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Supplemental Data

**Detecting and Characterizing Genomic Signatures
of Positive Selection in Global Populations**

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Input Data

Samples from Phases 2 and 3 of the International HapMap Project

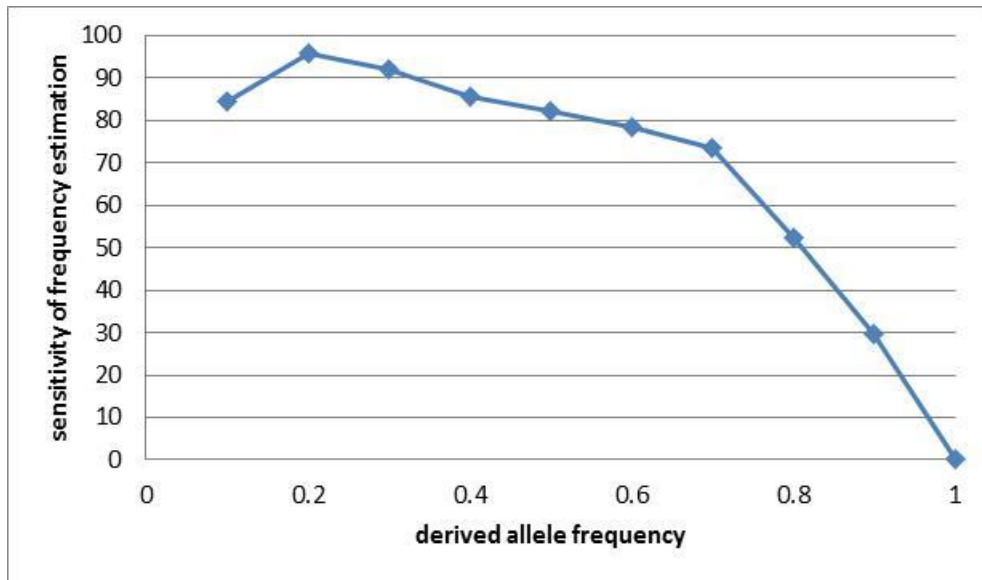
Phase 2 of the International HapMap Project surveyed around 3.1 million polymorphisms in four populations from three continents¹, consisting of 30 Utah parent-offspring trios from the CEPH collection with ancestry from Northern and Western Europe (CEU); 30 Yoruban trios from Ibadan, Nigeria in West Africa (YRI); 45 unrelated Han Chinese from Beijing, China (CHB) and 45 unrelated Japanese from Tokyo, Japan (JPT). In the positive selection analysis, only unrelated individuals from the four population groups were used, and this excluded the offsprings in the CEU and YRI trios, resulting in a sample size of 60 unrelated individuals in each of the two populations. Haplotypes for Phase 2 of the HapMap have been inferred with an updated version of PHASE^{2,3} that allows genotype data from both unrelated individuals and trios to be phased, and were downloaded from the HapMap resource.

Phase 3 of the International HapMap Project surveyed 1,301 individuals from eleven populations⁴ with two commercial genotyping microarrays: Affymetrix SNP6.0 and Illumina 1M. The two arrays assayed 2,007,788 SNPs of which 268,667 SNPs overlap between the two platforms. We considered only unrelated individuals from the eleven populations, which consisted of: (i) 53 individuals of African ancestry in Southwest USA (ASW); (ii) 113 Utah residents with Northern and Western European ancestry from the CEPH collection (CEU); (iii) 84 Han Chinese from Beijing, China (CHB); (iv) 85 Chinese in Metropolitan Denver, Colorado (CHD); (v) 88 Gujarati Indians in Houston, Texas (GIH); (vi) 86 Japanese from Tokyo, Japan (JPT); (vii) 90 Luhya from Webuye, Kenya (LWK); (viii) 50 individuals with Mexican ancestry in Los Angeles, California (MXL); (ix) 143 Maasai in Kinyawa, Kenya (MKK); (x) 88 Toscani in Italia (TSI); (xi) 113 Yoruban from Ibadan, Nigeria (YRI). A consensus set of 1,525,445 SNPs that are present across all eleven populations are used in the positive selection analysis. The phasing of the samples in HapMap Phase 3 was performed with IMPUTE v2^{4,5} and were downloaded from the HapMap resource.

Singapore Genome Variation Project

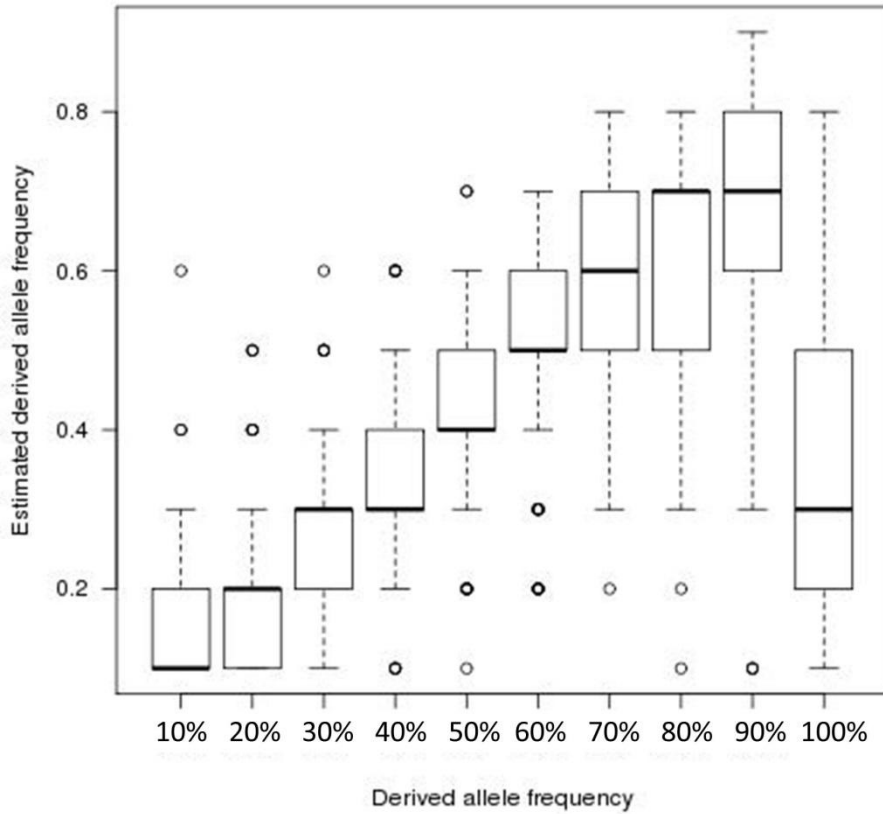
The Singapore Genome Variation Project (SGVP) surveyed 292 individuals from the three major ethnic groups in Singapore consisting of Chinese, Malays and Asian Indians⁶. Each sample was assayed on the Affymetrix SNP 6.0 and Illumina 1M genotyping microarrays, and post-QC genetic data for a final set of 96 Chinese (CHS), 89 Malays (MAS) and 83 Indians (INS) was released. This consists of 1,584,040 autosomal SNPs for CHS, 1,580,905 autosomal SNPs for MAS and 1,583,454 autosomal SNPs for INS. The SGVP samples were phased using the program *fastPHASE* (version 1.3)⁷ and were downloaded from the SGVP resource.

Figure S1. Power of HaploPS to Infer the Frequency of the Selected Allele



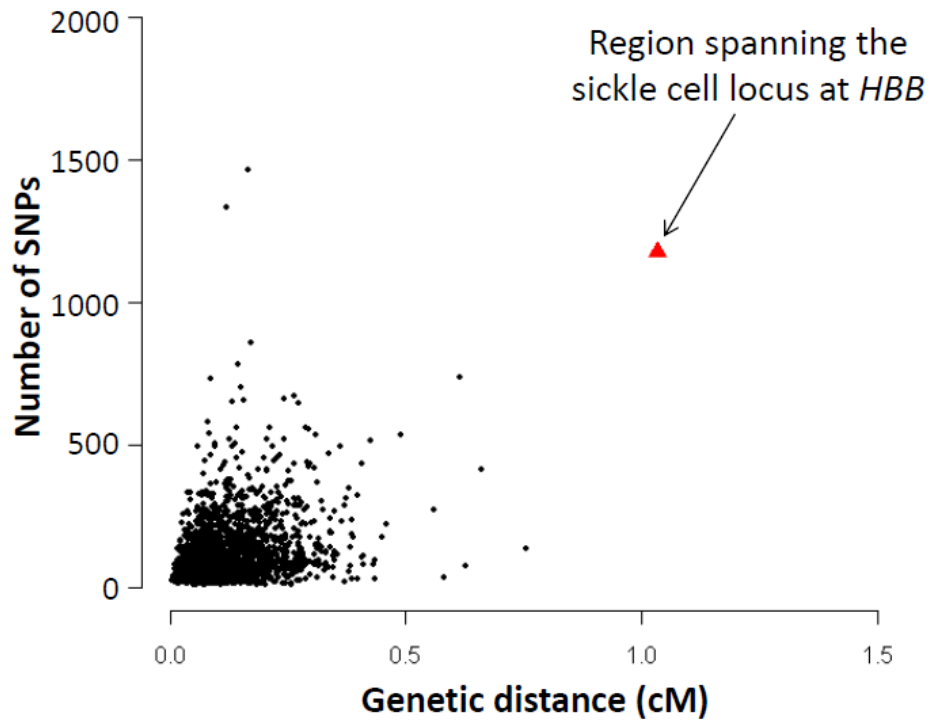
Assessment of the statistical power of haploPS to infer the frequencies of the simulated alleles under positive selection. Power here is quantified by the ability of haploPS to infer the frequency of the derived allele within 10% the actual simulation frequency out of 200 iterations at each derived allele frequency.

Figure S2. Boxplots of the Estimated Derived Allele Frequencies



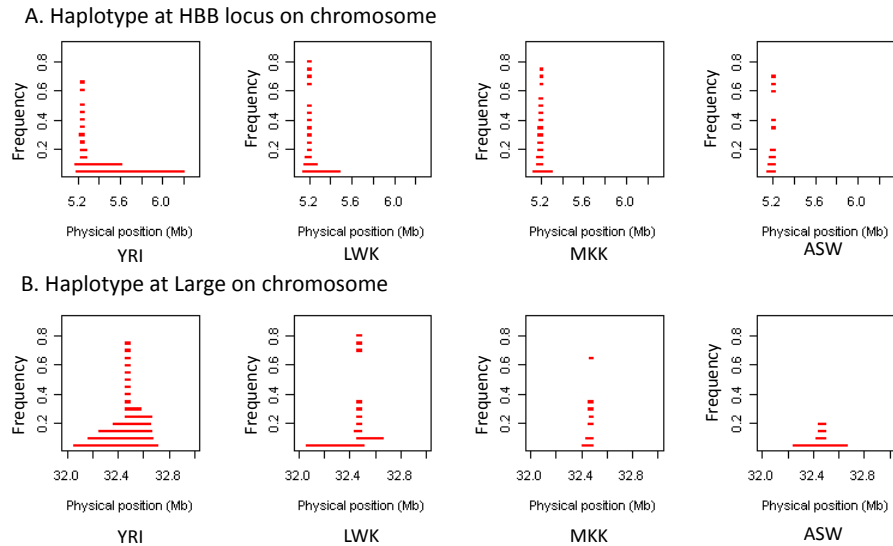
Distributions of the derived allele frequencies as estimated by haploPS, with the lower and upper edges of the each box represent the first and third quartile of the respective distribution. Each boxplot is tabulated from signals that have been successfully identified from the 200 iterations in the power simulations.

Figure S3. Positive Control of HaploPS Definition at *HBB*



Summary of the longest haplotypes at focal SNPs on chromosome 11 in YRI, at a core haplotype frequency of 5%. HaploPS defines a signal of positive selection as a region with both long genetic distance and carrying a large number of SNPs. The positive selection signal spanning the sickle-cell locus (HbS) at *HBB* is denoted by the red triangle.

Figure S4. Positive Selection at *HBB* and *LARGE* in Africa



HaploPS analyses performed across a range of core haplotype frequencies from 5% to 80% at the *HBB* (panel A) and *LARGE* (panel B) loci in the four populations with African ancestry (ASW, LWK, MKK and YRI). These two positively selected loci *HBB* and *LARGE* in the Yoruba data in Phase 2 of HapMap (YRI) are well-established to be genuinely under evolutionary pressure of selection. The sickle-cell locus *HBB* is under balancing selection for the almost ten-fold protection against malaria⁹ and the recessive sickle-cell anemia. The fitness benefit of the sickle-cell allele against childhood mortality by malaria implies the genomic background that the sickle-cell allele resides on enjoys a hitch-hiking advantage on being present in the population. This means the selection signal at *HBB* in YRI is one of the positive controls for selection metrics (Fig. S3), and the frequency of the sickle-cell allele is known to be at 12.5% in the YRI database in HapMap 2. The other known functional region is the *LARGE* locus on chromosome 22 that encodes for a protein essential for infection by the Lassa virus to cause Lassa hemorrhagic fever in Nigeria¹⁰. Together, these two regions present the strongest evidence of positive natural selection in YRI. However, these signals are not ubiquitously identified by every selection metric, especially *HBB* as the frequency of the signal is particularly low¹¹. HaploPS successfully located the selection signals at both loci and even provided an accurate estimate of the frequency of the selected variant (Fig. 3, Fig. S4, Table S1). In addressing the origin and segregation of selection signals, we are interested to address whether any of the other three populations with African ancestry are subjected to the same evolutionary pressure as Nigerian populations in regards to malaria and Lassa hemorrhagic fever. A detailed survey of haploPS analyses suggest that there were no evidence of positive selection at either *HBB* or *LARGE* in the Kenyan Maasai in Kinyawa (MKK), and in the African American population (ASW). For the Kenyan Luhya in Webuye (LWK), there seems to be a possible long haplotype at *HBB* with a core haplotype frequency of 5%, although when assessed against the genome-wide distribution of haplotype lengths of 5% frequency in LWK, this was not defined to be empirically significant (Fig. S4). There was no evidence of a long haplotype at *LARGE* for LWK. For *LARGE*, the absence of any selection signals in the two Kenyan populations can be explained by the endemicity of Lassa fever in West Africa only, and not in East Africa. Thus, without a selective pressure exerted by the viral hemorrhagic fever, there is no genomic advantage for the beneficial mutation to persist in the population. However, the absence of positive selection at *HBB* in the

two Kenyan populations is intriguing, given that malaria is similarly endemic in East Africa. We noted that there have not been any prior reports of positive selection in the vicinity of the sickle cell locus in the HapMap3 populations of the Luhya (LWK) and the Maasai (MKK). Previous reports on the frequency of the sickle-cell allele in Kenya cited figures in the range of 6.4%¹¹ to 7.8%^{12,13}. It is possible that the Luhya and Maasai samples in HapMap 3 did not include enough individuals who are carriers of the sickle-cell allele, given that the sickle-cell variant rs334 was not assayed in HapMap 3.

Table S1. Regions Identified by HaploPS to Be Positively Selected in the 14 Populations

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
1	103182146	103534051	0.1915	351905	147	4.10E-02	0.6	GIH
1	103321085	103514336	0.0974	193251	71	1.81E-02	0.9	MAS
1	113733222	114260718	0.1161	527496	192	3.24E-02	0.4	LWK
1	117122430	117153794	0.1643	31364	17	8.55E-03	0.95	INS
1	120146624	120488638	0.4207	342014	103	3.01E-02	0.55	MEX
1	120272947	120488638	0.1762	215691	40	4.57E-02	0.8	CEU
1	120287414	120488638	0.1762	201224	30	4.13E-02	0.85	TSI
1	144723881	145368810	5.1537	644929	301	1.60E-02	0.2	CHS
1	145830625	149622482	4.2394	3791857	568	2.29E-02	0.05	CHB
1	145865184	146183314	1.8739	318130	3	4.85E-02	0.95	INS
1	146268901	147468611	1.4185	1199710	20	3.43E-02	0.7	CEU
1	146268901	147468611	1.4186	1199710	20	2.54E-02	0.7	MEX
1	146273276	147327306	1.3949	1054030	17	3.12E-02	0.75	TSI
1	146292711	149282492	2.6598	2989781	408	1.54E-02	0.15	GIH
1	153077307	154135249	0.3295	1057942	279	2.02E-02	0.55	CHB
1	153077751	153253417	0.1719	175666	70	2.28E-02	0.9	JPT
1	153084311	153248332	0.2466	164021	69	5.80E-03	0.85	MAS
1	164724784	165688387	1.0403	963603	533	1.61E-02	0.2	MEX
1	167066523	167096615	0.1763	30092	21	3.51E-02	0.95	CHS
1	167346043	167744666	0.2124	398623	212	4.57E-02	0.6	MAS
1	169265406	169493840	0.5492	228434	204	4.66E-02	0.4	TSI
1	170912521	171363586	0.4753	451065	147	3.75E-02	0.6	CHB
1	170921000	171203259	0.2808	282259	77	2.32E-02	0.8	CHD
1	170958743	171203325	0.2338	244582	61	3.30E-02	0.85	JPT
1	174678225	175269861	0.5409	591636	294	1.99E-02	0.45	CHS
1	174682558	175278023	0.6356	595465	274	7.98E-03	0.5	CHB
1	174694380	175266826	0.5247	572446	263	2.34E-02	0.5	CHD
1	184448779	184487313	0.0298	38534	26	3.68E-02	0.8	LWK
1	188022869	188107700	0.2611	84831	67	6.37E-03	0.75	MEX
1	197460751	199404123	2.2950	1943372	969	3.48E-02	0.05	LWK
1	203025773	203137611	0.1752	111838	63	4.14E-02	0.75	TSI
1	234751417	234888470	0.3902	137053	125	3.20E-02	0.55	CEU
1	243053004	243113535	0.3504	60531	25	2.25E-02	0.8	MEX
2	8898471	9145966	0.2268	247495	105	1.72E-02	0.65	MEX
2	9270479	9691129	0.1903	420650	212	8.93E-03	0.75	CHS
2	9464256	9686972	0.3027	222716	77	8.76E-03	0.85	CHB
2	9471731	9671890	0.2166	200159	65	2.57E-02	0.85	CHD
2	9471731	9654635	0.2097	182904	60	2.88E-03	0.95	JPT
2	17314637	17855011	0.1873	540374	226	1.61E-02	0.7	JPT
2	17321779	17882568	0.2244	560789	243	3.69E-03	0.75	CHB
2	17414064	17897251	0.1628	483187	209	1.57E-02	0.75	CHD
2	17420013	17897251	0.1911	477238	224	3.84E-02	0.6	MAS
2	17761807	17894867	0.1374	133060	87	3.68E-02	0.85	CHS
2	21536938	22345904	0.6738	808966	227	4.14E-02	0.45	CHD
2	21536938	21865421	0.3141	328483	117	4.67E-02	0.55	MEX
2	21638566	21726948	0.1629	88382	42	2.88E-03	0.9	INS
2	21638566	21769279	0.0730	130713	53	2.04E-02	0.9	TSI
2	21796630	22127772	0.2693	331142	84	4.81E-02	0.7	MAS
2	22202044	22282185	0.1897	80141	16	2.39E-02	0.95	MAS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
2	22230520	22329742	0.1905	99222	28	1.99E-02	0.95	JPT
2	23738673	24485626	0.1872	746953	214	4.78E-02	0.65	CHD
2	25784609	26108767	0.3245	324158	77	4.17E-02	0.75	JPT
2	26013878	26216756	0.2483	202878	63	4.57E-02	0.8	CHS
2	41414230	41498236	0.1289	84006	40	2.46E-02	0.9	MAS
2	43282562	43910360	0.5401	627798	344	1.68E-02	0.45	CHD
2	43301099	43710431	0.1705	409332	191	4.06E-02	0.65	MAS
2	43301270	43958429	0.5232	657159	385	7.78E-03	0.45	CHS
2	43766724	43907627	0.2571	140903	113	3.99E-02	0.75	JPT
2	59756517	60928565	1.1773	1172048	634	2.97E-02	0.05	ASW
2	72209026	73015059	0.2996	806033	203	3.16E-02	0.5	TSI
2	72209811	72867344	0.1949	657533	164	3.14E-04	0.95	CHD
2	72215468	72361148	0.1447	145680	65	7.59E-03	0.85	INS
2	72221698	72385119	0.1241	163421	68	4.21E-02	0.8	GIH
2	72226494	72867344	0.1278	640850	159	1.77E-03	0.95	CHB
2	72226494	72867344	0.1278	640850	159	1.73E-03	0.95	JPT
2	72353883	72982189	0.0440	628306	140	9.07E-03	0.95	MAS
2	72361148	72984675	0.0291	623527	137	4.75E-02	0.95	CHS
2	72376277	72847001	0.0088	470724	99	4.77E-02	0.9	INS
2	73355048	73975731	0.3602	620683	184	4.09E-02	0.45	GIH
2	74061870	74085759	0.3471	23889	11	5.27E-03	0.95	INS
2	74334167	74703461	0.1481	369294	147	4.44E-02	0.65	TSI
2	74342206	74672115	0.0584	329909	135	2.59E-02	0.8	CEU
2	82366308	83231718	0.1462	865410	276	4.44E-02	0.55	GIH
2	82935950	83474238	0.2047	538288	182	3.34E-02	0.7	CHB
2	82961206	83211007	0.0412	249801	98	4.11E-02	0.85	INS
2	84222108	84993676	0.6195	771568	313	3.50E-02	0.4	CHB
2	84403907	84995378	0.3382	591471	230	4.50E-02	0.55	CHD
2	84422129	84975918	0.1938	553789	222	4.47E-02	0.65	CHS
2	84422129	84995378	0.3221	573249	220	4.10E-02	0.6	JPT
2	84759174	84946512	0.2537	187338	89	1.70E-02	0.75	MAS
2	86292111	87724232	1.1214	1432121	255	3.56E-02	0.35	JPT
2	86292581	88092105	1.8349	1799524	259	1.15E-02	0.35	CHD
2	86414037	88077079	1.8076	1663042	184	3.17E-03	0.5	CHB
2	96926278	98000626	0.2049	1074348	179	3.57E-02	0.55	GIH
2	108279191	109360822	0.8644	1081631	432	2.60E-02	0.1	LWK
2	108286633	108910484	0.4048	623851	186	5.83E-03	0.7	JPT
2	108292004	108337783	0.2400	45779	33	3.31E-02	0.9	CHB
2	108309635	108775208	0.1452	465573	121	7.15E-03	0.9	CHD
2	108310880	108711916	0.1008	401036	125	2.15E-02	0.9	CHS
2	118670171	118715400	0.2891	45229	19	2.51E-02	0.95	CHB
2	118670171	118715400	0.2891	45229	19	2.52E-02	0.95	CHD
2	118670171	118715400	0.2891	45229	19	2.40E-02	0.95	JPT
2	118670171	118715400	0.2891	45229	19	2.90E-02	0.85	MEX
2	121388588	121448505	0.2279	59917	43	4.94E-02	0.75	CEU
2	121388588	121448505	0.2279	59917	43	1.42E-02	0.9	CHB
2	121388588	121448505	0.2279	59917	43	4.87E-02	0.85	CHD
2	121388588	121448505	0.2279	59917	43	3.41E-02	0.75	GIH
2	121388588	121448505	0.2279	59917	43	2.32E-02	0.9	JPT

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
2	121388588	121446440	0.1226	57852	43	2.51E-02	0.9	MAS
2	121388588	121441888	0.2008	53300	37	1.21E-03	0.9	MEX
2	121388588	121448505	0.2279	59917	43	3.20E-02	0.75	TSI
2	125298395	126077652	0.1823	779257	278	1.26E-02	0.65	CHS
2	125417976	126070212	0.2022	652236	209	2.10E-02	0.7	CHD
2	125451613	126047813	0.1828	596200	188	4.25E-02	0.7	JPT
2	127669524	128337564	0.2738	668040	258	4.24E-02	0.45	MEX
2	130850530	131247669	0.4683	397139	25	2.38E-02	0.9	CHB
2	130850530	131247669	0.4683	397139	25	5.18E-03	0.95	CHD
2	130850530	131247669	0.4683	397139	25	2.86E-02	0.9	JPT
2	130859606	131201105	0.4468	341499	11	1.58E-02	0.95	CEU
2	130859606	131201105	0.4468	341499	11	1.11E-02	0.95	GIH
2	130859606	131198948	0.4295	339342	10	7.28E-03	0.95	MEX
2	130859606	131198948	0.4295	339342	10	2.12E-02	0.95	TSI
2	134098567	134504147	0.6352	405580	288	8.23E-03	0.2	MKK
2	135472099	135936301	0.0805	464202	143	1.79E-02	0.65	MKK
2	136104943	136505448	0.1419	400505	155	1.31E-02	0.75	CEU
2	136123915	136505448	0.1253	381533	149	2.98E-03	0.65	MKK
2	136797619	137528542	0.5349	730923	458	3.68E-03	0.2	MKK
2	137000875	138727290	1.5415	1726415	928	3.58E-02	0.05	CEU
2	149306956	149514117	0.2556	207161	23	2.03E-02	0.95	CHB
2	149306956	149514117	0.2556	207161	23	2.00E-02	0.95	CHD
2	149306956	149551286	0.2932	244330	33	2.91E-02	0.9	JPT
2	149306956	149551286	0.2932	244330	33	3.05E-02	0.75	MEX
2	149311497	149551286	0.1786	239789	32	3.05E-02	0.85	GIH
2	152198704	152445136	0.1825	246432	91	1.84E-02	0.7	MEX
2	157831816	157993623	0.4013	161807	65	3.27E-02	0.65	TSI
2	158735634	159294924	0.3378	559290	325	2.52E-02	0.4	INS
2	158811474	159285585	0.2194	474111	219	3.78E-02	0.5	GIH
2	167559968	168222918	0.7741	662950	235	2.94E-02	0.35	CEU
2	177356061	177598359	0.1468	242298	171	2.20E-02	0.7	MAS
2	177362003	177567092	0.1381	205089	142	4.39E-03	0.9	CHD
2	177388309	177567092	0.1323	178783	128	3.73E-03	0.95	CHS
2	177399743	177579250	0.1125	179507	120	5.26E-03	0.95	CHB
2	177400818	177558481	0.1089	157663	105	1.13E-02	0.95	JPT
2	177856534	178265165	0.2982	408631	221	3.79E-02	0.45	GIH
2	177915087	178265165	0.2146	350078	189	1.14E-02	0.65	CEU
2	177915087	178265165	0.2146	350078	189	4.15E-03	0.65	TSI
2	177934255	178264821	0.2043	330566	183	3.75E-03	0.65	MEX
2	190201049	190654845	0.3367	453796	177	3.35E-03	0.6	INS
2	190201887	190652296	0.2605	450409	179	3.29E-02	0.55	CEU
2	190213032	190656930	0.2889	443898	174	3.74E-02	0.5	GIH
2	191938312	192046963	0.2077	108651	45	7.81E-03	0.85	CEU
2	191938312	192046963	0.2077	108651	45	1.93E-03	0.9	GIH
2	191938312	192046963	0.2077	108651	45	9.15E-03	0.8	MEX
2	191938312	192046963	0.2077	108651	45	1.51E-03	0.9	TSI
2	192463422	192574023	0.3298	110601	55	4.68E-02	0.8	JPT
2	194601790	194931785	0.4403	329995	70	2.05E-02	0.4	ASW
2	194601790	194888312	0.4339	286522	59	4.53E-02	0.4	LWK

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
2	194601790	194901244	0.4376	299454	62	2.39E-02	0.45	YRI
2	194702813	194855676	0.3558	152863	28	3.28E-02	0.9	JPT
2	194702813	194855676	0.3558	152863	28	4.13E-02	0.75	MEX
2	194702813	194836382	0.1166	133569	24	2.50E-02	0.75	MKK
2	194789155	195056515	0.5554	267360	62	2.28E-02	0.65	TSI
2	196447175	196778627	0.2161	331452	123	4.84E-02	0.6	GIH
2	196449571	196778687	0.2177	329116	122	2.46E-02	0.65	CEU
2	196982600	197308539	0.3151	325939	123	3.78E-02	0.55	MEX
2	197006467	197209016	0.2999	202549	83	1.75E-02	0.8	CHB
2	197006467	197209016	0.2999	202549	83	6.05E-03	0.85	CHD
2	197006467	197224108	0.3396	217641	86	9.94E-03	0.8	CHS
2	197010693	197541775	0.4104	531082	175	8.48E-03	0.55	TSI
2	197012239	197190293	0.2528	178054	66	1.78E-02	0.75	CEU
2	197012239	197231211	0.3058	218972	82	2.05E-02	0.8	JPT
2	197018052	197524529	0.2597	506477	165	2.28E-02	0.55	GIH
2	197018052	197571429	0.1842	553377	196	3.53E-02	0.55	INS
2	197018052	197520866	0.0911	502814	167	4.47E-02	0.75	MAS
2	197473294	197749763	0.2245	276469	124	1.93E-02	0.8	JPT
2	198885068	199007099	0.2184	122031	37	1.65E-02	0.9	CHS
2	205911536	205996132	0.2853	84596	47	4.67E-02	0.7	CEU
2	205969388	206051091	0.5039	81703	27	2.95E-03	0.95	JPT
2	205971826	206051091	0.4620	79265	25	4.97E-03	0.95	CHB
2	205971826	206051304	0.4631	79478	26	4.69E-03	0.95	CHD
2	205971826	206051304	0.4631	79478	26	1.32E-02	0.8	MEX
2	205996132	206051091	0.2610	54959	19	1.81E-02	0.95	CHS
2	205998621	206051304	0.2347	52683	16	3.78E-02	0.9	GIH
2	205998621	206051304	0.3155	52683	18	7.13E-03	0.9	INS
2	208754345	208801314	0.1824	46969	24	4.06E-02	0.9	MAS
2	212929356	213112634	0.2004	183278	101	2.45E-02	0.8	CHS
2	212966867	213137308	0.2229	170441	87	2.88E-02	0.8	CHD
2	212978686	213137308	0.1976	158622	85	4.95E-02	0.8	CHB
2	213120671	213265529	0.2551	144858	79	6.22E-03	0.85	CHS
2	213121476	213267474	0.2526	145998	74	1.59E-02	0.85	JPT
2	213130009	213267474	0.1473	137465	79	4.11E-02	0.8	MAS
2	218187505	218244054	0.1751	56549	31	9.70E-03	0.95	CHS
2	218974448	219391887	0.2793	417439	186	4.20E-02	0.5	MEX
2	218980048	219406248	0.2610	426200	190	1.52E-02	0.7	CHB
2	218980048	219427976	0.2821	447928	192	1.03E-02	0.55	GIH
2	218991341	219406248	0.2557	414907	187	3.53E-02	0.65	JPT
2	219202788	219391887	0.2307	189099	99	2.04E-02	0.8	CHD
2	219223187	219389845	0.1681	166658	73	3.28E-02	0.8	MAS
2	236862764	236894573	0.1973	31809	13	4.09E-02	0.95	CEU
2	236862764	237108998	0.4420	246234	93	1.85E-02	0.6	GIH
2	236866495	237075397	0.3594	208902	89	9.02E-03	0.65	INS
2	236903235	237067304	0.1598	164069	68	1.82E-02	0.85	MAS
3	413656	440476	0.1350	26820	26	1.21E-02	0.95	GIH
3	413656	440476	0.1350	26820	26	3.19E-02	0.9	MEX
3	413656	440476	0.1350	26820	26	1.58E-02	0.95	TSI
3	415028	440476	0.1377	25448	24	4.89E-02	0.9	INS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
3	1106724	1132509	0.2869	25785	13	4.03E-02	0.95	CHS
3	11918454	12463027	0.4991	544573	361	3.79E-02	0.3	GIH
3	12469794	12716219	0.1817	246425	115	6.97E-03	0.85	CHS
3	19090335	19193162	0.2509	102827	26	1.49E-02	0.9	MAS
3	19098536	19193162	0.2316	94626	21	3.15E-02	0.85	INS
3	25701532	25912179	0.3257	210647	77	3.45E-02	0.65	CEU
3	25701532	25873417	0.1881	171885	62	3.37E-02	0.75	TSI
3	25703411	26333045	0.4811	629634	225	3.19E-02	0.4	GIH
3	25817330	25924304	0.1900	106974	35	4.00E-02	0.9	CHB
3	25817330	25924304	0.1900	106974	35	3.41E-02	0.9	CHD
3	25899702	26304269	0.3095	404567	149	2.15E-02	0.55	TSI
3	25905208	26106154	0.2226	200946	65	2.98E-02	0.85	JPT
3	25905266	25967254	0.3826	61988	22	5.62E-03	0.95	CHS
3	25912179	26314085	0.1693	401906	144	1.19E-02	0.75	MAS
3	25937362	26170980	0.1056	233618	74	1.88E-02	0.95	CHB
3	27002501	27573522	0.2282	571021	212	2.82E-02	0.65	CHD
3	44121527	44923774	0.3341	802247	237	2.73E-02	0.6	JPT
3	44172262	45089306	0.1480	917044	295	3.34E-02	0.65	CHB
3	44173853	45072513	0.1375	898660	283	2.78E-02	0.65	CHD
3	48393218	52043776	0.4605	3650558	986	2.39E-02	0.2	MEX
3	48608249	49334947	0.0359	726698	167	1.85E-02	0.9	GIH
3	48633471	49710750	0.0425	1077279	316	3.98E-02	0.55	INS
3	48694642	49696536	0.0718	1001894	297	5.56E-03	0.9	CHS
3	48696044	49713949	0.0411	1017905	230	4.32E-02	0.85	CHB
3	48696044	49710750	0.0409	1014706	229	1.86E-02	0.9	CHD
3	48696044	49713949	0.0411	1017905	230	2.11E-02	0.85	JPT
3	48794672	49710750	0.0259	916078	263	2.13E-02	0.85	MAS
3	49811711	52045995	0.3436	2234284	632	3.54E-02	0.25	GIH
3	58038371	58132899	0.1129	94528	67	2.05E-02	0.95	JPT
3	71495528	71720870	0.2967	225342	92	1.66E-02	0.8	JPT
3	72991962	73054439	0.1591	62477	30	3.57E-02	0.95	JPT
3	81566114	82116868	0.1650	550754	204	4.90E-02	0.55	INS
3	88179714	88379497	0.1353	199783	66	2.77E-02	0.8	INS
3	97669944	98810257	0.2628	1140313	268	4.67E-02	0.55	CHB
3	98390686	98792499	0.0819	401813	93	4.24E-02	0.8	GIH
3	100857841	101536850	0.1555	679009	274	4.78E-02	0.25	ASW
3	103385279	103498009	0.3874	112730	22	9.49E-03	0.95	CHB
3	103385279	103457196	0.2893	71917	15	4.79E-02	0.95	CHD
3	103385279	103457196	0.2128	71917	17	4.27E-02	0.95	CHS
3	103385279	103678351	0.5088	293072	70	4.05E-02	0.6	GIH
3	103385279	103457196	0.2893	71917	15	4.75E-02	0.95	JPT
3	103385279	103677465	0.1841	292186	81	1.77E-02	0.8	MAS
3	106127254	106288374	0.2074	161120	97	2.28E-02	0.75	MAS
3	106133970	106323341	0.1889	189371	98	3.54E-02	0.8	CHD
3	108708626	109044673	0.2407	336047	131	1.91E-02	0.7	MAS
3	108708695	109038156	0.1502	329461	109	2.72E-02	0.85	CHD
3	108715787	109037143	0.1474	321356	106	1.47E-02	0.9	CHB
3	108716017	108944421	0.1184	228404	82	2.29E-02	0.9	CHS
3	111990953	112312597	0.1880	321644	90	2.74E-02	0.7	TSI

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
3	112000633	112415016	0.2391	414383	108	2.04E-02	0.65	GIH
3	112008263	112415016	0.2306	406753	107	5.36E-03	0.75	CEU
3	120874113	123188532	1.6210	2314419	860	1.60E-02	0.1	MEX
3	121630988	121909440	0.8449	278452	68	3.27E-02	0.65	CHB
3	124935751	125005136	0.2133	69385	33	2.03E-02	0.85	CEU
3	124935751	125005136	0.2134	69385	33	4.62E-02	0.8	TSI
3	130551345	131129379	0.3213	578034	224	2.54E-02	0.5	CEU
3	136774788	138242936	0.5137	1468148	385	3.21E-02	0.4	CHD
3	136776805	137409312	0.4193	632507	165	3.95E-02	0.6	CHB
3	136855017	136908456	0.2486	53439	13	2.13E-02	0.95	MAS
3	137452445	138173081	0.0851	720636	240	1.66E-02	0.7	MAS
3	140513473	140730216	0.1717	216743	106	4.26E-02	0.8	CHD
3	140513473	140726150	0.1613	212677	104	2.30E-02	0.85	JPT
3	140514463	140730216	0.1577	215753	122	3.77E-02	0.8	CHS
3	142152832	142247462	0.0828	94630	37	4.26E-02	0.9	INS
3	142156882	142257543	0.1284	100661	35	2.76E-02	0.9	GIH
3	176705455	176973364	0.2819	267909	96	3.81E-02	0.75	JPT
3	176705455	176990147	0.7478	284692	116	4.87E-02	0.5	MAS
3	176707153	176980160	0.4440	273007	114	3.92E-02	0.65	CHS
3	176750257	176993163	0.4370	242906	83	3.58E-02	0.7	CHB
3	181834498	181856917	0.3775	22419	7	3.81E-02	0.95	MAS
3	190126423	190162775	0.2536	36352	24	3.38E-02	0.85	TSI
3	190129902	190162775	0.1508	32873	23	1.65E-02	0.95	CEU
3	196411317	196886423	0.4665	475106	80	3.98E-02	0.7	CHD
3	198784962	199049392	0.4210	264430	62	4.03E-02	0.75	CHB
3	198819718	199050651	0.3952	230933	52	1.02E-02	0.8	MAS
4	16362961	16426378	0.1574	63417	26	3.96E-02	0.9	CEU
4	28546678	28738406	0.1782	191728	92	3.83E-02	0.75	MAS
4	29512150	29765991	0.3786	253841	77	3.32E-02	0.6	MEX
4	29791393	29999351	0.3623	207958	83	3.08E-02	0.6	INS
4	32843099	34026565	0.6883	1183466	283	4.42E-02	0.4	CHS
4	32985041	33087910	0.6371	102869	35	1.37E-02	0.85	CHB
4	32986285	33099678	0.6352	113393	35	2.90E-02	0.45	ASW
4	32986285	33099678	0.6352	113393	35	2.30E-02	0.7	CEU
4	32986285	33087910	0.6332	101625	34	1.11E-02	0.85	CHD
4	32986285	33087910	0.6332	101625	34	1.60E-02	0.85	JPT
4	32986285	33099678	0.6352	113393	35	4.91E-02	0.65	MEX
4	32986285	33099678	0.6352	113393	35	1.69E-02	0.5	MKK
4	33059304	33099678	0.4870	40374	8	3.04E-02	0.95	TSI
4	33099678	34525359	0.6171	1425681	340	2.90E-02	0.4	CHB
4	33159145	34025092	0.2676	865947	172	4.74E-02	0.5	INS
4	33319009	34218766	0.2669	899757	203	3.78E-02	0.5	MEX
4	33319755	34025092	0.1386	705337	122	1.05E-02	0.75	GIH
4	33589951	34025092	0.1227	435141	78	4.83E-02	0.8	CEU
4	33761093	34041146	0.1610	280053	54	3.92E-02	0.8	TSI
4	41515032	41865830	0.2515	350798	148	8.17E-04	0.9	CHS
4	41515452	41811551	0.3306	296099	108	3.66E-04	0.95	CHB
4	41515452	41805211	0.3286	289759	97	2.16E-03	0.9	JPT
4	41521093	41860745	0.1538	339652	143	2.37E-02	0.65	INS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
4	41536091	41869567	0.1700	333476	128	1.41E-02	0.7	GIH
4	41544763	41895846	0.3390	351083	131	3.15E-02	0.55	TSI
4	41589703	41805211	0.1002	215508	73	4.08E-02	0.8	MEX
4	41596774	41891962	0.2970	295188	115	1.29E-02	0.65	CEU
4	41609348	41808557	0.0917	199209	76	2.35E-02	0.95	CHD
4	41629343	41701960	0.1209	72617	33	7.97E-03	0.95	MAS
4	45743877	47892524	0.9681	2148647	768	3.69E-02	0.05	ASW
4	53360612	54789386	1.2084	1428774	662	2.09E-02	0.05	ASW
4	55724939	55874640	0.3554	149701	60	2.02E-02	0.7	CEU
4	55724939	55874640	0.3554	149701	60	3.49E-02	0.65	MEX
4	60541497	60931841	0.1966	390344	129	4.81E-02	0.6	MEX
4	60541497	60888130	0.1741	346633	107	2.65E-02	0.7	TSI
4	68727369	68808109	0.2233	80740	32	2.62E-02	0.9	CHS
4	71739848	71786731	0.1821	46883	22	2.78E-02	0.95	CHS
4	76711587	77053289	0.3522	341702	159	3.16E-02	0.6	MAS
4	79707294	80104287	0.2654	396993	147	1.35E-02	0.6	TSI
4	80164473	80327205	0.3230	162732	56	1.39E-02	0.8	MAS
4	80168007	80408129	0.3629	240122	77	5.47E-03	0.7	INS
4	81426987	82160480	0.3010	733493	206	2.18E-02	0.5	MEX
4	81433599	82190265	0.2337	756666	224	2.42E-02	0.55	CEU
4	99808544	102349248	1.1372	2540704	1284	4.92E-02	0.05	MAS
4	100103668	100548716	0.2712	445048	268	1.89E-02	0.6	JPT
4	100195669	101415496	0.9469	1219827	586	5.75E-03	0.1	LWK
4	106708008	107092002	0.3106	383994	153	2.25E-02	0.55	MEX
4	106708112	107097080	0.3150	388968	154	3.70E-03	0.8	CHB
4	106708112	107106612	0.3405	398500	155	2.39E-03	0.8	CHD
4	106724392	107092002	0.1509	367610	171	6.35E-03	0.85	CHS
4	106725693	107097080	0.3005	371387	146	3.71E-02	0.55	CEU
4	106727975	107016278	0.1535	288303	121	7.79E-03	0.75	GIH
4	106727975	106891647	0.1562	163672	84	2.32E-02	0.8	MAS
4	106735477	107092002	0.1116	356525	141	3.84E-02	0.85	JPT
4	109730949	111434015	2.0368	1703066	771	2.71E-02	0.05	GIH
4	135551435	135768238	0.0991	216803	65	2.95E-02	0.95	CHB
4	135551435	135768238	0.0991	216803	65	3.21E-02	0.95	JPT
4	135640588	135700560	0.1774	59972	30	2.02E-02	0.9	MAS
4	143137205	143449084	0.2942	311879	168	2.21E-02	0.55	TSI
4	143139928	143448364	0.2894	308436	162	1.10E-02	0.6	CEU
4	143645481	144496236	0.3382	850755	264	2.58E-02	0.55	CHB
4	143656669	144161308	0.2947	504639	154	4.79E-02	0.65	CHD
4	143656669	144476163	0.2764	819494	265	4.31E-02	0.55	CHS
4	143802374	144641172	0.3094	838798	265	1.60E-02	0.6	JPT
4	158643549	158909796	0.3038	266247	111	2.04E-02	0.6	MEX
4	158831135	160094038	0.9408	1262903	375	2.82E-02	0.3	CHB
4	158949009	159353131	0.4001	404122	133	3.54E-02	0.65	JPT
4	158957384	159348081	0.4124	390697	146	2.48E-02	0.65	CHS
4	158957384	159348067	0.4320	390683	146	2.08E-02	0.6	MAS
4	158960909	159390104	0.4014	429195	138	2.90E-02	0.65	CHD
4	159414320	159999694	0.3895	585374	174	4.39E-02	0.55	MAS
4	165712136	165779292	0.2656	67156	29	3.58E-02	0.8	GIH

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
4	165712136	165778796	0.2440	66660	28	3.54E-02	0.8	MEX
4	165737752	165779292	0.2066	41540	14	4.57E-02	0.9	INS
4	170409932	170949741	0.3670	539809	173	2.21E-02	0.65	JPT
4	170432455	171014643	0.4826	582188	188	3.44E-02	0.55	CHD
4	170439942	170998573	0.3386	558631	179	2.49E-02	0.5	MEX
4	176457478	176722600	0.2497	265122	70	1.62E-02	0.75	CEU
5	11790940	11893590	0.1817	102650	58	3.04E-03	0.85	INS
5	11796161	11902590	0.1129	106429	58	2.11E-03	0.95	CEU
5	11796161	11902590	0.1129	106429	58	3.84E-02	0.85	GIH
5	11796161	11902590	0.1129	106429	58	1.08E-02	0.85	MEX
5	11796161	11902590	0.1129	106429	58	4.77E-03	0.9	TSI
5	15008153	16638349	1.3624	1630196	731	3.38E-02	0.05	MKK
5	38471062	38509906	0.1853	38844	19	4.18E-02	0.9	GIH
5	41665720	43748636	0.5697	2082916	667	4.65E-02	0.25	CHD
5	43652877	43740313	0.0144	87436	25	4.80E-02	0.8	MKK
5	43822280	43983865	0.0359	161585	36	4.82E-02	0.7	MKK
5	56766427	56785344	0.7338	18917	10	1.68E-02	0.9	CHS
5	97055633	97284375	0.2851	228742	65	1.64E-02	0.7	MEX
5	109032696	109270627	0.2003	237931	88	4.10E-02	0.4	ASW
5	109040175	109271870	0.1999	231695	88	2.10E-02	0.45	MKK
5	109630568	110382458	0.3215	751890	262	8.59E-03	0.5	MEX
5	109637952	110264681	0.1771	626729	219	2.17E-03	0.7	GIH
5	109637952	110426932	0.2316	788980	274	4.77E-03	0.6	TSI
5	109641683	110264681	0.0630	622998	240	3.12E-02	0.65	INS
5	109651498	109875243	0.0563	223745	89	4.62E-02	0.85	CEU
5	111976016	113082398	0.8651	1106382	629	4.24E-02	0.2	JPT
5	112716022	113162918	0.3104	446896	284	1.85E-02	0.45	INS
5	115398981	115753690	0.2345	354709	208	1.91E-02	0.55	TSI
5	117373324	117689639	0.2497	316315	130	3.61E-04	0.95	CHD
5	117375429	117596426	0.1587	220997	96	3.49E-03	0.95	CHB
5	117375429	117701041	0.2916	325612	158	1.32E-04	0.95	CHS
5	117375429	117592166	0.1560	216737	94	3.74E-03	0.95	JPT
5	117553872	117690181	0.0709	136309	68	4.62E-02	0.9	MAS
5	119697356	119896183	0.1935	198827	75	2.88E-02	0.85	CHB
5	119725911	119896183	0.2260	170272	79	2.79E-03	0.9	CHS
5	124389487	124519221	0.2407	129734	71	4.68E-02	0.8	CHB
5	129475677	131360659	0.2958	1884982	501	2.60E-02	0.35	CEU
5	129718181	131368130	0.1740	1649949	425	4.42E-02	0.45	TSI
5	134875534	137766939	2.0471	2891405	1371	9.69E-03	0.05	LWK
5	142148160	142402160	0.3717	254000	167	3.70E-02	0.5	CEU
5	142219472	142481021	0.3523	261549	165	3.93E-02	0.5	TSI
6	9632690	9873879	0.2846	241189	97	2.67E-02	0.75	CHS
6	25308447	28900456	1.3335	3592009	1819	1.33E-02	0.05	GIH
6	26232282	26662947	0.2731	430665	311	3.94E-02	0.55	JPT
6	26433867	27407504	0.2583	973637	375	2.47E-02	0.5	CHD
6	26445243	27293771	0.3237	848528	398	7.48E-03	0.4	INS
6	26449041	27404491	0.2393	955450	444	1.78E-02	0.5	CHS
6	26586906	27301074	0.0666	714168	236	4.66E-02	0.65	MAS
6	26661252	29937545	0.6745	3276293	1872	2.23E-02	0.05	MKK

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
6	27458360	28569200	0.1607	1110840	561	4.58E-02	0.35	MEX
6	27886961	28519223	0.0940	632262	359	2.91E-02	0.6	CEU
6	27896921	28550085	0.1012	653164	369	3.54E-02	0.55	TSI
6	28630674	30338107	0.6657	1707433	1557	3.98E-02	0.05	ASW
6	29470272	30279806	0.5032	809534	1062	9.95E-03	0.2	GIH
6	29607395	30453097	0.5086	845702	1090	6.08E-03	0.1	YRI
6	29638607	31677499	0.8643	2038892	3467	2.00E-02	0.05	CHS
6	29657422	31428789	1.1987	1771367	2147	1.14E-02	0.05	CHD
6	29831140	30197407	0.3091	366267	471	4.48E-02	0.15	LWK
6	29835002	30440139	0.3774	605137	748	1.78E-02	0.25	CEU
6	29838902	30453850	0.3771	614948	771	4.33E-02	0.25	JPT
6	29942930	32040156	1.4243	2097226	2295	5.11E-03	0.05	CHB
6	30476436	31736712	1.0327	1260276	1437	3.96E-02	0.05	TSI
6	30553455	31452273	0.7122	898818	1035	1.58E-02	0.15	GIH
6	31094506	32481163	1.0265	1386657	1489	2.45E-02	0.1	JPT
6	31126427	31451583	0.3635	325156	478	1.96E-03	0.2	ASW
6	31317489	31543098	0.3235	225609	274	4.81E-02	0.2	YRI
6	31515983	32950669	0.9608	1434686	1458	1.16E-02	0.1	CEU
6	33073726	33758599	0.6617	684873	554	5.66E-04	0.2	LWK
6	33153478	33207188	0.0830	53710	113	4.28E-02	0.55	YRI
6	33245381	33961049	0.5521	715668	457	3.00E-02	0.1	ASW
6	33283553	33945294	0.4734	661741	412	1.86E-02	0.15	YRI
6	33434412	35693077	2.0223	2258665	1077	3.01E-02	0.05	JPT
6	34186441	36235447	1.0923	2049006	777	1.74E-02	0.15	MEX
6	34771576	35822582	0.3499	1051006	436	3.77E-02	0.15	LWK
6	48495088	49774340	0.4418	1279252	421	1.74E-02	0.35	MEX
6	69720601	70604664	0.4067	884063	372	2.99E-02	0.15	LWK
6	69850800	70124723	0.1102	273923	117	2.91E-02	0.8	MAS
6	73809079	73916332	0.2071	107253	55	3.41E-02	0.75	GIH
6	73861595	73916332	0.1773	54737	36	2.36E-02	0.85	TSI
6	73863130	73913789	0.0693	50659	33	4.01E-02	0.95	CEU
6	73863130	73916332	0.1866	53202	37	3.58E-02	0.8	INS
6	88762834	88878455	0.3961	115621	43	2.86E-02	0.75	MAS
6	103976702	104092929	0.2727	116227	53	3.71E-02	0.7	INS
6	105639472	105742097	0.1770	102625	75	2.59E-02	0.8	MAS
6	105645907	105737023	0.2270	91116	66	1.45E-02	0.85	CHS
6	105975823	106058765	0.2399	82942	33	1.94E-02	0.9	CHS
6	120403970	122054906	0.9244	1650936	619	2.52E-03	0.1	ASW
6	124039525	124190847	0.3182	151322	71	1.63E-02	0.7	CEU
6	124039525	124178889	0.2789	139364	63	2.67E-02	0.7	TSI
6	124100953	124140135	0.3298	39182	10	3.57E-02	0.9	INS
6	125756107	125832721	0.2435	76614	45	1.09E-02	0.9	CHB
6	125756107	125832721	0.2435	76614	45	3.95E-02	0.85	CHD
6	125756107	125832721	0.2244	76614	38	4.99E-02	0.85	CHS
6	125756107	125832721	0.2435	76614	45	2.44E-03	0.95	JPT
6	129217882	129567166	0.2457	349284	158	3.63E-02	0.7	CHB
6	129217882	129567166	0.2457	349284	158	3.94E-02	0.7	JPT
6	129221234	129575312	0.2597	354078	160	3.31E-02	0.55	MEX
6	129241476	129455026	0.1159	213550	115	3.05E-02	0.8	MAS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
6	132632478	134596031	3.0453	1963553	1049	2.27E-03	0.05	LWK
6	158563514	158892410	0.1922	328896	159	2.48E-02	0.4	YRI
7	4024062	4115363	0.1984	91301	57	4.40E-02	0.85	CHD
7	19038306	19094932	0.2143	56626	17	1.43E-02	0.95	CEU
7	19038306	19094932	0.2143	56626	17	3.96E-02	0.9	GIH
7	19038306	19094932	0.2143	56626	17	2.20E-02	0.9	MEX
7	19038306	19094932	0.2143	56626	17	4.36E-02	0.9	TSI
7	20333053	20453361	0.3433	120308	87	1.56E-02	0.4	LWK
7	20357908	20453361	0.2574	95453	72	3.25E-02	0.45	MKK
7	29887937	30143369	0.2847	255432	120	1.68E-02	0.7	MAS
7	30213539	30444581	0.2205	231042	102	2.77E-02	0.8	CHB
7	30213539	30373970	0.1042	160431	61	3.93E-02	0.85	GIH
7	30213539	30444581	0.2205	231042	102	3.34E-02	0.8	JPT
7	30213539	30442258	0.4223	228719	93	1.16E-02	0.7	MAS
7	41352948	42057053	1.1096	704105	368	2.33E-02	0.1	LWK
7	47119915	47885203	1.4054	765288	473	4.73E-03	0.1	LWK
7	71951080	72434199	0.1261	483119	30	1.58E-02	0.7	MKK
7	72395959	72494205	0.2864	98246	19	6.86E-03	0.7	ASW
7	72400365	72494366	0.2863	94001	15	2.03E-02	0.75	YRI
7	73714429	74897267	0.6344	1182838	26	3.17E-02	0.85	CHB
7	73714429	74896316	0.6338	1181887	25	1.64E-02	0.9	JPT
7	74030155	74897267	0.5258	867112	7	3.80E-02	0.95	TSI
7	80118802	80681876	1.3316	563074	280	1.30E-02	0.15	YRI
7	87059734	87423695	0.1986	363961	140	3.59E-02	0.6	INS
7	91894910	92086012	0.2708	191102	61	3.56E-02	0.7	GIH
7	98536310	99260475	0.4679	724165	228	4.02E-02	0.4	MEX
7	98696103	99267779	0.1656	571676	166	1.19E-02	0.7	CEU
7	98715203	99203387	0.0843	488184	145	2.43E-02	0.75	TSI
7	111910801	112533491	0.6930	622690	210	2.21E-02	0.5	CHB
7	111917245	112625852	0.6449	708607	240	3.80E-02	0.45	CHD
7	111943958	112413077	0.2386	469119	144	9.31E-03	0.8	JPT
7	112424175	112640609	0.3569	216434	79	3.10E-02	0.75	JPT
7	117344604	120416717	1.0057	3072113	824	4.92E-02	0.05	MKK
7	118278239	119103185	0.1700	824946	174	1.51E-02	0.65	GIH
7	118795593	118867387	0.1904	71794	18	2.74E-02	0.9	INS
7	119383405	119783126	0.1137	399721	79	3.80E-02	0.8	GIH
7	119679297	120053694	0.1336	374397	121	2.68E-02	0.7	INS
7	119791151	119982844	0.0710	191693	67	2.85E-02	0.9	GIH
7	126630537	127617350	0.3734	986813	566	2.16E-02	0.35	MAS
7	126647066	127610096	0.3863	963030	503	2.06E-02	0.4	CHB
7	126716840	127589178	0.2746	872338	477	2.23E-02	0.45	CHS
7	126720180	127631331	0.3210	911151	442	2.42E-02	0.45	CHD
7	126735606	127628256	0.2695	892650	432	1.52E-02	0.5	JPT
7	131171022	131264503	0.1159	93481	71	1.71E-02	0.95	CHB
7	131171022	131264503	0.1159	93481	71	1.43E-02	0.95	JPT
7	131173326	131264503	0.0965	91177	70	2.67E-02	0.95	CHD
7	135427316	135522487	0.3112	95171	65	3.08E-02	0.8	CHB
7	135427316	135522487	0.3112	95171	65	3.86E-02	0.8	JPT
7	135435920	135522487	0.2623	86567	64	4.64E-02	0.8	CHD

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
7	135479126	135518370	0.1699	39244	44	1.89E-02	0.9	CHS
7	136091036	136183912	0.1962	92876	25	2.96E-02	0.9	MAS
7	136791784	136978915	0.1869	187131	83	6.30E-03	0.8	CEU
7	136834047	136978915	0.1632	144868	69	6.71E-03	0.85	TSI
7	136867054	136981473	0.1361	114419	57	1.28E-02	0.9	MAS
7	142255340	142399886	0.2056	144546	105	4.78E-03	0.9	CHB
7	142255340	142357842	0.1774	102502	77	2.40E-02	0.8	MAS
7	142267304	142335539	0.0611	68235	61	3.02E-02	0.85	MEX
7	142338604	142547945	0.1876	209341	84	2.16E-02	0.7	MEX
7	142347184	142547945	0.1823	200761	79	5.54E-03	0.9	CHD
7	142350718	142547754	0.1440	197036	78	3.10E-02	0.75	INS
7	142361476	142549290	0.1488	187814	68	3.32E-03	0.95	CHS
7	142361476	142549290	0.1663	187814	69	2.95E-03	0.9	MAS
7	142363600	142549290	0.1806	185690	60	4.79E-02	0.75	GIH
7	142363600	142549290	0.1806	185690	60	4.30E-03	0.95	JPT
7	143852325	143906857	0.3313	54532	18	2.37E-02	0.95	CHB
7	143852325	143908526	0.3750	56201	19	1.68E-02	0.95	CHD
7	143852325	143908526	0.3750	56201	19	1.67E-02	0.95	JPT
7	143853833	143908526	0.7545	54693	17	3.88E-02	0.8	CHS
7	143858588	143906857	0.2740	48269	15	2.99E-02	0.9	GIH
7	145991850	146059148	0.1622	67298	45	3.46E-02	0.8	INS
8	4468075	4734293	0.5874	266218	355	4.87E-02	0.3	MEX
8	9423238	9726911	0.1371	303673	125	3.36E-02	0.45	ASW
8	10870500	11128546	0.5528	258046	154	1.57E-02	0.5	MEX
8	10953933	11128546	0.2942	174613	105	1.30E-02	0.8	CHB
8	10955803	11129662	0.2938	173859	105	1.46E-02	0.8	JPT
8	10961779	11109959	0.1275	148180	88	2.02E-02	0.9	CHD
8	10961779	11129662	0.2234	167883	116	1.46E-02	0.8	CHS
8	11434265	11507031	0.5034	72766	52	1.34E-02	0.8	CHS
8	11434265	11507982	0.3442	73717	56	4.14E-02	0.8	JPT
8	11928738	12595527	2.7375	666789	6	1.84E-02	0.9	CHB
8	11928738	12583900	2.7228	655162	5	1.54E-02	0.95	CHD
8	11928738	12575194	2.7190	646456	4	3.30E-02	0.95	JPT
8	16233288	16441711	0.2733	208423	79	2.69E-02	0.65	MEX
8	16256455	16409289	0.2029	152834	59	4.74E-02	0.75	CEU
8	42262896	42443137	0.0696	180241	64	1.62E-02	0.85	MEX
8	50427166	51138284	0.1367	711118	258	3.23E-02	0.55	MEX
8	50428283	51320466	0.1552	892183	321	6.62E-03	0.7	JPT
8	50442166	51233532	0.1477	791366	287	5.65E-03	0.75	CHB
8	50443270	50816259	0.0731	372989	116	3.54E-02	0.8	TSI
8	50444713	51142873	0.1258	698160	257	2.53E-02	0.7	CHD
8	50444713	51109255	0.0828	664542	261	2.76E-02	0.75	CHS
8	50444713	51502012	0.1766	1057299	429	2.27E-02	0.5	MAS
8	58170835	58371459	0.2290	200624	79	2.60E-02	0.7	GIH
8	58211816	58393502	0.2285	181686	76	4.99E-02	0.65	MEX
8	59428857	62040177	2.3690	2611320	1162	5.16E-03	0.05	GIH
8	66841775	67126543	0.2235	284768	99	5.57E-03	0.8	MAS
8	82214785	82315105	0.1874	100320	30	9.19E-03	0.95	CHS
8	82218220	82315105	0.1452	96885	29	7.07E-03	0.95	MAS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
8	82333477	82390493	0.2847	57016	19	2.57E-02	0.95	CHB
8	82333477	82390493	0.2847	57016	19	2.63E-02	0.95	CHD
8	82333477	82390493	0.1536	57016	24	4.35E-02	0.95	CHS
8	82333477	82390493	0.2847	57016	19	2.45E-02	0.95	JPT
8	94330163	96316049	2.0191	1985886	889	1.46E-02	0.05	GIH
8	99569926	101062323	0.1250	1492397	484	1.89E-02	0.45	INS
8	99934477	100895039	0.0503	960562	335	3.39E-02	0.6	GIH
8	100502644	100895039	0.0324	392395	177	4.89E-02	0.55	YRI
8	111526351	111757796	0.3008	231445	77	1.89E-02	0.8	CHS
8	129601852	129661717	0.2032	59865	35	7.42E-03	0.95	JPT
8	129603855	129641731	0.1779	37876	26	3.44E-02	0.95	CHB
8	129603855	129666059	0.2574	62204	34	2.02E-02	0.9	CHD
8	139005674	139158337	0.1879	152663	87	1.95E-02	0.85	CHB
8	139005674	139158337	0.1879	152663	87	1.70E-02	0.85	JPT
8	139044879	139156857	0.1500	111978	77	3.32E-02	0.85	CHS
8	139044879	139106414	0.1129	61535	31	1.42E-02	0.95	MAS
8	139045840	139156386	0.1553	110546	68	6.13E-03	0.95	CHD
9	13800014	13869572	0.1859	69558	82	4.49E-02	0.8	CHS
9	13819452	13907453	0.2203	88001	84	3.79E-02	0.8	CHB
9	13819452	13892765	0.1910	73313	71	3.46E-02	0.85	JPT
9	13898391	13964008	0.1854	65617	58	1.62E-02	0.85	MAS
9	13909776	13964008	0.2190	54232	46	3.41E-02	0.85	CHS
9	17848979	17905817	0.2081	56838	45	4.06E-02	0.85	CHS
9	19523872	19555588	0.2460	31716	15	3.56E-03	0.95	INS
9	30064416	30970218	0.3722	905802	333	5.00E-02	0.15	ASW
9	73585441	73722438	0.1704	136997	26	3.92E-02	0.85	MEX
9	90080934	90294520	0.2663	213586	61	3.49E-02	0.7	TSI
9	90830146	90867761	0.2346	37615	27	1.37E-02	0.95	CHB
9	90830146	90867761	0.2346	37615	27	1.40E-02	0.95	CHD
9	90830146	90869638	0.2688	39492	28	8.16E-03	0.95	JPT
9	90831383	90956526	0.1333	125143	59	3.89E-02	0.9	CHS
9	90831383	90867761	0.1132	36378	30	1.75E-02	0.95	MAS
9	91500477	91584522	0.2870	84045	37	2.67E-03	0.9	MAS
9	91515255	91586235	0.2385	70980	17	3.16E-02	0.95	CHS
9	99607955	99791583	0.1110	183628	78	4.10E-02	0.55	MKK
9	99607955	99780936	0.1107	172981	73	3.10E-02	0.6	YRI
9	99692403	99779709	0.0746	87306	36	4.24E-02	0.7	LWK
9	106985636	107247018	0.3501	261382	116	8.18E-03	0.8	CHB
9	106985636	107247018	0.3501	261382	116	2.48E-03	0.85	JPT
9	106985636	107247018	0.3501	261382	116	3.32E-02	0.55	MEX
9	106989995	107247018	0.3337	257023	120	3.93E-02	0.55	INS
9	107001111	107247018	0.2942	245907	110	9.73E-03	0.8	CHD
9	107021818	107237687	0.2305	215869	94	1.23E-02	0.7	TSI
9	107113735	107237687	0.2236	123952	41	4.51E-02	0.8	MAS
9	107200685	107245083	0.5489	44398	19	5.09E-03	0.95	CHS
9	110170570	110412429	0.3924	241859	162	4.70E-02	0.6	CHB
9	110181693	110410567	0.2787	228874	181	3.67E-02	0.65	CHS
9	114400326	114441827	0.2036	41501	11	4.79E-02	0.8	LWK
9	119523830	119576672	0.2747	52842	56	7.07E-03	0.85	MAS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
9	121665047	121691605	0.2726	26558	13	4.94E-02	0.9	GIH
9	121665047	121691719	0.2827	26672	15	8.74E-03	0.95	MAS
9	124145611	124199342	0.2183	53731	78	4.52E-02	0.8	CHB
9	124149760	124199342	0.1836	49582	77	2.87E-02	0.85	JPT
9	124174237	124205046	0.1941	30809	67	2.53E-02	0.75	GIH
9	124525569	124594587	0.2106	69018	22	2.62E-02	0.9	CEU
9	124525569	124594587	0.2106	69018	22	2.10E-02	0.9	TSI
9	125483780	125753232	0.1163	269452	110	3.78E-02	0.8	MAS
9	127818983	129529564	2.0208	1710581	815	2.00E-02	0.05	GIH
9	130420046	130529272	0.1884	109226	32	3.47E-02	0.85	CEU
9	139557213	139853982	0.1990	296769	117	2.97E-02	0.8	JPT
10	2983411	3058270	0.2425	74859	59	7.82E-03	0.9	CHB
10	2983411	3058270	0.2425	74859	59	2.64E-02	0.85	CHD
10	2983411	3059355	0.2815	75944	63	1.76E-02	0.85	JPT
10	2983411	3058270	0.2161	74859	56	3.35E-02	0.8	MAS
10	2983411	3058270	0.2425	74859	59	1.91E-02	0.75	TSI
10	2983482	3058270	0.2422	74788	58	8.80E-03	0.8	CEU
10	2983482	3058486	0.2495	75004	59	3.51E-02	0.7	MEX
10	5923951	6027850	0.3861	103899	97	3.93E-02	0.55	MEX
10	7467074	7505211	0.2588	38137	15	1.15E-02	0.95	MAS
10	22715863	22830890	0.1566	115027	52	3.31E-02	0.85	MAS
10	22719183	22830890	0.2774	111707	56	2.50E-02	0.85	CHB
10	22719183	22830890	0.2774	111707	56	2.03E-02	0.85	CHD
10	22719183	22787162	0.0272	67979	37	4.59E-02	0.95	GIH
10	22719183	22830890	0.2774	111707	56	2.56E-02	0.85	JPT
10	22719183	22830890	0.2774	111707	56	8.92E-03	0.75	MEX
10	22719183	22830890	0.2774	111707	56	5.70E-03	0.8	TSI
10	22763535	22818373	0.2241	54838	33	1.74E-02	0.85	CEU
10	22899536	23122833	0.1766	223297	133	4.06E-02	0.7	MAS
10	24368938	24435153	0.1699	66215	20	4.86E-02	0.95	CHS
10	37874382	38408617	0.0534	534235	179	3.48E-02	0.5	YRI
10	45535772	45928700	2.1869	392928	5	3.73E-02	0.85	INS
10	55537663	55873747	0.1655	336084	236	1.98E-02	0.7	CHS
10	55540301	55878340	0.3003	338039	205	1.94E-02	0.65	CHB
10	55576118	55878340	0.2766	302222	180	1.51E-02	0.7	CHD
10	55645372	55877503	0.2065	232131	116	2.94E-02	0.8	JPT
10	58454974	58683042	0.3289	228068	106	8.41E-03	0.8	CHS
10	59100707	59382097	0.2436	281390	117	3.38E-02	0.6	MEX
10	59239732	59493843	0.3694	254111	170	4.72E-02	0.6	CHS
10	59241443	59475057	0.2568	233614	139	4.66E-02	0.7	CHB
10	59244741	59493843	0.2560	249102	144	4.30E-02	0.7	CHD
10	59244741	59495589	0.2280	250848	169	3.66E-02	0.65	MAS
10	65461949	65683554	0.2705	221605	96	2.99E-02	0.65	CEU
10	65461949	65892784	0.3927	430835	132	3.73E-02	0.6	MAS
10	65461949	65701100	0.2733	239151	108	2.95E-02	0.6	MEX
10	65463876	65701100	0.2000	237224	107	3.61E-02	0.65	TSI
10	68760010	69578163	0.4240	818153	263	3.46E-02	0.4	TSI
10	74416452	75076147	0.1212	659695	178	5.58E-03	0.8	TSI
10	74427256	74672001	0.0153	244745	74	4.67E-02	0.85	MEX

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
10	74806089	75076147	0.0909	270058	69	3.59E-02	0.85	CEU
10	78672427	79205306	1.0243	532879	352	3.39E-02	0.1	LWK
10	83978741	84315167	0.2474	336426	158	3.17E-02	0.55	GIH
10	86833539	87064857	0.1178	231318	130	3.92E-02	0.7	GIH
10	86883236	87277788	0.4033	394552	215	4.92E-02	0.55	JPT
10	92947202	95385717	2.1427	2438515	1056	3.21E-02	0.05	JPT
10	93078168	93277560	0.0819	199392	55	3.73E-02	0.9	GIH
10	94492224	94858444	0.2224	366220	216	3.71E-02	0.65	CHB
10	94492718	94856668	0.2871	363950	219	3.35E-02	0.6	CHS
10	94492718	94832203	0.2054	339485	203	1.48E-02	0.65	MAS
10	94836083	95141612	0.4026	305529	196	4.59E-02	0.55	CHD
10	101788336	102352105	0.4446	563769	254	3.16E-02	0.2	YRI
10	102454123	102574587	0.2027	120464	60	4.62E-02	0.85	CHB
10	104573922	104793052	0.0275	219130	79	3.91E-02	0.65	LWK
10	106546794	107547879	0.3886	1001085	534	1.61E-02	0.4	CHB
10	107026591	107474816	0.2243	448225	198	2.36E-02	0.7	CHD
10	107163031	107413259	0.1791	250228	114	2.73E-02	0.8	CHS
10	118103897	118208925	0.1264	105028	59	2.53E-02	0.85	GIH
10	118188266	118341404	0.1643	153138	69	2.18E-02	0.8	CEU
10	118188266	118340939	0.1445	152673	67	3.68E-02	0.8	TSI
10	118221091	118340939	0.1443	119848	55	4.34E-02	0.8	INS
10	121867472	121881512	0.1570	14040	11	4.83E-02	0.95	MEX
11	5188141	5598602	0.9991	410461	485	2.10E-02	0.1	YRI
11	23668389	23735797	0.1270	67408	35	4.52E-02	0.9	MAS
11	23679619	23735797	0.1844	56178	27	1.35E-02	0.95	CHS
11	25062167	25185866	0.2552	123699	64	4.82E-02	0.8	CHD
11	25062726	25229215	0.3719	166489	81	2.74E-02	0.75	CHB
11	25064349	25232451	0.4468	168102	81	3.66E-02	0.7	JPT
11	25119121	25163804	0.1806	44683	36	2.84E-02	0.9	CHS
11	25143560	25353119	0.2100	209559	115	4.52E-02	0.7	MAS
11	25196163	25598001	0.2994	401838	170	1.76E-02	0.7	CHD
11	25226911	25586941	0.2250	360030	170	1.05E-02	0.75	CHS
11	33650124	35010976	2.8184	1360852	937	1.36E-02	0.05	LWK
11	37668746	38202461	0.2831	533715	171	1.86E-02	0.7	CHD
11	37668746	38180677	0.2637	511931	167	2.43E-02	0.7	JPT
11	37793512	38135306	0.2270	341794	122	1.76E-02	0.8	CHB
11	37911272	37995486	0.1629	84214	27	3.85E-02	0.9	MAS
11	39626026	39946041	0.2145	320015	162	1.64E-02	0.6	MEX
11	41561200	41636767	0.2393	75567	33	3.55E-02	0.85	MAS
11	60635491	61027771	0.1312	392280	119	1.27E-02	0.9	CHD
11	60635491	61027771	0.0833	392280	140	3.00E-02	0.9	CHS
11	60637432	61028885	0.1312	391453	117	1.87E-02	0.9	CHB
11	60643489	61027771	0.1302	384282	115	3.21E-03	0.95	JPT
11	60772098	61136437	0.2566	364339	128	2.63E-02	0.6	TSI
11	60775218	61006342	0.0670	231124	78	3.40E-02	0.9	MAS
11	64095162	64348255	0.2687	253093	90	3.41E-02	0.65	CEU
11	64095162	64354588	0.2709	259426	92	1.94E-02	0.65	TSI
11	64896352	67806752	1.4200	2910400	808	5.87E-03	0.15	MEX
11	66594721	66948025	0.1096	353304	88	2.89E-02	0.8	GIH

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
11	66594721	66949131	0.2014	354410	113	8.22E-03	0.7	INS
11	67834242	68186263	0.3458	352021	141	4.43E-02	0.5	INS
11	77584034	78035685	0.3477	451651	154	1.98E-02	0.55	CEU
11	87892236	90630763	1.3291	2738527	980	4.40E-02	0.05	CEU
11	91676379	91849773	0.1748	173394	80	1.76E-02	0.75	GIH
11	91681501	91851009	0.1710	169508	80	4.19E-03	0.8	MEX
11	110023638	110209636	0.1832	185998	110	4.38E-03	0.5	LWK
11	129450904	129530155	0.1366	79251	40	3.05E-02	0.85	INS
12	951166	1459724	0.2932	508558	171	1.62E-02	0.7	JPT
12	15629793	15997790	0.2343	367997	145	6.29E-03	0.65	GIH
12	20876496	21011482	0.1093	134986	110	1.89E-02	0.75	INS
12	21308563	21399445	0.0834	90882	140	1.60E-02	0.75	MEX
12	33401684	34649300	0.1170	1247616	373	4.55E-02	0.55	MAS
12	36252688	39010297	0.7117	2757609	859	1.57E-02	0.2	MEX
12	41159574	44136773	2.1492	2977199	1263	4.42E-03	0.05	GIH
12	42489168	43107122	0.3713	617954	218	4.26E-02	0.55	CHB
12	42491285	43188531	0.3866	697246	240	1.62E-02	0.6	JPT
12	42597744	44321443	1.3276	1723699	657	1.91E-02	0.15	MEX
12	42881817	42987551	0.1881	105734	44	4.33E-02	0.75	INS
12	47959425	48451957	0.3605	492532	162	1.20E-02	0.7	CHS
12	47964796	48470263	0.2768	505467	163	4.58E-03	0.8	CHB
12	47964796	48470263	0.2768	505467	163	2.65E-02	0.7	CHD
12	48009848	48453169	0.1556	443321	145	2.91E-02	0.8	JPT
12	53412716	53547320	1.0220	134604	38	4.80E-02	0.6	MAS
12	57508987	57599418	0.2151	90431	56	4.32E-02	0.75	CEU
12	57525875	57750720	0.2666	224845	119	1.02E-02	0.65	TSI
12	65809611	65863997	0.1337	54386	28	1.25E-02	0.95	MAS
12	74752497	75123705	1.6156	371208	51	1.23E-02	0.65	MAS
12	78272240	78648427	0.3308	376187	112	4.58E-02	0.55	MEX
12	78401205	78652724	0.1742	251519	69	2.11E-02	0.55	YRI
12	78638266	78934970	0.2562	296704	70	1.42E-02	0.75	CEU
12	81099873	81575401	0.4072	475528	123	2.18E-02	0.35	YRI
12	86870158	87428895	0.3787	558737	174	1.86E-02	0.65	CHB
12	86871331	87412346	0.2339	541015	187	1.68E-02	0.7	CHS
12	86871331	87414712	0.4687	543381	181	2.17E-02	0.55	MAS
12	86881127	87414712	0.2295	533585	170	3.69E-02	0.7	CHD
12	86937549	87688096	0.2249	750547	226	3.02E-02	0.5	GIH
12	87342610	87864243	0.1786	521633	158	2.73E-02	0.65	CEU
12	87342610	87674375	0.1011	331765	98	2.67E-02	0.8	TSI
12	87367958	87723114	0.1126	355156	103	1.01E-02	0.8	MEX
12	87539269	87723114	0.2901	183845	56	8.36E-04	0.85	INS
12	98739698	98995242	0.1066	255544	96	4.95E-02	0.9	CHB
12	98739698	99296032	0.2067	556334	174	4.52E-03	0.8	CHD
12	98739698	99146849	0.2023	407151	145	1.16E-02	0.8	CHS
12	98739698	99296032	0.2067	556334	174	7.76E-04	0.9	JPT
12	102087154	103950819	2.7210	1863665	1360	1.47E-03	0.05	MKK
12	105745057	107306065	1.8284	1561008	777	1.34E-02	0.05	MKK
12	107481335	109460058	1.4976	1978723	715	3.01E-02	0.05	MKK
12	108665528	111807450	1.2601	3141922	923	1.92E-02	0.1	CHD

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
12	109807801	112446668	1.8748	2638867	934	2.05E-02	0.05	CHB
12	109841394	112515629	2.2217	2674235	955	3.97E-02	0.05	JPT
12	110032708	111072108	0.2302	1039400	343	3.62E-02	0.45	TSI
12	112328277	112375934	0.2266	47657	18	3.01E-02	0.95	CHS
12	112343834	112381135	0.1397	37301	14	4.02E-02	0.8	ASW
12	115670030	115828659	0.3157	158629	65	3.44E-02	0.65	MEX
12	121979264	122623065	0.4520	643801	153	8.71E-03	0.55	GIH
12	122405005	122828031	0.5376	423026	111	4.58E-02	0.5	MEX
12	122406541	122891313	0.5615	484772	133	7.65E-03	0.7	CHD
12	122406541	122842862	0.5426	436321	119	6.01E-04	0.9	JPT
12	122483546	122834234	0.1883	350688	154	1.12E-02	0.8	CHS
12	122499063	122577028	0.1396	77965	35	3.03E-02	0.9	MAS
12	122579359	122885054	0.1685	305695	126	3.60E-02	0.8	CHB
12	125520182	125630940	0.2537	110758	61	2.52E-02	0.85	CHB
12	125520182	125629813	0.2361	109631	59	4.14E-02	0.7	MEX
12	125522079	125632409	0.2811	110330	66	4.77E-02	0.8	JPT
12	127379351	127404601	0.2478	25250	19	4.28E-02	0.9	MAS
13	18847861	19386212	0.1806	538351	145	4.11E-02	0.75	CHB
13	18850959	19386212	0.1795	535253	143	2.20E-02	0.8	JPT
13	20705752	20753294	0.2217	47542	19	4.83E-02	0.95	CHD
13	20705752	20768166	0.2332	62414	28	1.21E-02	0.95	JPT
13	37775636	37860369	0.1528	84733	37	4.92E-02	0.85	CEU
13	37775636	37860369	0.1528	84733	37	4.35E-02	0.85	TSI
13	56453118	57152774	0.2888	699656	203	2.58E-02	0.25	ASW
13	56527759	57001072	0.0670	473313	127	4.08E-02	0.55	YRI
13	60292838	60493429	0.2399	200591	115	3.08E-02	0.7	MAS
13	60293427	60493599	0.1878	200172	105	4.87E-02	0.8	JPT
13	94479016	94587642	0.3346	108626	152	3.86E-02	0.5	GIH
13	102951017	103143536	0.1717	192519	120	3.80E-02	0.65	MEX
13	103648238	103714539	0.0983	66301	33	3.97E-02	0.9	INS
14	19284747	19453079	0.4512	168332	4	4.75E-02	0.95	MKK
14	23863737	24661742	1.1994	798005	543	4.81E-02	0.15	MEX
14	49021100	49473932	0.2799	452832	146	3.00E-02	0.7	JPT
14	59829480	60684493	0.2169	855013	229	1.63E-02	0.3	LWK
14	61014730	61131283	0.3460	116553	131	3.04E-02	0.55	TSI
14	62331615	63079242	0.7213	747627	356	4.11E-02	0.1	ASW
14	62757045	62837633	0.1854	80588	56	1.28E-02	0.8	INS
14	62821120	62954737	0.1987	133617	79	2.42E-02	0.7	MEX
14	62856527	62971047	0.1527	114520	56	4.45E-02	0.8	TSI
14	62858991	62967839	0.2031	108848	59	2.34E-02	0.75	INS
14	62962494	63137946	0.1824	175452	62	2.32E-02	0.75	MEX
14	65502497	66967075	0.3841	1464578	516	2.72E-02	0.3	MEX
14	65660573	66967453	0.2764	1306880	428	8.82E-04	0.55	TSI
14	65689881	66960075	0.2566	1270194	416	1.16E-03	0.55	CEU
14	65920022	66979795	0.2323	1059773	366	3.32E-02	0.25	MKK
14	76948436	77059691	0.1758	111255	59	3.66E-02	0.85	CHS
14	101638726	101737014	0.1136	98288	28	2.44E-02	0.95	MAS
14	105156965	105997070	1.4388	840105	6	2.17E-02	0.95	CEU
14	105156965	105692103	0.6963	535138	5	4.45E-02	0.95	GIH

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
14	105156965	105692103	0.6963	535138	5	4.80E-02	0.95	MEX
14	105156965	105997070	1.4388	840105	6	3.81E-02	0.9	TSI
15	18453936	19322563	4.3229	868627	3	3.31E-02	0.9	ASW
15	18453936	19322563	4.3229	868627	3	4.67E-02	0.95	CEU
15	18453936	19322563	4.3229	868627	3	4.21E-02	0.95	GIH
15	18453936	19884656	5.1923	1430720	6	8.39E-03	0.8	LWK
15	18453936	19884656	5.1923	1430720	6	4.29E-02	0.75	MEX
15	18453936	19322563	4.3229	868627	3	4.16E-02	0.9	MKK
15	18453936	19322563	4.3229	868627	3	2.27E-02	0.95	YRI
15	26029250	26809337	1.8403	780087	67	1.84E-02	0.5	TSI
15	26039328	26809337	1.8380	770009	55	1.78E-02	0.5	MEX
15	26203954	26812158	1.8484	608204	6	3.79E-02	0.85	CEU
15	28081081	30713357	3.3900	2632276	691	4.77E-02	0.05	MEX
15	28141595	29110106	1.0052	968511	153	2.61E-03	0.6	MAS
15	28153539	29085644	2.0002	932105	137	2.28E-02	0.35	INS
15	28157206	28971039	0.6212	813833	40	3.32E-02	0.75	CHB
15	28157206	29038940	0.6352	881734	75	5.93E-03	0.8	CHD
15	28157206	28843762	1.3626	686556	37	4.28E-03	0.8	CHS
15	28157206	28971039	0.6212	813833	40	2.32E-02	0.8	JPT
15	34210025	34375288	0.2920	165263	67	3.29E-02	0.8	CHB
15	40233690	42886577	0.6753	2652887	796	2.13E-02	0.2	JPT
15	40676339	42280859	0.2464	1604520	459	3.03E-02	0.4	CEU
15	42925286	43171957	0.3957	246671	65	2.91E-03	0.75	INS
15	43928463	44076751	0.2095	148288	74	2.57E-02	0.85	CHB
15	43928463	44059275	0.1881	130812	67	8.11E-03	0.9	CHD
15	43928463	44059275	0.1881	130812	67	4.04E-02	0.85	JPT
15	43928463	44055830	0.2520	127367	69	5.46E-03	0.85	MAS
15	43961704	44085712	0.2796	124008	70	7.77E-03	0.85	CHS
15	46146961	46304763	0.1538	157802	44	6.53E-03	0.9	CEU
15	46146961	46305485	0.1568	158524	45	4.92E-02	0.8	GIH
15	46146961	46305485	0.1568	158524	45	1.78E-02	0.85	TSI
15	46464675	46732970	0.1794	268295	142	2.24E-02	0.65	TSI
15	46473467	46736370	0.3893	262903	144	1.26E-02	0.55	INS
15	46473602	46782678	0.2612	309076	159	2.51E-02	0.55	GIH
15	46479901	46782678	0.2137	302777	158	1.47E-02	0.65	CEU
15	61567335	61969444	0.1506	402109	148	1.62E-02	0.85	CHB
15	61567335	61971073	0.1518	403738	149	2.77E-02	0.8	CHD
15	61567335	61936702	0.1152	369367	125	2.44E-02	0.9	JPT
15	61567683	61928089	0.0826	360406	116	4.58E-02	0.9	CHS
15	61567683	62058713	0.1673	491030	196	3.48E-02	0.65	MAS
15	61971415	62134999	0.3453	163584	109	1.85E-02	0.75	CHB
15	61999328	62941185	0.1593	941857	315	3.33E-02	0.6	CHS
15	62122278	62938688	0.3338	816410	233	2.69E-03	0.7	JPT
15	62303982	62934451	0.1670	630469	166	1.16E-02	0.8	CHD
15	62424589	62904700	0.1571	480111	129	4.10E-02	0.8	CHB
15	67440101	67644716	0.0749	204615	85	4.00E-02	0.85	TSI
15	69835470	70570555	0.1513	735085	243	3.75E-03	0.6	MEX
15	69880666	70775924	0.1557	895258	304	3.01E-03	0.6	INS
15	69884515	70762555	0.1677	878040	260	4.25E-03	0.7	CEU

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
15	69884515	70794003	0.1729	909488	268	1.42E-02	0.6	GIH
15	69916180	70794946	0.1446	878766	255	1.05E-02	0.65	TSI
15	80192696	81230621	0.8151	1037925	156	4.54E-02	0.2	LWK
15	80194449	81225246	0.8125	1030797	149	2.54E-02	0.25	YRI
15	88274514	88345490	0.1953	70976	18	4.27E-02	0.9	GIH
16	2062129	2167369	0.2584	105240	27	1.22E-02	0.9	MAS
16	2309072	2681813	0.5602	372741	80	4.46E-02	0.65	CHS
16	2309072	2370177	0.4459	61105	18	4.65E-02	0.85	MAS
16	2310040	2361830	0.2876	51790	21	3.15E-02	0.85	GIH
16	2462716	2582204	0.4979	119488	7	3.23E-02	0.95	MAS
16	2466655	2716804	0.5021	250149	43	2.53E-02	0.8	CHB
16	2466655	2665257	0.3583	198602	21	4.64E-02	0.9	CHD
16	2587877	2716804	0.3117	128927	43	1.95E-02	0.8	MAS
16	10816814	11432620	1.1110	615806	393	4.24E-02	0.2	MEX
16	13548359	13717292	0.3067	168933	118	4.43E-02	0.7	CHD
16	16161071	17820991	3.9103	1659920	608	4.40E-02	0.05	CHB
16	16190572	17614150	3.4628	1423578	478	1.13E-02	0.15	CHD
16	17350498	17437122	0.1937	86624	45	4.57E-02	0.85	CHS
16	21694617	22581356	0.8432	886739	135	1.09E-02	0.5	CEU
16	22847999	23024529	0.2653	176530	109	2.62E-02	0.4	YRI
16	23296041	23484768	0.2053	188727	74	1.51E-02	0.75	TSI
16	30435633	31101443	0.2609	665810	160	1.03E-02	0.75	CHS
16	30435773	31101443	0.1711	665670	134	2.86E-02	0.8	CHB
16	30435773	31098039	0.1708	662266	133	2.27E-02	0.8	CHD
16	30435773	31098039	0.1708	662266	133	3.63E-02	0.8	JPT
16	31844443	32066096	1.1384	221653	13	5.56E-03	0.9	MAS
16	32786914	33735555	3.9148	948641	6	4.42E-03	0.95	MAS
16	33756065	34069209	0.6162	313144	6	4.42E-02	0.95	MAS
16	46630304	47028216	0.1897	397912	140	2.09E-02	0.8	JPT
16	46643346	47028216	0.1787	384870	133	1.93E-02	0.8	CHD
16	46730905	47028216	0.1022	297311	111	1.03E-02	0.95	CHB
16	64345386	64441540	0.1947	96154	73	3.22E-02	0.85	CHB
16	64345386	64443954	0.2364	98568	75	4.15E-02	0.8	CHD
16	64345386	64443954	0.2364	98568	75	7.03E-03	0.9	JPT
16	64951891	68198345	1.2741	3246454	1017	4.47E-02	0.05	CEU
16	65700132	66902197	0.1356	1202065	319	2.17E-02	0.65	CHD
16	65701796	66901470	0.0612	1199674	354	4.63E-02	0.7	CHS
16	65729363	66582351	0.0988	852988	226	1.08E-02	0.85	JPT
16	65744712	66860911	0.1180	1116199	290	2.93E-02	0.7	CHB
16	65966681	66777470	0.1194	810789	218	3.80E-02	0.65	MAS
16	66049749	66247253	0.0479	197504	39	3.18E-02	0.9	MEX
16	77322312	77341734	0.5596	19422	12	3.83E-02	0.9	CHS
16	78324333	78505139	0.2315	180806	169	3.43E-02	0.55	MEX
16	81789713	81814269	0.3063	24556	27	3.60E-02	0.9	CHB
16	81789713	81816668	0.3348	26955	33	4.08E-02	0.85	CHD
17	10919861	10959235	0.1681	39374	15	4.77E-02	0.95	CEU
17	10919861	10968233	0.1991	48372	20	1.60E-02	0.9	MEX
17	10919861	10968233	0.1991	48372	20	3.51E-02	0.9	TSI
17	16366419	16412415	0.1447	45996	16	2.37E-02	0.95	INS

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
17	16474703	18694595	2.0689	2219892	665	2.36E-02	0.1	JPT
17	18825740	19358320	0.4509	532580	109	4.09E-02	0.55	TSI
17	18864543	19141092	0.1736	276549	14	4.98E-02	0.75	ASW
17	18864543	19112789	0.1725	248246	6	3.56E-02	0.95	LWK
17	18864543	19141092	0.1736	276549	14	4.39E-02	0.8	YRI
17	19741141	20457372	0.2153	716231	130	3.34E-02	0.75	CHB
17	19744839	20457372	0.2111	712533	129	3.52E-02	0.75	CHD
17	19816932	20466453	0.6106	649521	132	2.13E-02	0.6	CHS
17	19816932	20455513	0.1867	638581	132	3.74E-02	0.7	MAS
17	24874328	26435699	0.2214	1561371	505	5.51E-03	0.45	MAS
17	24935404	25960929	0.2074	1025525	305	4.45E-02	0.45	MEX
17	25574940	26419872	0.2755	844932	218	4.71E-02	0.6	CHB
17	25577112	26419872	0.2719	842760	214	4.03E-02	0.6	CHD
17	27315068	27444641	0.1579	129573	25	9.04E-03	0.95	MAS
17	31097011	31310634	0.1996	213623	81	3.90E-02	0.7	CEU
17	31097011	31310634	0.1996	213623	81	1.07E-02	0.75	TSI
17	33323919	33746729	1.5324	422810	19	4.28E-02	0.7	MAS
17	50951865	51173778	0.6917	221913	151	3.62E-02	0.4	INS
17	51276135	51409524	0.0871	133389	67	4.79E-02	0.85	CEU
17	53206418	53607488	0.7899	401070	206	4.45E-02	0.4	MAS
17	53311424	53502268	0.3613	190844	71	4.34E-03	0.9	JPT
17	53315647	53435448	0.3022	119801	47	6.11E-03	0.9	CHB
17	53346331	53403839	0.2602	57508	30	2.28E-02	0.9	CHS
17	53356034	53435448	0.2624	79414	29	3.17E-02	0.9	CHD
17	55573663	56600056	0.2885	1026393	227	1.48E-02	0.65	CHB
17	55573663	56018758	0.1899	445095	116	4.48E-02	0.75	CHS
17	55947947	56595255	0.1907	647308	128	1.65E-02	0.8	CHD
17	55959243	56505015	0.1538	545772	118	3.50E-02	0.75	MAS
17	55999122	56179349	0.1279	180227	27	1.80E-02	0.95	CEU
17	55999122	56490310	0.1465	491188	89	4.61E-03	0.85	GIH
17	55999122	56179349	0.1279	180227	27	1.36E-03	0.95	MEX
17	55999122	56179349	0.1279	180227	27	1.61E-02	0.95	TSI
17	56018758	56164550	0.0747	145792	39	4.13E-02	0.9	INS
17	56192719	56332539	0.0250	139820	31	3.85E-02	0.95	INS
17	58321149	58902680	0.1648	581531	115	4.42E-02	0.8	CHD
17	58321902	58903970	0.2614	582068	133	3.71E-02	0.7	CHS
17	59019747	59119256	0.1923	99509	30	4.90E-02	0.9	CHS
17	59875697	60493874	0.4516	618177	124	3.26E-02	0.65	JPT
17	59935620	60411795	0.1906	476175	77	6.49E-03	0.8	GIH
17	59985216	60493874	0.2697	508658	88	6.29E-03	0.85	CHD
17	59985216	60103123	0.1399	117907	34	2.47E-02	0.95	CHS
17	59985216	60103123	0.1703	117907	34	1.43E-02	0.9	MAS
17	60590698	60794308	0.3313	203610	133	3.66E-02	0.55	CEU
17	61345212	61634187	0.1396	288975	121	4.67E-02	0.75	MAS
17	63206575	63658822	0.3658	452247	65	3.95E-02	0.65	TSI
18	6147072	6244886	0.3244	97814	29	5.64E-03	0.95	CHB
18	6147072	6244886	0.3244	97814	29	5.35E-03	0.95	CHD
18	6147072	6230094	0.2771	83022	27	8.49E-03	0.95	JPT
18	6175410	6244886	0.2632	69476	16	1.18E-02	0.95	CEU

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
18	6175410	6230094	0.2159	54684	14	1.82E-02	0.95	GIH
18	6175410	6244886	0.2632	69476	16	2.09E-03	0.95	MEX
18	6175410	6244886	0.2632	69476	16	3.43E-02	0.9	TSI
18	7466415	7678197	0.3024	211782	120	2.67E-02	0.6	CEU
18	19465852	19883782	0.2365	417930	168	4.18E-02	0.55	TSI
18	30336115	30584024	0.2846	247909	104	2.96E-03	0.85	CHS
18	30337737	30593430	0.1036	255693	104	2.57E-02	0.85	MAS
18	30339720	30570172	0.1518	230452	89	3.74E-02	0.85	CHB
18	30367899	30579424	0.1469	211525	90	2.13E-02	0.75	MEX
18	30410744	30579424	0.1424	168680	74	3.77E-02	0.9	JPT
18	37545935	37604290	0.1786	58355	25	3.73E-02	0.9	MAS
18	64430875	64543625	0.2741	112750	67	2.65E-02	0.7	GIH
18	64780832	64928523	0.2159	147691	90	7.54E-04	0.85	GIH
18	64780832	64928523	0.2159	147691	90	4.92E-03	0.75	MEX
18	64785439	64922370	0.1994	136931	85	2.75E-04	0.9	CEU
18	64785439	64915926	0.1972	130487	80	2.35E-04	0.95	TSI
18	65840051	66022491	0.1899	182440	57	4.80E-02	0.85	CHD
19	1211286	1259057	0.2627	47771	19	1.76E-02	0.95	CHS
19	15186310	15431931	0.2384	245621	63	3.19E-02	0.45	ASW
19	15186310	15436801	0.2420	250491	64	4.41E-02	0.45	LWK
19	22522613	22789147	0.2334	266534	94	4.51E-02	0.65	CEU
19	22586511	23046994	0.1169	460483	147	4.66E-02	0.65	INS
19	42400700	43168897	0.2098	768197	238	2.88E-02	0.25	ASW
19	47285556	47598754	0.1358	313198	59	1.45E-02	0.6	LWK
19	47305035	47598754	0.1351	293719	56	2.38E-02	0.6	MKK
19	47473625	47574506	0.0756	100881	31	8.23E-03	0.7	ASW
19	47473625	47574506	0.0756	100881	31	1.41E-02	0.8	YRI
19	47568462	48034098	0.4441	465636	78	4.84E-02	0.7	CHD
19	47586321	48034098	0.4041	447777	72	3.25E-02	0.75	CHB
19	47586321	47895347	0.2689	309026	69	8.61E-03	0.75	GIH
19	47586321	48034098	0.4041	447777	72	1.57E-02	0.65	MEX
19	47586321	48034098	0.4041	447777	72	1.36E-03	0.8	TSI
19	47602928	48064226	0.3897	461298	70	4.44E-04	0.85	CEU
19	47605759	48034098	0.3771	428339	68	4.40E-02	0.75	JPT
20	7654428	7835679	0.2624	181251	68	3.38E-02	0.7	CEU
20	16442919	16458024	0.0670	15105	16	3.13E-02	0.9	LWK
20	16442919	16458024	0.0670	15105	16	6.70E-03	0.95	YRI
20	22434585	22540307	0.2153	105722	65	3.68E-02	0.7	MEX
20	22434585	22540307	0.2153	105722	65	2.02E-02	0.75	TSI
20	22436754	22529268	0.1485	92514	60	1.78E-03	0.9	CEU
20	24665867	24975078	0.3898	309211	187	2.82E-02	0.6	CHS
20	24745175	24980075	0.1381	234900	118	2.61E-02	0.85	CHD
20	24746856	24980075	0.1376	233219	117	4.04E-02	0.85	CHB
20	29982229	30569050	0.4041	586821	198	4.80E-02	0.55	CHS
20	29985593	30522023	0.3325	536430	174	1.21E-02	0.7	CHD
20	30959371	31254824	0.4295	295453	196	1.74E-02	0.6	CHS
20	30965993	31164994	0.3229	199001	146	4.11E-02	0.65	CHD
20	31155737	31254213	0.3162	98476	55	4.93E-02	0.65	MEX
20	33254942	34313778	0.2712	1058836	367	3.62E-02	0.5	CHB

chr	start	end	gened	pyhsd	n.snp	adjusted haploPS score	f	pop
20	33618155	34331565	0.1765	713410	245	3.83E-02	0.65	JPT
20	33637025	34140324	0.0984	503299	160	2.97E-02	0.75	CEU
20	33657468	34291873	0.1078	634405	215	7.50E-03	0.65	MEX
20	33671011	33965521	0.0323	294510	92	4.33E-02	0.55	ASW
20	52491840	52648939	0.2776	157099	67	4.80E-02	0.8	JPT
20	52496348	52648939	0.2764	152591	65	3.98E-02	0.8	CHD
20	52496348	52557704	0.1550	61356	17	3.05E-02	0.95	GIH
20	52496348	52590434	0.1901	94086	28	4.50E-02	0.85	TSI
21	16750162	16923481	0.6172	173319	62	4.92E-03	0.85	CHB
21	16750162	16925832	0.3143	175670	54	4.06E-02	0.75	MAS
21	16752075	16768363	0.3072	16288	14	4.02E-02	0.9	CEU
21	16752075	16804202	0.3586	52127	21	4.53E-02	0.9	CHD
21	16752075	16765240	0.2857	13165	12	4.88E-02	0.9	GIH
21	16752075	16790643	0.3413	38568	19	1.95E-02	0.95	JPT
21	16752075	16768363	0.3072	16288	14	2.06E-02	0.9	MEX
21	16752075	16768363	0.3072	16288	14	3.55E-02	0.9	TSI
21	16755601	16925832	0.2946	170231	52	3.11E-02	0.7	INS
22	20683066	20724144	0.2329	41078	32	3.19E-02	0.9	CHD
22	20690650	20723606	0.1612	32956	33	3.00E-02	0.85	INS
22	20704853	20723606	0.2725	18753	25	1.68E-03	0.95	MAS
22	21366105	21725684	1.2891	359579	79	4.35E-02	0.55	JPT
22	24995807	25022186	0.2186	26379	33	9.02E-03	0.9	MAS
22	29863796	30767340	0.2579	903544	349	4.03E-02	0.2	YRI
22	31464399	31853431	0.6799	389032	278	3.00E-02	0.15	LWK
22	32377427	32645294	0.4662	267867	241	3.34E-02	0.2	YRI
22	34158300	34221048	0.5968	62748	5	4.35E-02	0.9	YRI
22	34871671	34977906	0.4734	106235	93	4.89E-02	0.65	CHB
22	37179366	37661254	0.6946	481888	168	4.25E-02	0.4	MEX
22	37964380	38213290	0.4260	248910	105	2.57E-02	0.7	JPT
22	38086931	38157499	0.2367	70568	37	4.81E-02	0.85	CHS
22	44988731	45199234	0.2027	210503	121	8.31E-04	0.95	CHD
22	45000658	45215256	0.3505	214598	118	1.10E-03	0.9	CHB
22	45000658	45202574	0.1787	201916	113	1.17E-03	0.95	JPT
22	45001048	45210629	0.2435	209581	116	1.48E-03	0.9	CHS
22	45001048	45063370	0.0266	62322	41	2.34E-02	0.95	GIH
22	45001048	45205702	0.1897	204654	113	9.32E-04	0.8	MEX
22	45005170	45210629	0.3331	205459	116	3.68E-04	0.9	MAS
22	45053267	45118765	0.1808	65498	17	5.11E-03	0.95	INS
22	48540686	48777213	0.3519	236527	68	3.65E-02	0.65	TSI
22	48550082	48777213	0.3224	227131	67	1.95E-02	0.7	CEU
22	48569166	48777213	0.3171	208047	60	2.45E-03	0.8	MEX

The start and end coordinates for each region are reported in NCBI Build 36 coordinates.

Table S2. MIM Numbers for Genes Presented in Table 2

Gene	MIM ID	Gene	MIM ID	Gene	MIM ID
<i>ZMYM6</i>	613567	<i>TUBB</i>	191130	<i>BAI3</i>	602684
<i>SFPQ</i>	605199	<i>FLOT1</i>	606998	<i>CUX2</i>	610648
<i>ZMYM4</i>	613568	<i>IER3</i>	602996	<i>FAM109A</i>	614239
<i>NCDN</i>	608458	<i>DDR1</i>	600408	<i>SH2B3</i>	605093
<i>PSMB2</i>	602175	<i>GTF2H4</i>	601760	<i>ATXN2</i>	601517
<i>TFAP2E</i>	614428	<i>TFIIH</i>	189972	<i>BRAP</i>	604986
<i>LHX8</i>	604425	<i>VARs2</i>	612802	<i>ACAD10</i>	611181
<i>ACMSD</i>	608889	<i>DPCR1</i>	613928	<i>ALDH2</i>	100650
<i>CCNT2</i>	603862	<i>HLA-C</i>	142840	<i>MAPKAPK5</i>	606723
<i>RAB3GAP1</i>	602536	<i>HLA-B</i>	142830	<i>ERP29</i>	602287
<i>UBXD2</i>	611216	<i>MICA</i>	600169	<i>C12orf30</i>	612755
<i>LCT</i>	603202	<i>HCP5</i>	604676	<i>C12orf51</i>	610762
<i>MCM6</i>	601806	<i>HLA-DOA</i>	142930	<i>NAP1</i>	609916
<i>DARS</i>	603084	<i>HLA-DPA1</i>	142880	<i>TRAFD1</i>	613197
<i>CXCR4</i>	162643	<i>HLA-DPB1</i>	142858	<i>RPL6</i>	603703
<i>OR13G1</i>	611677	<i>COL11A2</i>	120290	<i>PTPN11</i>	176876
<i>UBD</i>	606050	<i>RXRb</i>	180246	<i>RHOJ</i>	607653
<i>GABBR1</i>	603540	<i>SLC39A7</i>	601416		
<i>MOG</i>	159465	<i>HSD17B8</i>	601417		
<i>ZFP57</i>	612192	<i>RING1</i>	602045		
<i>HLA-F</i>	143110	<i>VPS52</i>	603443		
<i>HLA-G</i>	142871	<i>RPS18</i>	180473		
<i>HLA-A</i>	142800	<i>B3GALT4</i>	603095		
<i>HLA-H</i>	613609	<i>WDR46</i>	611440		
<i>ZNRD1</i>	607525	<i>PFDN6</i>	605660		
<i>PPP1R11</i>	606670	<i>RGL2</i>	602306		
<i>PPP1R10</i>	603771	<i>TAPBP</i>	607081		
<i>RNF39</i>	607524	<i>ZBTB22</i>	611439		
<i>TRIM31</i>	609316	<i>DAXX</i>	603186		
<i>TRIM10</i>	605701	<i>KIFC1</i>	603763		
<i>TRIM15</i>	126200	<i>PHF1</i>	602881		
<i>TRIM26</i>	600830	<i>SYNGAP1</i>	603384		
<i>TRIM39</i>	605700	<i>BAK1</i>	600516		
<i>GNL1</i>	143024	<i>C6orf125</i>	614461		
<i>PRR3</i>	607147	<i>ITPR3</i>	147267		
<i>MRPS18B</i>	611982	<i>SBP1</i>	610902		
<i>DHX16</i>	603405	<i>IP6K3</i>	606993		
<i>MDC1</i>	607593	<i>EYS</i>	612424		

MIM numbers for the genes present in the 10 regions identified by haploPS with positive selection signals in multiple populations, and where the haplotype similarity index (HSI) are less than 0.90. This indicates that the haplotypes carrying the advantageous variant(s) at each of these 10 regions in the different populations are significantly different and thus suggestive of convergent evolution of multiple mutation events, either at the same variant or at different variants in the same genomic region. This information is an extension of Table 2 in the main text.

Table S3. Positive Selection Survey with Physical Distance

Chr	Start	End	Adj. P-value	Pop.	Frequency	Genes
1	171,791,702	173,246,946	1.17×10^{-3}	ASW	0.15	<i>SLC9A11, ANKRD45, KLHL20, CENPL, DARS2, GAS5, SNORD81, SNORD47, SNORD80, SNORD79, SNORD78, SNORD44, SNORD77, SNORD76, SNORD75, SNORD74, ZBTB37, DQ593451, SERPINC1, RC3H1, RABGAP1L, GPR52, IDN4-GGTR7, KIAA0471, CACYBP, MRPS14</i>
	172,215,955	173,189,969	2.04×10^{-3}	CEU	0.50	
	171,881,574	173,299,764	1.75×10^{-2}	CHB	0.30	
	172,148,516	173,303,662	4.28×10^{-2}	CHD	0.35	
	172,148,516	173,288,426	2.24×10^{-2}	CHS	0.35	
	172,150,698	173,189,969	5.09×10^{-4}	GIH	0.50	
	172,170,360	173,217,691	1.64×10^{-3}	INS	0.40	
	172,147,375	173,255,586	6.77×10^{-3}	JPT	0.45	
	172,020,658	172,501,666	2.45×10^{-2}	LWK	0.30	
	172,159,283	173,089,655	6.79×10^{-3}	MAS	0.45	
	172,342,803	172,749,056	1.98×10^{-2}	MKK	0.35	
	172,122,860	173,189,969	2.73×10^{-4}	MXL	0.50	
	171,791,702	173,244,726	7.57×10^{-7}	YRI	0.25	
16	45,158,679	45,262,450	1.17×10^{-3}	ASW	0.70	<i>SHCBP1, VPS35, ORC6L, ORC6, MYLK3, C16orf87, GPT2, DNAJA2, NETO2, ITFG1</i>
	45,158,679	45,354,669	1.17×10^{-3}	CEU	0.80	
	45,158,679	45,554,058	1.17×10^{-3}	CHB	0.75	
	45,158,679	45,511,849	1.17×10^{-3}	CHD	0.75	
	45,158,679	45,440,451	1.17×10^{-3}	GIH	0.70	
	45,337,768	46,092,753	1.17×10^{-3}	INS	0.45	
	45,365,022	45,827,459	1.17×10^{-3}	JPT	0.80	
	45,580,279	45,825,707	1.17×10^{-3}	MAS	0.75	
	45,158,679	45,354,669	1.17×10^{-3}	MXL	0.75	
	45,158,679	45,354,669	1.17×10^{-3}	TSI	0.75	

Positive selected regions identified by haploPS analysis with the use of physical distance, where at least ten of the fourteen populations exhibit evidence of positive selection and the genomic regions have not been previously reported by positive selection surveys with LRH/iHS and XP-EHH. A genomic region that is positively selected in the three population panels in Phase 2 of the HapMap can artificially lower the extent of heterozygosity in the region, resulting in an underestimate of genetic recombination and hence genetic distance. As iHS, XP-EHH and haploPS rely on the population-averaged genetic distance from HapMap to quantify haplotype lengths, regions that are positively selected in all the populations will not be successfully identified by any of these metrics. We thus re-perform the haploPS analyses using physical distance to quantify haplotype length instead of genetic distance. Here, we prioritize the loci that emerged with evidence of positive selection in at ten of the fourteen populations (i.e. more than 70% of the populations), and have not been previously identified with the haploPS analysis using genetic distance. As the purpose is to discover novel selection regions that would not have been detected by metrics that rely on genetic distance, we also excluded regions that have emerged from previous reports on positive selection with LRH/iHS or XP-EHH^{10,14-17}. Our analysis of positive selection with the use of physical distance identified two novel genomic regions that exhibited evidence of long haplotypes. The region on chromosome 1 spans between 171.8Mb and 173.2Mb, and the signal is found in 13 of the 14 populations (except TSI). The genes that are common to all 13 populations are the RAB GTPase-activating protein 1-like (*RABGAP1L*) and the G protein-coupled receptor 52 (*GPR52*). The second region is located on chromosome 16, spans between 45.1Mb and 46.0Mb, and the signal is found in 10 of the 14 populations (except CHS, LWK, MKK and YRI).

Table S4. Segregation of Positively Selected Pigmentation Genes across Global Populations

Population	<i>KITLG</i>	<i>SLC24A5</i>	<i>ADAM17</i>	<i>ADAMTS20</i>	<i>HERC2/OCA2</i>
CEU	X	X			X
TSI	X	X			X
MXL	X			X	X
GIH	X	X		X	
INS				X	
CHB	X		X	X	
CHD	X		X		
CHS	X		X		
JPT			X	X	
MAS	X				
ASW					
LWK					
MKK					
YRI					

Presence of haploPS positive selection signals at six skin pigmentation genes across the fourteen HapMap and SGVP populations. The pigmentation gene that is selected in a particular population is shown with an “X”. We surveyed six pigmentation genes that have been consistently identified by a variety of metrics for detecting positive selection in the ten non-African populations, and checked whether haploPS identified a selection signal in each of these genes for each of the populations. These genes are *KITLG*, *SLC24A5*, *ADAM17*, *ADAMTS20*, *OCA2* and *HERC2*. Under the assumption that haploPS is sufficiently sensitive to identify most of the positive selection signatures when they exist, we can evaluate whether certain pigmentation genes are selected only in some populations but not others. For example, haploPS identified selection signals at *ADAM17* in all four East Asian populations (CHB, CHD, CHS and JPT) but not the others, while *SLC24A5* was selected only in the Europeans (CEU, TSI) and Gujarati Indians (GIH). *HERC2* was selected only in the Europeans (CEU, TSI) and Mexicans (MXL). *KITLG* was selected in almost all the non-African populations except South Asian Indians (INS) and the Japanese (JPT). The distribution of the signal at *ADAMTS20* was less consistent, being selected in both Asian Indian populations (GIH, INS), a handful of East Asian populations (CHB, JPT), and the Mexicans (MXL).

Table S5. False Positive Rates (FPRs) of the Different LRH Methods for Detecting Positive Selection in Simulated Populations with Bottlenecks

Inbreeding coefficient	haploPS (1%)	iHS	XP-EHH
0.1	0%	43.7%	6.3%
0.2	1.2%	27.4%	7.1%
0.3	6.7%	16.8%	9.7%

To evaluate the effects of bottlenecks on haploPS, a range of simulations with different bottleneck intensities was performed. The simulation was performed using the program *cosi* (http://www.broadinstitute.org/~sfs/cosi/cosi_1.2.tar). The three population model is similar to the “cosi” demographic model, except there was no migration and the population size is kept constant at 10,000. A single bottleneck was introduced into the European population 1,950 generations before the split between Europe and Asia. We simulated 1,000 regions of 100kb for each bottleneck intensity setting. Three bottleneck intensities were employed with corresponding inbreeding coefficients of 0.1, 0.2 and 0.3. The same 2,000 null simulations for generating the null distribution of haploPS scores in the power simulations were used to identify the haploPS threshold for defining significance. The haploPS scores that corresponded to the bottom 1% of the score distribution in the 2,000 null simulations for Africa were used as the thresholds. In the simulations with bottlenecks, any region with a haploPS score below each of these thresholds will be considered a false positive finding. The false positive rate is defined as the proportion of the 1,000 simulated regions with a significant finding. The same approach of comparing against the null distributions of iHS and XP-EHH were used to generate the threshold for defining significance at the top 1% of the respective distributions.

References

1. Frazer, K.A. *et al.* A second generation human haplotype map of over 3.1 million SNPs. *Nature* 449, 851-61 (2007).
2. Stephens, M., Smith, N.J. & Donnelly, P. A new statistical method for haplotype reconstruction from population data. *Am J Hum Genet* 68, 978-89 (2001).
3. Marchini, J. *et al.* A comparison of phasing algorithms for trios and unrelated individuals. *Am J Hum Genet* 78, 437-50 (2006).
4. Altshuler, D.M. *et al.* Integrating common and rare genetic variation in diverse human populations. *Nature* 467, 52-8 (2010).
5. Howie, B.N., Donnelly, P. & Marchini, J. A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. *PLoS Genet* 5, e1000529 (2009).
6. Teo, Y.Y. *et al.* Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. *Genome Res* 19, 2154-62 (2009).
7. Scheet, P. & Stephens, M. A fast and flexible statistical model for large-scale population genotype data: applications to inferring missing genotypes and haplotypic phase. *Am J Hum Genet* 78, 629-44 (2006).
8. McVean, G.A. *et al.* The fine-scale structure of recombination rate variation in the human genome. *Science* 304, 581-4 (2004).
9. Jallow, M. *et al.* Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nat Genet* (2009).
10. Sabeti, P.C. *et al.* Positive natural selection in the human lineage. *Science* 312, 1614-20 (2006).
11. Clark, T.G. *et al.* Tumor necrosis factor and lymphotoxin-alpha polymorphisms and severe malaria in African populations. *J Infect Dis* 199, 569-75 (2009).
12. A global network for investigating the genomic epidemiology of malaria. *Nature* 456, 732-7 (2008).
13. Piel, F.B. *et al.* Global distribution of the sickle cell gene and geographical confirmation of the malaria hypothesis. *Nat Commun* 1, 104 (2010).
14. Sabeti, P.C. *et al.* Detecting recent positive selection in the human genome from haplotype structure. *Nature* 419, 832-7 (2002).
15. Voight, B.F., Kudravalli, S., Wen, X. & Pritchard, J.K. A map of recent positive selection in the human genome. *PLoS Biol* 4, e72 (2006).
16. Grossman, S.R. *et al.* A composite of multiple signals distinguishes causal variants in regions of positive selection. *Science* 327, 883-6 (2010).
17. Sabeti, P.C. *et al.* Genome-wide detection and characterization of positive selection in human populations. *Nature* 449, 913-8 (2007).