

Supplementary table 1- Characteristic of selected SNPs

#	Gene Symbol	Gene Name	Chromosome	NCBI SNP Reference	Cytogenetic Band	SNP Type	Location on NCBI Assembly
<b>Chromosome 1</b>							
1	NOTCH2	notch 2	1	rs10923931	1p12a	Intron	120517959
2	MTHFR;CLCN6	methylenetetrahydrofolate reductase (NAD(P)H);chloride channel; voltage-sensitive 6	1	rs1801133	1p36.22a	Mis-sense Mutation	11856378
3	LEPR	leptin receptor	1	rs2025804	1p31.3b	Intron	65946121
4	ADAM30	ADAM metallopeptidase domain 30	1	rs2641348	1p12a	Mis-sense Mutation	120437884
5	APOA2;FCER1G; TOMM40L;NR1I 3;NDUFS2	apolipoprotein A-II;Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide;translocase of outer mitochondrial membrane 40 homolog (yeast)-like;nuclear receptor subfamily 1; group I; member 3;NADH dehydrogenase (ubiquinone) Fe-S protein 2; 49kDa (NADH-coenzyme Q reductase)	1	rs5082	1q23.3a	Intron	161193683
<b>Chromosome 2</b>							
6			2	rs7566605	2q14.2a	Intergenic/Unknown	118836025
7	THADA	thyroid adenoma associated	2	rs7578597	2p21e	Mis-sense Mutation	43732823
8	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	2	rs10490072	2p16.1a	Intergenic/Unknown	60669931
<b>Chromosome 3</b>							
9	PPARG	peroxisome proliferator-activated receptor gamma	3	rs1801282	3p25.2b	INTRON	12393125
10	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	3	rs4402960	3q27.2b	Intron	185511687
<b>Chromosome 4</b>							
11	FABP2	fatty acid binding protein 2; intestinal	4	rs1799883	4q26f	Mis-sense Mutation	120241902
12	PPARGC1A	peroxisome proliferator-activated receptor gamma; coactivator 1 alpha	4	rs8192678	4p15.2c	Mis-sense Mutation	23815662
<b>Chromosome 5</b>							
13	ADRB2	adrenoceptor beta 2; surface	5	rs1042713	5q32d	Mis-sense Mutation	148206440
14	ADRB2	adrenoceptor beta 2; surface	5	rs1042714	5q32d	Mis-sense Mutation	148206473
<b>Chromosome 6</b>							
15	PPARD	peroxisome proliferator-activated receptor delta	6	rs2016520	6p21.31c	INTRON	35378778
16	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	6	rs4712523	6p22.3c	Intron	20657564
17	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	6	rs10946398	6p22.3c	Intron	20661034
18	EDN1	endothelin 1	6	rs5370	6p24.1b	Mis-sense Mutation	12296255



39	FTO	fat mass and obesity associated	16	rs3751812	16q12.2a	Intron	53818460
40	FTO	fat mass and obesity associated	16	rs8050136	16q12.2a	Intron	53816275
41	FTO	fat mass and obesity associated	16	rs9939609	16q12.2a	Intron	53820527

Supplementary table 2 - Allele frequencies used for PCA with 12 populations

SNP	Allele	KZ	ASW	CEU	CHB	CHD	GIH	JPT	LWK	MEX	MKK	TSI	YRI
rs1042713	A	0.42	0.57	0.36	0.55	0.58	0.43	0.44	0.52	0.45	0.54	0.34	0.5
rs10811661	C	0.28	0.09	0.2	0.42	0.44	0.09	0.48	0.06	0.11	0.1	0.19	0.02
rs1111875	C	0.41	0.77	0.58	0.32	0.31	0.41	0.35	0.81	0.64	0.76	0.6	0.87
rs2641348	G	0.05	0.35	0.37	0.02	0.02	0.22	0.02	0.46	0.1	0.36	0.08	0.38
rs13266634	T	0.37	0.19	0.24	0.47	0.44	0.23	0.44	0.06	0.19	0.05	0.25	0.07
rs4712523	G	0.32	0.6	0.34	0.42	0.41	0.23	0.41	0.66	0.31	0.54	0.28	0.69
rs1801133	A	0.28	0.12	0.31	0.48	0.34	0.17	0.36	0.09	0.42	0.08	0.46	0.09
rs2016520	C	0.22	0.29	0.22	0.27	0.39	0.2	0.23	0.29	0.07	0.28	0.24	0.31
rs2025804	A	0.36	0.83	0.62	0.16	0.11	0.79	0.15	0.78	0.65	0.85	0.73	0.77
rs2165241	T	0.26	0.19	0.44	0.08	0.08	0.37	0.16	0.18	0.42	0.23	0.47	0.25
rs2383208	G	0.28	0.24	0.21	0.4	0.41	0.09	0.45	0.21	0.14	0.32	0.19	0.12
rs3761847	G	0.46	0.47	0.48	0.47	0.49	0.31	0.42	0.74	0.46	0.66	0.4	0.59
rs4506565	T	0.15	0.49	0.3	0.07	0.04	0.3	0.03	0.51	0.28	0.4	0.39	0.44
rs10923931	T	0.05	0.35	0.09	0.02	0.02	0.21	0.02	0.46	0.09	0.36	0.07	0.38
rs5370	T	0.25	0.13	0.22	0.3	0.28	0.49	0.27	0.13	0.19	0.19	0.2	0.18
rs7578597	C	0.06	0.27	0.12	0.14	0.01	0.17	0.01	0.36	0.02	0.19	0.06	0.33
rs9465871	C	0.3	0.54	0.16	0.5	0.52	0.22	0.56	0.45	0.32	0.46	0.16	0.61
rs7756992	G	0.33	0.54	0.28	0.48	0.51	0.24	0.46	0.58	0.34	0.59	0.24	0.61
rs7961581	C	0.25	0.17	0.25	0.17	0.19	0.36	0.23	0.2	0.15	0.2	0.4	0.17
rs8050136	A	0.26	0.45	0.46	0.14	0.16	0.26	0.18	0.49	0.2	0.52	0.46	0.46
rs8192678	T	0.38	0.07	0.35	0.4	0.4	0.3	0.53	0.02	0.21	0.08	0.43	0.04

Supplementary table 3 - Matrix of genetic distances for the studied populations

A) Angular distance or Edwards' distance:

	ASW	CEU	CHB	CHD	GIH	JPT	KZ	LWK	MEX	MKK	TSI
CEU	0.15135614										
CHB	0.23066719	0.18022859									
CHD	0.24362309	0.19298444	0.05732912								
GIH	0.16089120	0.09630197	0.19915958	0.21316660							
JPT	0.24654170	0.18330974	0.06511821	0.04798831	0.20673438						
KZ	0.18900253	0.10391896	0.09533130	0.10366025	0.12744616	0.09345392					
LWK	0.08029194	0.19333967	0.27438191	0.28604772	0.20601726	0.29115715	0.23478776				
MEX	0.16201984	0.09728707	0.17115117	0.18212642	0.11461837	0.17257188	0.10373429	0.20861930			
MKK	0.06480021	0.15882162	0.24433926	0.25181510	0.17251790	0.25404563	0.19781683	0.06262348	0.17323236		
TSI	0.17761894	0.07543911	0.18609004	0.19813192	0.10751941	0.18445890	0.10721422	0.22118015	0.09773708	0.18363797	
YRI	0.08035576	0.19508018	0.27025024	0.28167963	0.20091409	0.28482226	0.23157116	0.05442719	0.20125377	0.07611173	0.21810801

B) Coancestry coefficient or Reynolds' distance:

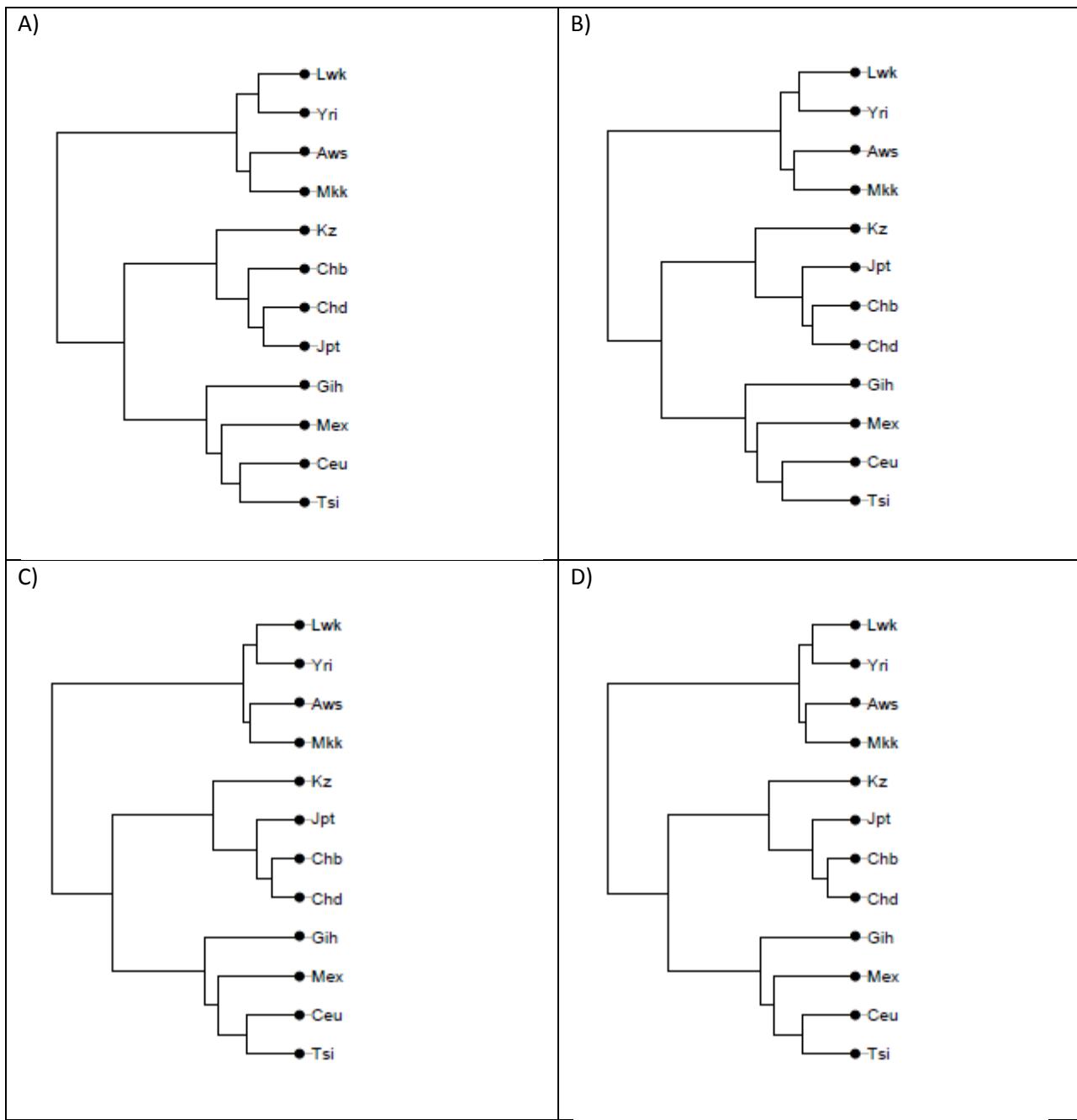
	ASW	CEU	CHB	CHD	GIH	JPT	KZ	LWK	MEX	MKK	TSI
CEU	0.29177703										
CHB	0.41835368	0.33667670									
CHD	0.42882114	0.35197291	0.08641653								
GIH	0.32235954	0.19146224	0.37078469	0.38645654							
JPT	0.43364040	0.33650127	0.10582187	0.10366666	0.37652616						
KZ	0.35491154	0.19985552	0.18758185	0.19927972	0.24283775	0.18294773					
LWK	0.14737572	0.35011659	0.47765763	0.48678810	0.39185143	0.49384736	0.41997984				
MEX	0.30725330	0.17974551	0.32930134	0.35181290	0.22050353	0.33883773	0.20891824	0.38239640			
MKK	0.12160400	0.29781734	0.43717590	0.44230161	0.33921827	0.44700046	0.36645546	0.12244792	0.32532009		
TSI	0.33662742	0.14489557	0.36097844	0.37981967	0.21081796	0.35730591	0.22548427	0.40039614	0.19504624	0.34439331	
YRI	0.12868645	0.35160370	0.46824529	0.47727071	0.38353495	0.48176875	0.41257001	0.11084471	0.36702836	0.14213688	0.39523572

C) Classical Euclidean distance or Rogers' distance:

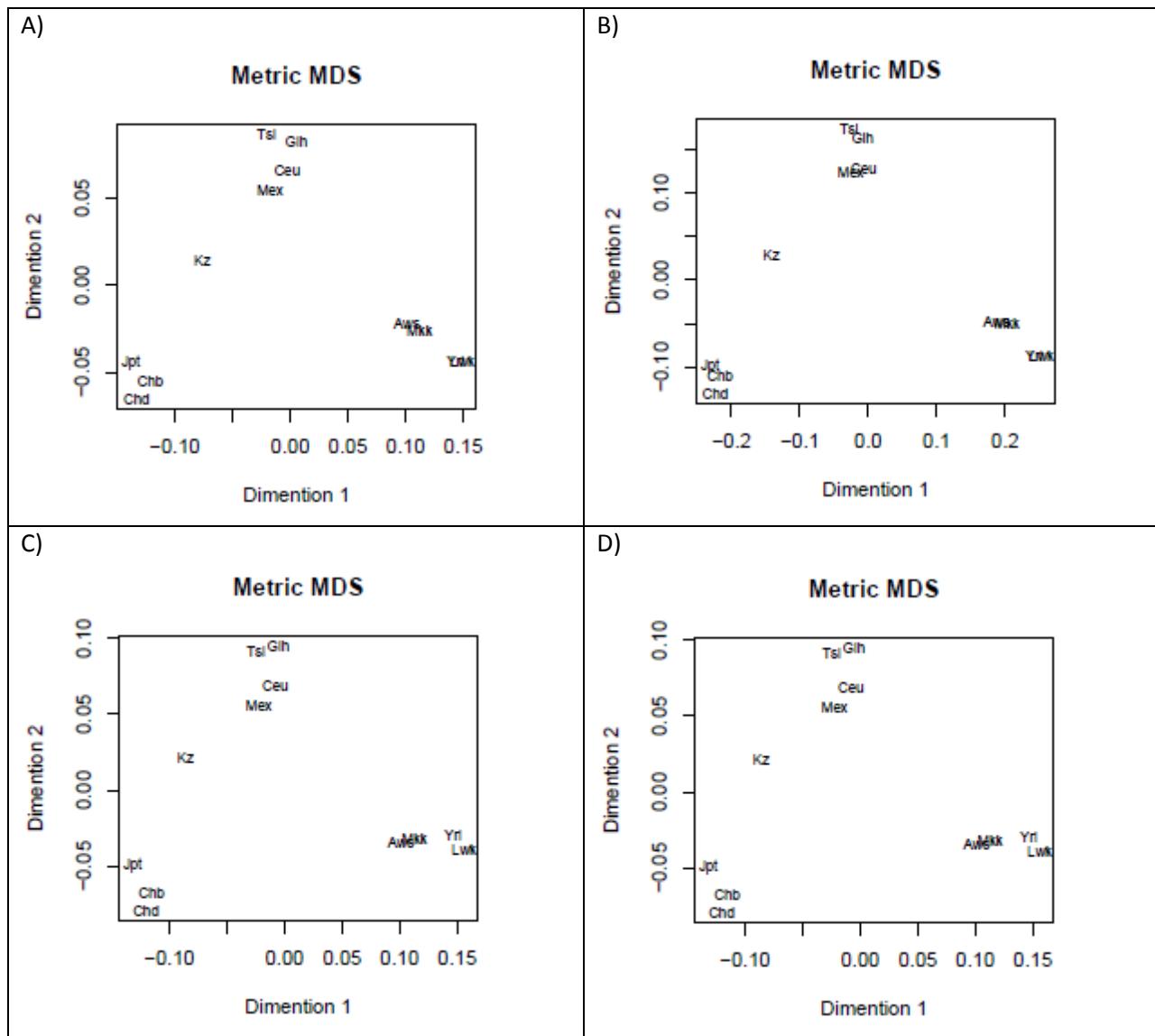
	ASW	CEU	CHB	CHD	GIH	JPT	KZ	LWK	MEX	MKK	TSI
CEU	0.15898888										
CHB	0.22048880	0.18240493									
CHD	0.22674180	0.18940729	0.03306038								
GIH	0.17843779	0.09938383	0.20777191	0.21878046							
JPT	0.23742620	0.17897422	0.05036538	0.04167268	0.20325132						
KZ	0.20207761	0.09467617	0.09915368	0.10141780	0.12202192	0.08819985					
LWK	0.06532088	0.19985795	0.27565384	0.28075032	0.22263215	0.28992237	0.24802603				
MEX	0.16779588	0.08480826	0.16931850	0.17723166	0.11118897	0.16765452	0.10235143	0.21423982			
MKK	0.05693782	0.16568977	0.23383499	0.24027003	0.18828276	0.25014844	0.20711168	0.05665838	0.17973258		
TSI	0.18558451	0.06238284	0.18991762	0.20409730	0.10958131	0.18370110	0.11159185	0.22861156	0.09461967	0.19385003	
YRI	0.06528110	0.19276134	0.26946432	0.27365981	0.20889159	0.27996259	0.24121547	0.05027547	0.19779903	0.06465247	0.21965910

D) Absolute genetics distance or Provesti 's distance:

	ASW	CEU	CHB	CHD	GIH	JPT	KZ	LWK	MEX	MKK	TSI
CEU	0.15898888										
CHB	0.22048880	0.18240493									
CHD	0.22674180	0.18940729	0.03306038								
GIH	0.17843779	0.09938383	0.20777191	0.21878046							
JPT	0.23742620	0.17897422	0.05036538	0.04167268	0.20325132						
KZ	0.20207761	0.09467617	0.09915368	0.10141780	0.12202192	0.08819985					
LWK	0.06532088	0.19985795	0.27565384	0.28075032	0.22263215	0.28992237	0.24802603				
MEX	0.16779588	0.08480826	0.16931850	0.17723166	0.11118897	0.16765452	0.10235143	0.21423982			
MKK	0.05693782	0.16568977	0.23383499	0.24027003	0.18828276	0.25014844	0.20711168	0.05665838	0.17973258		
TSI	0.18558451	0.06238284	0.18991762	0.20409730	0.10958131	0.18370110	0.11159185	0.22861156	0.09461967	0.19385003	
YRI	0.06528110	0.19276134	0.26946432	0.27365981	0.20889159	0.27996259	0.24121547	0.05027547	0.19779903	0.06465247	0.21965910



Supplementary Figure 1 - The dendograms based on matrices of genetic distances measured by different methods: A) angular distance or Edwards' distance; B) coancestry coefficient of Edwards' distance; C) classical Euclidean distance or Rogers's distance; D) absolute genetics distance or Provesti's distance



Supplementary Figure 2 - Multidimensional scaling representation of the A) angular distance or Edwards' distance; B) coancestry coefficient of Edwards' distance; C) classical Euclidean distance or Rogers's distance; D) absolute genetics distance or Provesti's distance between studied population