yourDNA Portal – Native American Ancestry Analysis of Each Chromosome for DKF

The following results from "yourDNAportal.com" purport to provide a detailed fine grained exploration of the ancestral results for each chromosome using different algorithms and reference samples. The author's assessment of this data will be provided at the end of the Results section below.

CHROMOSOME ANALYSIS

A) MODERN NATIVE AMERICAN REFERENCE GROUPS - RESULTS:

Chromosynthesis

Native American Modern Chromosynthesis

Explore your DNA via the power of Chromosynthesis!

By utilising chromosomal analysis, you can dig deeper into the more obscure areas of your ancestry. The fine detail of a chromosomal test, looks at each chromosome individually, allowing you to capture ancestry that may be missed by other tests.

Chromosynthesis is an excellent tool for capturing even the most distant ancestry. Each chromosome contains unique information and can have a very different autosomal profile. Usually the first 10 chromosomes are the most relevant, while the last 2 are less informative. A small percentage (1% of a chromosome) equals approximately 0.045% of the entire autosome. By analysing each chromosome, we can reveal both a deeper and more detailed ancestry than other tests.



Speculative results

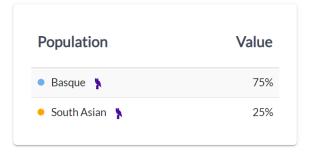
Conservative results

Population Value **Population** Value Basque 50% Basque 75% North-Western European 37.5% North-Western European \u00e8 25% Central Mediterranean 6.25% Chipewyan Saskatchewan Canada \$ 6.25%

Speculative results

Conservative results

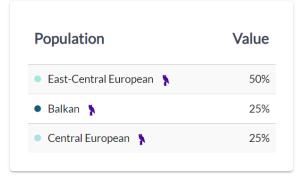
75%
18.75%
6.25%



Chromosome 22

Speculative results





B) GENOMEWIDE ANALYSIS USING MODERN NA REFERENCE SAMPLES:

Chromosynthesis

Native American Genomewide Chromosynthesis

Explore your DNA via the power of Chromosynthesis!

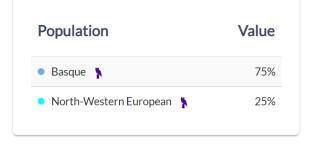
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Speculative results

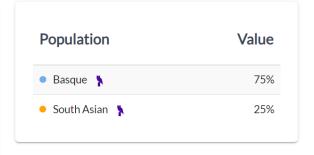




Speculative results

Conservative results

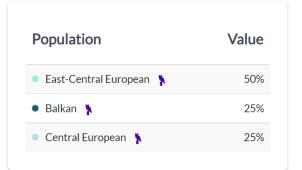
Population	Value
Basque	75%
South Asian	18.75%
Native American	6.25%



Chromosome 22

Speculative results





C) ANCIENT NA REFERENCE GROUPS - RESULTS:

Chromosynthesis

Native American Ancient Chromosynthesis

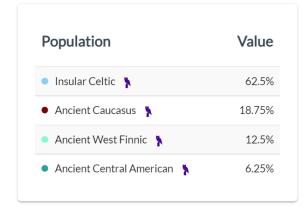
Explore your DNA via the power of Chromosynthesis!

By utilising chromosomal analysis, you can dig deeper into the more obscure areas of your ancestry. The fine detail of a chromosomal test, looks at each chromosome individually, allowing you to capture ancestry that may be missed by other tests.

Chromosynthesis is an excellent tool for capturing even the most distant ancestry. Each chromosome contains unique information and can have a very different autosomal profile. Usually the first 10 chromosomes are the most relevant, while the last 2 are less informative. A small percentage (1% of a chromosome) equals approximately 0.045% of the entire autosome. By analysing each chromosome, we can reveal both a deeper and more detailed ancestry than other tests.

Chromosome 1

Speculative results





Speculative results

Conservative results

Value
75%
18.75%
6.25%

Population	Value
Ancient West Mediterranean	75%
Insular Celtic	25%

Chromosome 7

Speculative results

Population	Value
• Insular Celtic 💃	37.5%
Mediterranean Neolithic Farmer	37.5%
Ancient Caucasus	12.5%
Ancient Patagonian	6.25%
Ancient West Mediterranean	6.25%

Population	Value
Ancient Caucasus	25%
Ancient West Mediterranean	25%
Insular Celtic	25%
Mediterranean Neolithic Farmer	25%

Speculative results

Conservative results

Population	Value
Mediterranean Neolithic Farmer	50%
Ancient Central American	12.5%
Ancient East Mediterranean	12.5%
Ancient West Mediterranean	12.5%
Ancient Oceanian	6.25%
Sub-Saharan African	6.25%

Population	Value
Mediterranean Neolithic Farmer	50%
Ancient Central American	25%
Ancient West Mediterranean	25%

Chromosome 16

Speculative results

Population	Value
Ancient West Finnic	50%
Ancient East Mediterranean	37.5%
Ancient North American	6.25%
Ancient South-Central Asian	6.25%

Population	Value
Ancient East Mediterranean	50%
Ancient West Finnic	50%

Speculative results

Conservative results

Value
56.25%
37.5%
6.25%

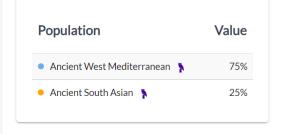
Population	Value
• Ancient Caucasus	50%
Ancient West Mediterranean	50%

Chromosome 18

Speculative results

Conservative results

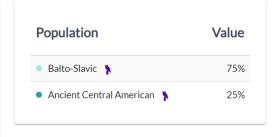
Population	Value
Ancient West Mediterranean	75%
Ancient South Asian	18.75%
Ancient West Amazonian	6.25%



Chromosome 22

Speculative results

Population	Value
Balto-Slavic	81.25%
Ancient Andean	6.25%
Ancient Central American	6.25%
Ancient South-Central Asian	6.25%



D) LANIAKEA ANALYSIS:



MODERN

Laniakea Global

Chromosynthesis

This test utilises Laniakea Global to give you a chromosome by chromosome analysis of your genetic identity. For each chromosome, you will get:

- 1. Admixture results
- 2. The populations most genetically similar
- 3. An estimation of ethnicity



Admixture Results

Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Northatlantic	30.69%
European Fennoscandian	27.94%
Mediterranean East	21.2%
European Germanic	12.64%
Asian Far-East	3.2%
Eurasian Alanic	1.67%
Native American South	1.54%
Native American Central	0.84%
European Atlantic	0.29%

Asian Far-East: 3.2%

The Asian Far-East component has its peak frequency in Japan, Korea and in eastern and north-eastern China. The component is fairly widespread and common throughout East Asia from the Philippines to Mongolia.

Native American South: 1.54%

The American South component has its frequency peak among the indigenous peoples of the Andes but is widespread and common throughout South America and more generally all the Americas.

Native American Central: 0.84%

The Native American Central component has its frequency peak in the descendants of the Mayan and Aztec peoples, however it is widespread and common in all the Americas.

Population	Value
Northern Celtogermanic	54%
Continental Celtogermanic	22.5%
• Finnish 💃	19%
Eastern North African	2%
• Arabic 🏌	1.5%
Japanese 🏌	0.5%
• Polynesian 🗼	0.5%



Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Fennoscandian	44.69%
European Atlantic	25.02%
European Northatlantic	16.82%
Mediterranean West	9.67%
Native American North	2.0%
African Rainforest	1.81%

Native American North: 2.0%

The Nativce American North component has its peak of frequency among the indigenous populations of Canada and the USA, but it is widespread and common in all the Americas, to a lesser extent also in Greenland and Siberia.



Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Fennoscandian	27.33%
European Central	25.34%
Mediterranean West	25.16%
Mediterranean East	6.46%
European Atlantic	5.56%
MENA Maghrebi	3.59%
MENA Mesopotamian	3.46%
European Northatlantic	1.59%
Asian Miao-Yi-Dai	1.52%

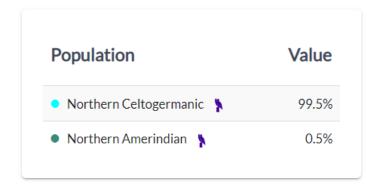
Asian Miao-Yi-Dai: 1.52%

The Miao-Yi-Dai component has its frequency peak in southern China but is widespread and common also in northern and western China, Taiwan and Japan, a good part of the Austronesian spectrum.



Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

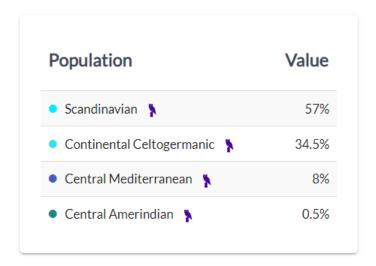
Admixture Population	Percentage
European Northatlantic	37.67%
European Germanic	28.52%
European Central	14.33%
European Eastern	10.17%
Eurasian Alanic	5.09%
Native American North	3.32%
African Khoisan	0.52%
Oceanian	0.38%



Admixture Results

Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Germanic	42.7%
European Central	17.66%
European Fennoscandian	12.91%
European Atlantic	9.62%
European Northatlantic	6.8%
Native American South	5.48%
Mediterranean East	2.46%
Asian Gedrosia	2.36%



Admixture Results

Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Central	49.75%
European Northatlantic	20.09%
European Atlantic	13.52%
European Fennoscandian	6.19%
Oceanian	3.46%
Asian Miao-Yi-Dai	3.07%
MENA Armenian	2.91%
European Germanic	1.01%



Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Northatlantic	28.59%
European Central	12.78%
European Atlantic	12.38%
European Fennoscandian	10.43%
MENA Mesopotamian	10.26%
Mediterranean East	9.74%
Native American North	6.99%
Eurasian Alanic	3.45%
Asian Miao-Yi-Dai	2.15%
Asian Tuvan	1.39%
Asian Siberian	1.34%
African Khoisan	0.48%

Population	Value
Northern Celtogermanic	73.5%
Southern Italian	21%
• Arctic	2.5%
Northern Amerindian	1%
• Levantine 💃	0.5%
Mongolian	0.5%
Northern Chinese	0.5%
Southern Chinese	0.5%





Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

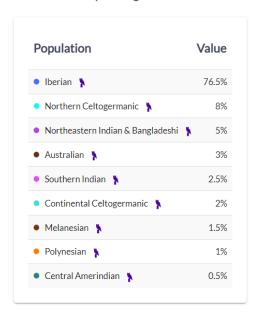
Admixture Population	Percentage
European Atlantic	27.08%
European Germanic	23.77%
MENA Mesopotamian	19.18%
MENA Armenian	13.31%
European Northatlantic	10.85%
Native American North	5.81%

Population	Value
Northern Celtogermanic	43%
• Iberian 🚶	17.5%
Central Mediterranean	14%
• Levantine 🚶	10%
Northern Italian	9.5%
• Arctic	2%
• Iranic 💃	1.5%
Northern Amerindian	1.5%
Eastern North African	1%

Admixture Results

Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Atlantic	37.2%
European Germanic	21.56%
Mediterranean East	12.14%
Asian Dravidian	9.37%
Oceanian	7.33%
Native American South	4.66%
European Northatlantic	3.41%
Asian Miao-Yi-Dai	2.23%
European Fennoscandian	2.11%



Admixture Results

Your admixture results are derived directly from the SNPs present in your file. They reveal the percentages that you share with the principal components of the populations present in the calculator, based on the frequency of alleles.

Admixture Population	Percentage
European Germanic	34.94%
European Fennoscandian	29.82%
European Northatlantic	17.25%
MENA Armenian	12.29%
Native American Central	3.14%
Mediterranean West	2.46%
MENA Arabian	0.09%

Analysis: The present author is unsure of how to interpret these results such that they make a valid and trustworthy contribution to the study of the ancestral composition of each chromosome (recalling that both the maternal and the paternal chromosomes are being combined here). Consistency (internal and external) is critical for arriving at a conclusion as to the merits of the data above. Clearly the results are somewhat "scattered" and vary from test procedure to test procedure, and are difficult to reconcile with data from other calculators (e.g., 23andMe, Gedmatch). For example, the array of ancestries (e.g., various Siberian groups, Southeast Asian) on chromosome 16 with the Laniakea calculator does not seem to be duplicated elsewhere. If those results were associated with chromosome 18, the results would make a lot more sense based on testing using different methodologies. It would seem that there is some tweaking of the components of their test procedures that are needed before any of the above results can be "taken to the bank".

Dr. David K. Faux 5 January 2023; 24 May 2023