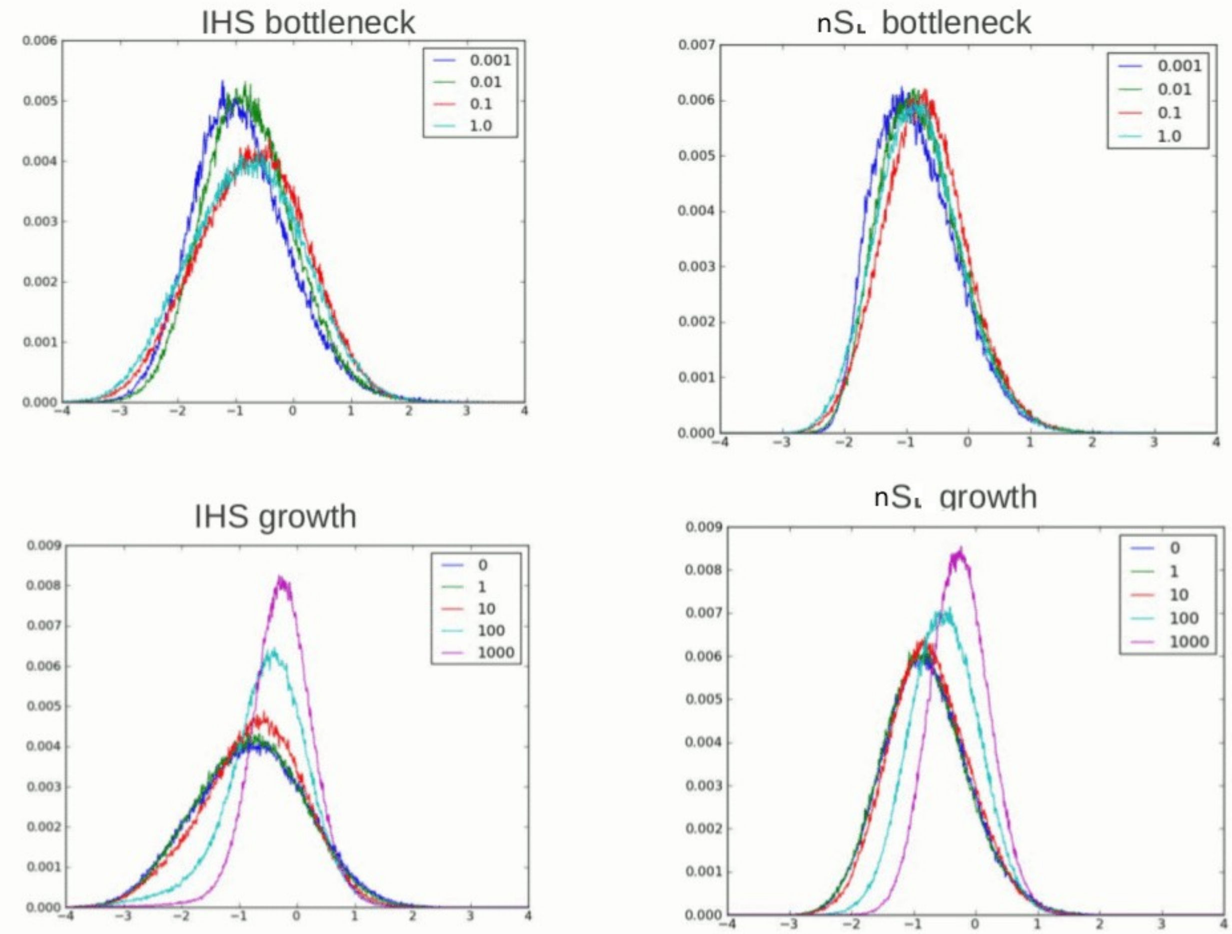
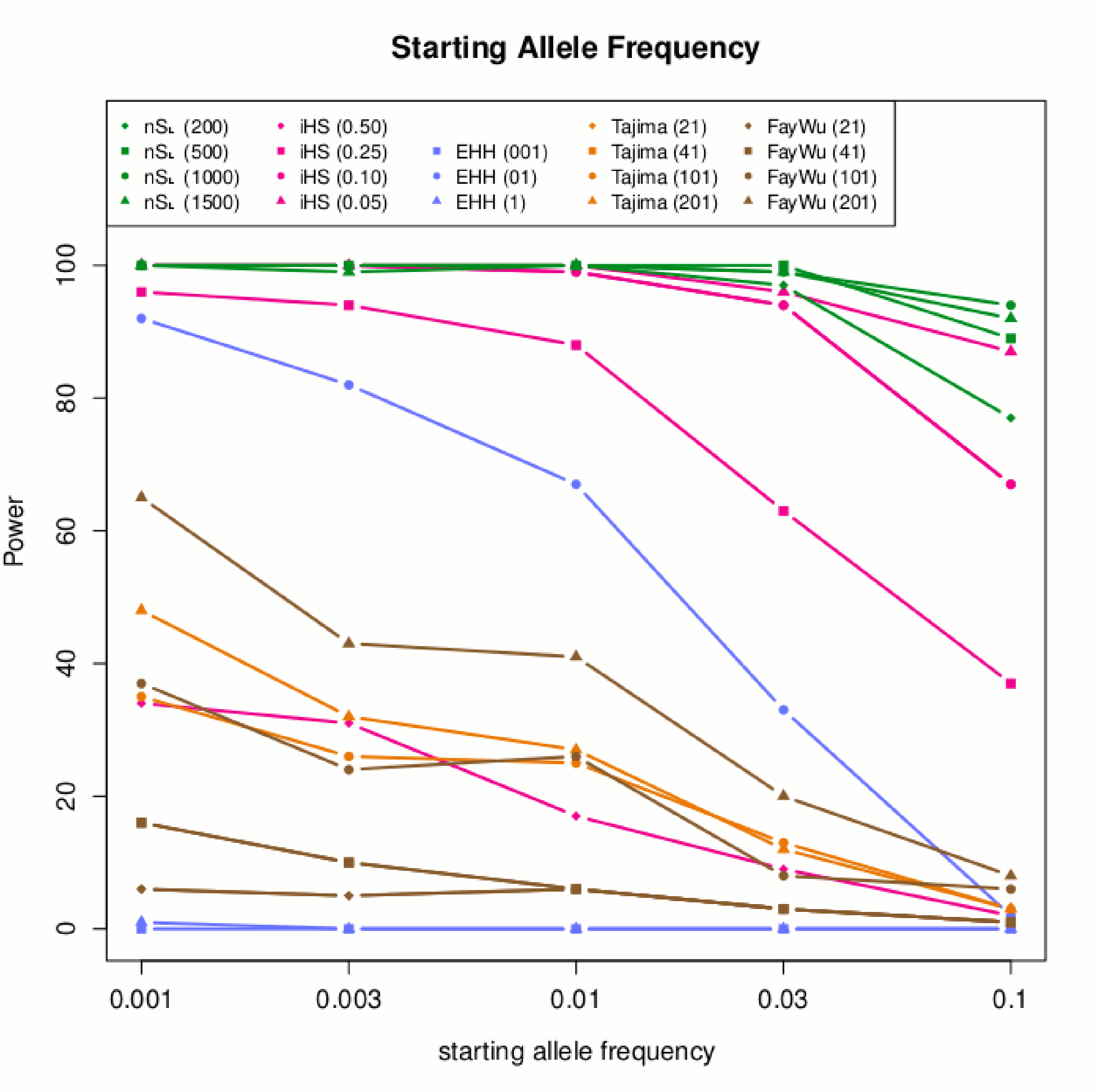
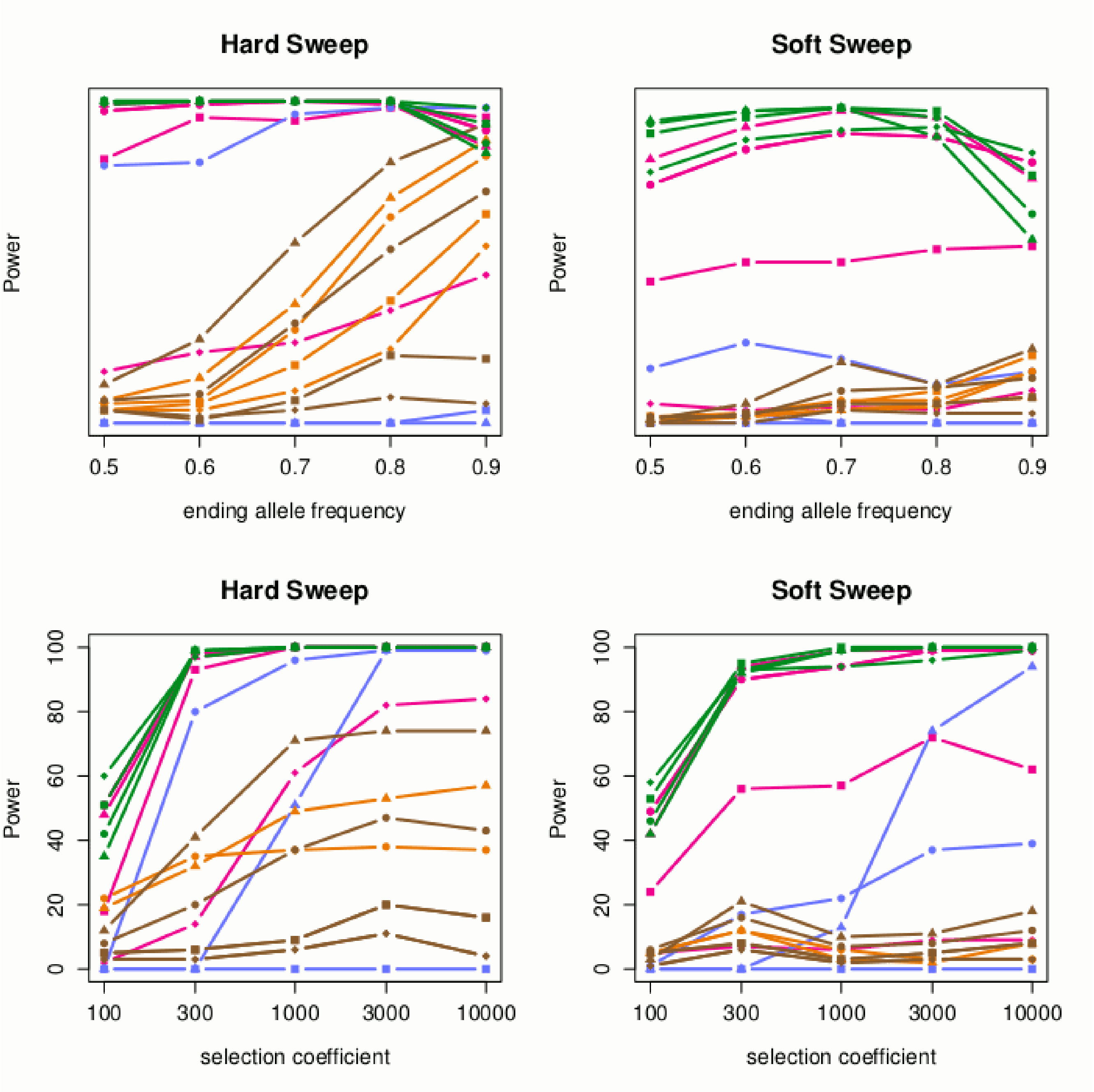
Supplementary Figure 1. Distribution of iHS and nS_L with population growth and population bottlenecks.



The top two panels show the distribution of iHS and nS_L under a range of bottleneck strengths (r = 0.001,0.01,0.1 and 1). Each color corresponds to a different bottleneck strength, as indicated in the embedded legend. The x-axis displays the score of iHS and nS_L (top left panel and top right panel, respectively). The bottom two panels show the distribution of iHS and nS_L for a range of growth rates (α=0,1,10,100,1000) in a model of exponential population growth. Each color corresponds to the growth rate indicated in the embedded legend.

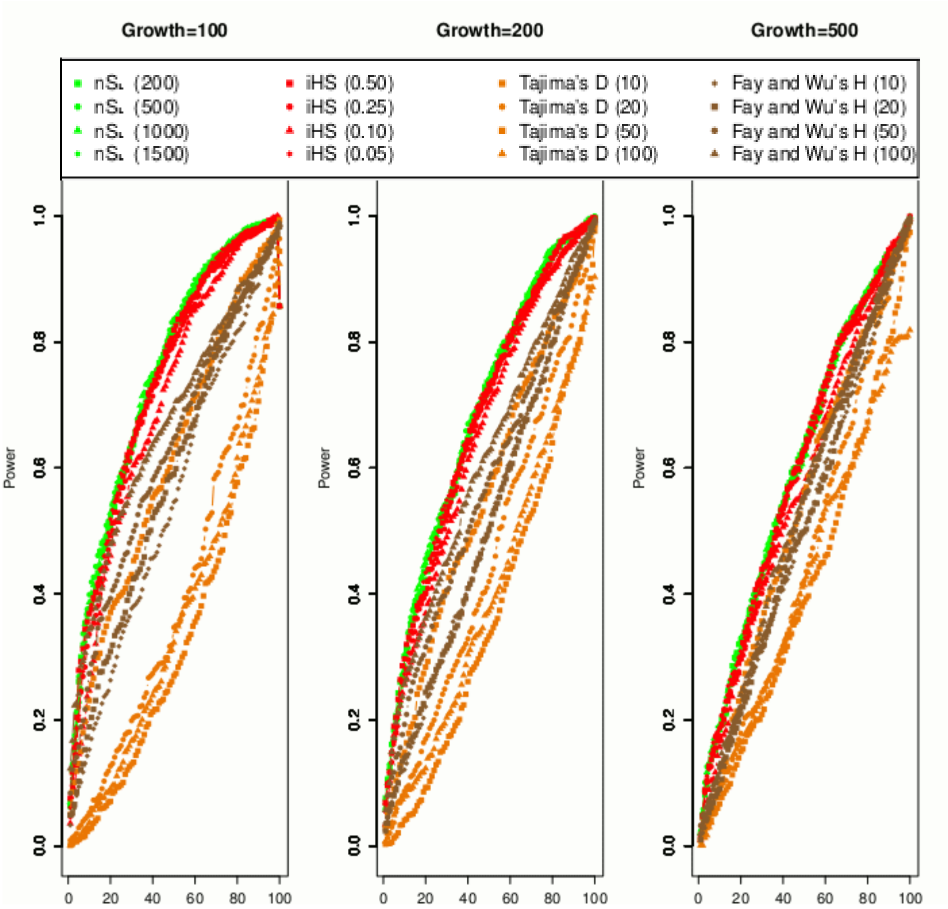
Supplementary Figure 2A and 2B. Power curves with selection.



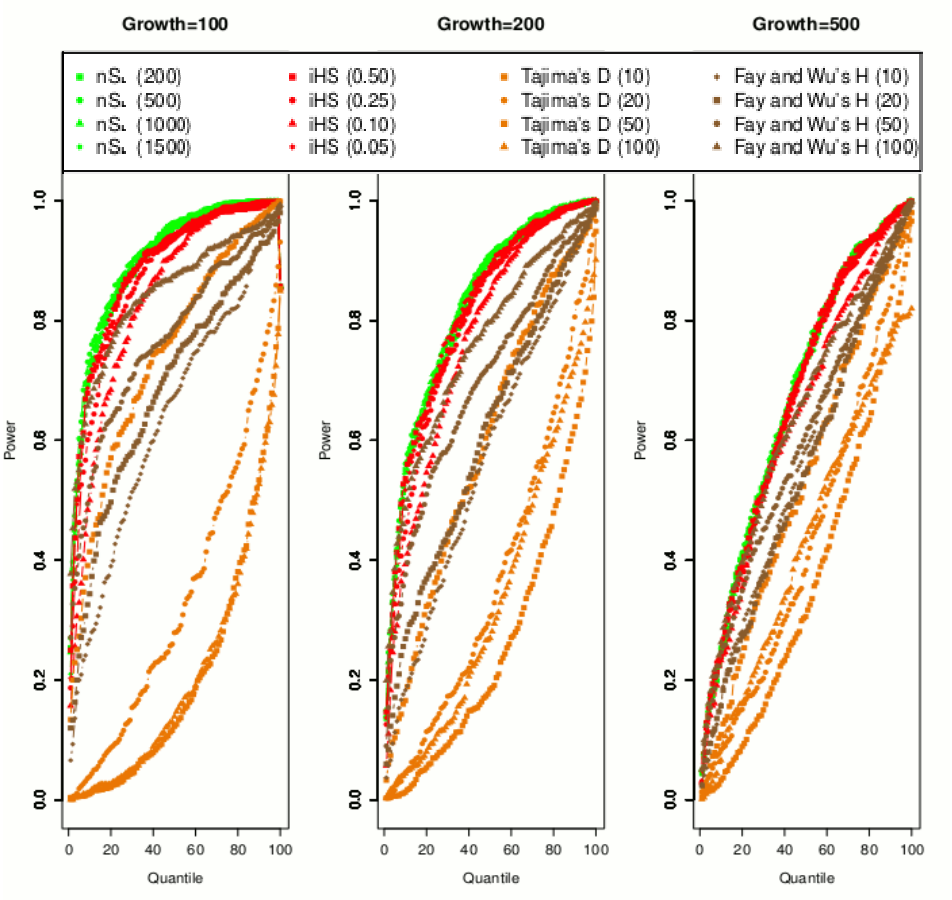


Supplementary Figure 2A shows the power of five methods (nS_L, iHS, EHH, Tajima's D and Fay and Wu's H) towards a range of starting allele frequencies (0.001-0.1). Power is defined as the proportion of simulations that reject the neutral null hypothesis at the 5% significance level. Each color corresponds to a method and symbols correspond to the window sizes used to run the methods (the specific window sizes used for the analysis are given in parenthesis). Supplementary Figure 2B is divided in four panels. The top two show the power of the five methods towards a range of ending allele frequencies (0.5-0.9). Power is again defined as the proportion of simulations rejecting the null hypothesis at the 5% significance level. The bottom two panels show the power of these methods towards a range of selection coefficients (100-10000). The color scheme and symbols in these panels correspond to the legend embedded in Supplementary Figure 2A.

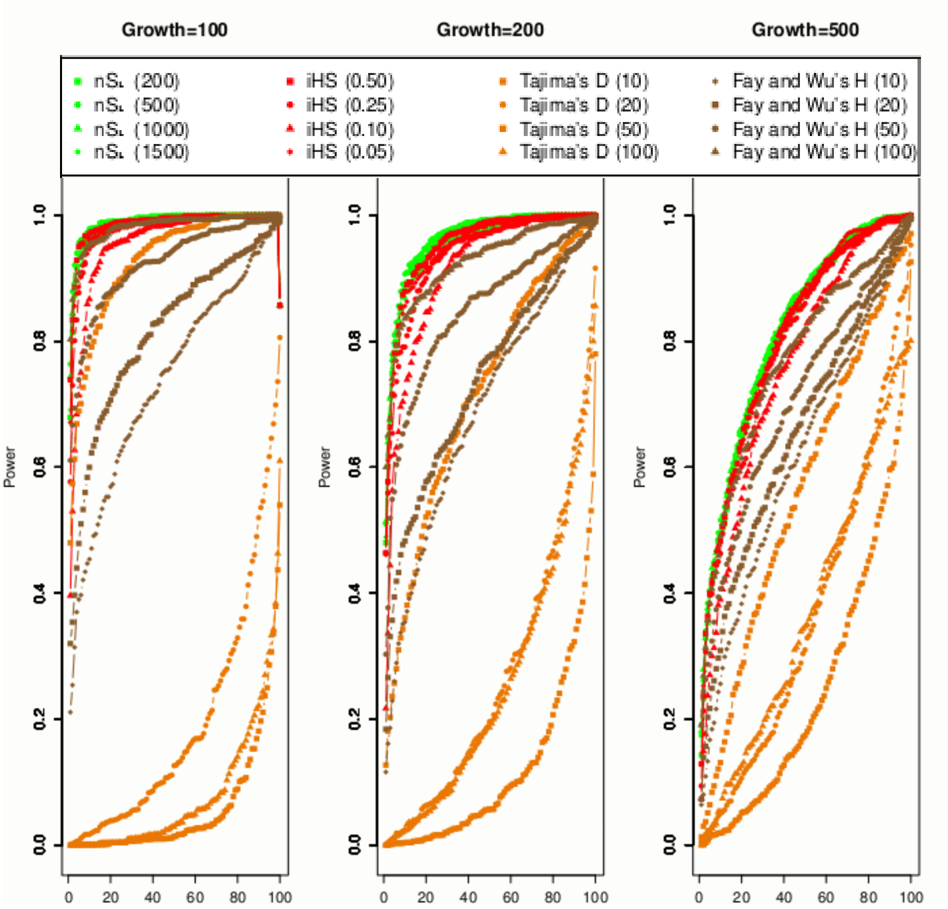
Supplementary Figure 2C. Power curves with selection (s=50) for three growth rates.



Supplementary Figure 2D. Power curves with selection (s=100) for three growth rates.

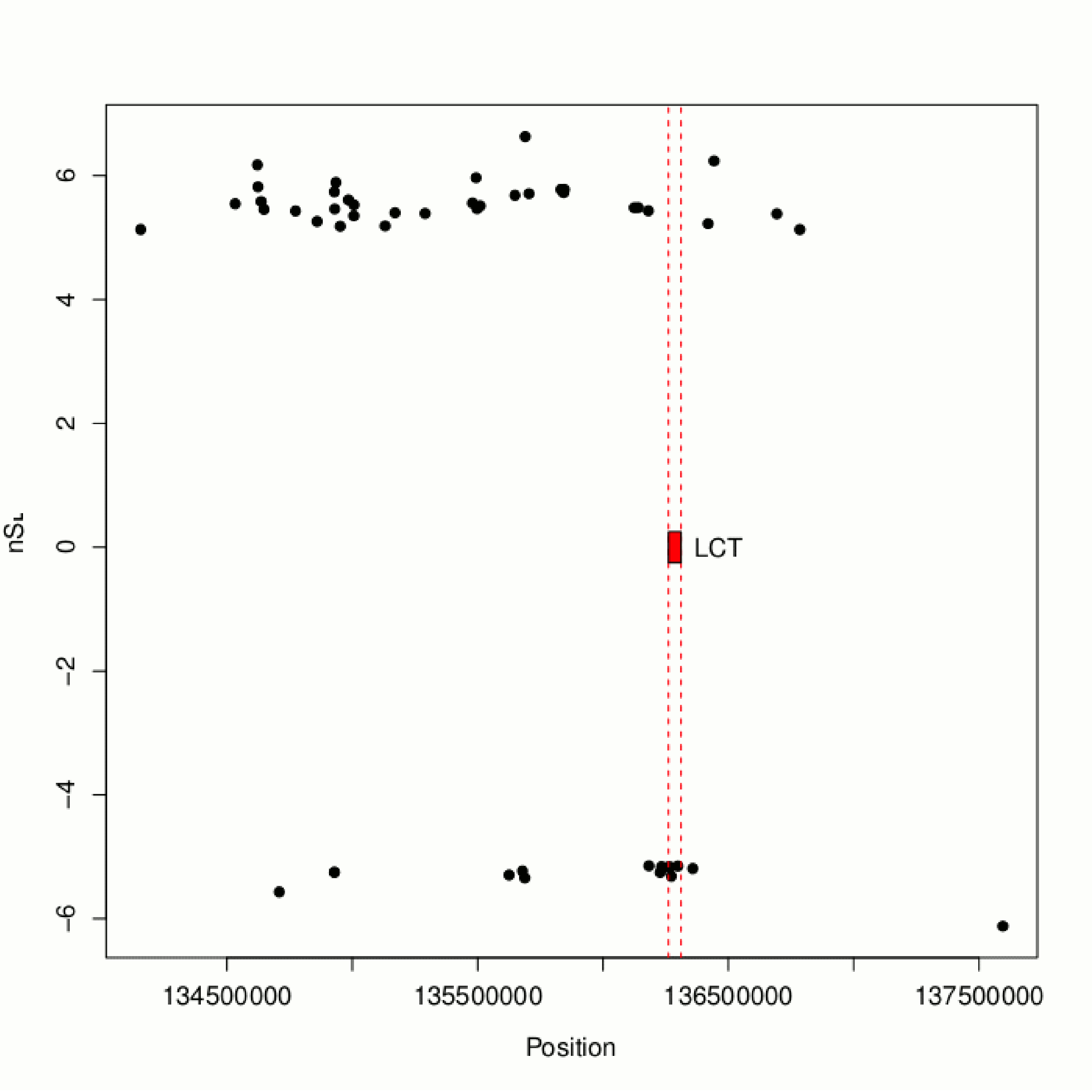


Supplementary Figure 2E. Power curves with selection (s=200) for three growth rates.



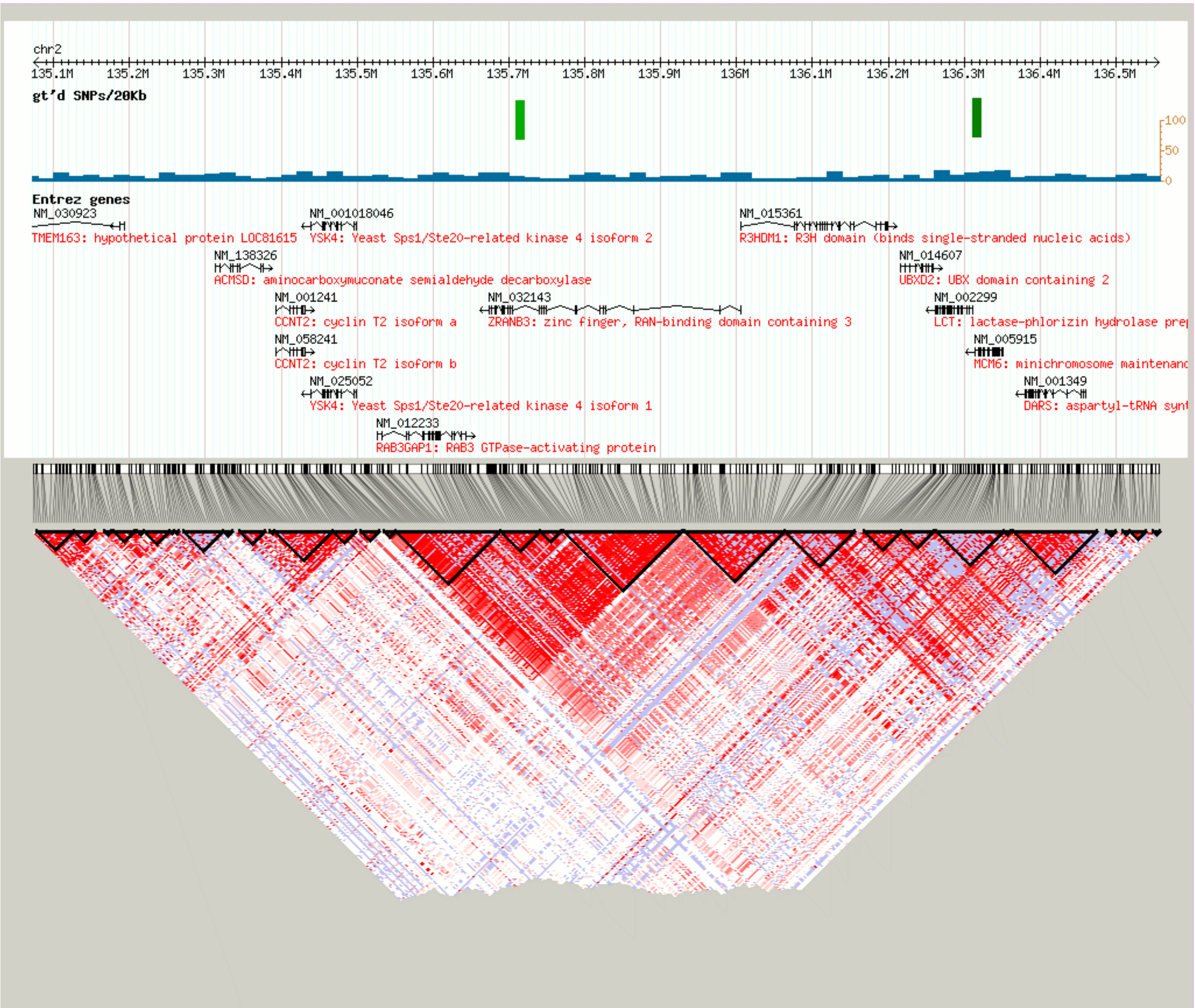
Supplementary Figure 2C, 2D and 2E show the power of four methods (nS$_L$, iHS, Tajima's D and Fay and Wu's H) for a selection coefficient (s) of 50, 100 and 200, respectively. Each figure contains three plots that correspond to three growth rates (α=100, 200 and 500). As in figure 2A and 2B, power is defined as the proportion of simulations that reject the neutral null hypothesis at the 5% significance level. The y-axis shows power, the x-axis shows the false positive rate. Each color corresponds to a method and symbols correspond to the window sizes used to run the methods (the specific window sizes used for the analysis are given after the underscore), as indicated by the legend embedded.

Supplementary Figure 3. Top 50 nS_L outliers in the MKK population.



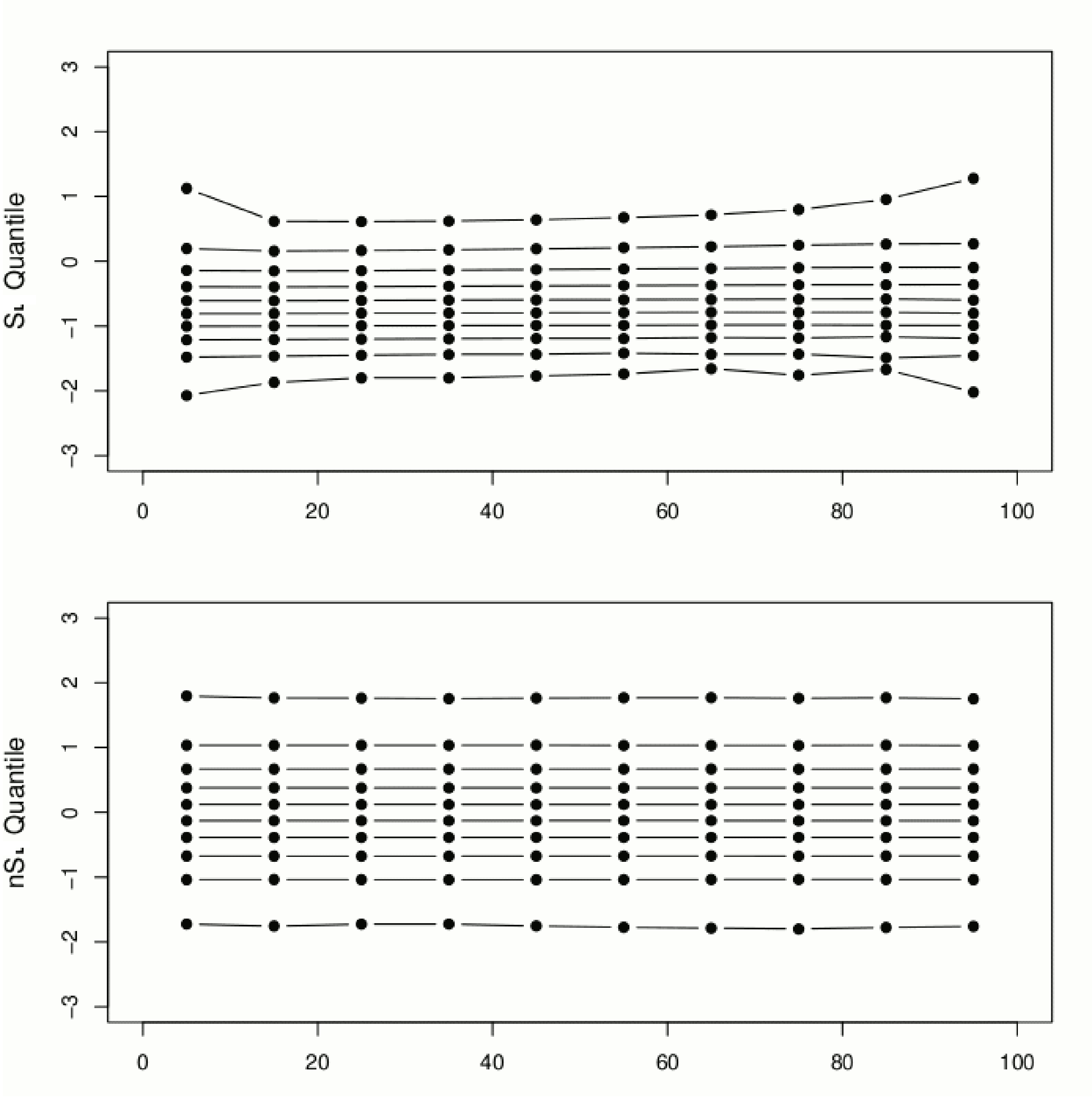
The y-axis shows nS_L score for the top 50 SNPs in the Maasai population (MKK). The x-axis shows the position of these SNPs. All of them are located within 3.4 MB in chromosome 2. This region contains the lactose resistance gene (LCT) (indicated with a red box), which has previously described to be under selection in the Maasai population.

Supplementary Figure 4. Linkage desiquilibrium (LD) plot for 1.4 MB centered at the top score in MKK.



The degree of LD along the region is shown by D' between pairs of SNPs. The brighter the color the higher the D' between the SNPs. The site with the highest score in MKK is located in *ZRANB3* (vertical light green bar). The approximate position of the sites previously described to be under positive selection in MKK is indicated by a vertical dark green line (5' extreme of *LCT*). Notice there is some LD between the *ZRANB3* and *LCT*.

Supplementary Figure 5. Dependency of nS_L on frequency.



The top panel (A) shows the non-standardized nS_L (y-axis) versus the Derived Allele Frequency (DAF) (x-axis). Values on the y-axis correspond to the nS_L score from 10th to the 100th percentile of the nS_L distribution in 10th increments (from top to bottom). The bottom panel (B) shows the quantile for nS_L standardized by frequency bins (y-axis) versus DAF (x-axis). Note the dependency of nS_L on DAF is highest for extreme DAFs and extreme nS_L quantilesed. Also note, standardization mitigates the dependency.

Supplementary Table 1. Samples used in this study.

Population label	**Population sample**	**Total number of samples**	**Non-closely related samples**
ASW	African ancestry in Southwest USA	83	42
CEU	Utah residents with Northern and Western European ancestry from the CEPH collection	165	107
CHB	Han Chinese in Beijing, China	84	84
JPT	Japanese in Tokyo, Japan	86	86
CHD	Chinese in Metropolitan Denver, Colorado	85	83
GIH	Gujarati Indians in Houston, Texas	88	83
LWK	Luhya in Webuye, Kenya	90	72
MEX	Mexican ancestry in Los Angeles, California	77	40
MKK	Maasai in Kinyawa, Kenya	171	53
TSI	Toscans in Italy	88	85
YRI	Yoruba in Ibadan, Nigeria	167	110
	Total	**1184**	**845**

Population label (as determined by the international HapMap project release 3), description of the population (brief description of the region of origin followed by country), original number of samples included in HapMap3 and number of samples used in this study after excluding individuals whose genome we estimated to be > 5% in IBD.

Supplementary Table 2. SNPs included in this study.

Chromosome	N_of_SNPs	SNPs in snp129OrthoPt2Pa2Rm2	Discordant allele in 2 or more species
1	115689	115217	4434
2	116430	115488	4241
3	96537	95771	3466
4	85772	85180	3067
5	87919	87158	3185
6	91357	90159	4219
7	75248	74512	3003
8	75272	74596	2862
9	62815	63007	2363
10	73832	73162	2834
11	70973	70206	3369
12	68525	67877	2804
13	51915	51295	2009
14	45474	45075	1639
15	42353	41961	1471
16	44648	44068	1913
17	38401	37842	1808
18	40824	40553	1534
19	26238	25510	2359
20	36258	35999	1449
21	19306	19125	838
22	20082	19706	1229
total	**1385868**	**1373467**	**56096**

List of the human autosomes, number of SNPs in each autosome (phased haplotype data from HapMap3); SNPs with corresponding allele information on the snp129OrthoPt2Pa2Rm2 from UCSC database and number of SNPs with discordant alleles in 2 or more species (includes SNPs with unavailable allele information and SNPs with discrepant alleles among species).

Supplementary Table 3. Total variation distance between the reference distribution and the distribution varying growth rate, bottleneck ratio, migration rate and recombination rate for five statistics.

	Growth rate (Ref=0)					Bottleneck ratio (Ref=1)					Migration rate (Ref=0)						Recombination rate (Ref=2000)					
	0	**1**	**10**	**100**	**1000**	**1**	**0.5**	**0.25**	**0.1**	**0.05**	**0**	**0.001**	**0.01**	**0.1**	**1**	**10**	**0**	**200**	**400**	**1000**	**2000**	**4000**
nSL_100	0.000	0.019	0.036	0.189	0.362	0.000	0.127	0.167	0.117	0.070	0.000	0.413	0.297	0.177	0.067	0.026	0.038	0.043	0.034	0.023	0.000	0.032
nSL_200	0.000	0.017	0.030	0.193	0.377	0.000	0.113	0.148	0.105	0.064	0.000	0.394	0.264	0.134	0.055	0.024	0.037	0.044	0.033	0.025	0.000	0.033
nSL_500	0.000	0.028	0.042	0.209	0.396	0.000	0.114	0.134	0.093	0.059	0.000	0.353	0.213	0.097	0.042	0.038	0.038	0.042	0.034	0.027	0.000	0.038
nSL_1000	0.000	0.034	0.064	0.229	0.404	0.000	0.121	0.140	0.102	0.072	0.000	0.326	0.178	0.083	0.037	0.047	0.050	0.052	0.042	0.032	0.000	0.042
nSL_1500	0.000	0.033	0.072	0.234	0.403	0.000	0.120	0.137	0.103	0.075	0.000	0.305	0.162	0.079	0.035	0.050	0.053	0.052	0.043	0.031	0.000	0.040
IHS_0.50	0.000	0.099	0.226	0.397	0.499	0.000	0.313	0.280	0.190	0.141	0.000	0.145	0.135	0.109	0.052	0.053	0.112	0.107	0.088	0.051	0.000	0.072
IHS_0.25	0.000	0.080	0.201	0.405	0.534	0.000	0.294	0.278	0.203	0.147	0.000	0.123	0.130	0.110	0.051	0.027	0.108	0.111	0.090	0.054	0.000	0.076
IHS_0.10	0.000	0.064	0.165	0.404	0.592	0.000	0.240	0.229	0.167	0.123	0.000	0.136	0.116	0.095	0.054	0.041	0.094	0.091	0.077	0.051	0.000	0.066
IHS_0.05	0.000	0.051	0.133	0.347	0.533	0.000	0.189	0.183	0.135	0.098	0.000	0.141	0.097	0.077	0.049	0.048	0.076	0.076	0.064	0.044	0.000	0.054
EHH_2	0.000	0.079	0.205	0.302	0.457	0.000	0.263	0.221	0.180	0.153	0.000	0.124	0.138	0.140	0.186	0.248	0.080	0.073	0.064	0.038	0.000	0.054
EHH_20	0.000	0.194	0.407	0.609	0.831	0.000	0.459	0.403	0.345	0.307	0.000	0.204	0.226	0.225	0.254	0.306	0.208	0.193	0.164	0.096	0.000	0.121
EHH_200	0.000	0.099	0.164	0.209	0.226	0.000	0.179	0.162	0.145	0.132	0.000	0.082	0.114	0.109	0.111	0.106	0.104	0.092	0.075	0.042	0.000	0.040
REHH_2	0.000	0.089	0.199	0.270	0.401	0.000	0.229	0.193	0.133	0.113	0.000	0.114	0.102	0.104	0.170	0.243	0.066	0.058	0.050	0.029	0.000	0.043
REHH_20	0.000	0.271	0.594	0.769	0.866	0.000	0.679	0.545	0.429	0.380	0.000	0.281	0.259	0.255	0.297	0.412	0.250	0.226	0.202	0.121	0.000	0.185
REHH_200	0.000	0.131	0.240	0.340	0.340	0.000	0.266	0.261	0.179	0.172	0.000	0.099	0.141	0.116	0.142	0.117	0.139	0.153	0.119	0.090	0.000	0.089
Tajima's D_21	0.000	0.201	0.562	0.840	0.934	0.000	0.434	0.170	0.045	0.056	0.000	0.410	0.335	0.270	0.144	0.049	0.077	0.067	0.057	0.033	0.000	0.040
Tajima's D_41	0.000	0.257	0.640	0.895	0.964	0.000	0.468	0.211	0.093	0.115	0.000	0.407	0.325	0.252	0.134	0.101	0.140	0.117	0.097	0.052	0.000	0.060
Tajima's D_101	0.000	0.354	0.728	0.936	0.981	0.000	0.527	0.287	0.198	0.232	0.000	0.397	0.298	0.192	0.130	0.219	0.257	0.206	0.166	0.084	0.000	0.086
Tajima's D_201	0.000	0.446	0.786	0.953	0.988	0.000	0.595	0.368	0.301	0.341	0.000	0.430	0.305	0.136	0.182	0.330	0.367	0.282	0.217	0.105	0.000	0.099
Fay and Wu's H_21	0.000	0.122	0.324	0.500	0.616	0.000	0.158	0.192	0.176	0.121	0.000	0.389	0.330	0.348	0.220	0.101	0.097	0.080	0.066	0.033	0.000	0.039
Fay and Wu's H_41	0.000	0.173	0.373	0.554	0.650	0.000	0.125	0.247	0.245	0.196	0.000	0.381	0.337	0.391	0.285	0.176	0.179	0.140	0.111	0.054	0.000	0.059
Fay and Wu's H_101	0.000	0.292	0.457	0.633	0.721	0.000	0.129	0.342	0.359	0.329	0.000	0.405	0.373	0.459	0.390	0.313	0.322	0.234	0.183	0.084	0.000	0.077
Fay and Wu's H_201	0.000	0.401	0.537	0.692	0.770	0.000	0.185	0.420	0.454	0.439	0.000	0.476	0.429	0.524	0.473	0.424	0.438	0.300	0.231	0.103	0.000	0.087

We computed each of the statistics with several window sizes (values after the underscore). For nS_L, Tajima's D, and Fay and Wu's H the window size is defined by the number of segregating sites. For iHS, the window size value gives the EHH threshold which sets the limits of integration. For EHH and rEHH the window size corresponds to the recombination rate distance over which the IBS of the haplotypes is judged. Values in the table range from 0 to 1. They correspond to the density of the distribution that does not overlap with the reference distribution. Values in bold and italics fall within the same range as the values obtained when testing nS_L. Shaded values are better than those obtained with nS_L.

Supplementary Table 4A and 4B. False positive rate for five statistics varying growth rate, bottleneck ratio, migration rate and recombination rate for two different significance levels (0.01 and 0.05).

A)

p-value=0.01	Growth rate (Ref=0)					Bottleneck ratio (Ref=1)					Migration rate (Ref=0)						Recombination rate (Ref=2000)				
	0	1	10	100	1000	1	0.5	0.25	0.1	0.05	0	0.001	0.01	0.1	1	10	0	200	400	1000	2000
nSL_100	0.0100	0.0148	0.0157	0.0025	0.0001	0.0100	0.0098	0.0083	0.0076	0.0081	0.0100	0.0067	0.0072	0.0046	0.0046	0.0144	0.0090	0.0084	0.0093	0.0100	0.0108
nSL_200	0.0100	0.0129	0.0113	0.0015	0.0000	0.0100	0.0088	0.0071	0.0061	0.0065	0.0100	0.0048	0.0056	0.0040	0.0046	0.0120	0.0114	0.0101	0.0108	0.0100	0.0093
nSL_500	0.0100	0.0122	0.0106	0.0017	0.0000	0.0100	0.0086	0.0071	0.0060	0.0072	0.0100	0.0036	0.0047	0.0038	0.0046	0.0107	0.0139	0.0118	0.0121	0.0100	0.0092
nSL_1000	0.0100	0.0120	0.0114	0.0019	0.0000	0.0100	0.0093	0.0075	0.0066	0.0080	0.0100	0.0045	0.0054	0.0046	0.0052	0.0114	0.0130	0.0112	0.0118	0.0100	0.0096
nSL_1500	0.0100	0.0115	0.0117	0.0025	0.0001	0.0100	0.0091	0.0077	0.0067	0.0083	0.0100	0.0052	0.0061	0.0051	0.0057	0.0122	0.0116	0.0106	0.0111	0.0100	0.0097
IHS_0.50	0.0100	0.0061	0.0013	0.0001	0.0000	0.0100	0.0059	0.0049	0.0029	0.0017	0.0100	0.0038	0.0052	0.0086	0.0095	0.0081	0.0185	0.0161	0.0139	0.0100	0.0063
IHS_0.25	0.0100	0.0072	0.0025	0.0001	0.0000	0.0100	0.0054	0.0032	0.0015	0.0016	0.0100	0.0020	0.0028	0.0042	0.0072	0.0111	0.0173	0.0171	0.0144	0.0100	0.0060
IHS_0.10	0.0100	0.0107	0.0108	0.0021	0.0004	0.0100	0.0093	0.0075	0.0055	0.0076	0.0100	0.0268	0.0065	0.0100	0.0154	0.0300	0.0104	0.0119	0.0109	0.0100	0.0085
IHS_0.05	0.0100	0.0116	0.0138	0.0034	0.0007	0.0100	0.0106	0.0092	0.0076	0.0107	0.0100	0.0280	0.0075	0.0113	0.0159	0.0306	0.0091	0.0108	0.0102	0.0100	0.0095
EHH_2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
EHH_20	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
EHH_200	0.0067	0.0048	0.0015	0.0001	0.0000	0.0067	0.0029	0.0021	0.0011	0.0010	0.0011	0.0002	0.0001	0.0002	0.0002	0.0002	0.0116	0.0134	0.0099	0.0067	0.0042
REHH_2	0.0081	0.0120	0.0217	0.0100	0.0066	0.0081	0.0131	0.0108	0.0093	0.0161	0.0075	0.0133	0.0094	0.0113	0.0244	0.0475	0.0075	0.0071	0.0072	0.0081	0.0093
REHH_20	0.0070	0.0127	0.0550	0.1120	0.0528	0.0070	0.0167	0.0208	0.0374	0.0836	0.0095	0.0368	0.0199	0.0191	0.0220	0.0414	0.0055	0.0049	0.0059	0.0070	0.0097
REHH_200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Tajima's D_21	0.0099	0.0129	0.0663	0.4683	0.8677	0.0099	0.0087	0.0150	0.0605	0.1914	0.0100	0.0023	0.0073	0.0209	0.0056	0.0025	0.0168	0.0154	0.0137	0.0099	0.0070
Tajima's D_41	0.0100	0.0134	0.0972	0.7247	0.9873	0.0100	0.0075	0.0153	0.0821	0.2969	0.0100	0.0010	0.0061	0.0205	0.0031	0.0007	0.0242	0.0210	0.0171	0.0100	0.0054
Tajima's D_101	0.0100	0.0170	0.2289	0.9771	1.0000	0.0100	0.0057	0.0159	0.1117	0.4306	0.0100	0.0005	0.0057	0.0189	0.0007	0.0000	0.0442	0.0328	0.0231	0.0100	0.0039
Tajima's D_201	0.0100	0.0226	0.4745	0.9998	1.0000	0.0100	0.0045	0.0146	0.1412	0.5241	0.0100	0.0006	0.0056	0.0167	0.0001	0.0000	0.0677	0.0444	0.0285	0.0100	0.0027
Fay and Wu's H_21	0.0100	0.0032	0.0002	0.0000	0.0000	0.0100	0.0097	0.0137	0.0179	0.0121	0.0100	0.0590	0.0563	0.0664	0.0221	0.0070	0.0125	0.0127	0.0116	0.0100	0.0080
Fay and Wu's H_41	0.0100	0.0023	0.0001	0.0000	0.0000	0.0100	0.0089	0.0144	0.0208	0.0139	0.0100	0.0581	0.0563	0.0757	0.0179	0.0033	0.0178	0.0165	0.0138	0.0100	0.0067
Fay and Wu's H_101	0.0100	0.0012	0.0000	0.0000	0.0000	0.0100	0.0074	0.0150	0.0236	0.0140	0.0100	0.0318	0.0505	0.0888	0.0087	0.0003	0.0299	0.0235	0.0180	0.0100	0.0047
Fay and Wu's H_201	0.0100	0.0007	0.0000	0.0000	0.0000	0.0100	0.0066	0.0172	0.0269	0.0117	0.0100	0.0249	0.0629	0.1000	0.0032	0.0000	0.0496	0.0338	0.0239	0.0100	0.0031

B)

p-value=0.05	Growth rate (Ref=0)					Bottleneck ratio (Ref=1)					Migration rate (Ref=0)						Recombination rate (Ref=2000)				
	0	1	10	100	1000	1	0.5	0.25	0.1	0.05	0	0.001	0.01	0.1	1	10	0	200	400	1000	2000
nSL_100	0.0500	0.0612	0.0529	0.0124	0.0009	0.0500	0.0416	0.0345	0.0302	0.0322	0.0499	0.0264	0.0271	0.0203	0.0292	0.0579	0.0509	0.0487	0.0500	0.0500	0.0474
nSL_200	0.0500	0.0564	0.0459	0.0100	0.0005	0.0500	0.0397	0.0333	0.0292	0.0309	0.0500	0.0218	0.0236	0.0202	0.0307	0.0535	0.0569	0.0538	0.0535	0.0500	0.0441
nSL_500	0.0500	0.0546	0.0486	0.0118	0.0006	0.0500	0.0407	0.0349	0.0314	0.0353	0.0500	0.0222	0.0245	0.0240	0.0328	0.0543	0.0573	0.0554	0.0542	0.0500	0.0448
nSL_1000	0.0500	0.0558	0.0546	0.0188	0.0021	0.0500	0.0431	0.0376	0.0351	0.0421	0.0500	0.0249	0.0270	0.0267	0.0344	0.0569	0.0561	0.0555	0.0534	0.0500	0.0475
nSL_1500	0.0500	0.0566	0.0588	0.0237	0.0038	0.0500	0.0450	0.0398	0.0384	0.0461	0.0500	0.0270	0.0292	0.0288	0.0359	0.0583	0.0536	0.0541	0.0518	0.0500	0.0487
IHS_0.50	0.0500	0.0356	0.0100	0.0008	0.0001	0.0500	0.0313	0.0249	0.0152	0.0090	0.0500	0.0162	0.0219	0.0319	0.0424	0.0382	0.0798	0.0727	0.0643	0.0500	0.0345
IHS_0.25	0.0500	0.0391	0.0148	0.0008	0.0000	0.0500	0.0279	0.0193	0.0102	0.0083	0.0500	0.0206	0.0204	0.0236	0.0379	0.0517	0.0753	0.0737	0.0656	0.0500	0.0331
IHS_0.10	0.0500	0.0469	0.0354	0.0086	0.0014	0.0500	0.0393	0.0326	0.0255	0.0259	0.0500	0.0784	0.0290	0.0378	0.0502	0.0792	0.0586	0.0574	0.0551	0.0500	0.0413
IHS_0.05	0.0500	0.0493	0.0400	0.0107	0.0017	0.0500	0.0422	0.0367	0.0303	0.0310	0.0500	0.0806	0.0326	0.0409	0.0513	0.0794	0.0548	0.0548	0.0533	0.0500	0.0438
EHH_2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
EHH_20	0.0170	0.0108	0.0019	0.0001	0.0000	0.0170	0.0047	0.0035	0.0020	0.0008	0.0319	0.0052	0.0087	0.0081	0.0066	0.0049	0.0319	0.0289	0.0254	0.0170	0.0090
EHH_200	0.0125	0.0083	0.0024	0.0002	0.0000	0.0125	0.0049	0.0036	0.0019	0.0014	0.0204	0.0047	0.0060	0.0070	0.0060	0.0061	0.0204	0.0224	0.0172	0.0125	0.0072
REHH_2	0.0414	0.0520	0.0702	0.0346	0.0231	0.0414	0.0526	0.0433	0.0351	0.0490	0.0387	0.0437	0.0410	0.0474	0.0833	0.1283	0.0387	0.0380	0.0388	0.0414	0.0434
REHH_20	0.0340	0.0486	0.1012	0.1271	0.0531	0.0340	0.0507	0.0562	0.0773	0.1244	0.0469	0.0754	0.0621	0.0586	0.0624	0.0905	0.0296	0.0289	0.0315	0.0340	0.0397
REHH_200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Tajima's D_21	0.0496	0.0755	0.3097	0.8535	0.9893	0.0496	0.0448	0.0618	0.1708	0.4323	0.0496	0.0194	0.0271	0.0508	0.0290	0.0252	0.0599	0.0612	0.0572	0.0496	0.0429
Tajima's D_41	0.0499	0.0820	0.4155	0.9670	0.9998	0.0499	0.0424	0.0634	0.1974	0.5037	0.0500	0.0123	0.0206	0.0490	0.0228	0.0148	0.0723	0.0712	0.0629	0.0499	0.0384
Tajima's D_101	0.0499	0.0982	0.6397	0.9993	1.0000	0.0499	0.0369	0.0643	0.2387	0.5846	0.0499	0.0042	0.0136	0.0450	0.0110	0.0033	0.0972	0.0888	0.0732	0.0499	0.0318
Tajima's D_201	0.0500	0.1225	0.8515	1.0000	1.0000	0.0500	0.0315	0.0644	0.2890	0.6839	0.0500	0.0019	0.0124	0.0411	0.0039	0.0004	0.1243	0.1086	0.0838	0.0500	0.0257
Fay and Wu's H_21	0.0498	0.0213	0.0025	0.0001	0.0000	0.0498	0.0551	0.0726	0.0898	0.0614	0.0499	0.2736	0.2539	0.2378	0.1065	0.0466	0.0544	0.0546	0.0523	0.0498	0.0454
Fay and Wu's H_41	0.0498	0.0167	0.0008	0.0000	0.0000	0.0498	0.0540	0.0767	0.0981	0.0638	0.0500	0.3521	0.3217	0.2836	0.1141	0.0383	0.0630	0.0604	0.0562	0.0498	0.0424
Fay and Wu's H_101	0.0500	0.0109	0.0001	0.0000	0.0000	0.0500	0.0505	0.0839	0.1107	0.0614	0.0500	0.4146	0.3745	0.3345	0.1100	0.0193	0.0860	0.0733	0.0642	0.0500	0.0343
Fay and Wu's H_201	0.0499	0.0067	0.0000	0.0000	0.0000	0.0499	0.0491	0.0945	0.1253	0.0533	0.0500	0.4268	0.3852	0.3737	0.0937	0.0061	0.1167	0.0899	0.0741	0.0499	0.0287

We computed each of the statistics using several window sizes (values after the underscore). For nS_L, Tajima's D, and Fay and Wu's H the window size is defined by the number of segregating sites. For iHS, the window size value gives the EHH threshold which sets the limits of integration. For EHH and rEHH the window size corresponds to the recombination rate distance over which the IBS of the haplotypes is judged. Values in the table range from 0 to 1. They correspond to the false positive rate respect to the standard neutral model. Notice that for some statistics the false positive rate is zero for all simulation conditions. This occurs because the most extreme value of the test statistic is found in a proportion larger than α, where α is the nominal significance level, under the standard neutral model.

Supplementary Table 5. Areas under the ROC curves.

	s=50			s=100			s=200		
	g=100	**g=200**	**g=500**	**g=100**	**g=200**	**g=500**	**g=100**	**g=200**	**g=500**
nSL_100	0.451	0.460	0.458	0.454	0.469	0.477	0.470	0.484	0.471
nSL_200	0.744	0.684	0.607	0.896	0.820	0.674	0.985	0.959	0.812
nSL_500	0.750	0.690	0.607	0.904	0.828	0.680	0.988	0.965	0.819
nSL_1000	0.746	0.687	0.604	0.898	0.825	0.677	0.985	0.961	0.818
nSL_1500	0.742	0.681	0.601	0.891	0.818	0.672	0.980	0.951	0.814
IHS_0.50	0.738	0.679	0.600	0.885	0.812	0.671	0.976	0.945	0.811
IHS_0.25	0.697	0.651	0.570	0.829	0.766	0.639	0.952	0.910	0.757
IHS_0.10	0.725	0.668	0.598	0.867	0.801	0.668	0.977	0.941	0.797
IHS_0.05	0.737	0.679	0.602	0.886	0.815	0.674	0.984	0.953	0.807
EHH_2	0.469	0.471	0.513	0.500	0.517	0.512	0.548	0.556	0.529
EHH_20	0.613	0.574	0.528	0.667	0.622	0.532	0.784	0.711	0.579
Tajima's D_10	0.610	0.559	0.540	0.741	0.596	0.532	0.928	0.717	0.559
Tajima's D_20	0.399	0.459	0.464	0.336	0.375	0.435	0.196	0.269	0.367
Tajima's D_50	0.330	0.376	0.417	0.206	0.268	0.370	0.059	0.120	0.253
Tajima's D_100	0.361	0.405	0.422	0.209	0.341	0.429	0.078	0.257	0.370
Fay and Wu's H_10	0.549	0.515	0.508	0.633	0.570	0.565	0.738	0.690	0.618
Fay and Wu's H_20	0.580	0.516	0.513	0.683	0.610	0.551	0.816	0.738	0.656
Fay and Wu's H_50	0.626	0.570	0.531	0.767	0.695	0.598	0.923	0.849	0.708
Fay and Wu's H_100	0.667	0.608	0.542	0.843	0.761	0.639	0.981	0.927	0.772

We show the area under the ROC curve for five statistics (nS_L, iHS, EHH, Tajima's D and Fay and Wu's H) under different combinations of selection strength and growth rate (s and g, respectively). We computed each of the statistics with several window sizes (values after the underscore). See the footnotes of Supplementary Tables 3 and 4A-4B for explanation on the window size.

Supplementary Table 6A. Top 30 nS_L outliers (< 1st or > 99th percentile) for the ASW population.

Population	SNPid	chr	Possition(bp)	Derived_Allele	DAF	nS_L	P-value	Function	Gene
ASW	rs17163742	chr01	221395906	C	11	5.14	1.00E-005	unknown	-
ASW	rs281364	chr17	19730045	G	6	5.04	1.00E-005	unknown	-
ASW	rs11292	chr10	102303597	G	25	4.8	1.00E-005	untranslated-3	HIF1AN
ASW	rs10073312	chr05	109249743	C	36	4.8	1.00E-005	unknown	-
ASW	rs8045580	chr16	22920077	G	12	4.72	1.00E-005	unknown	-
ASW	rs9788794	chr16	22921536	T	12	4.72	1.00E-005	unknown	-
ASW	rs12913601	chr15	71861953	T	14	-4.71	1.00E-005	unknown	-
ASW	rs4850505	chr02	194561636	G	12	4.62	1.00E-005	unknown	-
ASW	rs7778364	chr07	32364158	C	11	4.61	1.00E-005	unknown	-
ASW	rs1440101	chr15	72011684	G	83	4.61	1.00E-005	intron	LOXL1
ASW	rs12832115	chr12	112326305	C	14	4.6	1.00E-005	near-gene-5	-
ASW	rs2489043	chr10	102324317	C	30	4.59	1.00E-005	unknown	-
ASW	rs12902790	chr15	71955281	C	79	4.57	1.00E-005	intron	TBC1D21
ASW	rs9850102	chr03	48541782	T	6	4.57	1.00E-005	intron	PFKFB4
ASW	rs4937385	chr11	110149742	C	42	4.56	1.00E-005	unknown	-
ASW	rs2034377	chr02	223648307	C	39	4.52	1.00E-005	unknown	-
ASW	rs2088762	chr19	21349675	C	30	4.52	1.00E-005	unknown	ZNF738
ASW	rs16897662	chr08	100835696	G	19	4.52	1.00E-005	intron	VPS13B
ASW	rs2209797	chr09	19581691	G	6	4.51	1.00E-005	intron	SLC24A2
ASW	rs10504836	chr08	88669709	C	7	4.5	1.00E-005	unknown	-
ASW	rs7833870	chr08	100860332	C	19	4.49	1.00E-005	missense	VPS13B
ASW	rs2012013	chr19	21333646	T	30	4.48	1.00E-005	unknown	ZNF738
ASW	rs11049953	chr12	29002747	C	6	4.44	1.00E-005	unknown	-
ASW	rs1440102	chr15	72029039	A	15	-4.43	1.00E-005	intron	LOXL1
ASW	rs489913	chr15	71432872	C	13	-4.41	1.00E-005	intron	HCN4
ASW	rs16971703	chr15	72243676	C	14	-4.41	1.00E-005	unknown	-
ASW	rs16953384	chr15	67558675	C	6	4.39	1.00E-005	unknown	-
ASW	rs7650727	chr03	101171666	C	52	4.38	1.00E-005	intron	FILIP1L
ASW	rs1452383	chr15	71932107	A	19	-4.38	1.00E-005	unknown	-

Supplementary Table 6B. Top 30 nS_L outliers (< 1st or > 99th percentile) for the CEU population.

Population	**SNPid**	**chr**	**Possition(bp)**	**Derived_Allele**	**DAF**	**nS_L**	**P-value**	**Function**	**Gene**
CEU	rs4954555	chr02	136509584	T	93	-5.74	1.00E-005	unknown	-
CEU	rs7371606	chr02	136523244	G	25	5.71	1.00E-005	unknown	-
CEU	rs12475139	chr02	136503121	A	23	5.69	1.00E-005	unknown	-
CEU	rs13404551	chr02	136438465	C	21	5.62	1.00E-005	intron	DARS
CEU	rs313528	chr02	136162339	A	21	5.56	1.00E-005	intron	R3HDM1
CEU	rs1446584	chr02	136136431	G	20	5.47	1.00E-005	intron	R3HDM1
CEU	rs4954566	chr02	136617983	T	29	5.46	1.00E-005	unknown	-
CEU	rs4954388	chr02	136524612	C	23	5.42	1.00E-005	unknown	-
CEU	rs4954557	chr02	136521871	T	23	5.42	1.00E-005	unknown	-
CEU	rs953387	chr02	136623640	C	29	5.33	1.00E-005	unknown	-
CEU	rs6715785	chr02	136626743	A	29	5.33	1.00E-005	unknown	-
CEU	rs10484008	chr14	88446316	G	2	5.25	0.000158	unknown	-
CEU	rs7752195	chr06	25527073	T	8	-5.23	1.00E-005	intron	LRRC16A
CEU	rs7774567	chr06	25533505	A	8	-5.17	1.00E-005	intron	LRRC16A
CEU	rs666614	chr02	135006923	C	50	5.11	1.00E-005	intron	TMEM163
CEU	rs655472	chr02	135006691	C	50	5.05	1.00E-005	intron	TMEM163
CEU	rs9295661	chr06	25558005	C	8	-5.04	1.00E-005	intron	LRRC16A
CEU	rs10193587	chr02	136641909	C	27	4.98	1.00E-005	unknown	-
CEU	rs2090660	chr02	136535189	T	20	4.97	1.00E-005	unknown	-
CEU	rs749873	chr02	136533558	T	70	-4.87	1.00E-005	unknown	-
CEU	rs7568884	chr02	136644790	T	26	4.85	1.00E-005	unknown	-
CEU	rs4954573	chr02	136643564	G	26	4.85	1.00E-005	unknown	-
CEU	rs12631710	chr03	125123110	T	1	4.82	1.00E-005	intron	CCDC14
CEU	rs1533649	chr02	136530579	A	19	4.81	1.00E-005	unknown	-
CEU	rs4523477	chr01	73249037	G	1	4.8	1.00E-005	unknown	-
CEU	rs2230591	chr03	49911630	A	1	4.79	1.00E-005	missense	MST1R
CEU	rs1592	chr02	135438613	C	39	4.79	1.00E-005	near-gene-3	-
CEU	rs1399859	chr08	53076300	A	17	4.79	1.00E-005	unknown	-
CEU	rs1399857	chr08	53076461	G	17	4.79	1.00E-005	unknown	-
CEU	rs6473675	chr08	53077062	T	17	4.79	1.00E-005	unknown	-

Supplementary Table 6C. Top 30 nS_L outliers (< 1st or > 99th percentile) for the CHB population.

Population	SNPid	chr	Possition(bp)	Derived_Allele	DAF	nS_L	P-value	Function	Gene
CHB	rs260705	chr02	108937872	G	2	6.32	1.60E-005	intron	EDAR
CHB	rs6934645	chr06	33014206	A	4	-5.2	0.025119	unknown	HLA-DMB
CHB	rs12206377	chr06	33017313	G	4	-5.2	0.025119	unknown	-
CHB	rs9848674	chr03	108884573	C	5	5.18	0.000631	intron	BBX
CHB	rs13159615	chr05	144139852	T	2	5.15	2.00E-004	unknown	-
CHB	rs9267785	chr06	32032848	T	5	-5.01	0.039811	unknown	RDBP
CHB	rs7598552	chr02	108306502	C	5	5.01	0.001	intron	SULT1C2P1
CHB	rs1879493	chr02	108304920	C	5	5	0.001	near-gene-5	-
CHB	rs10209570	chr02	108610389	T	4	4.99	0.000794	intron	-
CHB	rs1821867	chr02	108577286	C	4	4.97	0.000631	intron	-
CHB	rs9819988	chr03	137107260	C	2	4.91	0.000316	unknown	-
CHB	rs7084981	chr10	94959756	T	5	4.85	0.001	unknown	-
CHB	rs28366175	chr06	32377556	C	5	-4.82	0.050119	unknown	C6orf10
CHB	rs9267661	chr06	31968555	T	5	-4.82	0.050119	unknown	EHMT2
CHB	rs2844648	chr06	31016693	C	7	-4.79	6.30E-005	unknown	-
CHB	rs13413437	chr02	108564962	C	95	-4.78	0.000126	unknown	-
CHB	rs6498703	chr16	17410330	A	7	4.77	1.00E-005	intron	XYLT1
CHB	rs12477830	chr02	108305167	G	93	-4.76	1.00E-005	untranslated-5	SULT1C2P1
CHB	rs17269356	chr02	108371267	C	5	4.76	0.001	unknown	-
CHB	rs12476238	chr02	108306768	C	93	-4.75	1.00E-005	intron	SULT1C2P1
CHB	rs1589912	chr02	108690108	A	5	4.74	0.001	unknown	-
CHB	rs4781986	chr16	17403825	C	10	4.74	1.00E-005	intron	XYLT1
CHB	rs4244304	chr10	94926318	C	10	4.73	1.00E-005	unknown	-
CHB	rs6716426	chr02	108680810	G	95	-4.72	0.000158	unknown	-
CHB	rs1907965	chr09	71703060	G	2	4.72	0.000398	intron	C9orf135
CHB	rs2247178	chr06	31024697	A	7	-4.7	1.00E-004	unknown	DPCR1
CHB	rs10179602	chr02	108451805	G	94	-4.7	0.000158	intron	GCC2
CHB	rs12438318	chr15	29467737	A	17	-4.68	1.00E-005	unknown	-
CHB	rs1973360	chr03	168999542	C	3	4.66	0.000501	intron	SERPINI1
CHB	rs12469016	chr02	108622967	G	95	-4.65	0.000158	intron	-

Supplementary Table 6D. Top 30 nS_L outliers (< 1st or > 99th percentile) for the CHD population.

Population	**SNPid**	**chr**	**Possition(bp)**	**Derived_Allele**	**DAF**	**nS_L**	**P-value**	**Function**	**Gene**
CHD	rs3800316	chr06	27364081	A	97	-5.5	1.00E-005	unknown	-
CHD	rs12613021	chr02	177530870	C	3	5.44	0.000251	unknown	-
CHD	rs6835296	chr04	143674737	C	3	5.29	0.000316	intron	INPP4B
CHD	rs10209570	chr02	108610389	T	2	5.2	0.000126	intron	-
CHD	rs911186	chr06	27258578	G	2	5.08	0.000158	unknown	-
CHD	rs10851487	chr15	29128753	G	4	4.84	0.001	intron	TRPM1
CHD	rs2854050	chr06	32293583	A	18	-4.82	1.00E-005	unknown	NOTCH4
CHD	rs9848674	chr03	108884573	C	6	4.8	1.00E-005	intron	BBX
CHD	rs4564548	chr16	17352536	C	11	4.7	1.00E-005	intron	XYLT1
CHD	rs11130186	chr03	49250832	A	1	4.68	1.00E-005	intron	CCDC36
CHD	rs9357105	chr06	31111902	A	10	-4.65	0.000316	unknown	-
CHD	rs9851055	chr03	108777698	T	8	4.62	1.00E-005	intron	BBX
CHD	rs1478894	chr08	11486163	C	8	4.57	1.00E-005	unknown	-
CHD	rs4781986	chr16	17403825	C	4	4.57	0.001259	intron	XYLT1
CHD	rs7168200	chr15	63009811	T	34	4.55	1.00E-005	intron	ANKDD1A
CHD	rs745767	chr02	177533661	A	97	-4.55	1.00E-004	unknown	-
CHD	rs631400	chr03	108820670	C	7	4.55	1.00E-005	intron	BBX
CHD	rs6900560	chr06	106035880	A	3	4.51	0.001	unknown	-
CHD	rs13281098	chr08	9316963	A	2	4.51	0.000398	unknown	-
CHD	rs3731640	chr02	26006297	G	8	4.49	1.00E-005	intron	KIF3C
CHD	rs7570544	chr02	108214569	G	30	4.48	1.00E-005	unknown	-
CHD	rs2966	chr06	33797498	C	10	4.48	1.00E-005	untranslated-3	IP6K3
CHD	rs2856437	chr06	32265342	A	18	-4.47	1.00E-005	unknown	PBX2
CHD	rs482542	chr01	164871465	G	2	4.47	0.000501	unknown	-
CHD	rs329921	chr03	108872594	C	5	4.47	0.001585	intron	BBX
CHD	rs12915207	chr15	47938432	G	2	4.47	0.000501	untranslated-3	ATP8B4
CHD	rs9480564	chr06	106015864	C	2	4.46	0.000501	unknown	-
CHD	rs2072134	chr12	111893559	A	18	-4.45	1.00E-005	untranslated-3	OAS3
CHD	rs12148990	chr16	17369496	A	7	4.43	1.00E-005	intron	XYLT1
CHD	rs855004	chr02	108133378	G	20	4.4	1.00E-005	unknown	-

Supplementary Table 6E. Top 30 nS_L outliers (< 1st or > 99th percentile) for the GIH population.

Population	SNPid	chr	Possition(bp)	Derived_Allele	DAF	nS_L	P-value	Function	Gene
GIH	rs2185770	chr06	73806676	G	10	5.4	1	intron	KCNQ5
GIH	rs4730954	chr07	119704394	G	5	5.37	1	intron	KCND2
GIH	rs12533932	chr07	119727006	G	5	5.29	1	intron	KCND2
GIH	rs3817874	chr22	45100920	G	6	5.18	1	intron	GTSE1
GIH	rs9267487	chr06	31619329	C	14	-5.09	1	unknown	P6V1G2-DDX3
GIH	rs28780106	chr06	30559494	A	23	-5.05	1	unknown	-
GIH	rs10819113	chr09	127884913	A	11	-5.04	1	unknown	-
GIH	rs10241520	chr07	119644092	A	92	-5.02	1	unknown	-
GIH	rs28732144	chr06	31664184	A	14	-5.01	1	unknown	LST1
GIH	rs2190184	chr07	119601105	C	93	-4.95	1	unknown	-
GIH	rs9654068	chr04	41727723	G	16	4.94	1	intron	SLC30A9
GIH	rs9291209	chr04	41727910	T	16	4.94	1	intron	SLC30A9
GIH	rs10134470	chr14	96663134	T	4	-4.91	1	unknown	-
GIH	rs4044210	chr22	45164979	C	11	4.86	1	missense	CELSR1
GIH	rs7672382	chr04	41869567	G	14	4.85	1	unknown	-
GIH	rs3093662	chr06	31652168	G	14	-4.81	1	unknown	TNF
GIH	rs13107768	chr04	41719739	A	16	4.76	1	intron	SLC30A9
GIH	rs11105028	chr12	87644447	G	4	4.73	1	unknown	-
GIH	rs17475879	chr06	30472487	T	22	-4.73	1	unknown	-
GIH	rs755407	chr09	125330375	T	26	4.72	1	intron	DENND1A
GIH	rs7290972	chr22	45174187	C	7	4.72	1	intron	CELSR1
GIH	rs3132689	chr06	29990509	G	24	-4.7	1	intron	-
GIH	rs11743225	chr05	117590170	A	22	4.68	1	unknown	-
GIH	rs2581442	chr04	41706570	T	16	4.68	1	intron	SLC30A9
GIH	rs15857	chr04	41717221	C	16	4.68	1	coding-synon	SLC30A9
GIH	rs6813397	chr04	41879586	G	14	4.65	1	unknown	-
GIH	rs7857782	chr09	125381131	G	20	4.64	1	intron	DENND1A
GIH	rs1155818	chr02	223608748	T	15	4.64	1	unknown	-
GIH	rs10953916	chr07	119886649	A	4	4.63	1	intron	KCND2
GIH	rs4355757	chr08	67083278	T	14	4.61	1	unknown	-

Supplementary Table 6F. Top 30 nS_L outliers (< 1st or > 99th percentile) for the JPT population.

Population	SNPid	chr	Possition(bp)	Derived_Allele	DAF	nS_L	P-value	Function	Gene
JPT	rs17356524	chr06	36370905	T	5	-6.21	0.000251	intron	PNPLA1
JPT	rs12724767	chr01	172515247	T	2	5.79	7.90E-005	intron	-
JPT	rs6088116	chr20	31178498	G	2	5.71	1.00E-004	unknown	-
JPT	rs1442493	chr04	100540388	G	23	5.57	1.00E-005	unknown	-
JPT	rs16869677	chr06	33984060	T	13	-5.47	1.00E-005	unknown	-
JPT	rs6912480	chr06	36737495	C	6	-5.45	1.00E-005	unknown	-
JPT	rs1535938	chr06	33959945	T	12	-5.44	1.00E-005	unknown	-
JPT	rs12197499	chr06	36322469	G	95	5.34	0.000251	intron	-
JPT	rs9469625	chr06	33989548	A	13	-5.3	1.00E-005	unknown	-
JPT	rs12191571	chr06	33988458	T	87	5.29	1.00E-005	unknown	-
JPT	rs27848	chr16	64438881	C	6	5.24	1.00E-005	unknown	-
JPT	rs1110528	chr16	64436948	G	6	5.2	1.00E-005	unknown	-
JPT	rs3128376	chr07	111916569	A	2	5.15	0.000251	intron	C7orf53
JPT	rs284789	chr04	100551080	A	23	5.15	1.00E-005	unknown	-
JPT	rs13196184	chr06	36314060	T	5	-5.14	0.025119	unknown	-
JPT	rs9296177	chr06	36305720	C	5	-5.08	0.025119	intron	BRPF3
JPT	rs7747793	chr06	36304140	A	5	-5.05	0.031623	intron	BRPF3
JPT	rs6921746	chr06	36817874	A	8	-5.03	1.60E-005	untranslated-3	CPNE5
JPT	rs2032506	chr06	36300204	T	5	-5.03	0.031623	intron	BRPF3
JPT	rs4236048	chr06	36299305	C	5	-5.03	0.031623	intron	BRPF3
JPT	rs3822969	chr06	36828736	A	8	-5.01	2.00E-005	intron	CPNE5
JPT	rs921656	chr02	108253437	A	20	4.98	1.00E-005	unknown	-
JPT	rs921659	chr02	108253651	C	20	4.98	1.00E-005	unknown	-
JPT	rs929056	chr06	36829606	T	92	4.96	1.00E-005	intron	CPNE5
JPT	rs11939328	chr04	99922259	A	19	4.96	1.00E-005	unknown	-
JPT	rs16889362	chr06	37073683	A	8	-4.9	2.50E-005	unknown	-
JPT	rs16889370	chr06	37076041	A	8	-4.89	3.20E-005	unknown	-
JPT	rs4241191	chr02	197190452	T	2	4.87	0.000398	unknown	-
JPT	rs4785862	chr16	64398663	C	6	4.85	0.001259	unknown	-
JPT	rs957644	chr01	163882781	T	3	4.83	0.000501	intron	MGST3

Supplementary Table 6G. Top 30 nS_L outliers (< 1st or > 99th percentile) for the LWK population.

Population	SNPid	chr	Possition(bp)	Derived_Allele	DAF	nS_L	P-value	Function	Gene
LWK	rs3763341	chr06	33086998	G	76	4.98	1.00E-005	unknown	-
LWK	rs10248243	chr07	47478639	C	22	-4.93	1.00E-005	intron	TNS3
LWK	rs10947368	chr06	33083319	T	22	-4.91	1.00E-005	unknown	HLA-DOA
LWK	rs12702428	chr07	48072734	G	15	-4.81	1.00E-005	unknown	-
LWK	rs7594789	chr02	12534521	A	13	-4.8	1.00E-005	unknown	-
LWK	rs10891158	chr11	110037558	T	17	4.77	1.00E-005	intron	ARHGAP2-
LWK	rs12692469	chr02	12221064	C	33	4.74	1.00E-005	unknown	-
LWK	rs17172879	chr07	47593038	T	26	-4.72	1.00E-005	unknown	-
LWK	rs3129304	chr06	33081721	C	24	-4.7	1.00E-005	unknown	HLA-DOA
LWK	rs3129303	chr06	33081856	C	24	-4.7	1.00E-005	unknown	HLA-DOA
LWK	rs2116263	chr06	33133471	A	22	-4.69	1.00E-005	unknown	-
LWK	rs9394174	chr06	33939650	T	18	-4.68	1.00E-005	unknown	-
LWK	rs4937385	chr11	110149742	C	28	4.67	1.00E-005	unknown	-
LWK	rs6006743	chr22	44184187	G	17	4.65	1.00E-005	intron	SMC1B
LWK	rs12282038	chr11	109994124	G	22	4.63	1.00E-005	intron	ARHGAP2-
LWK	rs943472	chr06	33846420	C	67	4.63	1.00E-005	unknown	-
LWK	rs16881634	chr07	47899539	C	83	4.6	1.00E-005	intron	PKD1L1
LWK	rs17131915	chr07	47900019	C	83	4.59	1.00E-005	missense	PKD1L1
LWK	rs1997125	chr07	48208860	G	13	-4.56	1.00E-005	intron	ABCA13
LWK	rs364950	chr06	33083874	A	61	4.53	1.00E-005	unknown	HLA-DOA
LWK	rs4551215	chr06	33133678	T	23	-4.53	1.00E-005	unknown	-
LWK	rs444821	chr06	33112913	T	62	4.51	1.00E-005	unknown	-
LWK	rs226118	chr11	110167354	T	22	4.5	1.00E-005	unknown	-
LWK	rs6925399	chr06	33610996	C	30	-4.5	1.00E-005	unknown	-
LWK	rs12192605	chr06	133463185	C	8	-4.47	1.00E-005	unknown	LOC285735
LWK	rs6819958	chr04	100879932	T	14	-4.45	1.00E-005	unknown	-
LWK	rs4312417	chr19	43489029	A	66	-4.45	1.00E-005	intron	YIF1B
LWK	rs721797	chr07	47638125	G	28	-4.4	1.00E-005	unknown	-
LWK	rs6908509	chr06	33408249	T	24	-4.39	1.00E-005	intron	-
LWK	rs2077943	chr11	110043499	C	28	4.39	1.00E-005	intron	ARHGAP2-

Supplementary Table 6H. Top 30 nS_L outliers (< 1st or > 99th percentile) for the MEX population.

Population	**SNPid**	**chr**	**Possition(bp)**	**Derived_Allele**	**DAF**	**nS_L**	**P-value**	**Function**	**Gene**
MEX	rs7290972	chr22	45174187	C	14	5.59	1.00E-005	intron	CELSR1
MEX	rs4744175	chr09	94909547	G	30	5.25	1.00E-005	intron	C9orf89
MEX	rs7141605	chr14	62950199	G	9	5.09	0.000794	intron	PPP2R5E
MEX	rs1255627	chr14	63035697	G	11	5.08	0.001259	intron	PPP2R5E
MEX	rs10992629	chr09	94894265	G	16	4.91	1.00E-005	unknown	-
MEX	rs11104982	chr12	87571073	T	5	4.88	0.000126	unknown	-
MEX	rs4044210	chr22	45164979	C	13	4.75	0.001585	missense	CELSR1
MEX	rs1797022	chr20	24000857	G	14	4.65	1.00E-005	unknown	-
MEX	rs1271559	chr14	62854512	G	11	4.61	0.001995	near-gene-5	-
MEX	rs907076	chr09	15433430	C	13	4.56	0.001995	intron	SNAPC3
MEX	rs10878563	chr12	65796686	G	11	4.55	0.001995	unknown	-
MEX	rs953493	chr12	38572369	C	28	-4.54	1.00E-005	intron	SLC2A13
MEX	rs4309576	chr02	152320491	G	20	4.53	1.00E-005	unknown	-
MEX	rs9836399	chr03	123294501	A	23	4.53	1.00E-005	intron	CD86
MEX	rs1149294	chr06	105758864	C	10	4.49	0.001995	unknown	-
MEX	rs3817874	chr22	45100920	G	14	4.49	1.00E-005	intron	GTSE1
MEX	rs4664502	chr02	152306061	G	20	4.49	1.00E-005	unknown	-
MEX	rs2115766	chr05	97076919	G	5	4.48	0.000316	unknown	-
MEX	rs17559800	chr12	38588213	G	28	-4.47	1.00E-005	intron	SLC2A13
MEX	rs6482215	chr10	22780705	A	9	4.45	0.001585	unknown	-
MEX	rs11564258	chr12	39078567	G	78	4.43	1.00E-005	unknown	-
MEX	rs669759	chr02	135007605	C	18	-4.43	1.00E-005	intron	TMEM163
MEX	rs10089519	chr08	129601300	A	26	4.39	1.00E-005	unknown	-
MEX	rs771205	chr01	149241732	T	6	4.38	0.001	ron,untranslate	FAM63A
MEX	rs12423682	chr12	38614682	T	28	-4.36	1.00E-005	intron	SLC2A13
MEX	rs17042744	chr02	21678327	G	10	4.36	0.001995	unknown	-
MEX	rs535458	chr12	38651650	A	28	-4.36	1.00E-005	intron	SLC2A13
MEX	rs17111530	chr14	80668665	C	10	4.36	0.001995	intron	TSHR
MEX	rs9831425	chr03	157722406	T	25	4.36	1.00E-005	intron	KCNAB1

Supplementary Table 6I. Top 30 nS_L outliers (< 1st or > 99th percentile) for the MKK population.

Population	**SNPid**	**chr**	**Possition(bp)**	**Derived_Allele**	**DAF**	**nS_L**	**P-value**	**Function**	**Gene**
MKK	rs16831455	chr02	135690238	G	16	6.63	1.00E-005	intron	ZRANB3
MKK	rs309154	chr02	136443037	C	25	6.24	1.00E-005	intron	DARS
MKK	rs6752874	chr02	134621845	C	70	6.17	1.00E-005	unknown	-
MKK	rs16838134	chr02	137595057	C	22	-6.12	1.00E-005	intron	THSD7B
MKK	rs13390171	chr02	135493974	A	25	5.97	1.00E-005	intron	YSK4
MKK	rs6430516	chr02	134935075	G	29	5.89	1.00E-005	intron	TMEM163
MKK	rs10928480	chr02	134624264	G	65	5.82	1.00E-005	unknown	-
MKK	rs9798267	chr02	135846261	G	23	5.78	1.00E-005	intron	ZRANB3
MKK	rs7577288	chr02	135831971	T	23	5.78	1.00E-005	intron	ZRANB3
MKK	rs637855	chr02	134928712	C	25	5.74	1.00E-005	unknown	-
MKK	rs6711370	chr02	135843570	C	23	5.73	1.00E-005	intron	ZRANB3
MKK	rs935615	chr02	135704886	T	9	5.71	1.00E-005	missense	ZRANB3
MKK	rs935614	chr02	135649190	G	12	5.68	1.00E-005	unknown	-
MKK	rs749460	chr02	134984725	C	29	5.61	1.00E-005	intron	TMEM163
MKK	rs10928484	chr02	134636634	A	64	5.58	1.00E-005	unknown	-
MKK	rs11674684	chr02	134708891	A	34	-5.57	1.00E-005	unknown	-
MKK	rs7582173	chr02	135479788	G	23	5.56	1.00E-005	intron	YSK4
MKK	rs1715008	chr02	134533486	C	16	5.55	1.00E-005	unknown	-
MKK	rs666614	chr02	135006923	C	36	5.53	1.00E-005	intron	TMEM163
MKK	rs11888951	chr02	135510315	C	25	5.51	1.00E-005	unknown	-
MKK	rs2289959	chr02	136140374	C	19	5.49	1.00E-005	intron	R3HDM1
MKK	rs16831899	chr02	136125291	A	17	5.48	1.00E-005	intron	R3HDM1
MKK	rs11900832	chr02	135498105	T	25	5.47	1.00E-005	intron	YSK4
MKK	rs610624	chr02	134930232	C	33	5.46	1.00E-005	untranslated-3	TMEM163
MKK	rs17712107	chr02	134648097	C	62	5.46	1.00E-005	unknown	-
MKK	rs10197046	chr02	136181435	C	20	5.43	1.00E-005	intron	R3HDM1
MKK	rs11887041	chr02	134773894	G	52	5.43	1.00E-005	intron	MGAT5
MKK	rs12691872	chr02	135170502	C	48	5.4	1.00E-005	intron	TMEM163
MKK	rs6757855	chr02	135290633	G	22	5.39	1.00E-005	unknown	-
MKK	rs7371043	chr02	136693406	C	56	5.39	1.00E-005	unknown	-

Supplementary Table 6J. Top 30 nS_L outliers (< 1st or > 99th percentile) for the TSI population.

Population	**SNPid**	**chr**	**Possition(bp)**	**Derived_Allele**	**DAF**	**nS_L**	**P-value**	**Function**	**Gene**
TSI	rs17135372	chr05	112532674	G	2	5.81	4.00E-005	intron	MCC
TSI	rs2255998	chr14	61121435	G	2	5.22	0.000126	intron	-
TSI	rs1251536	chr01	76206653	A	2	5.07	0.000158	unknown	-
TSI	rs35407	chr05	33982328	A	2	5.05	0.000158	ron,untranslate	SLC45A2
TSI	rs7225869	chr17	60828075	A	9	4.92	1.00E-005	unknown	-
TSI	rs6769309	chr03	40475755	T	2	4.85	2.00E-004	intron	RPL14
TSI	rs3829073	chr09	2117883	C	11	4.73	1.00E-005	intron	SMARCA2
TSI	rs8043050	chr15	46464675	C	2	4.68	0.000251	unknown	-
TSI	rs1088673	chr14	61075401	C	12	4.68	1.00E-005	intron	PRKCH
TSI	rs2105073	chr14	61100961	G	5	4.66	1.00E-005	unknown	-
TSI	rs4766558	chr12	110148444	G	28	4.66	1.00E-005	intron	CUX2
TSI	rs933305	chr12	110222670	A	20	4.65	1.00E-005	intron	CUX2
TSI	rs475107	chr18	7536294	G	28	4.63	1.00E-005	unknown	-
TSI	rs3094005	chr06	31573026	T	6	-4.62	1.00E-005	unknown	-
TSI	rs4664502	chr02	152306061	G	18	4.57	1.00E-005	unknown	-
TSI	rs4309576	chr02	152320491	G	17	4.56	1.00E-005	unknown	-
TSI	rs17016066	chr12	87722428	A	1	4.55	1.00E-005	unknown	-
TSI	rs7434698	chr04	8762299	T	4	4.54	0.000631	unknown	-
TSI	rs2971426	chr01	35370701	A	11	4.53	1.00E-005	unknown	-
TSI	rs11143833	chr09	70623561	A	2	4.53	0.000316	intron	PIP5K1B
TSI	rs1634721	chr06	31085659	A	4	-4.48	0.031623	unknown	PBMUCL1
TSI	rs554825	chr18	7476106	G	30	4.48	1.00E-005	unknown	-
TSI	rs519282	chr01	65259671	G	8	4.45	1.00E-005	unknown	-
TSI	rs535857	chr01	65264782	G	8	4.45	1.00E-005	unknown	-
TSI	rs6930572	chr06	31536148	G	4	-4.44	0.031623	unknown	-
TSI	rs6716286	chr02	152284682	C	16	4.42	1.00E-005	intron	NEB
TSI	rs998460	chr04	34138953	T	4	4.42	0.001	unknown	-
TSI	rs10456396	chr06	31612525	A	4	-4.39	0.039811	unknown	DDX39B
TSI	rs1482184	chr08	122604920	C	10	4.39	1.00E-005	unknown	-
TSI	rs9514153	chr13	102997576	C	18	4.38	1.00E-005	unknown	-

Supplementary Table 6K. Top 30 nS_L outliers (< 1st or > 99th percentile) for the YRI population.

Population	SNPid	chr	Possition(bp)	Derived_Allele	DAF	nS_L	P-value	Function	Gene
YRI	rs1394121	chr16	22856080	C	19	5.45	1.00E-005	unknown	-
YRI	rs853040	chr07	80482597	G	16	-5.28	1.00E-005	unknown	-
YRI	rs10281727	chr07	80410578	T	21	-4.99	1.00E-005	unknown	-
YRI	rs7193968	chr16	69230453	G	2	4.94	5.00E-005	unknown	IL34
YRI	rs17292844	chr20	15067797	C	2	4.91	6.30E-005	intron	-
YRI	rs4312417	chr19	43489029	A	78	-4.85	1.00E-005	intron	YIF1B
YRI	rs11880532	chr19	43550883	T	80	-4.83	1.00E-005	intron	CATSPERG
YRI	rs2866908	chr04	108124957	A	14	4.83	1.00E-005	intron	DKK2
YRI	rs7120391	chr11	5187483	C	22	-4.82	1.00E-005	unknown	-
YRI	rs10231365	chr07	20398110	C	25	4.82	1.00E-005	intron	ITGB8
YRI	rs2413395	chr22	34984662	A	7	4.82	1.00E-005	intron	APOL1
YRI	rs2489043	chr10	102324317	C	25	4.81	1.00E-005	unknown	-
YRI	rs2270095	chr19	43532736	T	81	-4.81	1.00E-005	intron	CATSPERG
YRI	rs8136512	chr22	32461239	C	28	-4.81	1.00E-005	intron	LARGE
YRI	rs6687226	chr01	160158180	A	1	4.76	1.00E-005	intron	ATF6
YRI	rs11292	chr10	102303597	G	20	4.73	1.00E-005	untranslated-3	HIF1AN
YRI	rs4821178	chr22	32441978	G	64	4.7	1.00E-005	intron	LARGE
YRI	rs10234980	chr07	79958990	T	25	-4.64	1.00E-005	intron	CD36
YRI	rs11881305	chr19	43496058	A	80	-4.63	1.00E-005	intron	YIF1B
YRI	rs2088762	chr19	21349675	C	24	4.63	1.00E-005	unknown	ZNF738
YRI	rs3130186	chr06	33164185	T	10	4.63	1.00E-005	unknown	-
YRI	rs12693718	chr02	194559758	C	21	4.62	1.00E-005	unknown	-
YRI	rs943472	chr06	33846420	C	70	4.62	1.00E-005	unknown	-
YRI	rs6925399	chr06	33610996	C	35	-4.6	1.00E-005	unknown	-
YRI	rs12609878	chr19	43574621	T	80	-4.6	1.00E-005	intron	SPRED3
YRI	rs2012013	chr19	21333646	T	24	4.59	1.00E-005	unknown	ZNF738
YRI	rs317775	chr11	5503226	A	12	-4.58	1.00E-005	unknown	-
YRI	rs6457736	chr06	33672390	T	56	4.58	1.00E-005	unknown	-
YRI	rs6929774	chr06	33670698	C	56	4.57	1.00E-005	near-gene-5	-
YRI	rs8045580	chr16	22920077	G	11	4.57	1.00E-005	unknown	-