

	Chr 2	Chr 9	Chr 10	Chr 14
Total Faux	238	112	95	51
Middle-East	18	9	6	3
America	1	0	0	2
Central-South Asia	17	6	1	2
Europe	202	96	87	43
East-Asia	0	1	1	0
Africa				

	HGDP00875 Maya	HGDP00953 Yakut	HGDP00948 Yakut	HGDP01060/1061 Pima
Total Candidates	1338	222	255	417
Middle-East	1	1	2	0
America	1309	0	7	422
Central-South Asia	2	16	9	0
Europe	2	0	2	0
East-Asia	23	204	234	4
Faux	1	1	1	1

Controls pop	Orcadian pop
Total Matches	1786
Middle-East	137
America	5
Central-South Asia	122
Europe	1500
East-Asia	9
Africa	
Faux	13

The Orcadian group was included in the analysis by Anders Palsen as a control procedure to better assess the author's matches. It should be noted that the Orcadian group is significantly different from other European populations in terms of its high relatedness to East Asia. Hellenthal et al., 2008 noted that they were outliers who have a large number of matches to the Near East, Central Asia, and East Asia in relation to other European populations. This can also be seen in the "Advanced Global Similarity" tool at 23andme where the Orcadians are the only population to arc off to the east instead of being tightly clustered like other European populations.

Hence it will be instructive to explore what is seen with the European population with the closest links to the east using the example of Chromosome 10. The above Native

American matches are to 3 Columbian, 1 Pima and 1 Maya. All of these groups are admixed to some degree, and this number of matches is miniscule in relation to the total of 1786 – but whether shared ancestry or random convergence is not entirely clear. In terms of the Chromosome 10 East Asian matches, while there are 6 Yakut blocks, they are very specific and very limited with 4 occurring between 105 and 108 Mb, and 2 in 67/69 and 71 Mb. These are not proximal to the author's match in the 91 to 95 Mb positions. There were also 1 Lahu, 1 Tu, and 1 Cambodian.

Due to the very low frequency matches to the Yakut in general, and in different regions of Chromosome 10, in the European population with the highest affinity to East Asia it does not appear that the author's Yakut match can be explained by European admixture.

Hellenthal et al. attribute this Orcadian matching (small as it is) to gene flow rather than convergence. However the analysis highlights the difficulty in obtaining 100% clear results no matter how deeply one digs. It largely boils down to a probability decision. Given the above analysis, and given the author's documented Native American genealogy, and given that the Yakut are the Asian group most closely related genetically to Native Americans, it is most parsimonious to accept the finding (particularly since as will be noted later that it is consistent with the different inheritance pattern of the X chromosome) that this block shared with the Yakut is a function of shared ancestry (identical by descent) going back 15,000 years or so. The same estimate could apply to the matches with the Pima and Maya since the time to most recent common ancestor may be about the same (the convergence times about equal) with the Yakut due to long genetic separations between say the Pima and the Mohawk, and the Mohawk and the Yakut.