

Supplementary III: candidate regions & SNPs and maximum EHHST values of genome-wide scans of HapMap phase II data

In this supplementary, we presented 21 candidate regions and related SNPs in Tables 1 — 15 for natural selection. To select a candidate SNP, we used four selection criteria as follows: 1) the selected SNP had high EHHST value of top one percentile, i.e., the EHHST value of the SNP was in the top one percentile of all SNPs of a chromosome in which the SNP was located, 2) the selected SNP had an allele which was likely to be newly derived by using the data from <http://hgw-ucsc.edu/selection/frontpage.html> of the University of Chicago (Voight et al. 2006), 3) the derived allele of the selected SNP had a high frequency which was larger than 0.5 in the tested population, 4) the derived allele of the selected SNP was likely to be highly differentiated among the three populations of CHB+JPT, CEU, and YRI, in terms of the F_{st} score of the SNP was in the top one percentile of all F_{st} scores of SNPs on a chromosome. A candidate region was selected if there was a long list of SNPs which satisfied the selection criteria. In the 21 candidate regions, 3 were close to regions reported in Sabeti et al. (2007), and 12 were not reported; we counted these 15 regions as new candidates. The remaining 6 regions were within regions reported in Sabeti et al. (2007). The region containing the least number of SNPs satisfying the criteria (7 SNPs) was located on chromosome 10, and it was reported in Table 10 because it was close to one candidate chr10:22.7 of Sabeti et al. (2007). Other regions contained 9 to 69 SNPs which satisfied the criteria.

In the Tables 16 and 17, we provided the maximum EHHST values and related SNP information of the HapMap Phase II data of the three populations chromosome by chromosome. In the neighbor regions of these SNPs, there was usually stretch of extended haplotype homozygosity and this could be an indication of positive selection. For instance, the Asian sample (CHB+JPT) was reported to have strong selection signal in the region of 72.6Mb on chromosome 2 (Sabeti et al. 2007). We confirmed this finding by identifying two SNPs rs7594350 and rs1400582, which had highest EHHST value 30805.837 (Table 16). The SNPs and their neighbor regions reported in the Tables 16 and 17 could be useful for further investigation.

Based on the information of Tables 16 and 17, we then compared allele frequencies of the SNPs reported in the Tables. Since selected alleles were likely to be highly differentiated between populations, we further selected the SNPs whose allele frequency was significantly different among the three samples and then determined the selected population.

References

- Voight BF, Kudaravalli S, Wen X, Pritchard JK. 2006. A map of recent positive selection in the human genome. *PLoS Biol* 4:e72.

Table 1: Regions and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 1 and chromosome 2 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile. In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chrms, Tested Popu., Genes	SNP Name	Position	Derived Allele Frequency			F_{st}	Pct	EHHST	Pct of
			CEU	CHB+JPT	YRI	Value	of F_{st}	Value	EHHST
Chrms 1, CHB+JPT*, <i>LHX8</i> (75,367-75,400kb), <i>SLC44A5</i> (75,440-75,849kb)	rs11162498	75329244	0.2167	0.8278	0.1167	0.541	0.9925	94.979	0.995
	rs11162513	75339512	0.2167	0.8333	0.1167	0.548	0.9931	105.252	0.9955
	rs6671729	75342043	0.2167	0.8278	0.1167	0.541	0.9925	106.522	0.9955
	rs12402007	75343282	0.2	0.8333	0.1167	0.5582	0.994	109.398	0.9957
	rs1007512	75344267	0.225	0.8333	0.1167	0.5431	0.9927	109.894	0.9957
	rs17096272	75355512	0.2167	0.8333	0.1167	0.548	0.9931	113.956	0.996
	rs6663002	75360138	0.2167	0.8333	0.1167	0.548	0.9931	113.721	0.9959
	rs10493552	75364816	0.2	0.8333	0.1167	0.5582	0.994	113.624	0.9959
	rs1526505	75371488	0.1917	0.8333	0.1167	0.5635	0.9944	112.276	0.9958
	rs12041465	75381637	0.1833	0.8333	0.1167	0.5689	0.9947	109.809	0.9957
	rs1144297	75512920	0.375	0.8889	0.0833	0.578	0.9953	71.381	0.9929
	Chrms 2, CHB+JPT*	rs12614724	17200074	0.2667	0.9444	0.175	0.6209	0.9967	842.262
rs1396074		17202963	0.2667	0.9444	0.1833	0.6148	0.9964	858.499	0.9989
rs2135974		17203557	0.2667	0.9444	0.1833	0.6148	0.9964	810.547	0.9989
rs11096723		17203869	0.2833	0.9444	0.1833	0.6059	0.9958	724.421	0.9987
rs16983283		17217851	0.0333	0.7389	0.0833	0.6022	0.9955	156.695	0.9901
rs7560778		17218020	0.0333	0.7389	0.0833	0.6022	0.9955	159.508	0.9903
rs4832711		17218488	0.0333	0.7389	0.0833	0.6022	0.9955	176.744	0.9913
rs1948984		17219024	0.025	0.7389	0.0833	0.6102	0.9961	180.468	0.9915
rs4832712		17219866	0.0417	0.7389	0.0917	0.5875	0.9941	215.376	0.9935
rs925140		17226171	0.0917	0.9333	0.4	0.6219	0.9968	247.588	0.9944
rs287294		17235190	0.0833	0.7556	0.1083	0.5564	0.9909	263.261	0.9949
rs12710631		17237305	0.0917	0.9333	0.4417	0.6126	0.9962	272.712	0.9952
rs1507985		17240320	0.0917	0.9333	0.4417	0.6126	0.9962	280.998	0.9954
rs2063164		17241504	0.0917	0.9333	0.4417	0.6126	0.9962	287.446	0.9955
rs7563222		17242000	0.0917	0.9333	0.45	0.6111	0.9962	291.606	0.9956
rs1507977		17246940	0.1	0.9333	0.4917	0.5975	0.9951	295.282	0.9957
rs13010278		17247913	0.1	0.9333	0.65	0.6065	0.9958	292.05	0.9956
rs1589272		17253381	0.1333	0.9389	0.7167	0.5971	0.9951	329.658	0.9963
rs989555		17265872	0.0917	0.9333	0.45	0.6111	0.9962	209.21	0.9933

Table 2: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 2 of the HapMap Phase II data.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 2, CHB+JPT	rs9309464	72387471	0.7917	0.9944	0.0083	0.8361	1	1991.005	0.9996
	rs7595180	72389198	0.7833	0.9944	0.0083	0.832	1	2189.058	0.9996
	rs6752122	72399186	0.7917	0.9944	0.0167	0.8274	1	3118.113	0.9997
	rs7558919	72402403	0.7917	0.9944	0.075	0.7671	0.9997	4341.774	0.9998
	rs6546764	72406443	0.7917	0.9944	0.0667	0.7757	0.9997	5394.427	0.9998
	rs11126366	72407800	0.7917	0.9944	0.1583	0.681	0.9987	7102.119	0.9999
	rs2420444	72419965	0.7917	0.9944	0.0083	0.8361	1	17750.731	1
	rs7594350	72425722	0.7917	0.9944	0.0083	0.8361	1	30805.837	1
	rs7558686	72432297	0.7917	0.9944	0.0667	0.7757	0.9997	7115.398	0.9999
	rs13390754	72437629	0.7917	0.9944	0.075	0.7671	0.9997	3637.12	0.9998
	rs598496	72438429	0.7917	0.9944	0.075	0.7671	0.9997	3123.944	0.9997
	rs598138	72438483	0.7917	0.9944	0.0667	0.7757	0.9997	2737.124	0.9997
	rs680495	72445746	0.7917	0.9944	0.0167	0.8274	1	1568.588	0.9995
	rs590252	72461324	0.7917	0.9944	0.0667	0.7757	0.9997	1292.252	0.9993
	rs641939	72464683	0.7917	0.9944	0.0083	0.8361	1	1220.543	0.9992
	rs630241	72475478	0.7917	0.9944	0.0583	0.7843	0.9998	334.55	0.9963
	rs628432	72477120	0.7917	0.9944	0.0167	0.8274	1	360.481	0.9967
	rs659833	72496496	0.7917	0.9944	0.0083	0.8361	1	390.677	0.997
	rs3115351	72496883	0.7917	0.9944	0.05	0.793	0.9998	407.716	0.9972
	rs640610	72504445	0.7917	0.9944	0.0417	0.8016	0.9999	446.569	0.9976
	rs590345	72534217	0.6917	0.9944	0.15	0.6504	0.9978	666.602	0.9986
	rs647242	72536445	0.7083	0.9944	0.125	0.6807	0.9986	716.327	0.9987
	rs2203679	72542046	0.7083	0.9944	0.0833	0.7234	0.9993	1013.56	0.9991
	rs653220	72561382	0.7083	0.9944	0.0083	0.801	0.9999	3219.831	0.9997
	rs6714595	72565756	0.7083	0.9944	0.0083	0.801	0.9999	1919.837	0.9996
	rs11686713	72662046	0.7083	0.9944	0.0417	0.7664	0.9996	178.415	0.9914
	rs11677707	72732262	0.7083	0.9944	0.025	0.7837	0.9998	362.72	0.9967
	rs6724529	72734249	0.7083	0.9944	0.025	0.7837	0.9998	375.546	0.9969
	rs4852886	72736040	0.7083	0.9944	0.0917	0.7148	0.9992	388.213	0.997
	rs11685114	72749123	0.7083	0.9944	0.0083	0.801	0.9999	408.743	0.9973
	rs4852891	72798521	0.725	0.9944	0.0167	0.7983	0.9999	405.396	0.9972
	rs7588400	72830661	0.725	0.9944	0.0167	0.7983	0.9999	306.541	0.9959
rs970577	72859087	0.8	0.9389	0.2	0.5623	0.9917	225.758	0.9938	
rs1876490	72905859	0.6833	0.9333	0.0167	0.7049	0.999	1588.944	0.9995	

Table 3: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 2 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 2, CHB+JPT*	rs1514999	103484100	0.475	0.9333	0.1	0.5993	0.9953	164.562	0.9907
	rs7595711	103519644	0.475	0.9333	0.1	0.5993	0.9953	588.34	0.9983
	rs6734144	103521977	0.475	0.9333	0.1	0.5993	0.9953	626.421	0.9985
	rs4851029	103526217	0.45	0.9333	0.1167	0.5873	0.9941	639.747	0.9985
	rs6721892	103529619	0.4583	0.9444	0.125	0.5933	0.9948	640.805	0.9985
	rs1983305	103530871	0.4583	0.9444	0.125	0.5933	0.9948	601.374	0.9984
	rs4851031	103531382	0.4583	0.9444	0.125	0.5933	0.9948	576.552	0.9983
	rs1451974	103540096	0.4583	0.9444	0.1333	0.5856	0.9939	363.404	0.9967
	rs7580027	103544809	0.4583	0.9389	0.125	0.5856	0.9939	269.354	0.9951
	rs6543217	103549697	0.4583	0.9444	0.125	0.5933	0.9948	261.158	0.9948
	rs6543218	103549969	0.4583	0.9444	0.125	0.5933	0.9948	251.652	0.9945
	rs13411937	103553084	0.4583	0.9444	0.125	0.5933	0.9948	234.368	0.9941
	rs7565635	103558332	0.4583	0.9444	0.1417	0.5779	0.9931	187.937	0.9919
	rs6738539	103562187	0.4583	0.9444	0.1417	0.5779	0.9931	172.925	0.9911
	rs7591265	103562871	0.4583	0.9444	0.125	0.5933	0.9948	168.412	0.9909
	rs6727525	103569144	0.4583	0.9444	0.125	0.5933	0.9948	275.921	0.9953
	rs1869073	103570952	0.4583	0.9444	0.1417	0.5779	0.9931	327.638	0.9962
	rs10188273	103575435	0.3917	0.9444	0.125	0.6091	0.996	384.636	0.997
	rs4851660	103584221	0.4583	0.9444	0.1417	0.5779	0.9931	441.44	0.9976
	rs10189533	103585672	0.4583	0.9444	0.1333	0.5856	0.9939	488.319	0.9979
	rs10192716	103586576	0.4583	0.9444	0.125	0.5933	0.9948	546.241	0.9982
	rs1451988	103589021	0.4583	0.9444	0.125	0.5933	0.9948	659.861	0.9986
	rs6543223	103594301	0.4583	0.9444	0.125	0.5933	0.9948	886.581	0.9989
	rs13396809	103595295	0.4667	0.9444	0.125	0.5919	0.9945	1067.541	0.9991
	rs7570362	103597727	0.4583	0.9444	0.125	0.5933	0.9948	1283.435	0.9993
	rs12328095	103603254	0.4583	0.9389	0.1417	0.5702	0.9923	1526.657	0.9994
	rs6719978	103604933	0.4583	0.9444	0.1333	0.5856	0.9939	1379.914	0.9994
	rs1584705	103606168	0.4583	0.9444	0.1417	0.5779	0.9931	1286.076	0.9993
	rs11123965	103606637	0.4583	0.9444	0.125	0.5933	0.9948	1188.888	0.9992
	rs11888473	103606852	0.4583	0.9444	0.1417	0.5779	0.9931	1091.811	0.9992

Table 4: Regions and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 2 and chromosome 3 of the HapMap Phase II data. * marked new regions; **abbreviations**: Chrms — Chromosome, Popu. — Population, Pct — percentile. In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 2, CHB+JPT <i>LIMS1</i> (108,571-108,670kb)	rs10179602	108451805	0.3833	0.8722	0.025	0.6124	0.9962	290.676	0.9956
	rs1053027	108457987	0.3833	0.8778	0.0917	0.5534	0.9905	349.171	0.9965
	rs2077472	108492518	0.3833	0.8944	0.1	0.567	0.9921	380.171	0.9969
	rs12613554	108527107	0.3917	0.8722	0.0167	0.619	0.9966	651.248	0.9985
	rs12473539	108531804	0.3917	0.8722	0.0833	0.552	0.9903	696.403	0.9987
	rs1469965	108536852	0.3917	0.8722	0.0833	0.552	0.9903	536.393	0.9981
	rs10179040	108552213	0.3917	0.8722	0.0833	0.552	0.9903	529.817	0.9981
	rs11123708	108562291	0.3917	0.8722	0.0833	0.552	0.9903	471.995	0.9978
	rs10187016	108563195	0.3833	0.8778	0.0833	0.5613	0.9915	461.466	0.9977
	rs13413437	108564962	0.3917	0.8722	0.0833	0.552	0.9903	427.252	0.9974
	rs13422997	108572896	0.3917	0.8722	0.0833	0.552	0.9903	195.172	0.9923
	rs7565372	108587342	0.3917	0.8722	0.0833	0.552	0.9903	200.544	0.9927
	rs6707379	108600999	0.3917	0.8722	0.075	0.5601	0.9914	199.593	0.9926
	rs12469016	108622967	0.3917	0.8722	0.075	0.5601	0.9914	500.032	0.9979
	Chrms, 3 CHB+JPT*	rs9827968	106178646	0.425	0.8556	0.0667	0.5404	0.9915	119.307
rs1503079		106241722	0.4917	0.9278	0.1333	0.5577	0.9933	230.958	0.9976
rs1566718		106244327	0.4917	0.9278	0.1417	0.5497	0.9926	226.533	0.9975
rs1566717		106250199	0.4917	0.9278	0.1417	0.5497	0.9925	203.063	0.9968
rs13090983		106250823	0.4917	0.9278	0.1417	0.5497	0.9926	193.69	0.9967
rs12633740		106252196	0.4917	0.9278	0.1417	0.5497	0.9926	175.793	0.9962
rs12637494		106256655	0.4917	0.9278	0.1417	0.5497	0.9925	162.694	0.9956
rs10933802		106256994	0.4917	0.9278	0.1417	0.5497	0.9925	155.645	0.9952
rs10933803		106257871	0.4917	0.9278	0.05	0.6401	0.9981	145.816	0.9947
rs2047806		106261500	0.525	0.9778	0.15	0.6091	0.9965	122.116	0.9933
rs2134526		106262934	0.4917	0.9278	0.1417	0.5497	0.9925	114.486	0.9927
rs6800325		106265702	0.5417	0.9778	0.1417	0.6161	0.9969	1473.75	0.9999
rs10933807		106267020	0.4917	0.9278	0.1417	0.5497	0.9925	1006.902	0.9997
rs2895296		106271452	0.4917	0.9278	0.1167	0.5737	0.9946	571.559	0.9993
rs1503084		106274502	0.4917	0.9278	0.1167	0.5737	0.9946	96.787	0.9912
rs10933809		106283040	0.4917	0.9278	0.1167	0.5737	0.9946	121.231	0.9932
rs1503085		106284786	0.4917	0.9278	0.1167	0.5737	0.9946	125.271	0.9934
rs1503075		106289543	0.4167	0.9056	0.0667	0.6051	0.9963	156.038	0.9953
rs1503158		106297795	0.3917	0.9056	0.0667	0.611	0.9966	167.596	0.9958
rs12492439		106299176	0.4	0.9056	0.0333	0.6418	0.9982	175.354	0.9962
rs870279		106305849	0.4	0.8889	0.075	0.5793	0.9951	174.778	0.9962
rs12492301		106306013	0.4	0.8889	0.0667	0.5874	0.9956	177.173	0.9963

Table 5: Two regions and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 4 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile. # marked region which was close to a candidate region found in Table 1, Sabeti et al. (2007).

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 4, CEU	rs10002222	33667869	0.9	0.6778	0.025	0.5912	0.9942	89.357	0.9941
	rs12645236	33691462	0.8667	0.6833	0.025	0.5671	0.9924	98.49	0.9948
	rs6821548	33706776	0.9	0.6833	0.025	0.594	0.9944	129.362	0.9965
	rs7665973	34073859	0.8917	0.9833	0.3333	0.5464	0.9905	259.032	0.999
	rs10031884	34074934	0.8833	0.9833	0.2417	0.6353	0.997	278.189	0.9991
	rs6830615	34077763	0.8833	0.9833	0.3083	0.566	0.9923	285.51	0.9992
	rs1364911	34078305	0.8833	0.9833	0.2167	0.6612	0.9981	290.995	0.9992
	rs6817183	34174660	0.8333	0.8167	0.025	0.64	0.9973	70.715	0.9917
	rs1842531	34179397	0.8333	0.8111	0.025	0.635	0.997	71.55	0.9918
	rs6847787	34183722	0.9333	0.8278	0.1333	0.6037	0.9949	75.518	0.9927
	rs6812860	34185807	0.975	0.9722	0.1417	0.8008	1	76.661	0.9929
	rs10033586	34190319	0.9	0.8167	0.125	0.5752	0.993	75.174	0.9926
	rs4859322	34198313	0.8333	0.8111	0.025	0.635	0.997	72.822	0.9921
rs4859283	34203697	0.8333	0.8111	0.025	0.635	0.997	72.773	0.9921	
Chrms 4, CHB+JPT*,#	rs714226	41521093	0.9333	0.9944	0.2417	0.6948	0.9988	58.06	0.994
	rs6840961	41522632	0.8417	0.9833	0.225	0.6237	0.9962	57.797	0.994
	rs9991121	41523790	0.85	0.9778	0.125	0.7251	0.9993	54.141	0.9934
	rs4623048	41528244	0.7583	0.9611	0.0167	0.7677	0.9999	53.418	0.9931
	rs9998239	41529367	0.9083	0.9722	0.2083	0.6728	0.9983	52.918	0.993
	rs6839376	41544538	0.8	0.9611	0.1	0.699	0.999	50.703	0.9925
	rs6447118	41550330	0.8	0.9611	0.1	0.699	0.999	49.738	0.9922
	rs7356183	41554214	0.8083	0.9611	0.1	0.7035	0.9991	49.412	0.9921
	rs7660832	41584424	0.7833	0.9611	0.2417	0.5411	0.99	45.336	0.9907
	rs2660335	41680446	0.7583	0.9667	0.0917	0.6951	0.9989	316.06	0.9991
	rs2581435	41685047	0.7583	0.9667	0.0917	0.6951	0.9989	367.83	0.9993
	rs4540084	41696545	0.7583	0.9667	0.0917	0.6951	0.9989	403.192	0.9994
	rs2660331	41696942	0.7583	0.9667	0.0917	0.6951	0.9989	415.118	0.9994
	rs2581455	41697890	0.7333	0.9667	0.0583	0.7201	0.9993	442.977	0.9994
	rs2660330	41698140	0.7667	0.9667	0.0917	0.6989	0.9989	470.647	0.9995
	rs1047626	41698428	0.7333	0.9667	0.0583	0.7201	0.9993	484.84	0.9995
	rs2581453	41698592	0.7583	0.9722	0.0917	0.7027	0.999	500.064	0.9995
	rs2660329	41700744	0.7583	0.9667	0.15	0.6336	0.9969	528.134	0.9995
	rs2660326	41701828	0.7583	0.9667	0.15	0.6336	0.9968	567.847	0.9996
	rs2660325	41701960	0.7583	0.9667	0.15	0.6336	0.9969	579.248	0.9996
	rs2581449	41701981	0.7583	0.9667	0.15	0.6336	0.9969	589.284	0.9996
	rs2581448	41702151	0.7583	0.9667	0.15	0.6336	0.9969	604.229	0.9996
	rs2660323	41702769	0.7583	0.9667	0.15	0.6336	0.9969	613.77	0.9996
	rs9884564	41703000	0.7333	0.9722	0.0333	0.754	0.9997	714.736	0.9997
	rs2581443	41703898	0.7583	0.9667	0.15	0.6336	0.9969	721.93	0.9998
	rs2660319	41705641	0.7333	0.9667	0.1	0.676	0.9985	719.208	0.9998
	rs2581441	41706727	0.7333	0.9667	0.0333	0.7467	0.9996	704.512	0.9997
	rs2581426	41712257	0.7333	0.9667	0.0333	0.7467	0.9996	664.02	0.9997
	rs2581424	41713389	0.7583	0.9667	0.15	0.6336	0.9969	630.272	0.9997

Table 6: Continuation of Table 5. In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 4, CHB+JPT <i>CCDC4</i> (41,808-41,850kb), <i>TMEM33</i> (41,632-41,653kb) <i>WDR21B</i> (41,679-41,680kb)	rs1848180	41713701	0.7333	0.9667	0.0333	0.7467	0.9996	612.026	0.9996
	rs10805092	41714239	0.7583	0.9667	0.15	0.6336	0.9968	593.444	0.9996
	rs2581420	41716994	0.7583	0.9667	0.15	0.6336	0.9968	525.486	0.9995
	rs10461065	41719050	0.7583	0.9667	0.15	0.6336	0.9969	477.692	0.9995
	rs10461059	41720699	0.7583	0.9667	0.15	0.6336	0.9968	421.18	0.9994
	rs9998823	41720912	0.7583	0.9722	0.15	0.6415	0.9973	408.751	0.9994
	rs4241695	41722202	0.7583	0.9667	0.15	0.6336	0.9969	396.399	0.9994
	rs9654067	41723554	0.7583	0.9667	0.15	0.6336	0.9968	373.813	0.9993
	rs3827588	41725973	0.7583	0.9667	0.15	0.6336	0.9968	343.577	0.9992
	rs3827590	41726194	0.7083	0.9722	0.15	0.6228	0.9961	334.513	0.9992
	rs3827591	41726229	0.7083	0.9667	0.15	0.6149	0.9957	325.588	0.9992
	rs4861155	41726781	0.7333	0.9667	0.0333	0.7467	0.9996	309.138	0.9991
	rs7683204	41728350	0.7583	0.9667	0.15	0.6336	0.9968	294.067	0.9991
	rs11725865	41731391	0.7667	0.9667	0.1417	0.646	0.9975	273.82	0.999
	rs10006383	41733603	0.7667	0.9667	0.1417	0.646	0.9976	43.632	0.9901
	rs12507609	41736854	0.7667	0.9667	0.15	0.6373	0.9972	44.266	0.9904
	rs4377621	41738061	0.7083	0.9667	0.0333	0.7375	0.9994	44.915	0.9906
	rs10433708	41745215	0.7667	0.9667	0.1417	0.646	0.9976	45.227	0.9907
	rs10938170	41750639	0.7667	0.9667	0.1417	0.646	0.9976	47.358	0.9914
	rs3804192	41761196	0.7667	0.9667	0.1417	0.646	0.9976	49.648	0.9922
	rs12647092	41766976	0.7083	0.9667	0.0333	0.7375	0.9994	59.678	0.9943
	rs10019356	41768229	0.7667	0.9667	0.15	0.6373	0.9972	60.754	0.9946
	rs4438791	41769322	0.7083	0.9667	0.0333	0.7375	0.9994	61.825	0.9947
	rs7660223	41775871	0.7667	0.9667	0.1	0.69	0.9988	71.182	0.9957
	rs11725543	41781944	0.7667	0.9667	0.1417	0.646	0.9975	73.344	0.9959
	rs10002107	41782303	0.7667	0.9667	0.1417	0.646	0.9975	74.775	0.996
	rs12511999	41786014	0.7083	0.9667	0.0333	0.7375	0.9994	76.895	0.9962
	rs6832890	41801295	0.7583	0.9667	0.0833	0.704	0.9991	83.865	0.9966
	rs6447128	41801872	0.75	0.9778	0.0833	0.7156	0.9992	86.149	0.9968
	rs7682049	41807491	0.675	0.95	0.0167	0.7234	0.9993	89.61	0.997
rs13756	41807998	0.675	0.95	0.0167	0.7234	0.9993	90.879	0.9971	
rs16854014	41812231	0.9333	0.9833	0.3667	0.5479	0.9907	100.079	0.9976	
rs2880666	41815266	0.675	0.95	0.0167	0.7234	0.9993	98.591	0.9975	
rs6447131	41824754	0.675	0.9556	0.05	0.6949	0.9988	101.828	0.9977	
rs6447132	41828823	0.6583	0.9556	0.0583	0.6817	0.9986	101.778	0.9977	
rs7664565	41829776	0.6667	0.9556	0.0583	0.6838	0.9987	101.689	0.9977	
rs6848386	41841414	0.675	0.9556	0.15	0.59	0.9941	101.398	0.9977	
rs6856819	41844970	0.6917	0.9556	0.2	0.543	0.9903	99.008	0.9975	
rs4861024	41847307	0.6917	0.9556	0.15	0.5944	0.9944	98.502	0.997	
rs4449446	41849931	0.6833	0.95	0.1583	0.5758	0.9931	96.958	0.997	

Table 7: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 5 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 5, CHB+JPT*	rs397317	117006587	0.6583	0.9722	0.025	0.7391	0.9996	92.618	0.9948
	rs267035	117010380	0.6583	0.9722	0.025	0.7391	0.9996	112.143	0.9964
	rs267033	117010655	0.6583	0.9722	0.025	0.7391	0.9996	107.01	0.996
	rs267030	117011477	0.6583	0.9722	0.025	0.7391	0.9996	119.091	0.9969
	rs192378	117011538	0.6583	0.9722	0.025	0.7391	0.9996	121.734	0.997
	rs197864	117014844	0.6583	0.9722	0.025	0.7391	0.9996	126.235	0.9971
	rs842002	117023413	0.6583	0.9722	0.025	0.7391	0.9996	92.058	0.9948
	rs842003	117023684	0.6583	0.9722	0.025	0.7391	0.9996	93.725	0.9949
	rs1686409	117030985	0.6583	0.9722	0.025	0.7391	0.9996	96.408	0.9952
	rs1686410	117030996	0.6583	0.9722	0.025	0.7391	0.9996	94.739	0.995
	rs10036241	117033421	0.7083	0.9667	0.15	0.6149	0.9968	87.005	0.9943
	rs2416472	117033845	0.6917	0.9667	0.0417	0.7233	0.9992	84.739	0.9941
	rs7714451	117037818	0.8333	0.9667	0.175	0.6463	0.9979	75.177	0.9927
	rs7724328	117515965	0.4083	0.9778	0.0917	0.6812	0.9988	773.232	0.9998
	rs4317366	117516317	0.4083	0.9778	0.0167	0.7513	0.9996	713.005	0.9998
	rs6872244	117517311	0.4083	0.9667	0.0167	0.7364	0.9993	644.77	0.9997
	rs1479207	117520698	0.4083	0.9778	0.0167	0.7513	0.9996	97.216	0.9953
	rs10079352	117522539	0.4083	0.9778	0.0167	0.7513	0.9996	103.815	0.9958
	rs4639272	117524321	0.4167	0.9778	0.1167	0.6568	0.9982	109.814	0.9963
	rs4401605	117524359	0.4167	0.9778	0.0167	0.7496	0.9996	110.889	0.9963
	rs7721999	117524545	0.425	0.9778	0.0167	0.7481	0.9996	111.909	0.9964
	rs2900117	117525764	0.5	0.9778	0.0333	0.7231	0.9992	116.02	0.9967
	rs734155	117531602	0.4917	0.9778	0.15	0.6125	0.9967	161.408	0.998
	rs13356156	117533769	0.4583	0.9778	0.0583	0.7027	0.999	164.766	0.9981
	rs1479196	117534564	0.4583	0.9778	0.0583	0.7027	0.999	168.118	0.9981
	rs1382721	117543368	0.5	0.9778	0.05	0.7066	0.999	187.399	0.9984
	rs1382720	117547386	0.4583	0.9778	0.05	0.7107	0.9991	199.031	0.9987
	rs6883098	117588162	0.5	0.9778	0.2167	0.5522	0.9925	192.883	0.9985
	rs1479225	117588467	0.5	0.9778	0.2083	0.5594	0.9935	192.319	0.9985
	rs6859099	117590938	0.475	0.9722	0.2167	0.5486	0.9922	187.462	0.9985
	rs1871367	117599244	0.4167	0.9667	0.0167	0.7347	0.9993	169.643	0.9982
	rs7341174	117620240	0.5833	0.9667	0.2167	0.5287	0.99	139.264	0.9974

Table 8: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 7 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 7, CEU*	rs7789561	119168428	0.7667	0.9611	0.1083	0.6736	0.9987	82.129	0.9962
	rs11978043	119170356	0.7667	0.9611	0.1083	0.6736	0.9987	85.747	0.9965
	rs1404083	119187663	0.7667	0.9611	0.1083	0.6736	0.9987	96.623	0.9973
	rs12706259	119197681	0.7667	0.9556	0.1083	0.6661	0.9984	90.741	0.9968
	rs13239182	119212898	0.7667	0.9611	0.0667	0.718	0.9995	90.151	0.9967
	rs12536246	119216218	0.7667	0.9611	0.0667	0.718	0.9995	89.162	0.9967
	rs6466713	119221432	0.7667	0.9611	0.1083	0.6736	0.9987	82.437	0.9963
	rs940412	119228681	0.7667	0.9611	0.1083	0.6736	0.9987	2036.208	1
	rs1916859	119230892	0.7667	0.9611	0.1083	0.6736	0.9987	920.089	0.9999

Table 9: Two regions and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 8 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile. In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 8, CEU*	rs6989187	50635491	0.8417	0.8667	0.1333	0.5726	0.9947	172.591	0.9949
	rs9643617	50652967	0.8417	0.8667	0.125	0.5819	0.9953	211.534	0.9965
	rs9643406	50670255	0.8417	0.8667	0.125	0.5819	0.9953	283.27	0.9984
	rs6992847	50671501	0.8417	0.8667	0.125	0.5819	0.9953	322.309	0.9989
	rs1352112	50935021	0.8417	0.8667	0.1667	0.5359	0.9909	119.764	0.9903
	rs9886451	50935477	0.8417	0.8667	0.1667	0.5359	0.9909	122.549	0.9906
	rs1552372	50935855	0.8417	0.8667	0.1667	0.5359	0.9909	125.42	0.9909
	rs9298228	50937171	0.8417	0.8667	0.1167	0.5911	0.9959	128.378	0.9912
	rs9298229	50937251	0.8417	0.8667	0.1667	0.5359	0.9909	131.424	0.9915
	rs10089399	50938876	0.8333	0.8667	0.1667	0.5305	0.9901	137.789	0.992
	rs10092384	50939034	0.8417	0.8667	0.1667	0.5359	0.9909	141.128	0.9923
	rs11785147	50940355	0.8417	0.8667	0.1667	0.5359	0.9909	152.275	0.9934
	rs13251355	50943725	0.9833	0.8667	0.2583	0.555	0.9935	173.889	0.9949
	Chrms 8, CEU* <i>PCMTD1</i> (52,893-52,936kb)	rs10464943	52876153	0.9083	0.5722	0.05	0.5327	0.9905	655.337
rs756484		52877010	0.9083	0.5722	0.0417	0.5417	0.9921	651.099	0.9998
rs10958298		52882635	0.9083	0.5722	0.0417	0.5417	0.9921	216.268	0.9967
rs13275235		52887958	0.9083	0.5722	0.0417	0.5417	0.9918	282.938	0.9984
rs4873608		52890882	0.9083	0.5722	0.0417	0.5417	0.9918	290.769	0.9984
rs13257067		52898125	0.9083	0.5722	0.0417	0.5417	0.9918	312.322	0.9988
rs753539		52904315	0.9083	0.5722	0.0417	0.5417	0.9921	329.594	0.9989
rs10504128		52911112	0.9083	0.5722	0.0417	0.5417	0.9918	467.469	0.9995
rs5002416		52913710	0.9083	0.5722	0.0417	0.5417	0.9921	419.255	0.9993
rs9298463		52915555	0.9083	0.5722	0.0417	0.5417	0.9921	600.776	0.9998
rs4259408		52921282	0.9083	0.5722	0.0417	0.5417	0.9918	303.701	0.9986
rs11784921		52922009	0.9083	0.5722	0.05	0.5327	0.9905	304.451	0.9987
rs11777885		52922275	0.9083	0.5722	0.0417	0.5417	0.9918	297.022	0.9985
rs6986984		52923371	0.9083	0.4444	0.0333	0.5439	0.9924	286.575	0.9984
rs10096943		52923543	0.9083	0.5722	0.0417	0.5417	0.9918	274.069	0.9983
rs4584139		52926708	0.9083	0.5722	0.0417	0.5417	0.9918	258.376	0.9981

Table 10: Three regions and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 10 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile. # marked region which was close to a candidate region found in Table 1, Sabeti et al. (2007). In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 10, CEU	rs10903907	3024509	0.9417	0.9222	0.1333	0.712	0.9994	123.177	0.9951
	rs12782126	3026072	0.9333	0.9667	0.2333	0.66	0.9985	123.316	0.9951
	rs11251627	3028967	0.9083	0.9333	0.0833	0.7515	0.9998	122.611	0.995
	rs10794981	3031809	0.9083	0.9333	0.2583	0.5649	0.9929	110.887	0.9942
	rs7911099	3034806	0.9083	0.9444	0.2	0.6421	0.9979	101.682	0.9937
	rs7914892	3035244	0.9083	0.9333	0.2	0.6272	0.9973	98.094	0.9934
	rs10903915	3035615	0.9083	0.95	0.2	0.6497	0.9981	83.167	0.9915
	rs11251634	3036588	0.9083	0.9333	0.0583	0.778	0.9999	80.906	0.9911
	rs10794985	3037529	0.9083	0.9333	0.225	0.6005	0.9955	78.628	0.9907
	rs10903916	3037704	0.9	0.9333	0.2	0.6205	0.9969	76.557	0.9904
Chrms 10, CEU*,#	rs12262786	23929695	0.8167	0.9389	0.1917	0.5804	0.9942	349.148	0.999
	rs7919210	23934980	0.825	0.9389	0.225	0.5496	0.9914	251.366	0.9983
	rs2050610	23935872	0.8167	0.9333	0.1917	0.573	0.9936	205.902	0.9978
	rs6482309	23942942	0.8583	0.9389	0.1833	0.6152	0.9966	100.332	0.9936
	rs7100887	23943388	0.8417	0.9389	0.1833	0.6043	0.9958	112.922	0.9943
	rs1415423	23945789	0.8583	0.9389	0.1833	0.6152	0.9965	119.354	0.9947
	rs1415421	23945921	0.8583	0.9389	0.1917	0.6063	0.996	131.722	0.9954
	Chrms 10, CHB+JPT <i>PCDH15</i> (55,233-56,231kb)	rs10825242	55554795	0.2333	0.9167	0.1833	0.5955	0.9951	98.568
rs12218327		55561007	0.225	0.9	0.125	0.6222	0.997	93.558	0.9954
rs9787578		55561682	0.325	0.9444	0.2167	0.5606	0.9925	93.514	0.9954
rs9787465		55562067	0.225	0.9056	0.2167	0.5626	0.9927	91.449	0.9953
rs4447073		55568150	0.325	0.9444	0.2167	0.5606	0.9925	85.253	0.995
rs11004104		55588365	0.2333	0.9444	0.1333	0.6706	0.9987	78.291	0.994
rs11004105		55589349	0.2333	0.9444	0.125	0.6771	0.9989	75.405	0.9935
rs4636568		55590392	0.2333	0.9444	0.1333	0.6706	0.9987	73.598	0.9932
rs11004106		55591311	0.2333	0.9444	0.1333	0.6706	0.9987	72.372	0.9929
rs11004107		55591322	0.225	0.9167	0.1083	0.6576	0.9984	67.084	0.9918
rs10763079		55605400	0.6917	0.9889	0.2417	0.5507	0.9914	64.178	0.9911
rs4935502		55625450	0.1583	0.8944	0.1667	0.6269	0.9973	121.242	0.9969
rs10825275		55640296	0.9417	0.9944	0.3167	0.6264	0.9973	225.536	0.9996
rs7093540		55641050	0.3417	0.9	0.1333	0.5585	0.9922	224.442	0.9996
rs11004141		55641433	0.1583	0.8667	0.1	0.6411	0.9978	223.228	0.9996
rs4935104		55646474	0.15	0.8556	0.1833	0.5711	0.9934	209.818	0.9994
rs1970519		55790948	0.225	0.8667	0.075	0.621	0.9969	157.962	0.9983
rs2028440		55796208	0.2333	0.8722	0.075	0.6235	0.997	137.462	0.9976
rs11004267		55806859	0.2417	0.8667	0.0417	0.6424	0.9979	81.592	0.9944
rs11004270		55817364	0.225	0.8667	0.0417	0.6511	0.9982	78.882	0.9941
rs11004275		55822846	0.2333	0.8667	0.0917	0.6018	0.9956	72.757	0.993
rs10825320		55826240	0.8583	0.9722	0.2583	0.5829	0.9944	72.754	0.993
rs2050998		55827170	0.8583	0.9722	0.2583	0.5829	0.9944	72.41	0.9929
rs2050999		55827214	0.2333	0.8667	0.0917	0.6018	0.9956	70.715	0.9927
rs9943342		55832701	0.2333	0.8667	0.0917	0.6018	0.9956	68.106	0.9921
rs2795918		55847021	0.325	0.9222	0.1167	0.6094	0.9962	65.802	0.9915
rs1219862		55860311	0.325	0.9222	0.0917	0.6313	0.9975	82.791	0.9945

Table 11: Two regions and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 11 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st}	Pct	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI	Value	of F_{st}		
Chrms 11, CHB+JPT*	rs821006	38066457	0.975	0.95	0.3417	0.5633	0.9944	74.432	0.9934
	rs821011	38082143	0.9833	0.95	0.3583	0.5551	0.9935	71.546	0.9929
	rs820905	38137367	0.9833	0.9611	0.3167	0.6152	0.9972	147.722	0.9983
	rs898911	38154147	0.9833	0.9611	0.3083	0.6238	0.998	98.601	0.9961
	rs10742415	38164195	0.9833	0.9833	0.3583	0.6092	0.9971	114.962	0.9974
	rs1381587	38165693	0.9833	0.9833	0.3667	0.6007	0.9968	114.432	0.9973
	rs6484977	38168478	0.9833	0.9833	0.3667	0.6007	0.9967	113.742	0.9973
	rs4755483	38176296	0.9833	0.9833	0.3667	0.6007	0.9967	112.905	0.9973
	rs4756422	38179004	0.9833	0.9833	0.3583	0.6092	0.9971	93.202	0.9955
	rs10836939	38180677	0.9833	0.9833	0.3583	0.6092	0.9971	93.267	0.9955
	rs10768362	38182171	0.9833	0.9833	0.3667	0.6007	0.9967	93.162	0.9955
	rs4756423	38182413	0.9833	0.9833	0.4167	0.5496	0.9929	92.888	0.9954
	rs10836940	38195060	0.9833	0.9833	0.35	0.6176	0.9977	83.28	0.9947
	rs1462245	38242568	0.9917	0.9833	0.4333	0.5428	0.9923	535.322	0.9997
	rs2045737	38263161	0.9833	0.8389	0.1917	0.5978	0.9966	58.564	0.9902
Chrms 11, CEU*	rs10742415	38164195	0.9833	0.9833	0.3583	0.6092	0.9971	89.663	0.9933
	rs1381587	38165693	0.9833	0.9833	0.3667	0.6007	0.9968	97.501	0.9946
	rs6484977	38168478	0.9833	0.9833	0.3667	0.6007	0.9967	108.643	0.9958
	rs4755483	38176296	0.9833	0.9833	0.3667	0.6007	0.9967	119.824	0.9965
	rs4756422	38179004	0.9833	0.9833	0.3583	0.6092	0.9971	117.061	0.9964
	rs10836939	38180677	0.9833	0.9833	0.3583	0.6092	0.9971	122.364	0.9966
	rs10768362	38182171	0.9833	0.9833	0.3667	0.6007	0.9967	123.988	0.9967
	rs4756423	38182413	0.9833	0.9833	0.4167	0.5496	0.9929	124.806	0.9967
	rs10836940	38195060	0.9833	0.9833	0.35	0.6176	0.9977	161.221	0.9977
	rs1462245	38242568	0.9917	0.9833	0.4333	0.5428	0.9923	90.075	0.9935
	rs1585555	38244083	0.9917	0.9833	0.4333	0.5428	0.9923	90.794	0.9937
	rs1599564	38244690	0.9917	0.9833	0.4333	0.5428	0.9922	90.319	0.9935
	rs2045737	38263161	0.9833	0.8389	0.1917	0.5978	0.9966	86.314	0.9927
	rs11034713	38391328	0.6667	0.0556	0.0333	0.555	0.9935	469.665	0.9995
	rs12786969	38395092	0.6667	0.0444	0.0083	0.5989	0.9966	418.25	0.9994
rs1435156	38448731	0.6833	0.0611	0.0083	0.5914	0.9963	86.225	0.9927	

Table 12: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 12 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile. In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 12, CHB+JPT* <i>TMEM117</i> (42,516-43,070kb)	rs2407788	42674621	0.875	0.8611	0.1833	0.5348	0.9907	44.893	0.9961
	rs842199	42743839	0.8167	0.8722	0.1583	0.5355	0.9908	38.057	0.9942
	rs7971340	42762284	0.9167	0.9833	0.3	0.6018	0.9961	44.539	0.996
	rs2638853	42763366	0.9167	0.8556	0.1333	0.6163	0.9971	41.135	0.9951
	rs17121310	42771080	0.9167	0.8556	0.2	0.5437	0.9918	41.819	0.9953
	rs1352935	42771425	0.9083	0.9556	0.3	0.5519	0.9924	45.644	0.9963
	rs7967957	42775258	0.9167	0.9556	0.2667	0.5941	0.9957	46.17	0.9964
	rs6582498	42782123	0.9167	0.9556	0.3	0.5589	0.993	47.269	0.9968
	rs17094092	42794527	0.9167	0.8556	0.2	0.5437	0.9918	46.661	0.9966
	rs12315961	42796636	0.9167	0.9556	0.275	0.5853	0.9953	50.398	0.9975
	rs11182423	42807802	0.9167	0.8556	0.1917	0.5527	0.9924	45.747	0.9963
	rs1643429	42879128	0.9167	0.8556	0.125	0.6254	0.9975	42.564	0.9955

Table 13: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 13 of the HapMap Phase II data. * marked new regions; **abbreviations:** Chrms — Chromosome, Popu. — Population, Pct — percentile.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 13, CHB+JPT*	rs4310736	63174790	0.825	0.9389	0.2583	0.5142	0.9907	41.525	0.99
	rs9539851	63177581	0.825	0.9389	0.2583	0.5142	0.9907	42.741	0.9906
	rs9539854	63181695	0.8333	0.9944	0.3417	0.5161	0.9909	45.613	0.9915
	rs9539855	63182064	0.8333	0.9944	0.3417	0.5161	0.9909	45.705	0.9915
	rs11843593	63185384	0.8333	0.9889	0.2833	0.5668	0.9946	45.658	0.9915
	rs9571012	63201277	0.9833	0.9444	0.2417	0.6679	0.9983	44.623	0.9912
	rs7985049	63203415	0.9917	0.9333	0.2833	0.6182	0.9973	45.249	0.9914
	rs4363749	63205262	0.9917	0.9333	0.2667	0.6354	0.9977	45.043	0.9913
	rs2807121	63286791	0.825	0.9333	0.2417	0.5244	0.9916	47.596	0.9919
	rs536914	63320940	0.9833	0.9333	0.2667	0.6265	0.9975	53.095	0.9934
	rs621541	63321216	0.9833	0.9333	0.2667	0.6265	0.9974	53.169	0.9934
	rs1686806	63322252	0.975	0.9333	0.2667	0.6178	0.9972	53.202	0.9934
	rs275913	63330923	0.9833	0.9333	0.2667	0.6265	0.9974	55.027	0.9942
	rs12428552	63336180	0.9833	0.9333	0.2667	0.6265	0.9975	54.179	0.9939
	rs824764	63338626	0.9833	0.9333	0.275	0.6178	0.9973	53.395	0.9935
	rs1095072	63347162	0.9833	0.9389	0.2667	0.6342	0.9976	54.375	0.994
	rs605874	63348614	0.9833	0.9389	0.2667	0.6342	0.9976	53.93	0.9938

Table 14: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 15 of the HapMap Phase II data.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 15, CHB+JPT	rs11635593	61799912	0.1167	0.9167	0.1917	0.6708	0.9967	96.004	0.9995
	rs7163401	61811844	0.0583	0.9167	0.1917	0.7184	0.9984	90.311	0.9994
	rs7172848	61818807	0.0583	0.9167	0.1917	0.7184	0.9984	86.486	0.9993
	rs7164301	61821430	0.0583	0.9167	0.1917	0.7184	0.9984	84.642	0.9993
	rs8037083	61853580	0.0583	0.9167	0.25	0.6868	0.9972	53.122	0.9982
	rs2414823	61860806	0.0583	0.9167	0.1917	0.7184	0.9984	49.036	0.9975
	rs7178111	61862564	0.1	0.9167	0.1833	0.6891	0.9972	48.503	0.9974
	rs6494433	61869963	0.0583	0.9167	0.1917	0.7184	0.9984	47.406	0.9971
	rs4984317	61871710	0.0583	0.9167	0.1917	0.7184	0.9984	46.265	0.9968
	rs4984318	61871736	0.0583	0.9167	0.1917	0.7184	0.9984	45.711	0.9967
	rs8027701	61878102	0.0667	0.9167	0.1917	0.7114	0.9979	43.451	0.9959
	rs6494436	61878357	0.0583	0.9167	0.2	0.7136	0.998	42.897	0.9956
	rs4776681	61886816	0.0583	0.9167	0.1917	0.7184	0.9984	39.216	0.9939
	rs7173437	61887845	0.0583	0.8833	0.1917	0.676	0.9968	38.332	0.9936
	rs2099921	61890902	0.0583	0.8833	0.1917	0.676	0.9968	37.811	0.9934
	rs7178104	61892636	0.0583	0.8889	0.1917	0.683	0.9971	35.796	0.9926
	rs7182375	61892683	0.0583	0.8889	0.3333	0.6153	0.9942	35.312	0.9924
	rs7165577	61904056	0.0583	0.8889	0.1833	0.688	0.9972	33.16	0.9909
	rs2053593	61905916	0.0583	0.8889	0.1917	0.683	0.9971	32.275	0.9901

Table 15: One region and SNPs which had highest EHHST values, strongest differentiations, and high derived allele frequency in the tested population (> 0.5) on chromosome 17 of the HapMap Phase II data. * marked new regions; **abbreviations**: Chrms — Chromosome, Popu. — Population, Pct — percentile. # marked region which was close to a candidate region found in Table 1, Sabeti et al. (2007). In the first column, the **Genes** provided names and positions of genes which were located in a region.

Chromosome, Tested Popu.	SNP Name	Position	Derived Allele Frequency			F_{st} Value	Pct of F_{st}	EHHST Value	Pct of EHHST
			CEU	CHB+JPT	YRI				
Chrms 17, CEU*,# <i>CA4</i> (55,582-55,592kb)	rs345187	55588298	0.9333	0.9389	0.175	0.6821	0.9972	48.386	0.9956
	rs345184	55594073	0.9417	0.9278	0.1667	0.6837	0.9972	50.526	0.9961
	rs2452542	55600976	0.85	0.7278	0.0333	0.5719	0.991	49.052	0.9958
	rs9891296	55630776	0.95	0.9222	0.275	0.5694	0.9908	53.405	0.9967
	rs9893536	55663144	0.95	0.9278	0.2667	0.5856	0.9921	51.67	0.9963
	rs8080640	55671729	0.95	0.9278	0.275	0.5767	0.9914	49.539	0.9959
	rs7216914	55678847	0.95	0.9278	0.2	0.6561	0.9963	48.49	0.9957
	rs237967	55686029	0.95	0.9278	0.275	0.5767	0.9914	44.898	0.9947
	rs237956	55695726	0.95	0.9278	0.2667	0.5856	0.9921	43.142	0.9938
	rs237954	55698601	0.95	0.9278	0.1917	0.6649	0.9965	40.97	0.9934

Table 16: Maximum extended haplotype-based homozygosity score test (EHHST) values of the HapMap Phase II data of three population across human genome, chromosome 1 to chromosome 11.

Chromosome	Sample	SNP	Position	Values
chromosome 1	CEU	rs9287131	192304513	1385.916
	CHB+JPT	rs10493514	73153100	5096.607
	YRI	rs2292275	161558841	72.873
chromosome 2	CEU	rs6739328	21650555	9178.164
	CEU	rs6547423	21651477	9178.164
	CEU	rs1477471	21651840	9178.164
	CHB+JPT	rs7594350	72425722	30805.837
	CHB+JPT	rs1400582	72474987	30805.837
	YRI	rs11883730	63445734	213.353
chromosome 3	CEU	rs341770	8954779	1345.997
	CHB+JPT	rs1386675	97865566	5371.473
	YRI	rs6763004	164851217	115.185
chromosome 4	CEU	rs1455724	60996026	1747.229
	CHB+JPT	rs6531808	86381856	2922.449
	YRI	rs4834160	128144330	53.851
chromosome 5	CEU	rs1054020	145505341	1557.327
	CHB+JPT	rs13182616	155717380	1649.290
	YRI	rs2431218	79905228	70.966
chromosome 6	CEU	rs3010521	48715542	628.272
	CHB+JPT	rs12202591	130680197	3719.419
	YRI	rs1264567	30474079	133.707
chromosome 7	CEU	rs17169262	136890892	8827.805
	CHB+JPT	rs11979882	90245236	1205.201
	YRI	rs569862	54641039	65.130
chromosome 8	CEU	rs2205153	91466385	1570.848
	CHB+JPT	rs13260166	50721620	1296.325
	YRI	rs16915414	51870380	87.408
chromosome 9	CEU	rs13291813	106392446	1408.915
	CHB+JPT	rs17810391	105983919	6384.794
	YRI	rs12004563	71920439	100.471
chromosome 10	CEU	rs7100458	74673099	5067.346
	CHB+JPT	rs2067732	86973092	280.070
	YRI	rs4623821	58998686	53.969
chromosome 11	CEU	rs11035187	39228629	3991.305
	CHB+JPT	rs2618296	37916220	8101.077
	YRI	rs4543965	37931669	64.632

Table 17: Maximum extended haplotype-based homozygosity score test (EHHST) values of the HapMap Phase II data of three population across human genome, chromosome 12 to chromosome 22.

Chromosome	Sample	SNP	Position	Values
chromosome 12	CEU	rs4149160	20905844	950.954
	CHB+JPT	rs10863071	84669944	4077.948
	YRI	rs12312066	66002935	94.098
chromosome 13	CEU	rs2231332	37822263	3292.477
	CHB+JPT	rs9506383	19282447	7783.522
	YRI	rs4884166	54667146	124.023
chromosome 14	CEU	rs1253642	51496904	1138.814
	CHB+JPT	rs10136790	67471698	5801.927
	CHB+JPT	rs10133262	67477691	5801.927
	YRI	rs7156228	59748861	58.875
chromosome 15	CEU	rs4404024	69734324	1101.560
	CHB+JPT	rs1472946	49011221	695.312
	YRI	rs12939	40363868	62.413
chromosome 16	CEU	rs2245201	77092871	235.138
	CHB+JPT	rs16969790	20173234	200.338
	YRI	rs2157854	22851261	96.901
chromosome 17	CEU	rs12450486	41620562	489.866
	CHB+JPT	rs12051550	20070138	832.638
	YRI	rs17175543	54158597	33.747
chromosome 18	CEU	rs9319771	64871413	4272.775
	CEU	rs10432227	64871622	4272.775
	CHB+JPT	rs2222394	18502286	372.659
	YRI	rs11664364	36269816	76.499
chromosome 19	CEU	rs978348	34008970	335.706
	CHB+JPT	rs16968285	33056093	224.119
	YRI	rs10422765	23730242	54.129
chromosome 20	CEU	rs184147	37751486	452.847
	CHB+JPT	rs4611702	40670251	293.510
	YRI	rs290429	52108753	63.020
chromosome 21	CEU	rs2027717	23329336	85.046
	CHB+JPT	rs2834997	35860466	826.522
	YRI	rs2070865	39637389	33.553
chromosome 22	CEU	rs5999761	33929534	1034.820
	CHB+JPT	rs17377643	40482934	260.948
	YRI	rs8142666	28754601	56.552