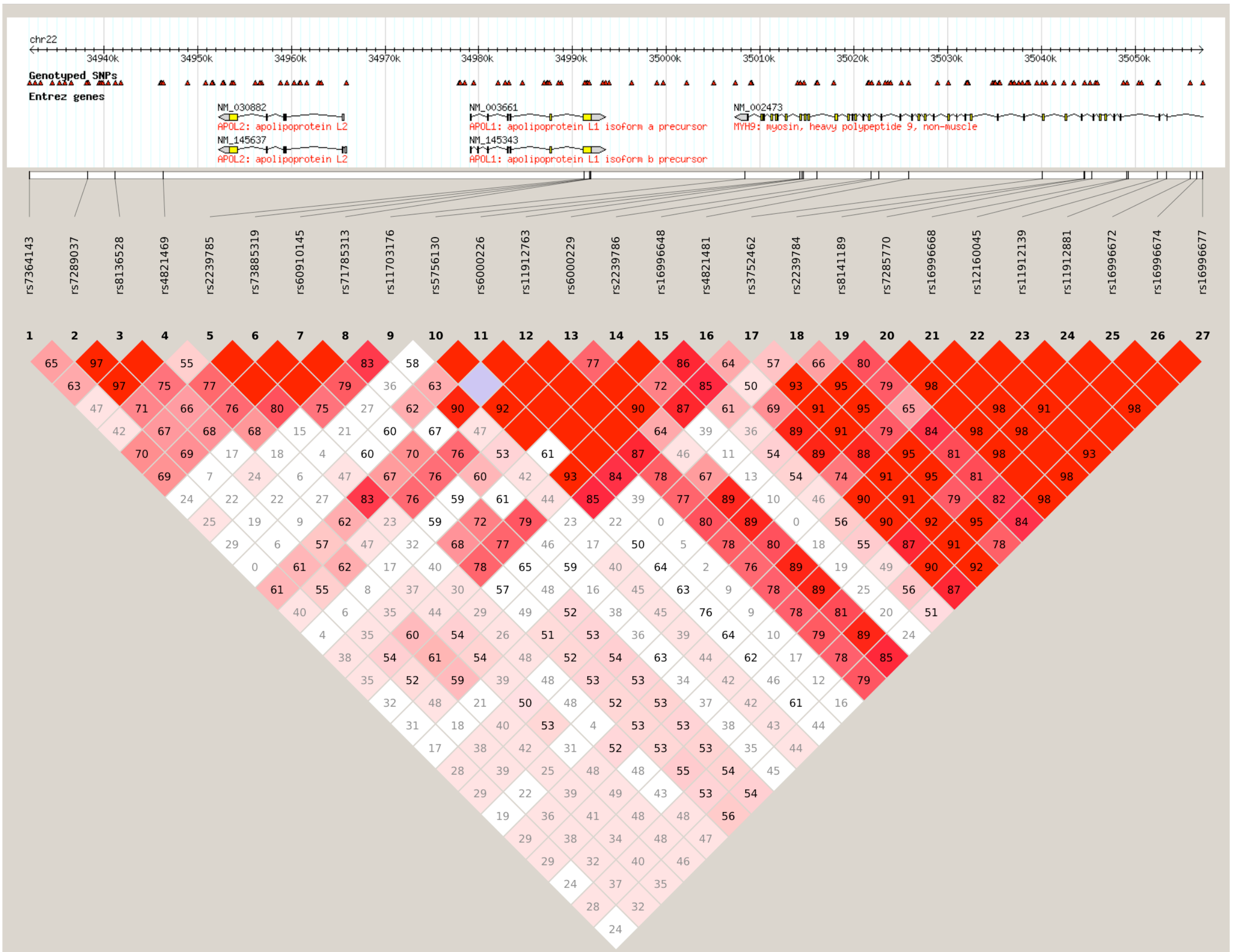

Figure S1. Linkage disequilibrium patterns (D') in African American controls from NIH (n=180) for the three disease associated variants and all of the variants we tested that are also present in HapMap (Figure created using Haploview) (S*11*).

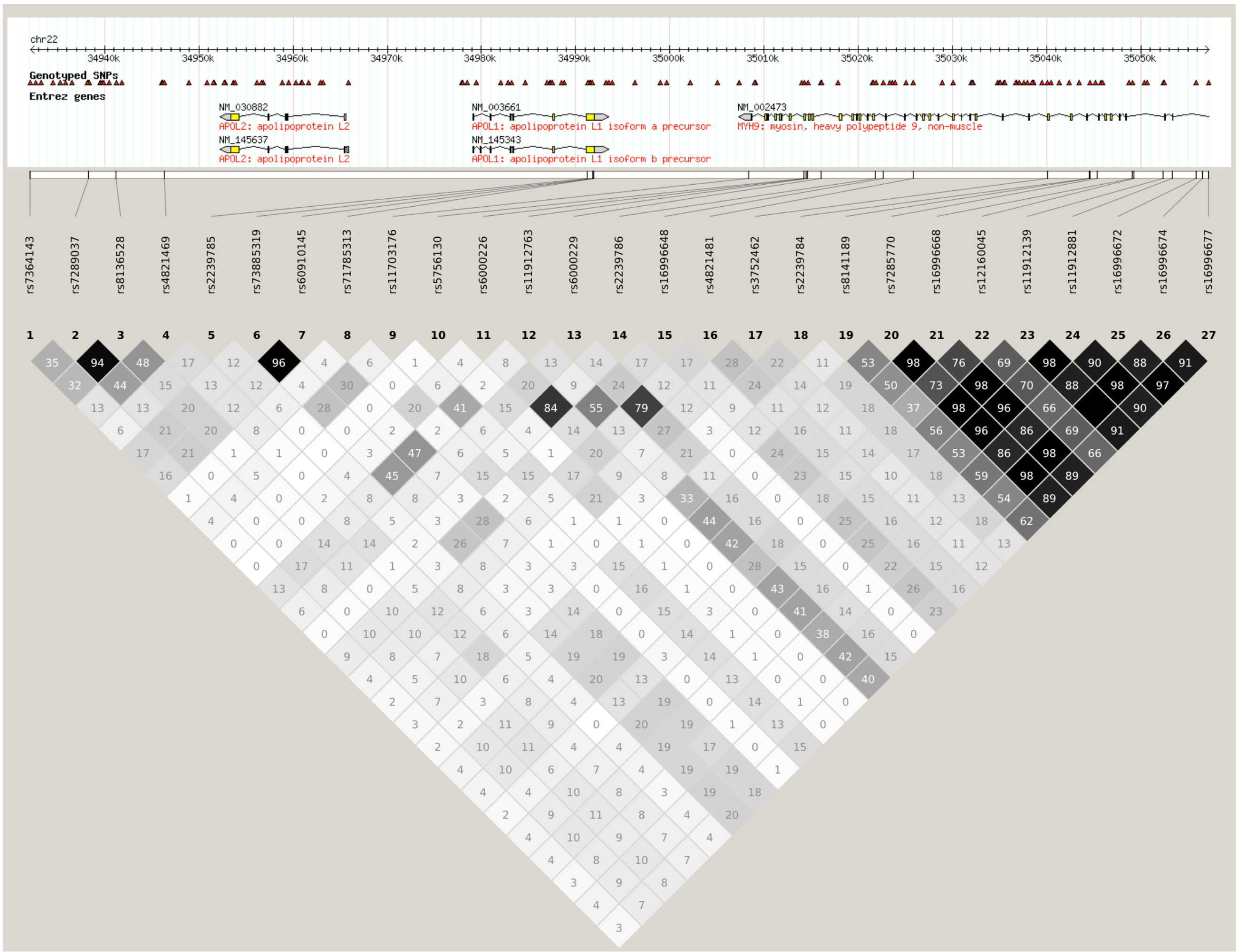

Figure S2. Linkage disequilibrium patterns (r^2) in African American controls from NIH (n=180) for the three disease associated variants and all of the variants we tested that are also present in HapMap (Figure created using Haploview) (S*11*).

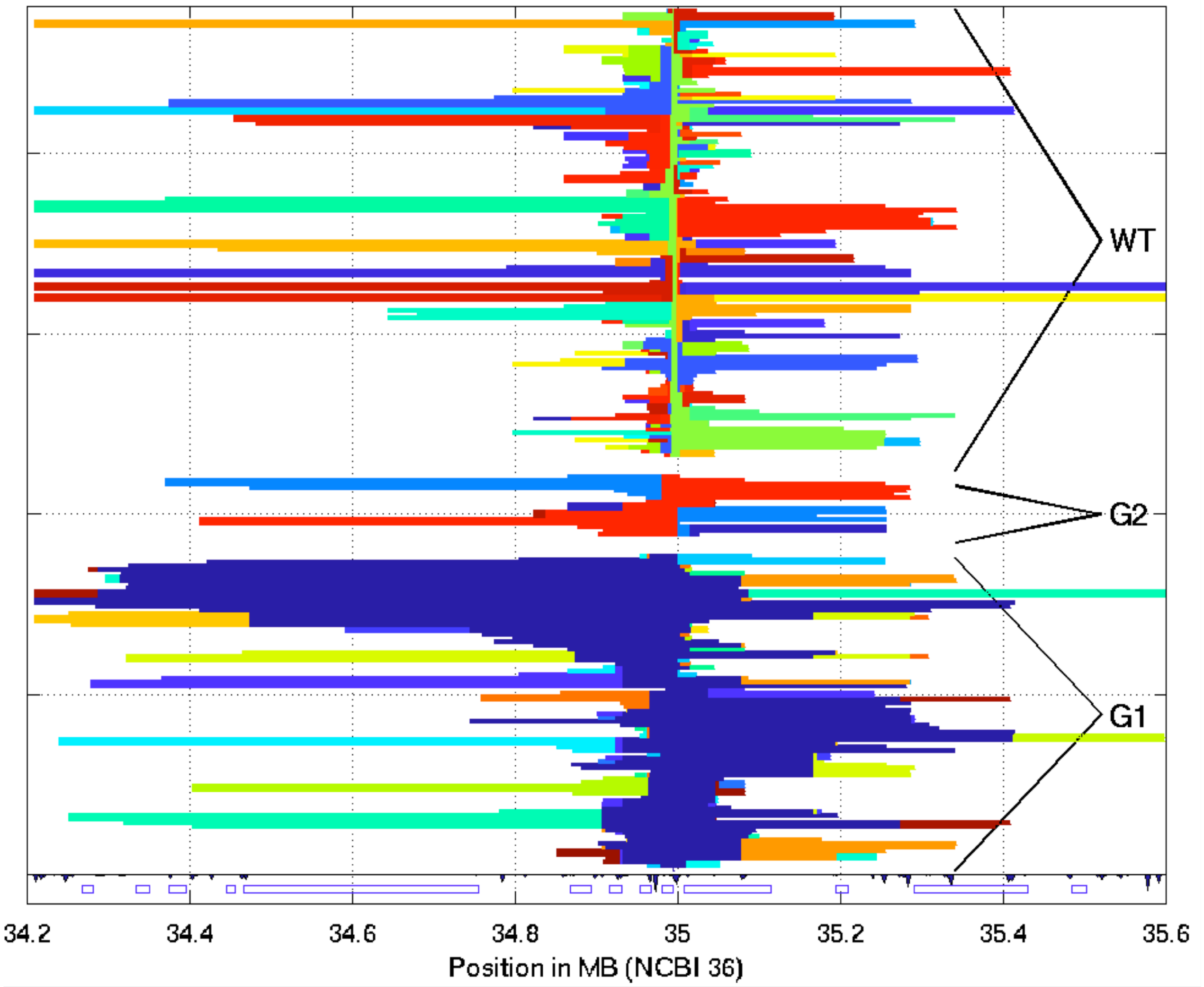

Figure S3. Haplotype structure in the Yoruba samples from Hapmap. The 230 chromosomes from the 167 Yoruba samples, a mix of trios, pairs, and unrelated samples, were divided in three groups according to the presence of the core alleles G1 (n=88), G2 (n=17), or the absence of either (n=125). Haplotypes were colored in such a way that chromosomes with the same color at a given position have the same haplotype from that position up to the position of the C-terminal part of APOL1, and their colors are different when this is not the case. Recombination hotspots ascertained from Hapmap are displayed below together with genes RASD2, MB, APOL6, APOL5, RBM9, APOL3, APOL4, APOL2, APOL1, MYH9, TXN2, CACNG2, and RABL4 (blue rectangles, from left to right). As suggested from the picture, patterns of linkage disequilibrium for G1 extend far from the linkage disequilibrium block containing APOL1, which leads to strong association with kidney disease for variants in MYH9, the closest gene to APOL1 by genetic distance.

Table S1. Association of variants on chromosome 22 with focal segmental glomerulosclerosis (FSGS) using Fisher's exact test and logistic regression conditioning first on rs73885319 and then on both rs73885319 and rs71785313.

Variant	Position (NCBI 36)	Derived allele	Ancestral allele	Frequency derived allele in affected (n=205)	Frequency derived allele in unaffected (n=180)	P-value for Fisher's exact test	P-value after conditioning on rs73885319	P-value after conditioning on rs73885319 and rs71785313
rs11089781	34886714	A	G	0.32	0.21	0.0013	0.925	0.2439
rs7364143	34932129	T	G	0.56	0.4	9.904e-06	0.9919	0.1461
rs7289037	34938336	A	G	0.53	0.33	5.118e-08	0.2779	0.8734
rs8136528	34941252	T	C	0.52	0.34	4.977e-07	0.5498	0.3631
rs4821469	34946391	C	T	0.3	0.49	9.835e-08	0.0545	0.3533
rs73885303	34953617	T	C	0	0	0.4759	0.9993	0.9993
rs10854687	34954365	A	C	0.51	0.3	4.117e-09	0.3387	0.4109
rs9622362	34986390	A	C	0.04	0.09	0.0149	0.8758	0.13
rs9622363	34986501	A	G	0.82	0.51	6.112e-20	0.0002	0.8217
rs41297245	34987686	A	G	0.01	0.05	0.0009	0.1298	0.5326
rs2239785	34991276	A	G	0.14	0.35	3.081e-12	0.0057	0.9337
rs136175	34991512	A	G	0.03	0.07	0.0171	0.2976	0.8123
rs73403889	34991637	A	G	0	0	1	0.9993	0.9993
rs16996616	34991837	A	G	0.03	0.08	0.0093	0.5397	0.3839
rs73885319	**34991852**	**G**	**A**	**0.53**	**0.19**	**1.070e-23**	**NaN**	**NaN**
rs60910145	**34991980**	**G**	**T**	**0.52**	**0.18**	**2.591e-23**	**0.6051**	**0.7417**
rs71785313	**34991997**	**D**	**I**	**0.23**	**0.15**	**0.0089**	**4.377e-07**	**NaN**
rs58384577	34993159	C	T	0.49	0.19	9.782e-18	0.1982	0.3419
rs60295735	34997100	A	G	0.5	0.2	9.128e-17	0.6759	0.9987
rs56277602	34998706	T	G	0.5	0.76	2.359e-13	0.3886	0.5788
rs73885325	35000629	T	A	0.49	0.25	6.903e-12	0.3589	0.5589
NA	35005098	A	G	0.44	0.22	1.482e-09	0.1207	0.285
rs73405714	35005359	G	A	0.44	0.22	9.451e-10	0.1746	0.3297
rs11703176	35008422	A	C	0.48	0.31	3.782e-06	0.0257	0.1264
rs58168942	35012680	A	G	0.4	0.19	2.652e-10	0.2972	0.4001
rs5756130	35014277	T	C	0.06	0.1	0.0814	0.2318	0.5038
rs6000226	35014513	T	C	0.32	0.26	0.0909	0.0001	0.1419
rs11912763	35014668	A	G	0.41	0.19	9.573e-12	0.4741	0.529

rs11549907	35014926	T	C	0.06	0.08	0.2976	0.9798	0.4356
rs6000229	35016105	T	C	0.2	0.36	5.378e-06	0.1074	0.9112
rs6000223	35017908	0	A	0	0	1	NaN	NaN
rs73405726	35018652	C	G	0.47	0.29	3.090e-07	0.1368	0.3053
rs73405727	35020433	T	C	0.42	0.19	2.243e-11	0.5361	0.5282
rs2239786	35021873	C	G	0.32	0.29	0.4288	0.0005	0.1924
rs16996648	35022698	C	T	0.47	0.29	3.090e-07	0.1368	0.3063
rs56339459	35023558	T	C	0.42	0.19	8.107e-12	0.3864	0.4316
rs4821481	35025888	T	C	0.17	0.36	4.398e-09	0.0037	0.2728
rs6000235	35026033	C	T	0.78	0.53	7.393e-13	0.0027	0.4815
rs3752462	35040129	T	C	0.13	0.28	1.820e-07	0.0031	0.1644
rs2239784	35044581	T	C	0.28	0.37	0.006	0.743	0.1031
rs8141189	35044656	T	A	0.43	0.3	0.0003	0.3762	0.5344
rs7285770	35045413	A	G	0.41	0.25	5.869e-06	0.3736	0.5092
rs55816447	35047283	T	C	0.42	0.25	7.291e-07	0.3485	0.4334
rs55670830	35049098	A	G	0.61	0.76	2.948e-05	0.2393	0.3437
rs16996668	35049131	G	C	0.42	0.25	2.920e-06	0.4054	0.5467
rs12160045	35049306	G	A	0.45	0.32	0.0004	0.1751	0.45
rs11912139	35052407	T	C	0.41	0.25	1.340e-06	0.289	0.3368
rs11912881	35053384	A	T	0.41	0.25	8.857e-06	0.3462	0.4146
rs16996672	35055916	T	C	0.45	0.27	1.611e-07	0.6268	0.8562
rs16996674	35056598	T	C	0.41	0.25	3.157e-06	0.3884	0.4494
rs16996677	35057229	A	G	0.45	0.26	6.587e-08	0.7119	0.954

Table S2. Association of variants on chromosome 22 with hypertension-attributed end-stage kidney disease (H-ESKD) using Fisher's exact test and logistic regression conditioning first on rs73885319 and then on both rs73885319 and rs71785313.

Variant	Position (NCBI 36)	Derived allele	Ancestral allele	Frequency derived allele in affected (n=1030)	Frequency derived allele in unaffected (n=1025)	P-value for Fisher's exact test	P-value after conditioning on rs73885319	P-value after conditioning on rs73885319 and rs71785313
rs5999985	34452302	A	G	0.05	0.04	0.3704	0.2828	0.2178
rs41283201	34452326	A	T	0.07	0.06	0.2551	0.3638	0.617
rs2157258	34672336	C	T	0.31	0.33	0.2308	0.0232	0.036
rs16996299	34778586	T	C	0.41	0.34	3.596e-06	0.0567	0.5757
rs6000152	34868999	A	G	0.08	0.07	0.329	0.2081	0.1121
rs7284379	34881360	T	C	0.28	0.19	7.393e-11	0.0045	0.0939
rs11089781	34886714	A	G	0.29	0.21	1.243e-10	0.0065	0.1118
rs132653	34886769	T	G	0.44	0.48	0.0154	0.5453	0.3879
rs6000173	34917169	T	G	0.26	0.34	2.776e-08	0.0008	0.0651
rs61730819	34917292	T	C	0.08	0.11	0.0005	0.1326	0.5655
rs2016708	34948899	T	C	0.42	0.25	1.031e-29	9.595e-06	0.044
rs1001293	34960895	T	C	0.45	0.31	2.796e-20	0.0063	0.3886
rs9622363	34986501	A	G	0.72	0.53	5.537e-34	6.124e-08	0.4915
rs136168	34990788	A	G	0.44	0.54	2.402e-10	0.0135	0.5
rs16996616	34991837	A	G	0.05	0.08	0.0007	0.5301	0.3903
rs73885319	**34991852**	**G**	**A**	**0.41**	**0.21**	**3.435e-40**	**NaN**	**NaN**
rs71785313	**34991988**	**D**	**I**	**0.21**	**0.13**	**7.056e-10**	**8.798e-18**	**NaN**
rs7078	35007860	G	A	0.1	0.15	3.958e-05	0.1648	0.97
rs12107	35007928	A	G	0.07	0.11	1.827e-05	0.0504	0.4258
rs16996639	35008348	A	G	0.1	0.08	0.062	0.0021	0.4986
rs11089787	35008399	G	C	0.48	0.38	1.715e-10	0.156	0.8759
rs735853	35009159	G	C	0.07	0.11	1.167e-06	0.0159	0.3515
rs58168942	35012680	A	G	0.34	0.2	5.203e-24	0.9944	0.6896
rs5756129	35014138	C	T	0.15	0.21	6.215e-07	0.061	0.8231
rs11912763	35014668	A	G	0.34	0.19	5.768e-24	0.3702	0.5297
rs56020676	35020066	C	T	0.4	0.26	1.136e-19	0.5497	0.459
rs73885341	35021424	A	G	0.4	0.27	4.573e-17	0.9711	0.6416
rs4821480	35025193	T	G	0.26	0.4	6.162e-21	6.763e-06	0.0965
rs2032487	35025374	T	C	0.25	0.38	3.872e-20	2.137e-05	0.1363

rs4821481	35025888	T	C	0.26	0.4	7.197e-21	8.516e-06	0.0962
rs2413396	35038030	C	T	0.28	0.42	1.124e-16	0.0006	0.6024
rs5750250	35038429	G	A	0.32	0.5	2.475e-26	4.145e-08	0.0163
rs3752462	35040129	T	C	0.19	0.27	6.410e-09	0.0287	0.7214
rs11912881	35053384	A	T	0.34	0.25	5.712e-11	0.8152	0.8574
rs16996674	35056598	T	C	0.34	0.23	7.141e-13	0.47	0.4214
rs16996677	35057229	A	G	0.36	0.27	1.943e-10	0.9985	0.9281

Table S3. Natural selection analysis of the APOL1 region. In the last seven columns are reported fixation index (F_{ST}) values for the Yoruba population (YRI) and the European poulation (CEU) from Hapmap, p-values for frequency differentiation according to the method described in Ayodo et al (S*9*), ΔDAF, iHH_D, iHH_A, iHS, and ΔiHH scores for these variants in the Yoruba popualation computed as described in Voight et al. (S*5*) and Grossman et al (S*6*).

Variant	Position (NCBI 36)	Derived allele	Ancestral allele	Frequency derived allele in YRI (n=167)	Frequency derived allele in CEU (n=165)	F_{ST}	P	ΔDAF	iHH_D	iHH_A	iHS	ΔiHH
rs12185880	34900774	G	C	0.14	0.02	0.0519	0.2959	0.12	0.1141	0.0458	0.6682	0.0682
rs132681	34904713	A	G	0.07	0.24	0.0567	0.2738	-0.17	0.2093	0.04	0.5043	0.1693
rs132683	34905610	A	G	0.67	0.28	0.1555	0.0664	0.39	0.0742	0.0946	1.5193	-0.0204
rs132686	34906596	G	A	0	0.3	0.1777	0.0495	-0.3	NaN	NaN	NaN	NaN
rs132688	34906886	A	G	0	0.29	0.1644	0.059	-0.29	NaN	NaN	NaN	NaN
rs6000164	34907077	T	C	0.12	0	0.0631	0.2473	0.12	0.1337	0.0523	1.0651	0.0813
rs132689	34907092	A	G	0.1	0.29	0.0578	0.2691	-0.19	0.1932	0.0467	0.4534	0.1465
rs5995235	34907888	T	C	0.33	0.04	0.1384	0.0836	0.29	0.0392	0.0921	2.0781	-0.0529
rs6000167	34908800	G	A	0.45	0.58	0.0177	0.5593	-0.12	0.0225	0.1531	2.9392	-0.1306
rs132692	34909112	C	T	0.97	0.72	0.118	0.1106	0.25	NaN	NaN	NaN	NaN
rs132693	34909507	A	G	0.01	0.23	0.1196	0.1082	-0.22	NaN	NaN	NaN	NaN
rs2239831	34913030	C	T	0.87	0.44	0.2054	0.0345	0.43	0.0647	0.1054	-0.7131	-0.0407
rs916338	34914376	T	C	0.01	0.24	0.1224	0.104	-0.23	NaN	NaN	NaN	NaN
rs132697	34914659	A	G	0.01	0.23	0.1139	0.1176	-0.22	NaN	NaN	NaN	NaN
rs8136064	34914892	G	T	0.02	0.04	0.0082	0.7165	-0.03	NaN	NaN	NaN	NaN
rs1053982	34915510	T	C	0.25	0.56	0.1017	0.1391	-0.31	0.0378	0.0958	2.4848	-0.0579
rs5756091	34915667	T	G	0.24	0.56	0.1078	0.1276	-0.32	0.0446	0.093	2.0092	-0.0484
rs5756093	34915917	A	G	0	0	NaN	NaN	0	NaN	NaN	NaN	NaN
rs6000172	34917148	G	A	0.24	0.54	0.0974	0.1479	-0.3	0.0466	0.0925	2.1149	-0.0459
rs6000174	34917225	A	G	0.24	0.54	0.0972	0.1486	-0.3	0.0466	0.0925	2.1149	-0.0459
rs2227167	34917432	A	G	0.24	0.54	0.099	0.1446	-0.3	0.0466	0.0925	2.1149	-0.0459
rs2269596	34920892	T	C	0.77	0.47	0.0986	0.1455	0.3	0.0911	0.0541	-1.8428	0.037
rs2007468	34921326	A	G	0.12	0.52	0.193	0.0406	-0.41	0.1469	0.0746	1.2289	0.0723
rs2007706	34922316	C	T	0.01	0.53	0.3359	0.0067	-0.51	NaN	NaN	NaN	NaN
rs132717	34926598	C	T	0.23	0.61	0.1443	0.0771	-0.37	0.09	0.1119	1.5478	-0.0219
rs132734	34927823	G	A	0.23	0.6	0.1483	0.073	-0.38	0.0891	0.1099	1.5004	-0.0208

rs132735	34927827	T	G	0.48	0.27	0.0503	0.3041	0.21	0.2457	0.0488	-1.3619	0.1969
rs5995251	34930704	T	A	0.39	0.38	0.0026	0.9279	0.02	0.0542	0.1867	2.1688	-0.1325
rs6000190	34930787	G	A	0.39	0.38	0.0026	0.9279	0.02	0.0542	0.1867	2.1688	-0.1325
rs5995252	34931145	T	C	0.4	0.37	0.0031	0.8933	0.03	0.0525	0.1896	2.0349	-0.1371
rs7364143	34932129	T	G	0.47	0.25	0.0542	0.2851	0.22	0.3243	0.0266	-1.758	0.2976
rs5995255	34932725	T	G	0.42	0.38	0.0043	0.831	0.04	0.0499	0.1933	2.1875	-0.1434
rs6000197	34933240	A	G	0.42	0.37	0.0049	0.8077	0.05	0.0473	0.2062	2.1831	-0.159
rs132744	34934551	T	C	0.48	0.07	0.2182	0.0293	0.42	0.3452	0.0288	-2.3276	0.3164
rs132745	34935277	C	T	0.15	0.24	0.0128	0.6296	-0.08	0.0793	0.0947	1.9529	-0.0154
rs132746	34935337	C	T	0.15	0.24	0.0141	0.6093	-0.09	0.0855	0.0934	1.8959	-0.0079
rs8142325	34935923	T	A	0.46	0	0.2967	0.0109	0.46	0.3925	0.0192	-2.367	0.3733
rs132749	34936575	T	C	0.81	0.5	0.1048	0.1331	0.31	0.0904	0.1129	1.7405	-0.0225
rs9610448	34938151	A	G	0.78	0.44	0.1246	0.1009	0.34	0.0726	0.121	1.8981	-0.0484
rs132750	34938295	C	T	0.03	0.23	0.0932	0.1573	-0.2	NaN	NaN	NaN	NaN
rs7289037	34938336	A	G	0.49	0.11	0.1744	0.0517	0.38	0.3518	0.0207	-2.3661	0.3311
rs11704479	34939580	A	G	0	0.08	0.0416	0.3522	-0.08	NaN	NaN	NaN	NaN
rs4820222	34939685	C	T	0.78	0.44	0.1246	0.1009	0.34	0.0946	0.1158	1.5535	-0.0211
rs6000199	34939878	A	G	0.08	0.11	0.0044	0.8251	-0.03	0.2801	0.0774	0.8319	0.2026
rs8140384	34940517	C	T	0.79	0.44	0.1336	0.0892	0.35	0.1038	0.1118	1.5156	-0.008
rs8136528	34941252	T	C	0.48	0.11	0.171	0.054	0.38	0.3518	0.0194	-2.4246	0.3324
rs5995259	34941809	A	G	0.18	0.33	0.0329	0.4116	-0.15	0.084	0.1061	1.9637	-0.0221
rs1315	34946081	C	A	0.1	0.23	0.031	0.4267	-0.13	0.1912	0.0844	1.2233	0.1068
rs4821467	34946146	A	G	0.49	0.11	0.1766	0.0502	0.38	0.3518	0.0186	-2.4632	0.3332
rs4821469	34946391	C	T	0.34	0.89	0.3225	0.008	-0.55	0.1697	0.0412	-2.097	0.1286
rs763086	34949003	G	A	0.66	0.34	0.1044	0.1339	0.32	0.0447	0.173	2.394	-0.1283
rs11703398	34950907	A	G	0.83	0.77	0.0086	0.7079	0.06	0.1014	0.0723	-1.5356	0.0291
rs2006259	34951559	A	C	0.65	0.34	0.0997	0.1433	0.31	0.0432	0.1763	2.3864	-0.1331
rs132757	34951655	T	C	0	0.24	0.1361	0.0862	-0.24	NaN	NaN	NaN	NaN
rs9619597	34952768	T	G	0	0.11	0.0587	0.2652	-0.11	NaN	NaN	NaN	NaN
rs129607	34952852	T	C	0.39	0.46	0.0063	0.7649	-0.06	0.0387	0.2083	2.7583	-0.1696
rs132760	34953677	T	C	0	0	NaN	NaN	0	NaN	NaN	NaN	NaN
rs7285167	34953866	A	G	0.46	0.11	0.1522	0.0694	0.35	0.4127	0.0167	-2.557	0.396
rs11089784	34956223	T	C	0.1	0.23	0.031	0.4267	-0.13	0.2071	0.0876	1.1779	0.1195
rs11703957	34956901	G	A	0.21	0.23	0.0026	0.9311	-0.02	0.0802	0.1216	2.0023	-0.0414
rs2010467	34958853	T	C	0.46	0.68	0.0527	0.2922	-0.22	0.2824	0.0449	-1.8381	0.2375
rs2010659	34959579	C	A	0.14	0.33	0.0535	0.2881	-0.19	0.1925	0.123	1.132	0.0695
rs9610462	34960296	A	C	0.14	0.33	0.0508	0.3013	-0.19	0.1925	0.123	1.132	0.0695

rs1001294	34960936	T	C	0.14	0.34	0.0541	0.2855	-0.19	0.1786	0.1247	1.6193	0.0539
rs2157249	34960985	T	C	0.86	0.66	0.0556	0.2786	0.2	0.1231	0.1925	-0.9876	-0.0694
rs2157250	34961637	G	A	0.05	0.21	0.0582	0.2673	-0.16	0.4548	0.1106	0.988	0.3442
rs136142	34962971	T	C	0.35	0.37	0.0027	0.9188	-0.02	0.1412	0.2709	1.7202	-0.1297
rs1557534	34963171	A	G	0.03	0.04	0.0028	0.9073	-0.01	NaN	NaN	NaN	NaN
rs136145	34965913	A	G	0.7	0.38	0.1048	0.1332	0.32	0.258	0.312	1.2744	-0.054
rs4821472	34977906	C	T	0.03	0.1	0.0262	0.4682	-0.08	NaN	NaN	NaN	NaN
rs5995271	34978039	T	G	0.07	0.09	0.004	0.8449	-0.02	0.2683	0.1797	1.7851	0.0886
rs5756115	34978498	G	A	0	0.23	0.1262	0.0987	-0.23	NaN	NaN	NaN	NaN
rs9610467	34979520	A	G	0.09	0.21	0.0271	0.4596	-0.11	0.1528	0.1642	2.168	-0.0114
rs7284919	34982110	C	T	0.07	0.18	0.0299	0.4355	-0.11	0.1255	0.1496	2.6268	-0.0242
rs136148	34982877	T	C	0.9	0.65	0.0929	0.158	0.25	0.1606	0.1107	-1.569	0.0499
rs4820224	34983221	A	G	0.01	0.1	0.0387	0.3701	-0.09	NaN	NaN	NaN	NaN
rs2413395	34984662	A	G	0.07	0	0.0392	0.3674	0.07	0.1679	0.1491	2.0733	0.0188
rs136159	34986969	T	C	0	0.23	0.1304	0.0932	-0.23	NaN	NaN	NaN	NaN
rs129423	34987275	T	C	0	0.22	0.1276	0.0969	-0.22	NaN	NaN	NaN	NaN
rs136161	34987378	C	G	0.8	0.44	0.1419	0.0796	0.36	0.1617	0.164	1.5058	-0.0022
rs713929	34987542	A	G	0	0.22	0.1276	0.0969	-0.22	NaN	NaN	NaN	NaN
rs713753	34988480	T	C	0.12	0.56	0.2252	0.0268	-0.45	0.2091	0.1315	1.5658	0.0776
rs4419330	34988801	C	T	0.12	0.04	0.019	0.5431	0.07	0.1707	0.1186	1.6238	0.0521
rs2239785	34991276	A	G	0.73	0.22	0.2612	0.017	0.51	0.0719	0.1722	2.3367	-0.1003
rs136174	34991482	C	A	0	0.22	0.1206	0.1066	-0.22	NaN	NaN	NaN	NaN
rs136175	34991512	A	G	1	0.78	0.1206	0.1066	0.22	NaN	NaN	NaN	NaN
rs136176	34991592	G	A	0	0.22	0.126	0.099	-0.22	NaN	NaN	NaN	NaN
rs136177	34991788	A	G	0.97	0.78	0.0853	0.1764	0.19	NaN	NaN	NaN	NaN
rs16996616	34991837	A	G	0.06	0.01	0.0229	0.4999	0.05	0.2036	0.0986	1.7291	0.105
rs73885319	**34991852**	**G**	**A**	**0.38**	**0**	**0.2349**	**0.0236**	**0.38**	**0.5129**	**0.0389**	**-2.3052**	**0.474**
rs60910145	**34991980**	**G**	**T**	**0.38**	**0**	**0.2349**	**0.0236**	**0.38**	**0.5129**	**0.0389**	**-2.3052**	**0.474**
rs71785313	**34991997**	**D**	**I**	**0.08**	**0**	**0.0436**	**0.3392**	**0.08**	**0.3833**	**0.1073**	**0.8937**	**0.276**
rs2012928	34993948	A	G	0.17	0.2	0.0035	0.8649	-0.03	0.1449	0.139	1.4612	0.0059
rs136183	34996271	T	C	0.34	0.49	0.0249	0.4801	-0.15	0.0817	0.2287	1.962	-0.147
rs4821475	34999041	C	T	0.37	0.77	0.1723	0.0532	-0.41	0.0869	0.1894	1.6174	-0.1026
rs9306308	34999716	A	T	0.02	0.19	0.0749	0.206	-0.17	NaN	NaN	NaN	NaN
rs136187	35002222	C	A	0.5	0.37	0.0204	0.5273	0.13	0.2527	0.0504	-1.6072	0.2023
rs136196	35005096	A	G	0.31	0.36	0.0043	0.8315	-0.04	0.0778	0.1304	1.4805	-0.0526
rs2481	35007346	A	G	0.09	0.14	0.0073	0.7391	-0.05	0.0715	0.0776	2.1868	-0.0061
rs735854	35009004	C	T	0.93	0.37	0.3508	0.0056	0.56	0.0609	0.0732	2.3478	-0.0123

rs5756129	35014038	C	T	0.21	0.23	0.0031	0.8916	-0.02	0.0903	0.0901	1.4315	0.0002
rs5756130	35014277	T	C	0.18	0.05	0.0415	0.3525	0.13	0.1303	0.0813	1.0676	0.049
rs2269529	35014300	C	T	0.03	0.18	0.0649	0.2405	-0.15	NaN	NaN	NaN	NaN
rs2269530	35014304	A	C	0.03	0.18	0.068	0.2292	-0.16	NaN	NaN	NaN	NaN
rs11912763	35014668	A	G	0.33	0	0.1975	0.0382	0.33	0.5054	0.0184	-3.1245	0.487
rs1476009	35016002	A	G	0.04	0.04	0.0024	0.9498	-0.01	NaN	NaN	NaN	NaN
rs6000229	35016105	T	C	0.72	0.01	0.5347	0.0006	0.7	0.0301	0.088	2.4195	-0.0579
rs6000233	35017908	C	T	0.36	0.01	0.1984	0.0378	0.35	0.0481	0.1097	1.6645	-0.0616
rs710181	35021553	A	C	0.02	0.05	0.0063	0.7647	-0.02	NaN	NaN	NaN	NaN
rs875725	35021637	C	T	0.07	0.01	0.0226	0.5031	0.06	0.0801	0.0426	1.5067	0.0375
rs2239786	35021873	C	G	0.29	0.02	0.1392	0.0827	0.27	0.0623	0.0821	1.4104	-0.0197
rs875726	35021915	A	G	0.19	0.7	0.2655	0.0161	-0.51	0.1101	0.0587	0.9695	0.0515
rs16996648	35022698	C	T	0.4	0.01	0.2282	0.0258	0.38	0.3122	0.0127	-3.1668	0.2995
rs9610486	35023388	A	G	0.19	0.7	0.2655	0.0161	-0.51	0.1101	0.059	0.9767	0.0512
rs5756133	35023926	A	T	0.09	0.65	0.3293	0.0073	-0.55	0.2674	0.0428	0.0834	0.2246
rs2187776	35025119	C	T	0.31	0.05	0.122	0.1047	0.26	0.0567	0.0873	1.3852	-0.0306
rs4821481	35025888	T	C	0.73	0.06	0.4761	0.0013	0.67	0.0336	0.0832	1.9913	-0.0496
rs2239787	35028938	A	C	0	0.04	0.019	0.5432	-0.04	NaN	NaN	NaN	NaN
rs9619601	35030121	A	G	0.96	0.96	0.0028	0.9121	0.01	NaN	NaN	NaN	NaN
rs8137674	35032048	A	G	0.99	1	0.0089	0.7018	-0.01	NaN	NaN	NaN	NaN
rs8138016	35032095	A	G	0.06	0.01	0.0164	0.5762	0.04	0.1404	0.0444	1.2423	0.0959
rs17806543	35034780	A	C	0	0.06	0.0344	0.4002	-0.06	NaN	NaN	NaN	NaN
rs2239781	35034987	T	C	0.02	0.19	0.083	0.1827	-0.17	NaN	NaN	NaN	NaN
rs2239782	35035050	A	G	0.05	0.24	0.07	0.222	-0.18	0.1129	0.0432	1.4986	0.0697
rs1557529	35035475	A	G	0.48	0.96	0.2784	0.0137	-0.47	0.1822	0.0084	-2.6592	0.1737
rs1557530	35035568	A	G	0.21	0.67	0.2206	0.0284	-0.46	0.0949	0.0551	0.9039	0.0398
rs2187777	35036688	T	C	0	0.04	0.0204	0.5276	-0.04	NaN	NaN	NaN	NaN
rs2157252	35036825	A	C	0.23	0.67	0.201	0.0365	-0.44	0.0732	0.0603	1.2577	0.0129
rs2157254	35037146	C	G	0.23	0.67	0.201	0.0365	-0.44	0.0732	0.0603	1.2577	0.0129
rs2157256	35037607	A	G	0.71	0.33	0.1481	0.0733	0.38	0.0764	0.0306	-1.2237	0.0458
rs2413396	35038030	C	T	0.33	0.9	0.3389	0.0065	-0.57	0.092	0.0187	-2.3259	0.0733
rs5750250	35038429	G	A	0.36	0.94	0.3757	0.0042	-0.58	0.1024	0.0145	-2.5454	0.088
rs3830104	35038570	C	T	0.03	0.08	0.0165	0.5753	-0.05	NaN	NaN	NaN	NaN
rs4820229	35038699	G	A	0.23	0.67	0.1973	0.0383	-0.44	0.0732	0.0607	1.2661	0.0124
rs4820230	35039485	G	A	0.71	0.32	0.1544	0.0674	0.39	0.0771	0.0305	-1.2352	0.0466
rs3752462	35040129	T	C	0.77	0.33	0.201	0.0365	0.44	0.0614	0.0732	-0.8358	-0.0118
rs4820232	35040487	G	A	0.25	0.67	0.181	0.0474	-0.42	0.0503	0.0668	1.6014	-0.0166

rs8141971	35041308	G	A	0.22	0.67	0.2095	0.0328	-0.45	0.0865	0.0587	1.0738	0.0278
rs5756152	35042418	A	G	0.42	0.04	0.1962	0.0389	0.37	0.2751	0.0175	-2.1833	0.2576
rs9610489	35043477	C	T	0.09	0.19	0.0204	0.5277	-0.09	0.0924	0.0466	1.3336	0.0458
rs2239784	35044581	T	C	0.3	0.91	0.3955	0.0033	-0.61	0.0739	0.0379	-1.0935	0.036
rs1005570	35045220	A	G	0.5	0.13	0.161	0.0617	0.37	0.1437	0.0305	-1.6247	0.1132
rs2071731	35048804	A	G	0.21	0.37	0.0309	0.4272	-0.15	0.0933	0.0505	0.645	0.0428
rs12159211	35049109	A	G	0.01	0.04	0.0108	0.6644	-0.03	NaN	NaN	NaN	NaN
rs5756154	35050370	T	C	0.3	0.55	0.0654	0.2385	-0.25	0.0603	0.0605	1.0802	-0.0002
rs5756156	35050725	T	C	0.25	0.54	0.0912	0.1618	-0.29	0.0892	0.0512	0.6283	0.0381
rs8136069	35052436	A	C	0.21	0.37	0.0324	0.4152	-0.16	0.0933	0.0472	0.569	0.0461
rs8136336	35052480	G	A	0.04	0.04	0.0022	0.9966	0	NaN	NaN	NaN	NaN
rs16996672	35055916	T	C	0.37	0	0.2267	0.0263	0.37	0.2783	0.0196	-2.0506	0.2587
rs16996677	35057229	A	G	0.37	0	0.219	0.029	0.36	0.2774	0.0197	-2.0454	0.2578
rs11704382	35058098	A	C	0	0.08	0.044	0.3378	-0.08	NaN	NaN	NaN	NaN
rs4820234	35059020	A	G	0.27	0.46	0.0412	0.3543	-0.19	0.078	0.0597	0.8686	0.0183
rs2413398	35060893	T	G	0.73	0.35	0.1453	0.0761	0.38	0.0578	0.0813	-0.2741	-0.0234
rs1557540	35062483	C	T	0.26	0.46	0.0432	0.3426	-0.19	0.0812	0.0583	0.8637	0.0229
rs713839	35063884	G	A	0.27	0.65	0.1419	0.0797	-0.37	0.0824	0.0635	0.8787	0.0189
rs739096	35071686	C	G	0.03	0.53	0.3181	0.0084	-0.5	NaN	NaN	NaN	NaN
rs6000244	35071832	T	C	0.06	0	0.0341	0.4023	0.06	0.257	0.0431	0.4544	0.2139
rs739097	35076025	G	A	0.65	0.54	0.0128	0.6303	0.1	0.0747	0.0846	0.9153	-0.0099
rs5756164	35078939	A	G	0.05	0.06	0.0026	0.9248	-0.01	0.1732	0.0451	1.1679	0.1281
rs11089788	35081047	A	C	0.44	0.51	0.0075	0.7353	-0.07	0.1615	0.0553	-0.3323	0.1062
rs136206	35085444	A	G	0.67	0.31	0.1317	0.0915	0.36	0.0557	0.0582	-0.1922	-0.0026
rs16996693	35086202	C	A	0.01	0.01	0.0027	0.9192	0	NaN	NaN	NaN	NaN
rs9306310	35088204	A	G	0.01	0.54	0.3558	0.0053	-0.53	NaN	NaN	NaN	NaN
rs136211	35088493	A	G	0.55	0.66	0.0143	0.6059	-0.11	0.1116	0.0282	-0.4026	0.0834
rs16996704	35094734	A	G	0.54	0.12	0.204	0.0351	0.42	0.0967	0.028	-0.5759	0.0687
rs933224	35095949	T	C	0.58	0.67	0.0092	0.6948	-0.08	0.1274	0.0226	-1.1861	0.1049
rs1883273	35099631	G	A	0.59	0.34	0.0645	0.2418	0.25	0.064	0.0234	-1.0759	0.0407
rs6000262	35099984	A	G	0.59	0.33	0.0672	0.2319	0.25	0.064	0.0234	-1.0759	0.0407

Table S4. Genotype for the Yoruba Hapmap samples.

Family ID	Individual ID	Father ID	Mother ID	Sex (1=male; 2=female)	rs73885319 (G1)	rs60910145 (G1)	rs71785313 (G2)
Y001	NA18484	NA18486	NA18488	2	GA	GT	II
Y002	NA18485	NA18487	NA18489	1	AA	TT	II
Y001	NA18486	0	0	1	GG	GG	II
Y002	NA18487	0	0	1	AA	TT	DI
Y001	NA18488	0	0	2	AA	TT	II
Y002	NA18489	0	0	2	GA	GT	II
Y003	NA18497	NA18498	NA18499	1	GG	GG	II
Y003	NA18498	0	0	1	GG	GG	II
Y003	NA18499	0	0	2	GA	GT	II
Y004	NA18500	NA18501	NA18502	1	GA	GT	II
Y004	NA18501	0	0	1	GA	GT	II
Y004	NA18502	0	0	2	AA	TT	DI
Y005	NA18503	NA18504	NA18505	1	GG	GG	II
Y005	NA18504	0	0	1	GA	GT	DI
Y005	NA18505	0	0	2	GG	GG	II
Y009	NA18506	NA18507	NA18508	1	GA	GT	II
Y009	NA18507	0	0	1	GA	GT	II
Y009	NA18508	0	0	2	GA	GT	II
Y010	NA18509	0	NA18511	1	GA	GT	II
Y010	NA18510	0	0	1	AA	TT	II
Y010	NA18511	0	0	2	GG	GG	II
Y013	NA18515	NA18516	NA18517	1	GA	GT	DI
Y013	NA18516	0	0	1	GA	GT	DI
Y013	NA18517	0	0	2	GG	GG	II
Y014	NA18518	NA18519	NA18520	2	GA	GT	II
Y014	NA18519	0	0	1	AA	TT	II
Y014	NA18520	0	0	2	GA	GT	II
Y016	NA18521	NA18522	NA18523	1	GA	GT	II
Y016	NA18522	0	0	1	GA	GT	II
Y016	NA18523	0	0	2	AA	TT	II
Y018	NA18852	0	0	2	AA	TT	II
Y018	NA18853	0	0	1	GA	GT	II
Y018	NA18854	NA18853	NA18852	1	AA	TT	II
Y023	NA18855	0	0	2	GA	GT	II
Y023	NA18856	0	0	1	GG	GG	II
Y023	NA18857	NA18856	NA18855	1	GG	GG	II
Y012	NA18858	0	0	2	AA	TT	DI
Y012	NA18859	0	0	1	AA	TT	II
Y012	NA18860	NA18859	NA18858	1	AA	TT	II
Y024	NA18861	0	0	2	GA	GT	II
Y024	NA18862	0	0	1	GG	GG	II
Y024	NA18863	NA18862	NA18861	1	GA	GT	II
Y007	NA18867	0	0	2	AA	TT	DI
Y007	NA18868	0	0	1	GA	GT	II
Y007	NA18869	NA18868	NA18867	1	AA	TT	DI
Y017	NA18870	0	0	2	GA	GT	DI
Y017	NA18871	0	0	1	GA	GT	II

Y017	NA18872	NA18871	NA18870	1	GA	GT	DI
Y019	NA18873	0	0	2	AA	TT	II
Y019	NA18874	0	0	1	GA	GT	DI
Y019	NA18875	NA18874	NA18873	2	GA	GT	II
Y025	NA18907	0	0	2	GA	GT	DI
Y025	NA18908	0	0	1	AA	TT	II
Y027	NA18909	0	0	2	GA	GT	DI
Y027	NA18910	0	0	1	GA	GT	II
Y027	NA18911	NA18910	NA18909	1	AA	TT	DI
Y028	NA18912	0	0	2	AA	TT	II
Y028	NA18913	0	0	1	AA	TT	DI
Y028	NA18914	NA18913	NA18912	1	AA	TT	II
Y030	NA18916	0	0	2	GA	GT	II
Y030	NA18917	0	0	1	GA	GT	DI
Y033	NA18923	0	0	1	AA	TT	II
Y033	NA18924	0	0	2	AA	TT	II
Y033	NA18925	NA18923	NA18924	1	AA	TT	II
Y030	NA18930	NA18917	NA18916	2	AA	TT	DI
Y036	NA18933	0	0	2	GA	GT	II
Y036	NA18934	0	0	1	AA	TT	II
Y036	NA18935	NA18934	NA18933	1	GA	GT	II
Y040	NA19092	0	0	1	AA	TT	II
Y040	NA19093	0	0	2	GA	GT	II
Y040	NA19094	NA19092	NA19093	2	AA	TT	II
Y041	NA19095	0	0	2	AA	TT	II
Y041	NA19096	0	0	1	GA	GT	II
Y041	NA19097	NA19096	NA19095	2	GA	GT	II
Y105	NA19098	0	0	1	GA	GT	II
Y105	NA19099	0	0	2	GA	GT	II
Y105	NA19100	NA19098	NA19099	2	AA	TT	II
Y042	NA19101	0	0	1	GA	GT	II
Y042	NA19102	0	0	2	AA	TT	DI
Y042	NA19103	NA19101	NA19102	1	AA	TT	II
Y006	NA19107	0	0	1	GA	GT	II
Y006	NA19108	0	0	2	GA	GT	II
Y006	NA19109	NA19107	NA19108	2	AA	TT	II
Y079	NA19113	0	0	1	GA	GT	DI
Y079	NA19114	0	0	2	GA	GT	II
Y079	NA19115	NA19113	NA19114	2	AA	TT	DI
Y060	NA19116	0	0	2	GG	GG	II
Y100	NA19117	0	0	1	AA	TT	DI
Y100	NA19118	0	0	2	0	0	0
Y060	NA19119	0	0	1	GA	GT	II
Y060	NA19120	NA19119	NA19116	1	GG	GG	II
Y061	NA19121	0	0	1	GA	GT	II
Y061	NA19122	0	0	2	AA	TT	II
Y061	NA19123	NA19121	NA19122	1	AA	TT	II
Y077	NA19127	0	0	2	GA	GT	II
Y077	NA19128	0	0	1	GA	GT	II
Y077	NA19129	NA19128	NA19127	2	GA	GT	II

Y101	NA19130	0	0	1	AA	TT	II
Y101	NA19131	0	0	2	GA	GT	II
Y101	NA19132	NA19130	NA19131	2	AA	TT	II
Y043	NA19137	0	0	2	GA	GT	II
Y043	NA19138	0	0	1	GA	GT	II
Y043	NA19139	NA19138	NA19137	1	GA	GT	II
Y071	NA19140	0	0	2	GA	GT	II
Y071	NA19141	0	0	1	GA	GT	II
Y071	NA19142	NA19141	NA19140	1	GG	GG	II
Y074	NA19143	0	0	2	GA	GT	II
Y074	NA19144	0	0	1	AA	TT	II
Y074	NA19145	NA19144	NA19143	1	AA	TT	II
Y075	NA19146	0	0	1	GA	GT	II
Y075	NA19147	0	0	2	GA	GT	II
Y075	NA19148	NA19146	NA19147	2	GA	GT	II
Y073	NA19149	0	0	2	GA	GT	II
Y073	NA19150	0	0	1	GA	GT	II
Y073	NA19151	NA19150	NA19149	2	GG	GG	II
Y072	NA19152	0	0	2	GA	GT	II
Y072	NA19153	0	0	1	AA	TT	II
Y072	NA19154	NA19153	NA19152	1	GA	GT	II
Y056	NA19159	0	0	2	AA	TT	II
Y056	NA19160	0	0	1	AA	TT	II
Y056	NA19161	NA19160	NA19159	1	AA	TT	II
Y047	NA19171	0	0	1	GA	GT	II
Y047	NA19172	0	0	2	GG	GG	II
Y047	NA19173	NA19171	NA19172	1	GA	GT	II
Y100	NA19174	NA19117	NA19118	1	AA	TT	II
Y044	NA19175	0	0	1	GA	GT	II
Y044	NA19176	0	0	2	AA	TT	II
Y044	NA19177	NA19175	NA19176	1	GA	GT	II
Y038	NA19178	0	0	1	AA	TT	DI
Y038	NA19179	0	0	2	GG	GG	II
Y038	NA19180	NA19178	NA19179	2	GA	GT	II
Y052	NA19181	0	0	1	GA	GT	II
Y052	NA19182	0	0	2	GG	GG	II
Y052	NA19183	NA19181	NA19182	2	GA	GT	II
Y039	NA19184	0	0	1	GA	GT	DI
Y039	NA19185	0	0	2	AA	TT	II
Y039	NA19186	NA19184	NA19185	1	AA	TT	DI
Y111	NA19189	0	0	1	GA	GT	II
Y111	NA19190	0	0	2	GG	GG	II
Y111	NA19191	NA19189	NA19190	1	GG	GG	II
Y112	NA19192	0	0	1	AA	TT	II
Y112	NA19193	0	0	2	AA	TT	II
Y112	NA19194	NA19192	NA19193	1	AA	TT	II
Y035	NA19197	0	0	2	GA	GT	II
Y035	NA19198	0	0	1	AA	TT	II
Y035	NA19199	NA19198	NA19197	2	AA	TT	II
Y045	NA19200	0	0	1	GA	GT	II

Y045	NA19201	0	0	2	AA	TT	II
Y045	NA19202	NA19200	NA19201	2	AA	TT	II
Y048	NA19203	0	0	1	AA	TT	II
Y048	NA19204	0	0	2	GG	GG	II
Y048	NA19205	NA19203	NA19204	1	GA	GT	II
Y051	NA19206	0	0	2	GG	GG	II
Y051	NA19207	0	0	1	AA	TT	II
Y051	NA19208	NA19207	NA19206	1	GA	GT	II
Y050	NA19209	0	0	2	AA	TT	II
Y050	NA19210	0	0	1	AA	TT	II
Y050	NA19211	NA19210	NA19209	1	AA	TT	II
Y110	NA19213	0	0	1	GA	GT	II
Y110	NA19214	0	0	2	AA	TT	II
Y110	NA19215	NA19213	NA19214	2	GA	GT	II
Y058	NA19221	NA19223	NA19222	2	AA	TT	DI
Y058	NA19222	0	0	2	AA	TT	II
Y058	NA19223	0	0	1	AA	TT	DD
Y057	NA19224	NA19226	NA19225	1	GA	GT	II
Y057	NA19225	0	0	2	GA	GT	II
Y057	NA19226	0	0	1	GA	GT	II
Y116	NA19235	0	0	2	AA	TT	II
Y116	NA19236	0	0	1	GA	GT	II
Y116	NA19237	NA19236	NA19235	2	AA	TT	II
Y117	NA19238	0	0	2	AA	TT	II
Y117	NA19239	0	0	1	GA	GT	II
Y117	NA19240	NA19239	NA19238	2	GA	GT	II
Y120	NA19247	0	0	2	GA	GT	II
Y120	NA19248	0	0	1	AA	TT	II
Y120	NA19249	NA19248	NA19247	1	GA	GT	II
Y025	NA19252	0	NA18907	1	AA	TT	DI
Y092	NA19256	0	0	1	GA	GT	II
Y092	NA19257	0	0	2	GG	GG	II
Y092	NA19258	NA19256	NA19257	1	GG	GG	II

Table S5. Genotype data for samples whose plasma was tested for trypanosomal lytic potential. Last column shows presence or absence of lytic activity in the plasma against Trypanosoma brucei rhodesiense.

Subject	rs73885319 (G1)	rs60910145 (G1)	rs71785313 (G2)	ETat1.2R lysis
1	AA	TT	II	-
2	AA	TT	II	-
3	GG	GG	II	+
4	AA	TT	II	-
5	AA	TT	II	-
6	GA	GT	II	+
7	GG	GG	II	+
8	GA	GT	II	+
9	AA	TT	DI	+
10	GA	GT	II	+
11	GA	GT	II	+
12	GA	GT	II	+
13	AA	TT	DI	+
14	GA	GT	DI	+
15	AA	TT	II	-
16	AA	TT	II	-
17	AA	TT	II	-
18	AA	TT	II	-
19	GA	GT	II	+
20	GA	GT	II	+
21	AA	TT	II	-
22	AA	TT	II	-
23	AA	TT	DI	+
24	AA	TT	DI	+
25	AA	TT	II	-
26	AA	TT	DI	+
27	GA	GT	II	+
28	AA	TT	II	-
29	GG	GT	II	+
30	GG	GG	II	+
31	AA	TT	II	-
32	AA	TT	DI	+
33	AA	TT	II	-
34	GG	GG	II	+
35	AA	TT	II	-
36	AA	TT	II	-
37	GA	GT	II	+
38	AA	TT	DI	+
39	AA	TT	II	-
40	AA	TT	II	-
41	AA	TT	II	-
42	GA	GT	II	+
43	GA	GT	DI	+
44	GG	GG	II	+

45	AA	TT	DI	+
46	GA	GT	II	+
47	GA	GT	DI	+
48	AA	TT	DI	+
49	AA	TT	II	-
50	AA	TT	II	-
51	AA	TT	DI	+
52	AA	TT	II	-
53	AA	TT	DI	+
54	AA	TT	DI	+
55	GA	GT	II	+
56	AA	TT	II	-
57	AA	TT	DI	+
58	GA	GT	II	+
59	AA	TT	II	-
60	AA	TT	DI	+
61	GA	GT	DI	+
62	AA	TT	DI	+
63	AA	TT	DI	+
64	AA	TT	II	-
65	AA	TT	DD	+
66	AA	TT	<NA>	-
67	AA	TT	II	-
68	GA	GT	II	+
69	GG	GG	II	+
70	GA	GT	DI	+
71	AA	TT	DI	+
72	AA	TT	II	-
73	AA	TT	DI	+
74	GA	GT	II	+
75	AA	TT	II	-

References:

S1. L. M. McKenzie *et al.*, NPHS2 variation in sporadic focal segmental glomerulosclerosis. *J Am Soc Nephrol* **18**, 2987 (Nov, 2007).

S2. M. S. Orloff *et al.*, Variants in the Wilms' tumor gene are associated with focal segmental glomerulosclerosis in the African American population. *Physiol Genomics* **21**, 212 (Apr 14, 2005).

S3. S. Purcell *et al.*, PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* **81**, 559 (Sep, 2007).

S4. B. I. Freedman *et al.*, Polymorphisms in the non-muscle myosin heavy chain 9 gene (MYH9) are strongly associated with end-stage renal disease historically attributed to hypertension in African Americans. *Kidney Int* **75**, 736 (Apr, 2009).

S5. B. F. Voight, S. Kudaravalli, X. Wen, J. K. Pritchard, A map of recent positive selection in the human genome. *PLoS Biol* **4**, e72 (Mar, 2006).

S6. S. R. Grossman *et al.*, A composite of multiple signals distinguishes causal variants in regions of positive selection. *Science* **327**, 883 (Feb 12, 2010).

S7. L. Lecordier *et al.*, C-terminal mutants of apolipoprotein L-I efficiently kill both Trypanosoma brucei brucei and Trypanosoma brucei rhodesiense. *PLoS Pathog* **5**, e1000685 (Dec, 2009).

S8. B. L. Browning, S. R. Browning, A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. *Am J Hum Genet* **84**, 210 (Feb, 2009).

S9. G. Ayodo *et al.*, Combining evidence of natural selection with association analysis increases power to detect malaria-resistance variants. *Am J Hum Genet* **81**, 234 (Aug, 2007).

S10. P. C. Sabeti *et al.*, Genome-wide detection and characterization of positive selection in human populations. *Nature* **449**, 913 (Oct 18, 2007).

S11. J. C. Barrett, B. Fry, J. Maller, M. J. Daly, Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics* **21**, 263 (Jan 15, 2005).