Supplementary information for "Standardized subsets of the HGDP-CEPH Human Genome Diversity Cell Line Panel, accounting for atypical and duplicated samples and pairs of close relatives"

The phrase "inferred to be cousins" in Supplementary Tables 6-15 means "inferred to be first cousins or other distant relatives." First cousins are not included in "inferred relative pairs" in the tables; the phrase "no other relationships" in the tables, however, means "no other FS, PO, HS, GG, AV, or CO relationships." A pair is listed in the tables if the likelihood ratio for the most likely relationship in comparison to "unrelated" exceeds 100. If the most likely relationship for a pair is HS, AV, GG, or CO, and if the likelihood ratio for this relationship and "unrelated" exceeds 100, other relationships (among HS, AV, GG, and CO) are also mentioned as secondary possibilities if their likelihoods are 10% or more of the likelihood of the most likely relationship (regardless of whether or not the likelihood ratios for these additional possibilities and "unrelated" exceed 100). The threshold of 10% was chosen for convenience; with a threshold considerably smaller than 10%, the tables would become unwieldy. For a given pair, if several alternative relationships are listed, the list proceeds in decreasing order of the likelihoods of the relationships. If CO is the most likely relationship for a pair of individuals, other relationships are only mentioned for that pair if they affect a decision about exclusion that utilizes inferred relationships for other pairs. Samples are indicated by identification numbers that were assigned by CEPH and that range from 1 to 1419.

Supplementary Web Resources

Marshfield Human Diversity Panel website, http://research.marshfieldclinic.org/genetics/Freq/FreqInfo.htm
Rosenberg Lab website, http://rosenberglab.bioinformatics.med.umich.edu
Rosenberg USC Diversity Panel website, http://www.cmb.usc.edu/people/noahr/diversity.html

Supplementary References

Ramachandran, S., Rosenberg, N. A., Zhivotovsky, L. A. & Feldman, M. W. (2004) Robustness of the inference of human population structure: a comparison of X-chromosomal and autosomal microsatellites. *Hum Genomics* **1**, 87-97.

Rosenberg, N. A. (2005) Algorithms for selecting informative marker panels for population assignment. *J Comput Biol* **12**, 1183-1201.

Rosenberg, N. A. & Calabrese, P. P. (2004) Polyploid and multilocus extensions of the Wahlund inequality. *Theor Pop Biol* **66**, 381-391.

Rosenberg, N. A., Li, L. M., Ward, R. & Pritchard, J. K. (2003b) Informativeness of genetic markers for inference of ancestry. *Am J Hum Genet* **73**, 1402-1422.

Zhivotovsky, L. A., Rosenberg, N. A. & Feldman, M. W. (2003) Features of evolution and expansion of modern humans, inferred from genomewide microsatellite markers. *Am J Hum Genet* **72**, 1171-1186.

Supplementary Table 1. Nine disjoint subsets into which 1066 samples can be subdivided.

Subset number	**Samples included**	**Explanation**
1	Japanese 1026	The individual is not in the diversity panel.
2	She 1331	The genotypes for this individual were excluded from data sent from the Mammalian Genotyping Service to Marc Feldman in March 2002, and were therefore not included in the data analyzed by Rosenberg *et al.* (2002). However, this individual is in the diversity panel and his genotypes do appear in the files of microsatellite genotypes posted on the Marshfield Human Diversity Panel website (the individual is male).
3	Biaka Pygmy 980 Japanese 770	These individuals were found by Rosenberg *et al.* (2002) to be extremely atypical and potentially mislabeled.
4	Herero 1028 Herero 1035 Ovambo 1031 Pedi 993 Sotho 994 Tswana 1030 Tswana 1034 Zulu 1033	These individuals are from populations in which only one or two individuals was included in the diversity panel.
5	Nilote 1410	This individual is the sole representative of his population and is not in the diversity panel (the individual is male).
6	Bedouin 652 Biaka Pygmy 1087 Biaka Pygmy 1092 Biaka Pygmy 981 Druze 589 Han 1022 Hezhen 1235 Italian 1154 Japanese 1025 Melanesian 826 Melanesian 659 Melanesian 979	Each of these samples is a duplicate of the sample in the corresponding position in the list in set 7.
7	Bedouin 650 Biaka Pygmy 452 Biaka Pygmy 457 Biaka Pygmy 472 Druze 583 Han 813 Hezhen 1233 Italian 1149 Japanese 762 Melanesian 657 Melanesian 658 Melanesian 660	Each of these samples is a duplicate of the sample in the corresponding position in the list in set 6. The individuals in set 7 are the ones with the smaller identification numbers in their duplicate pairs.
8	Hazara 111 Pathan 220	These samples, from Pakistan, are duplicates of each other but are listed with different population labels.
9	All 1027 individuals not in subsets 1-8.	

Supplementary Table 2. Combinations of subsets from Supplementary Table 1 that are studied in various settings.

Description	**Subsets from Supplementary Table 1 that are included**
Included in HGDP-CEPH Human Genome Diversity Cell Line Panel	2 3 4 6 7 8 9
Genotyped by Marshfield for microsatellites from screening set 10	1 2 3 4 5 6 7 8 9
Analyzed in Rosenberg *et al.* (2002)	1 3 6 7 8 9
Genotyped by Marshfield for microsatellites from screening sets 13 and 52	2 3 4 6 7 8 9
Genotyped by Marshfield for indel markers from screening set 100	1 2 3 4 5 6 7 8 9
Included in H1048 (see Supplementary Table 4)	2 4 7 9

The samples analyzed in the Rosenberg *et al.* (2002) paper are identical to those analyzed in Rosenberg *et al.* (2003), Rosenberg *et al.* (2003b), Zhivotovsky *et al.* (2003), Ramachandran *et al.* (2004), Rosenberg & Calabrese (2004), and Rosenberg (2005). The exact data used in the Rosenberg *et al.* (2002) paper are located on the Rosenberg Lab website and were previously located on the Rosenberg USC Diversity Panel website. An article that refers to Rosenberg *et al.* (2002) and to either of these websites very likely used this same set of individuals. An article that references the Marshfield Human Diversity Panel website would likely have used a slightly different combination of individuals. In the table, “Marshfield” refers to the Mammalian Genotyping Service at the Center for Medical Genetics, Marshfield Medical Research Foundation.

Supplementary Table 3. Duplicate pairs, adapted from Mountain & Ramakrishnan (2005, Table 1).

Member of duplicate pair retained in H1048	**Member of duplicate pair excluded from H1048**	**Proportion-of-shared-alleles distance between the pair**
Bedouin 650	Bedouin 652	0.004
Biaka Pygmy 452	Biaka Pygmy 1087	0.016
Biaka Pygmy 457	Biaka Pygmy 1092	0.006
Biaka Pygmy 472	Biaka Pygmy 981	0.006
Druze 583	Druze 589	0.014
Han 813	Han 1022	0.008
Hezhen 1233	Hezhen 1235	0.004
Italian 1149*	Italian 1154	0.003
Japanese 762	Japanese 1025	0.009
Melanesian 657	Melanesian 826	0.003
Melanesian 658	Melanesian 659	0.007
Melanesian 660	Melanesian 979	0.006
	Hazara 111 Pathan 220	0.017

* This corrects a typographical error in Mountain & Ramakrishnan (2005).

This analysis is based on the 377 microsatellite loci studied by Rosenberg *et al.* (2002) and utilizes the proportion-of-shared-alleles distance as described in Mountain & Cavalli-Sforza (1997).

Supplementary Table 4. The H1048 data set.

Subset (from Supplementary Table 1)	Reason for exclusion from H1048
1	Not in the diversity panel
3	Correct population labels are unknown
5	Not in the diversity panel
6	Duplicates; the convention is to discard duplicates with larger identification numbers
8	Duplicates; the correct population label is unknown

Supplementary Table 5. The 11 of 783 loci from Ramachandran *et al.* (2005) and Rosenberg *et al.* (2005) that were not used in the RELPAIR analysis.

Locus	**Reason for exclusion**
D20S201*	Uncertain/unknown map position
D11S4463*	Uncertain/unknown map position
ATA43C09M	Bioinformatics error
GATA12A08P	Bioinformatics error
GATA143C02	Uncertain/unknown map position
GATA71E06	Uncertain/unknown map position
GTTT002P	Bioinformatics error
TAT028P	Bioinformatics error
TTA008P	Bioinformatics error
TTTA075P	Bioinformatics error
TTTTA002	Uncertain/unknown map position

* These loci were omitted in Rosenberg & Calabrese (2004) for the same reason. The other nine loci in the table are among those that have been genotyped more recently and that were not considered in Rosenberg *et al.* (2002). The bioinformatics errors that caused loci to be excluded were generally of an inconsequential nature, such as typographical errors that led to a loss of information about map position. These errors were discovered only after the analysis was performed, and the exclusion of these loci is not expected to substantially influence the calculations.

Supplementary Table 6. Inferred relative pairs for (sub-Saharan) Africa.

Population	Inferred relative pairs	Comments	Individuals excluded from H971	Individuals excluded from H952
Bantu (S. Africa)		No relationships in this population.		
Bantu (Kenya)	(1411, 1413) FS	No other relationships involving 1411, 1413. (1412, 1418) are inferred to be cousins. No other relationships in this population.	1413	1413
Mandenka	(913, 919) HS or AV (915, 916) AV or HS	No other relationships involving 913, 919. No other relationships involving 915, 916. (908, 1285) are inferred to be cousins. No other relationships in this population		919 916
Yoruba	(920, 921) FS (922, 923) FS (922, 925) PO (923, 925) PO	No other relationships involving 920, 921. No other relationships involving 922, 923, 925. It seems safe to infer that 925 (f) is a parent and that 922 (f) and 923 (m) are her offspring. No other relationships in this population.	921 922 923	921 922 923
San	(987, 988) PO	No other relationships in this population.	988	988
Mbuti Pygmy	(982, 983) PO (468, 471) PO (468, 984) AV or HS	No other relationships involving 982, 983. No other relationships involving 468, 471, 984. No other relationships in this population.	983 468	983 468
Biaka Pygmy	(473, 1089) PO (466, 1088) FS (1085, 1088) AV, CO, or HS (465, 1085) HS, AV, or CO (477, 1093) PO (457, 1093) PO (1084, 1093) FS (477, 1084) GG, HS, CO, or AV (457, 477) GG or HS (457, 1084) AV, HS, or CO (451, 464) PO (472, 1091) AV, HS, or CO (448, 461) AV or HS	No other relationships involving 473, 1089. (466, 1085), (465, 466), (465, 1088), (455, 1085) are inferred to be cousins. No other relationships involving 455, 465, 466, 1085, 1088. It is likely that 1093 (m) is a parent of 457 (m) and 477 (m), who are half sibs, and that 1084 (f) is a full sib of 1093. No other relationships involving 457, 477, 1084, 1093. (451, 1091), (451, 472) are inferred to be cousins. (451, 1091) has a higher relative likelihood for grandparent/grandchild than (451, 472) has for any non-cousin relationship. No other relationships involving 451, 464, 472, 1091. (448, 460) are inferred to be cousins. No other relationships involving 448, 460, 461. (453, 479) are inferred to be cousins. No other relationships in this population.	1089 1088 477 1093 451	1089 1088 1085 477 1093 1084 451 1091 448

Supplementary Table 7. Inferred relative pairs for Europe.

Population	**Inferred relative pairs**	**Comments**	**Individuals excluded from H971**	**Individuals excluded from H952**
Orcadian	(794, 801) PO	No other relationships in this population.	801	801
Adygei		No relationships in this population.		
Russian		No relationships in this population.		
Basque		No relationships in this population.		
French	(511, 532) FS	No other relationships in this population.	532	532
Italian		No relationships in this population.		
Sardinian		No relationships in this population.		
Tuscan		No relationships in this population.		

Supplementary Table 8. Inferred relative pairs for the Middle East.

Population	Inferred relative pairs	Comments	Individuals excluded from H971	Individuals excluded from H952
Mozabite	(1280, 1281) FS	No other relationships in this population.	1281	1281
Bedouin	(616, 633) PO (617, 635) AV or HS	No other relationships involving 616, 633. (617, 619) are inferred to be cousins. No other relationships involving 617, 619, 635. Nine additional cousin pairs – (610, 612), (614, 615), (614, 626), (614, 642), (615, 626), (615, 628), (618, 701), (622, 642), (630, 631) – but otherwise no other relationships in this population.	633	633 617
Druze	(571, 592) PO (569, 603) FS (568, 585) HS or AV (590, 605) FS (570, 591) AV or HS	No other relationships involving 571, 592. (569, 585), (585, 603), (577, 585), (568, 577) are inferred to be cousins. No other relationships involving 568, 569, 577, 585, 603. (581, 605), (573, 605), (581, 590), (558, 590) are inferred to be cousins. (581, 604) are inferred to be cousins. No other relationships involving 558, 573, 581, 590, 605. No other relationships involving 570, 591. Nine additional cousin pairs – (557, 565), (557, 578), (557, 594), (559, 584), (562, 594), (564, 594), (567, 588), (575, 583), (575, 604) – but otherwise no other relationships in this population.	592 603 605	592 603 585 605 570
Palestinian	(694, 695) FS (681, 684) HS or AV (682, 743) AV or HS (723, 743) AV or HS (726, 728) AV or HS (693, 742) AV or HS	No other relationships involving 694, 695. (681, 734) are inferred to be cousins. No other relationships involving 681, 684, 734. (682, 723) are inferred to be cousins. No other relationships involving 682, 723, 743. No other relationships involving 726, 728. (679, 693), (679, 742) are inferred to be cousins. No other relationships involving 679, 693, 742. Ten additional cousin pairs – (675, 737), (677, 724), (678, 735), (683, 690), (688, 727), (691, 746), (696, 730), (697, 733), (724, 725), (732, 735) – but otherwise no other relationships in this population.	695	695 681 743 728 742

Supplementary Table 9. Inferred relative pairs for Central/South Asia.

Population	Inferred relative pairs	Comments	Individuals excluded from H971	Individuals excluded from H952
Balochi	(82, 84) FS	No other relationships in this population.	84	84
Brahui		No relationships in this population.		
Makrani		(154, 157) are inferred to be cousins. No other relationships in this population.		
Sindhi	(167, 203) PO	No other relationships involving 167, 203. (173, 175) are inferred to be cousins. No other relationships in this population.	203	203
Pathan		No relationships in this population.		
Burusho		No relationships in this population.		
Hazara	(106, 113) FS (112, 128) HS or AV	No other relationships involving 106, 113. No other relationships involving 112, 128. Five additional cousin pairs – (102, 105), (102, 108), (104, 118), (105, 108), (121, 122) – but otherwise no other relationships in this population.	113	113 128
Uygur		No relationships in this population.		
Kalash	(288, 292) PO (321, 326) HS, AV, CO, or GG	(292, 328) are inferred to be cousins. No other relationships involving 288, 292, 328. (286, 321), (286, 319) are inferred to be cousins. No other relationships involving 286, 319, 321, 326. Two additional cousin pairs – (267, 277), (274, 313) – but otherwise no other relationships in this population.	292	292 321

Supplementary Table 10. Inferred relative pairs for East Asia.

Population	**Inferred relative pairs**	**Comments**	**Individuals excluded from H971**	**Individuals excluded from H952**
Han		No relationships in this population.		
Han (N. China)		No relationships in this population.		
Dai		No relationships in this population.		
Daur		No relationships in this population.		
Hezhen		No relationships in this population.		
Lahu	(1321, 1325) FS (1323, 1324) PO	No other relationships involving 1321, 1325. No other relationships involving 1323, 1324. No other relationships in this population.	1325 1324	1325 1324
Miao		No relationships in this population.		
Oroqen	(1203, 1210) FS	No other relationships in this population.	1210	1210
She		No relationships in this population.		
Tujia		No relationships in this population.		
Tu		No relationships in this population.		
Xibo		No relationships in this population.		
Yi		No relationships in this population.		
Mongola		No relationships in this population.		
Naxi	(1340, 1343) FS	No other relationships involving 1340, 1343. (1339, 1342) are inferred to be cousins. No other relationships in this population.	1343	1343
Cambodian	(713, 718) PO	No other relationships in this population.	718	718
Japanese		No relationships in this population.		
Yakut		No relationships in this population.		

Supplementary Table 11. Inferred relative pairs for Oceania.

Population	Inferred relative pairs	Comments	Individuals excluded from H971	Individuals excluded from H952
Melanesian	(660, 789) PO (660, 824) PO (788, 789) PO (788, 824) PO (789, 824) FS	No other relationships involving 660, 788, 789, 824. 660, 788, 789, 824 is a family with parents 660 (f) and 788 (m), and offspring 789 (m) and 824 (m).	789 824	789 824
	(655, 657) PO (656, 657) PO	No other relationships involving 655, 656, 657. 655 (m) and 656 (f) are parents and 657 (f) is their offspring.	657	657
	(658, 978) FS (658, 664) PO (664, 978) GG	No other relationships involving 658, 664, 978. 978 cannot be both the full sib of 658 and the grandparent or grandchild of 664. The likelihood of an avuncular relationship for (664, 978) is small but not negligible in comparison with a grandparent/grandchild relationship. It is likely that 658 (f) is a parent of 664 (f) and that 978 (f) is the full sib of 658 and the aunt of 664.	658	658 978
	(490, 662) PO (490, 663) PO	(491, 663) are inferred to be cousins. No other relationships involving 490, 491, 662, 663. 662 (m) and 663 (f) are the parents of 490 (m).	490	490
	(661, 825) FS (661, 823) GG, HS, or CO	(823, 825) are inferred to be cousins. No other relationships involving 661, 823, 825. If (661, 825) are full sibs, then 823 must have the same relationship to both 661 and 825. Avuncular and half sibs both have likelihoods >10% of the likelihood of cousins for (823, 825). Half sibs and cousins both have likelihoods >10% of the likelihood of grandparent/grandchild for (661, 823). No other relationships in this population.	825	825 823
Papuan		No relationships in this population.		

Supplementary Table 12. Inferred relative pairs for Colombian and Maya.

Population	**Inferred relative pairs**	**Comments**	**Individuals excluded from H971**	**Individuals excluded from H952**
Colombian	(709, 710) PO (707, 708) PO (705, 706) PO (793, 970) PO (703, 793) PO (702, 792) FS (704, 827) PO	(705, 709), (707, 709), (705, 707), (705, 708) are inferred to be cousins. No other relationships involving 705, 706, 707, 708, 709, 710. No other relationships involving 703, 793, 970. 703 (m) and 970 (f) are parents and 793 (f) is their offspring. No other relationships involving 702, 792. No other relationships involving 704, 827. No other relationships in this population.	709 707 705 793 792 827	709 707 705 793 792 827
Maya	(862, 867) PO (858, 866) PO (866, 867) AV or HS (876, 878) FS (854, 874) HS, AV, or GG	(862, 866), (858, 867) are inferred to be cousins. No other relationships involving 876, 878. (865, 874), (873, 874), (865, 873) are inferred to be cousins. No other relationships involving 854, 873, 874. Two additional cousin pairs – (859, 865), (868, 869) – but otherwise no other relationships in this population.	867 866 878	867 866 878 874

In the Maya population, previously reported family information (Howard Cann, pers. comm.) suggested certain relative pairs. A reported HS relationship between 858 and 865 was not supported by the analysis. The other reported relationships – PO relationship between 858 and 866, and FS relationship between 876 and 878 – were confirmed. The reported polarity of the PO relationship, with 866 as the parent and 858 as the offspring, was consistent with the analysis, but could not be confirmed. All other inferred relationships were not among those that were previously reported.

Supplementary Table 13. Inferred relative pairs for Karitiana.

Population	Inferred relative pairs	Comments	Individuals excluded from H971	Individuals excluded from H952
Karitiana	(1016, 1018) PO (1007, 1016) FS (999, 1007) PO (997, 999) PO (1004, 1012) PO (1004, 1007) FS (1007, 1018) GG or CO (1004, 1018) GG (1004, 1016) FS (1005, 997) FS (1005, 1006) HS, AV, or GG (1004, 1017) GG, CO, HS, or AV (1014, 1017) PO	It is likely that 997, 999, 1004, 1007, 1012, 1016, 1018 are an extended family, that 1016 (f) is a parent of 1018 (f), 1004 (m) is a parent of 1012 (m), 997 (m) and 1007 (f) are the parents of 999 (f), and that 1004, 1007, 1016 are full sibs. 1005 is the full sib of 997 and 1006 is related by some second-degree relationship to 1005. 1014 and 1017 are somehow linked into this pedigree. No other non-cousin relationships involving 997, 999, 1004, 1014, 1005, 1006, 1006, 1012, 1016, 1017, 1018.	997 1004 1005 1007 1016 1017	997 1004 1005 1007 1016 1017
	(998, 1000) FS (998, 1011) FS (998, 1008) FS (1008, 1011) FS (1000, 1008) GG, FS, or HS (1000, 1011) CO, HS, AV, or GG	No other first-degree relationships involving 998, 1000, 1008, 1011. (1008, 1011) was inferred to be a parent/offspring pair according to allele sharing but a full sib pair according to RELPAIR. The inference from allele sharing is likely to be more reliable. According to the reported relationships (Howard Cann, pers. comm.), 998 (m), 1000 (m), and 1008 (f) are full sibs and 1011 (f) is the offspring of 1008.	1000 1008 1011	1000 1008 1011
	(995, 996) FS	No other non-cousin relationships involving 995, 996. No other first-degree relationships in this population.	996	996

In the Karitiana population, there are many relative pairs, and for convenience, some second-degree relative pairs are not listed in the table. The relationships in Karitiana differ substantially from the proposed list based on reported family relationships (Howard Cann, pers. comm.). That list does have the FS relationship between 1004, 1007, and 1016, as well as all of the inferred PO relationships except between 1014 and 1017. However, a reported PO relationship between 995 and 1014 was not confirmed, nor was a reported HS relationship of 995 to 1004, 1007, and 1016. The analysis was consistent with a reported HS relationship for 1005 and 1006. It was also consistent with the reported FS relationship of 998, 1000, and 1008; the allele sharing but not the RELPAIR analysis was consistent with the report that 1008 is a parent of 1011. The reported HS relationship of 1010 and 1011 was not supported by RELPAIR, nor was the reported FS relationship of 996 and 1017.

Supplementary Table 14. Inferred relative pairs for Pima.

Population	Inferred relative pairs	Comments	Individuals excluded from H971	Individuals excluded from H952
Pima	(1047, 1049) PO (1048, 1049) PO (1037, 1039) PO (1037, 1040) PO (1038, 1039) PO (1038, 1040) PO (1039, 1040) FS (1048, 1050) FS (1048, 1038) FS (1038, 1050) FS (1048, 1052) PO (1050, 1052) PO (1038, 1052) PO	No other non-cousin relationships involving 1037, 1038, 1039, 1040, 1047, 1048, 1049, 1050, 1052. 1047 (m) and 1048 (f) are the parents of 1049 (f). 1037 (m) and 1038 (f) are the parents of 1039 (m) and 1040 (m). 1038 (f), 1048 (f), and 1050 (m) are full sibs and are the offspring of 1052 (m). Several other cousin and grandparent/grandchild relationships involving this pedigree are also inferred. Not all of these relationships are consistent with the inferred pedigree but the inferences about first-degree relationships are taken to be more reliable.	1048 1049 1052 1038 1039 1040	1048 1049 1052 1038 1039 1040
	(1054, 1055) PO	(1054, 1056) are inferred to be cousins. No other relationships involving 1054, 1055, 1056.	1054	1054
	(1043, 1046) PO (1044, 1046) PO (1043, 1045) PO (1044, 1045) PO (1045, 1046) FS	(1043, 1044), (1043, 1053), (1042, 1046) are inferred to be cousins. No other relationships involving 1043, 1044, 1045, 1046. 1043 (m) and 1044 (f) are the parents of 1045 (m) and 1046 (f).	1045 1046	1045 1046
	(1041, 1042) PO (1041, 1053) GG, HS, or AV	No other non-cousin relationships involving 1041, 1042, 1053.	1042	1042
	(1060, 1061) FS	(1037, 1061) are inferred to be cousins. No other relationships involving 1060, 1061.	1061	1061
		No other non-cousin relationships in this population.		

In this population, there are many relationship pairs, and for convenience, only first-degree relatives are listed for the large pedigree that includes 1037, 1038, 1039, 1040, 1047, 1048, 1049, 1050, 1052. All of the previously reported relationships in Pima (Howard Cann, pers. comm.) were confirmed, except that the polarity of two PO relationships could not be inferred: the reported relationships listed 1041 as a parent of 1042 and 1054 as a parent of 1055. Several relationships in addition to those previously reported were also identified. In particular, these included the FS relationship between 1038, 1048, and 1050 and the PO relationships between 1038 and 1052, and between 1048 and 1052.

Supplementary Table 15. Inferred relative pairs for Surui.

Population	**Inferred relative pairs**	**Comments**	**Individuals excluded from H971**	**Individuals excluded from H952**
Surui	(839, 840) FS (839, 841) FS (839, 842) FS (839, 850) FS (840, 841) FS (840, 842) FS (840, 850) FS (841, 842) FS (841, 850) FS (842, 850) FS (837, 839) PO (837, 840) PO (837, 841) GG (837, 842) PO (837, 850) PO (838, 839) PO (838, 840) PO (838, 841) AV, HS, or GG (838, 842) GG, HS, or AV (838, 850) GG or HS	It is likely that 837, 838, 839, 840, 841, 842, 850 is a family with parents 837 (m) and 838 (f) and offspring 839 (m), 840 (f), 841 (f), 842 (m), 850 (f). All ten parent/offspring pairs in this family are identified by allele sharing, although only six are identified by RELPAIR. All ten full sib relationships are identified both by allele sharing and by RELPAIR. Reported information (Howard Cann, pers. comm.) had suggested that 837 (m) is a parent of 839, 840, 841, 842, 850.	839 840 841 842 850	839 840 841 842 850
	(838, 851) FS (833, 851) PO (830, 851) PO	(830, 833) are inferred to be cousins. Reported information (Howard Cann, pers. comm.) suggested that they are half sibs. It is likely but not certain that 851 (m) is the full sib of 838 (f) and a parent of 830 (f) and 833 (f).	851 830	851 830 833
	(843, 848) PO (846, 848) PO	(843, 846) are inferred to be unrelated. Therefore it seems likely that 843 (m) and 846 (f) are the parents of 848 (f).	848	848
	(833, 834) FS (834, 835) FS (844, 852) FS (844, 847) FS	(834, 835) and (833, 834) but not (833, 835) are inferred to be FS, inconsistent with the transitivity of the FS relation. Neither 834 nor 835 was inferred to have a PO relationship with 851, a putative parent (offspring?) of 833. 834, however, but not 835, was inferred to have a GG relationship with 851. Other questionable relationships include: (850, 851) are inferred to be GG or CO; (844, 847) and (844, 852) but not (847, 852) are inferred to be FS, when (844, 847) was a putative PO pair by allele sharing; (832, 844) are inferred to be GG, CO, or HS; (835, 843) GG, HS, or AV; (830, 832) are inferred to be AV or HS – reported information suggested that these individuals are HS. No other first-degree relationships in this population.	834 835 844 847	834 835 844 847

In the Surui population, there are many relative pairs, and for convenience, some second-degree relative pairs are not listed in the table. Most of the reported family relationships in Surui (Howard Cann, pers. comm.) were confirmed. In particular, 837 was seen to be a parent of 839, 840, 841, 842, and 850. 851 was seen to have PO relationships with 830 and 833, but 830 and 833 were not seen to have a relationship that could enable inference of polarity; to be very conservative, 830 was excluded along with 851 from data set H971. The analysis was consistent with the reported HS relationship for 830 and 832, but AV had a higher likelihood than HS. Notable previously unknown relationships include the fact that 838 is likely to be the other parent of 839, 840, 841, 842, and 850.

Supplementary Table 16. Concordance of allele-sharing and RELPAIR analyses.

Population	Sample size in H1048	Number of PO pairs (allele sharing)	Number of PO pairs (RELPAIR)	Number of FS pairs (allele sharing)	Number of FS pairs (RELPAIR)
Adygei	17	0	0	0	0
Balochi	25	0	0	1	1
Bantu (Kenya)	12	0	0	1	1
Bantu (S. Africa)	8	0	0	0	0
Basque	24	0	0	0	0
Bedouin	48	1	1	0	0
Biaka Pygmy	32	4	4	2	2
Brahui	25	0	0	0	0
Burusho	25	0	0	0	0
Cambodian	11	1	1	0	0
Colombian	13	6	6	1	1
Dai	10	0	0	0	0
Daur	10	0	0	0	0
Druze	47	1	1	2	2
French	29	0	0	1	1
Han	34	0	0	0	0
Han (N. China)	10	0	0	0	0
Hazara	24	0	0	1	1
Hezhen	9	0	0	0	0
Italian	13	0	0	0	0
Japanese	29	0	0	0	0
Kalash	25	1	1	0	0
Karitiana	24	6	5	6	9
Lahu	10	1	1	1	1
Makrani	25	0	0	0	0
Mandenka	24	0	0	0	0
Maya	25	2	2	1	1
Mbuti Pygmy	15	2	2	0	0
Melanesian	19	9	9	3	3
Miao	10	0	0	0	0
Mongola	10	0	0	0	0
Mozabite	30	0	0	1	1
Naxi	10	0	0	1	1
Orcadian	16	1	1	0	0
Oroqen	10	0	0	1	1
Palestinian	51	0	0	1	1
Papuan	17	0	0	0	0
Pathan	24	0	0	0	0
Pima	25	15	15	6	6
Russian	25	0	0	0	0
San	7	1	1	0	0
Sardinian	28	0	0	0	0
She	10	0	0	0	0
Sindhi	25	1	1	0	0
Surui	21	15	10	14	15
Tu	10	0	0	0	0
Tujia	10	0	0	0	0
Tuscan	8	0	0	0	0
Uygur	10	0	0	0	0
Xibo	9	0	0	0	0
Yakut	25	0	0	0	0
Yi	10	0	0	0	0
Yoruba	25	2	2	2	2
Total	**1048**	**69**	**63**	**46**	**50**

Supplementary Table 17. 69 inferred parent/offspring pairs in H1048.

Population	First individual			Second individual			Method of inference: allele sharing (A) or RELPAIR (R)
	Identification number	Sex	Parent (P), offspring (O), or uncertain (U)	Identification number	Sex	Parent (P), offspring (O), or uncertain (U)	
Bedouin	616	M	U	633	F	U	A,R
Biaka Pygmy	451	M	U	464	M	U	A,R
Biaka Pygmy	457	M	O	1093	M	P	A,R
Biaka Pygmy	473	M	U	1089	M	U	A,R
Biaka Pygmy	477	M	O	1093	M	P	A,R
Cambodian	713	F	U	718	F	U	A,R
Colombian	703	M	P	793	F	O	A,R
Colombian	704	F	U	827	F	U	A,R
Colombian	705	M	U	706	F	U	A,R
Colombian	707	F	U	708	F	U	A,R
Colombian	709	M	U	710	M	U	A,R
Colombian	793	F	O	970	F	P	A,R
Druze	571	F	U	592	F	U	A,R
Kalash	288	M	U	292	M	U	A,R
Karitiana	997	M	P	999	F	O	A,R
Karitiana	999	F	O	1007	F	P	A,R
Karitiana	1004	M	P	1012	M	O	A,R
Karitiana	1008	F	U	1011	F	U	A
Karitiana	1014	F	U	1017	F	U	A,R
Karitiana	1016	F	P	1018	F	O	A,R
Lahu	1323	F	U	1324	F	U	A,R
Maya	858	F	U	866	F	U	A,R
Maya	862	F	U	867	F	U	A,R
Mbuti Pygmy	468	M	U	471	F	U	A,R
Mbuti Pygmy	982	M	U	983	M	U	A,R
Melanesian	490	M	O	662	M	P	A,R
Melanesian	490	M	O	663	F	P	A,R
Melanesian	655	M	P	657	F	O	A,R
Melanesian	656	F	P	657	F	O	A,R
Melanesian	658	F	U	664	F	U	A,R
Melanesian	660	F	P	789	M	O	A,R
Melanesian	660	F	P	824	M	O	A,R
Melanesian	788	M	P	789	M	O	A,R
Melanesian	788	M	P	824	M	O	A,R
Orcadian	794	F	U	801	F	U	A,R
Pima	1037	M	P	1039	M	O	A,R
Pima	1037	M	P	1040	M	O	A,R
Pima	1038	F	P	1039	M	O	A,R
Pima	1038	F	P	1040	M	O	A,R
Pima	1038	F	O	1052	M	P	A,R
Pima	1041	F	U	1042	M	U	A,R
Pima	1043	M	P	1045	M	O	A,R
Pima	1043	M	P	1046	F	O	A,R
Pima	1044	F	P	1045	M	O	A,R
Pima	1044	F	P	1046	F	O	A,R
Pima	1047	M	P	1049	F	O	A,R

Pima	1048	F	P	1049	F	O	A,R
Pima	1048	F	O	1052	M	P	A,R
Pima	1050	M	O	1052	M	P	A,R
Pima	1054	F	U	1055	M	U	A,R
San	987	M	U	988	M	U	A,R
Sindhi	167	M	U	203	M	U	A,R
Surui	830	F	U	851	M	U	A,R
Surui	833	F	U	851	M	U	A,R
Surui	837	M	P	839	M	O	A,R
Surui	837	M	P	840	F	O	A,R
Surui	837	M	P	841	F	O	A
Surui	837	M	P	842	M	O	A,R
Surui	837	M	P	850	F	O	A,R
Surui	838	F	P	839	M	O	A,R
Surui	838	F	P	840	F	O	A,R
Surui	838	F	P	841	F	O	A
Surui	838	F	P	842	M	O	A
Surui	838	F	P	850	F	O	A
Surui	843	M	P	848	F	O	A,R
Surui	844	M	U	847	M	U	A
Surui	846	F	P	848	F	O	A,R
Yoruba	922	F	O	925	F	P	A,R
Yoruba	923	M	O	925	F	P	A,R

The relationship for Melanesians 658 and 664 is listed as being of uncertain polarity, but it is likely that 658 is a parent and 664 is her offspring. It is also likely that Surui 844 is a parent and 847 is his offspring.

Supplementary Table 18. 46 inferred full sib pairs in H1048.

Population	First individual		Second individual		Method of inference: allele sharing (A) or RELPAIR (R)
	Identification number	Sex	Identification number	Sex	
Balochi	82	M	84	M	A,R
Bantu (Kenya)	1411	M	1413	M	A,R
Biaka Pygmy	466	M	1088	M	A,R
Biaka Pygmy	1084	F	1093	M	A,R
Colombian	702	F	792	M	A,R
Druze	569	F	603	M	A,R
Druze	590	F	605	M	A,R
French	511	M	532	F	A,R
Hazara	106	M	113	M	A,R
Karitiana	995	F	996	F	A,R
Karitiana	998	M	1000	M	A,R
Karitiana	998	M	1008	F	A,R
Karitiana	1004	M	1007	F	A,R
Karitiana	1004	M	1016	F	A,R
Karitiana	1007	F	1016	F	A,R
Lahu	1321	M	1325	F	A,R
Maya	876	F	878	M	A,R
Melanesian	658	F	978	F	A,R
Melanesian	661	F	825	F	A,R
Melanesian	789	M	824	M	A,R
Mozabite	1280	F	1281	F	A,R
Naxi	1340	M	1343	M	A,R
Oroqen	1203	M	1210	M	A,R
Palestinian	694	F	695	F	A,R
Pima	1038	F	1048	F	A,R
Pima	1038	F	1050	M	A,R
Pima	1039	M	1040	M	A,R
Pima	1045	M	1046	F	A,R
Pima	1048	F	1050	M	A,R
Pima	1060	M	1061	M	A,R
Surui	833	F	834	M	A,R
Surui	834	M	835	M	A,R
Surui	838	F	851	M	A,R
Surui	839	M	840	F	A,R
Surui	839	M	841	F	A,R
Surui	839	M	842	M	A,R
Surui	839	M	850	F	A,R
Surui	840	F	841	F	A,R
Surui	840	F	842	M	A,R
Surui	840	F	850	F	A,R
Surui	841	F	842	M	A,R
Surui	841	F	850	F	A,R
Surui	842	M	850	F	A,R
Surui	844	M	852	F	A,R
Yoruba	920	F	921	F	A,R
Yoruba	922	F	923	M	A,R

Surui pairs (833, 834) and (834, 835) but not (833, 835) were inferred to be full sibs. For at least one of these three pairs, the relationship must have been incorrectly inferred.

Supplementary Table 19. 34 inferred second-degree relative pairs in H1048.

Population	First individual			Second individual			Method of inference: allele sharing (A) or RELPAIR (R)
	Identification number	Sex	Half sib (H), aunt or uncle (A), niece or nephew (N), grandparent (G), grandchild (C), or uncertain (U)	Identification number	Sex	Half sib (H), aunt or uncle (A), niece or nephew (N), grandparent (G), grandchild (C), or uncertain (U)	
Bedouin	617	M	U	635	F	U	R
Biaka Pygmy	448	M	U	461	M	U	R
Biaka Pygmy	457	M	N	1084	F	A	R
Biaka Pygmy	457	M	H	477	M	H	R
Biaka Pygmy	465	M	U	1085	F	U	R
Biaka Pygmy	472	M	U	1091	M	U	R
Biaka Pygmy	477	M	N	1084	F	A	R
Biaka Pygmy	1085	F	U	1088	M	U	R
Druze	568	F	U	585	F	U	R
Druze	570	F	U	591	F	U	R
Hazara	112	M	U	128	M	U	R
Kalash	321	M	U	326	M	U	R
Mandenka	913	M	U	919	M	U	R
Mandenka	915	F	U	916	F	U	R
Maya	854	F	U	874	F	U	R
Maya	866	F	U	867	F	U	R
Mbuti Pygmy	468	M	U	984	M	U	R
Melanesian	661	F	U	823	M	U	R
Melanesian	664	F	U	978	F	U	R
Palestinian	681	F	U	684	F	U	R
Palestinian	682	F	U	743	F	U	R
Palestinian	693	F	U	742	F	U	R
Palestinian	723	M	U	743	F	U	R
Palestinian	726	M	U	728	M	U	R
Pima	1038	F	A	1049	F	N	R
Pima	1039	M	N	1048	F	A	R
Pima	1039	M	N	1050	M	A	R
Pima	1039	M	C	1052	M	G	R
Pima	1040	M	N	1048	F	A	R
Pima	1040	M	N	1050	M	A	R
Pima	1040	M	C	1052	M	G	R
Pima	1041	F	U	1053	F	U	R
Pima	1049	F	N	1050	M	A	R
Pima	1049	F	C	1052	M	G	R

The type of second-degree relationship is regarded as certain only if a single type of relationship is compatible with the pairs that appear in Supplementary Tables 17 and 18 (and with the lack of appearance of any other pairs in those tables). Due to the considerable uncertainty in Karitiana and Surui, no pairs are listed for these populations. Some pairs listed with uncertain relationship might not actually be second-degree relatives, and some second-degree pairs might not have been identified. Melanesians 664 and 978 are listed as having an uncertain relationship, but it is likely that 978 is an aunt and that 664 is her niece.

Supplementary Table 20. 17 inferred parent/parent/offspring trios in H1048.

Population	Identification number of father	Identification number of mother	Identification number of offspring	Sex of offspring	Method of inference: allele sharing (A) or RELPAIR (R)
Colombian	703	970	793	F	A,R
Karitiana	997	1007	999	F	A,R
Melanesian	655	656	657	F	A,R
Melanesian	662	663	490	M	A,R
Melanesian	788	660	789	M	A,R
Melanesian	788	660	824	M	A,R
Pima	1037	1038	1039	M	A,R
Pima	1037	1038	1040	M	A,R
Pima	1043	1044	1045	M	A,R
Pima	1043	1044	1046	F	A,R
Pima	1047	1048	1049	F	A,R
Surui	837	838	839	M	A,R
Surui	837	838	840	F	A,R
Surui	837	838	841	F	A
Surui	837	838	842	M	A
Surui	837	838	850	F	A
Surui	843	846	848	F	A,R

H1048 includes several sets that contain two parents and two or more of their offspring: Melanesians 660, 788, 789, 824; Pima 1037, 1038, 1039, 1040; Pima 1043, 1044, 1045, 1046; and Surui 837, 838, 839, 840, 841, 842, 850.

Supplementary Table 21. Numbers of individuals excluded from H1048 in H971 and H952.

Population	Sample size in H1048	Number of individuals excluded from H1048 in H971	Sample size in H971	Number of individuals excluded from H1048 in H952	Sample size in H952
Adygei	17	0	17	0	17
Balochi	25	1	24	1	24
Bantu (Kenya)	12	1	11	1	11
Bantu (S. Africa)	8	0	8	0	8
Basque	24	0	24	0	24
Bedouin	48	1	47	2	46
Biaka Pygmy	32	5	27	9	23
Brahui	25	0	25	0	25
Burusho	25	0	25	0	25
Cambodian	11	1	10	1	10
Colombian	13	6	7	6	7
Dai	10	0	10	0	10
Daur	10	0	10	0	10
Druze	47	3	44	5	42
French	29	1	28	1	28
Han	34	0	34	0	34
Han (N. China)	10	0	10	0	10
Hazara	24	1	23	2	22
Hezhen	9	0	9	0	9
Italian	13	0	13	0	13
Japanese	29	0	29	0	29
Kalash	25	1	24	2	23
Karitiana	24	10	14	10	14
Lahu	10	2	8	2	8
Makrani	25	0	25	0	25
Mandenka	24	0	24	2	22
Maya	25	3	22	4	21
Mbuti Pygmy	15	2	13	2	13
Melanesian	19	6	13	8	11
Miao	10	0	10	0	10
Mongola	10	0	10	0	10
Mozabite	30	1	29	1	29
Naxi	10	1	9	1	9
Orcadian	16	1	15	1	15
Oroqen	10	1	9	1	9
Palestinian	51	1	50	5	46
Papuan	17	0	17	0	17
Pathan	24	0	24	0	24
Pima	25	11	14	11	14
Russian	25	0	25	0	25
San	7	1	6	1	6
Sardinian	28	0	28	0	28
She	10	0	10	0	10
Sindhi	25	1	24	1	24
Surui	21	12	9	13	8
Tu	10	0	10	0	10
Tujia	10	0	10	0	10
Tuscan	8	0	8	0	8
Uygur	10	0	10	0	10
Xibo	9	0	9	0	9
Yakut	25	0	25	0	25
Yi	10	0	10	0	10
Yoruba	25	3	22	3	22
Total	**1048**	**77**	**971**	**96**	**952**

Supplementary Table 22. The 77 individuals included in H1048 but not in H971.

Population	Individuals in H1048 but not in H971
Balochi	84
Hazara	113
Sindhi	203
Kalash	292
Biaka Pygmy	451
Mbuti Pygmy	468
Biaka Pygmy	477
Melanesian	490
French	532
Druze	592
Druze	603
Druze	605
Bedouin	633
Melanesian	657
Melanesian	658
Palestinian	695
Colombian	705
Colombian	707
Colombian	709
Cambodian	718
Melanesian	789
Colombian	792
Colombian	793
Orcadian	801
Melanesian	824
Melanesian	825
Colombian	827
Surui	830
Surui	834
Surui	835
Surui	839
Surui	840
Surui	841
Surui	842
Surui	844
Surui	847

Population	Individuals in H1048 but not in H971 (continued)
Surui	848
Surui	850
Surui	851
Maya	866
Maya	867
Maya	878
Yoruba	921
Yoruba	922
Yoruba	923
Mbuti Pygmy	983
San	988
Karitiana	996
Karitiana	997
Karitiana	1000
Karitiana	1004
Karitiana	1005
Karitiana	1007
Karitiana	1008
Karitiana	1011
Karitiana	1016
Karitiana	1017
Pima	1038
Pima	1039
Pima	1040
Pima	1042
Pima	1045
Pima	1046
Pima	1048
Pima	1049
Pima	1052
Pima	1054
Pima	1061
Biaka Pygmy	1088
Biaka Pygmy	1089
Biaka Pygmy	1093
Oroqen	1210
Mozabite	1281
Lahu	1324
Lahu	1325
Naxi	1343
Bantu (Kenya)	1413

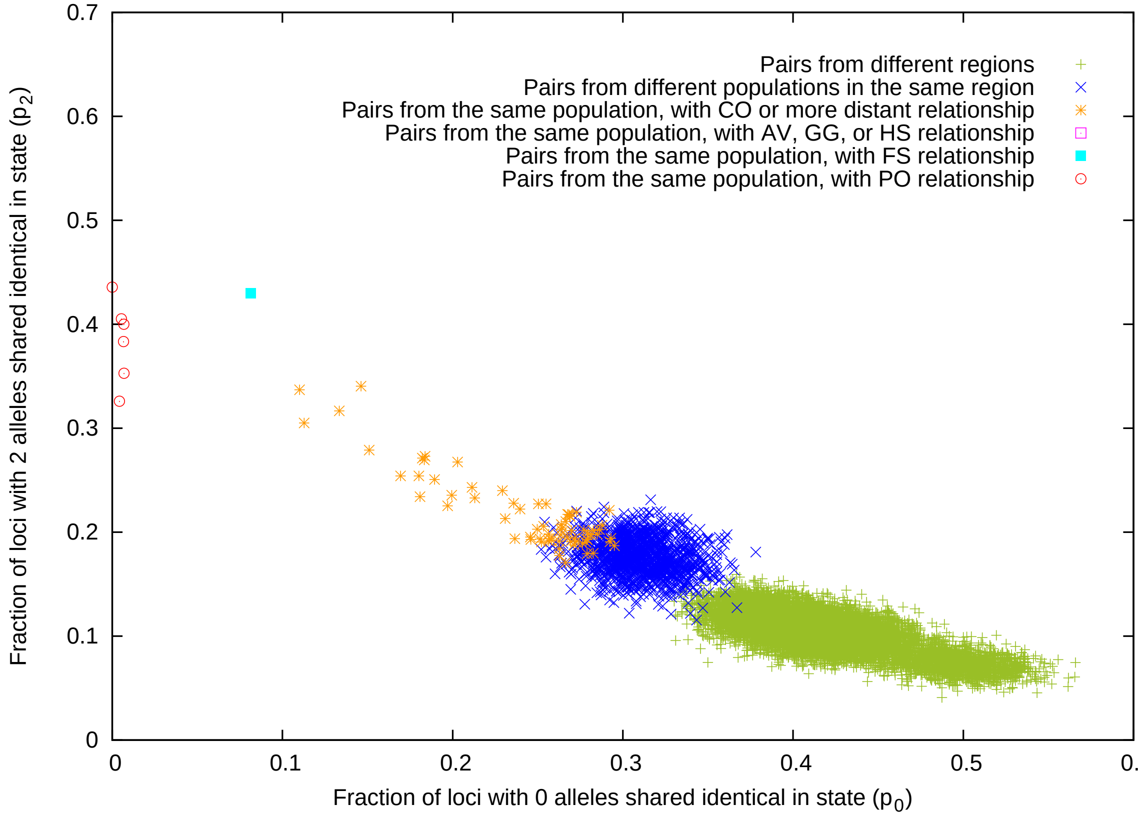
Supplementary Table 23. The 96 individuals included in H1048 but not in H952.

Population	Individuals in H1048 but not in H952
Balochi	84
Hazara	113
Hazara	128
Sindhi	203
Kalash	292
Kalash	321
Biaka Pygmy	448
Biaka Pygmy	451
Mbuti Pygmy	468
Biaka Pygmy	477
Melanesian	490
French	532
Druze	570
Druze	585
Druze	592
Druze	603
Druze	605
Bedouin	617
Bedouin	633
Melanesian	657
Melanesian	658
Palestinian	681
Palestinian	695
Colombian	705
Colombian	707
Colombian	709
Cambodian	718
Palestinian	728
Palestinian	742
Palestinian	743
Melanesian	789
Colombian	792
Colombian	793
Orcadian	801
Melanesian	823
Melanesian	824
Melanesian	825
Colombian	827
Surui	830
Surui	833
Surui	834
Surui	835
Surui	839
Surui	840
Surui	841
Surui	842
Surui	844
Surui	847

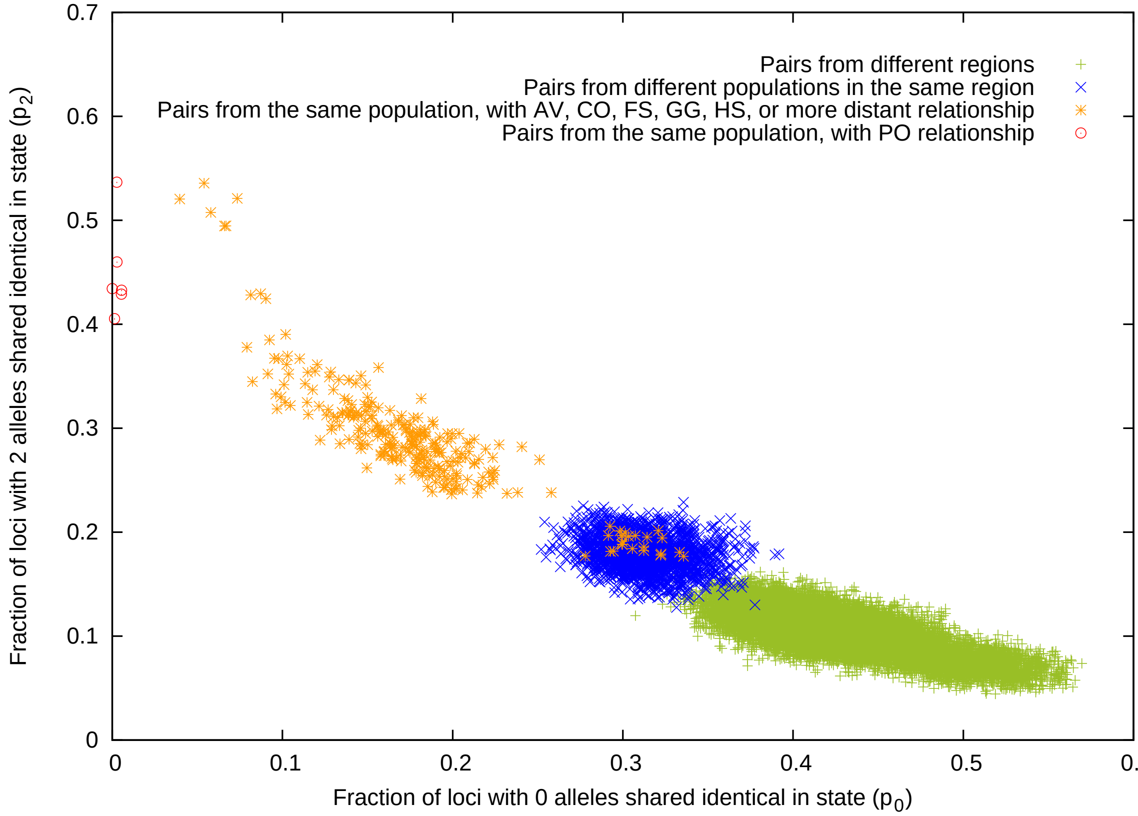
Population	Individuals in H1048 but not in H952 (continued)
Surui	848
Surui	850
Surui	851
Maya	866
Maya	867
Maya	874
Maya	878
Mandenka	916
Mandenka	919
Yoruba	921
Yoruba	922
Yoruba	923
Melanesian	978
Mbuti Pygmy	983
San	988
Karitiana	996
Karitiana	997
Karitiana	1000
Karitiana	1004
Karitiana	1005
Karitiana	1007
Karitiana	1008
Karitiana	1011
Karitiana	1016
Karitiana	1017
Pima	1038
Pima	1039
Pima	1040
Pima	1042
Pima	1045
Pima	1046
Pima	1048
Pima	1049
Pima	1052
Pima	1054
Pima	1061
Biaka Pygmy	1084
Biaka Pygmy	1085
Biaka Pygmy	1088
Biaka Pygmy	1089
Biaka Pygmy	1091
Biaka Pygmy	1093
Oroqen	1210
Mozabite	1281
Lahu	1324
Lahu	1325
Naxi	1343
Bantu (Kenya)	1413

Supplementary Table 24. Regional sample sizes for data sets H1048, H971, and H952.

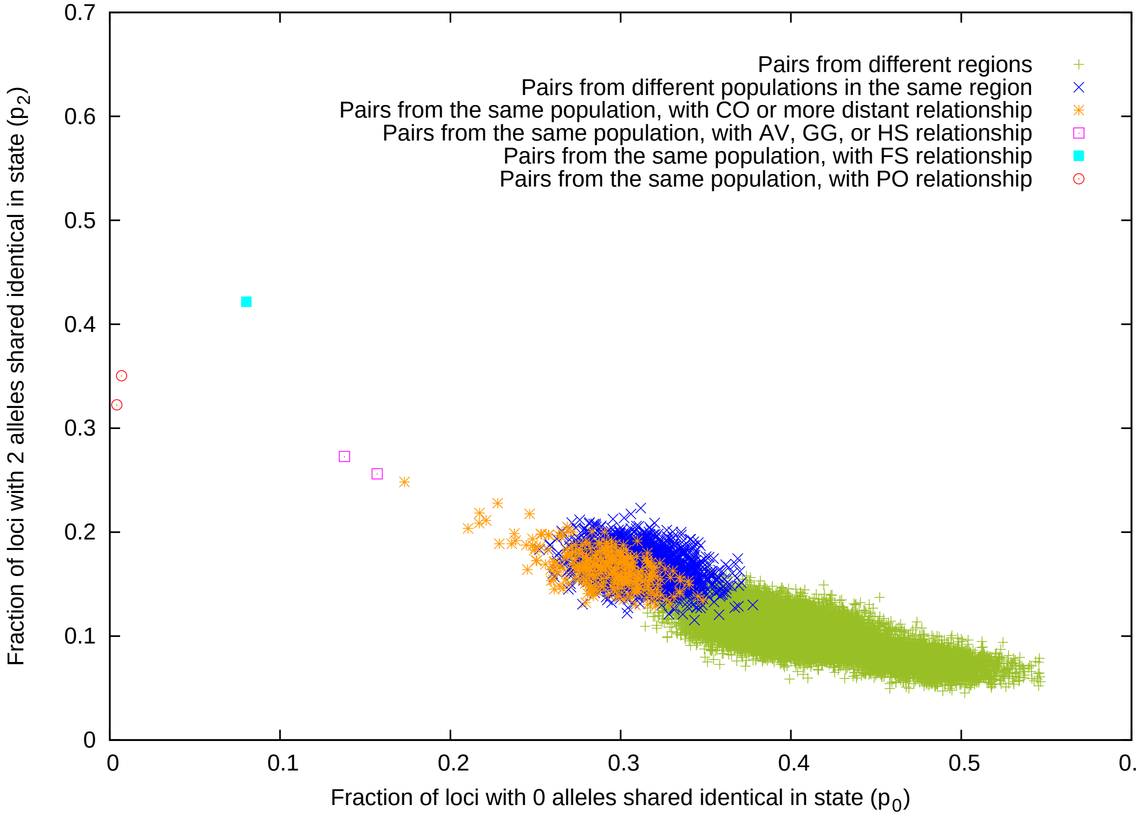
Region	**H1048**	**H971**	**H952**
Africa	123	111	105
Europe	160	158	158
Middle East	176	170	163
Central/South Asia	208	204	202
East Asia	237	232	232
Oceania	36	30	28
America	108	66	64
Total	**1048**	**971**	**952**



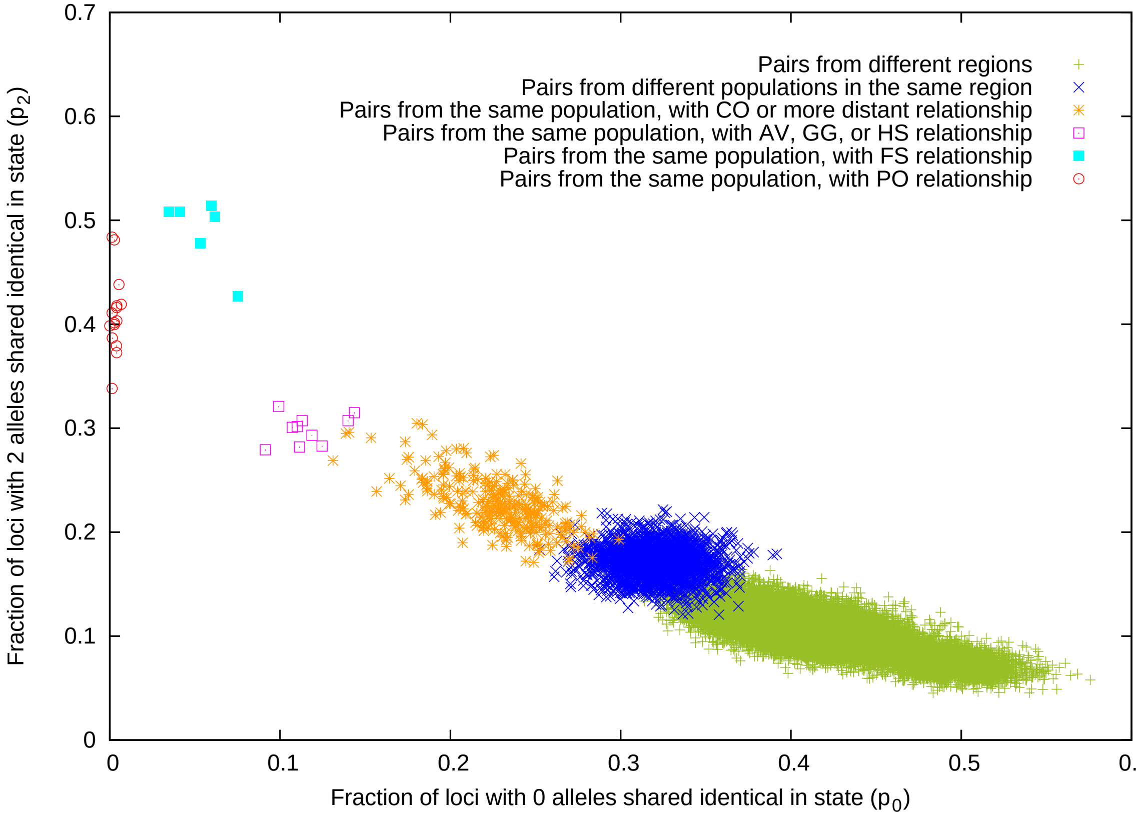
Supplementary Figure 2. Allele sharing for pairs of individuals from H1048 in which at least one member of the pair is from the Colombian population. The plot contains six parent/offspring pairs and one full sib pair.



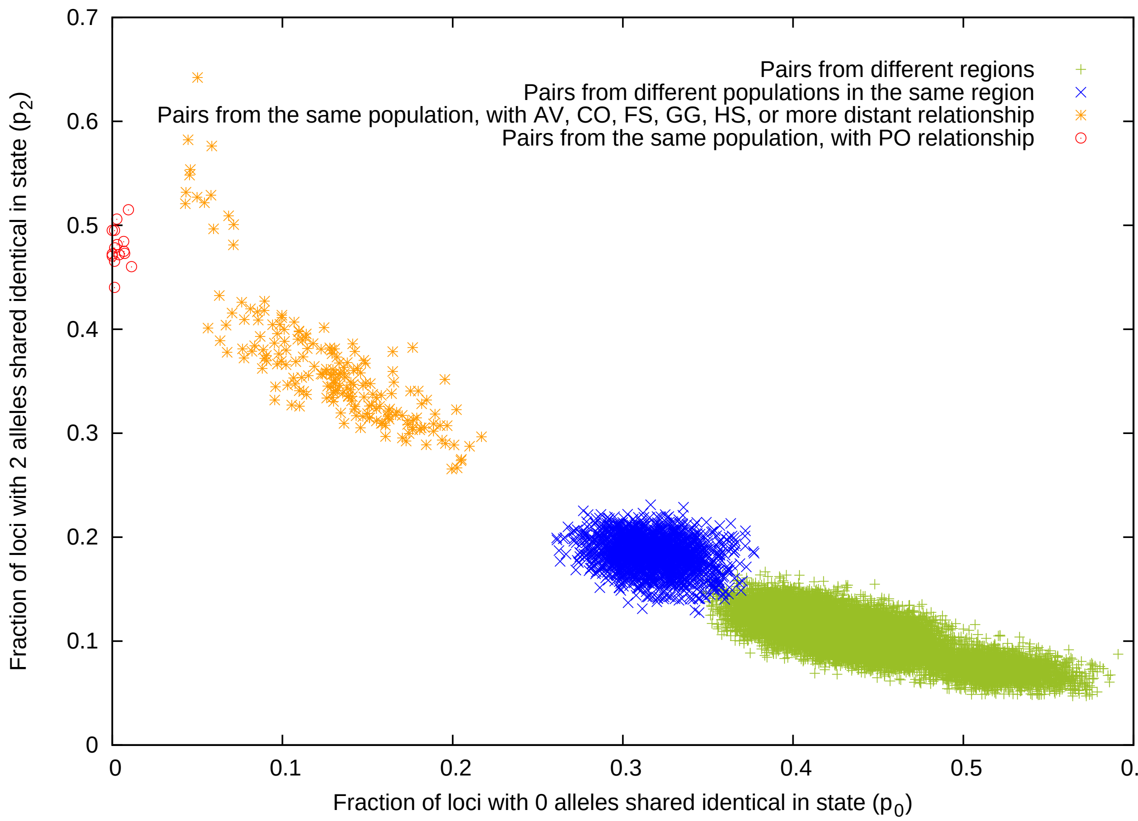
Supplementary Figure 3. Allele sharing for pairs of individuals from H1048 in which at least one member of the pair is from the Karitiana population. Because the confidence placed in specific relationship inferences was lower in this population than in other populations, all pairs from the Karitiana population except for parent/offspring pairs were plotted with the same symbol. The plot contains six parent/offspring pairs.



Supplementary Figure 4. Allele sharing for pairs of individuals from H1048 in which at least one member of the pair is from the Maya population. The plot contains two parent/offspring pairs, one full sib pair, and two pairs with second-degree relationships.



Supplementary Figure 5. Allele sharing for pairs of individuals from H1048 in which at least one member of the pair is from the Pima population. The plot contains 15 parent/offspring pairs, six full sib pairs, and 10 pairs with second-degree relationships.



Supplementary Figure 6. Allele sharing for pairs of individuals from H1048 in which at least one member of the pair is from the Surui population. Because the confidence placed in specific relationship inferences was smaller in this population than in other populations, all pairs from the Surui population except for parent/offspring pairs were plotted with the same symbol. The plot contains 15 parent/offspring pairs.