deCODEme

world america europe africa south west asia east asia oceania discussion

Genetic atlas

Here, we present a comparison of your genetic code with that of people from all over the world. This comparison is based on several hundred thousand genetic variants and more than 1000 reference individuals from 50 different populations worldwide. The seven images above show the percentage of your genotypes that are shared with each of these populations, represented by a brown bar. The scale of genetic similarity shown is from 50% - 90%. The exact percentage for any one population can be viewed as tooltip information for its bar.

The number on the righthand side of the bar represents the rank of each population in terms of genetic similarity to you, with "1" indicating the greatest similarity. The first image shows a map of the world with the 50 worldwide populations grouped into six different regions and your average similarity to each of the six regions. The remaining images show more detailed maps of the six regions, presenting information about your genetic similarity to individual populations.

So where do i come from?

Tracing your exact geographical origin is a near impossible task and those claiming to be able to do so may often be providing more speculative results than factual. However, you will be able to use the results from the genetic similarity comparison to discover your ancestry in the broad sense of ethnicity.

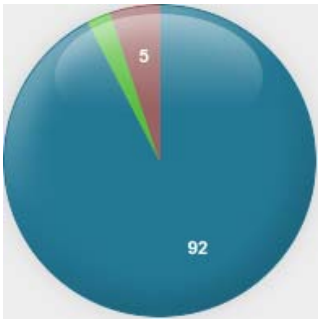
We assess your genetic similarity to 50 different populations from all over the world. The greater your similarity to a particular population, the more likely you have ancestors that belonged to that group in the past. We plan to add more populations in the near future to allow for a more precise evaluation of your genetic relationship to world populations.

How does it work?

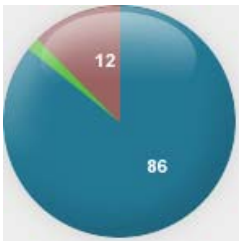
When we compare your genome with each of the reference individuals, we divide the genome into large segments and estimate the total fraction of the genome you share with them. We then calculate the average fraction you share with each of the 50 populations to which these individuals belong.

Note that because all humans are genetically very similar, you will always share a substantial fraction of your genome with all the different populations. However, in most cases, there will be subtle but sufficient differences in the average fraction shared with the 50 worldwide populations, such that we can reliably

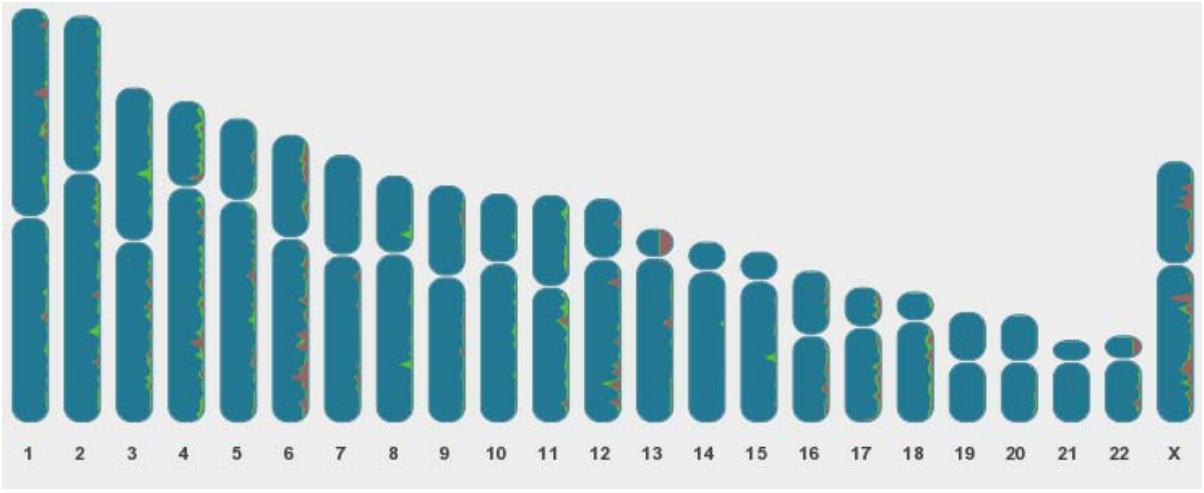
rank your genetic similarity and pick out the ones to which you have the strongest relationship.



chromosomes 1 to 22



x chromosome



ancestral make up of your chromosomes

Ancestral origins

Using your deCODEme Genetic Scan results, we use a well-established computer program to match your chromosomes, segment by segment, to one of three different ancestral groups of humans - Africans, Europeans and East Asians. By doing this, we are virtually reconstructing the geographical distribution of your ancestors back hundreds and even thousands of generations.

Here, we provide separate estimates of ancestry for your 22 autosomal chromosomes and your X chromosome(s). While all your ancestors had an equal chance of contributing genetic material to your autosomal chromosomes, your X chromosome (s) were more likely to receive contributions from your female ancestors.

We also examine the ancestry of two very special parts of your genome, mitochondrial DNA (mtDNA) and the Y chromosome (carried only by men).

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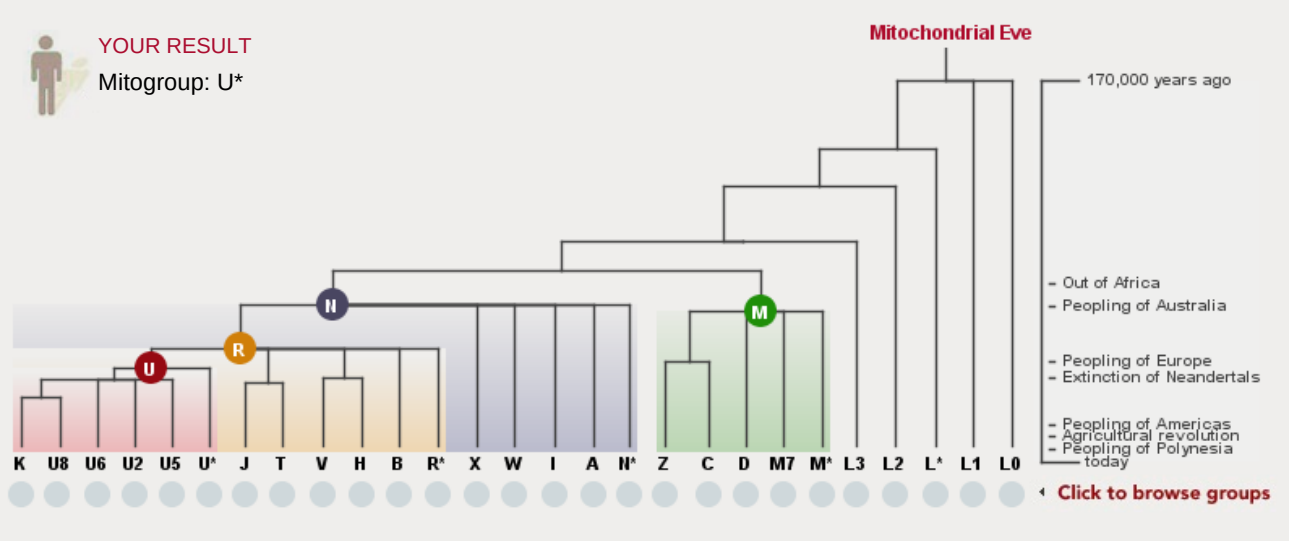
mitogroup info | users in group | allele frequencies | about mitogroup ancestry | discussion



Female line analysis: Your mitogroup is U*

3.6% of deCODEme users are a member of this group.

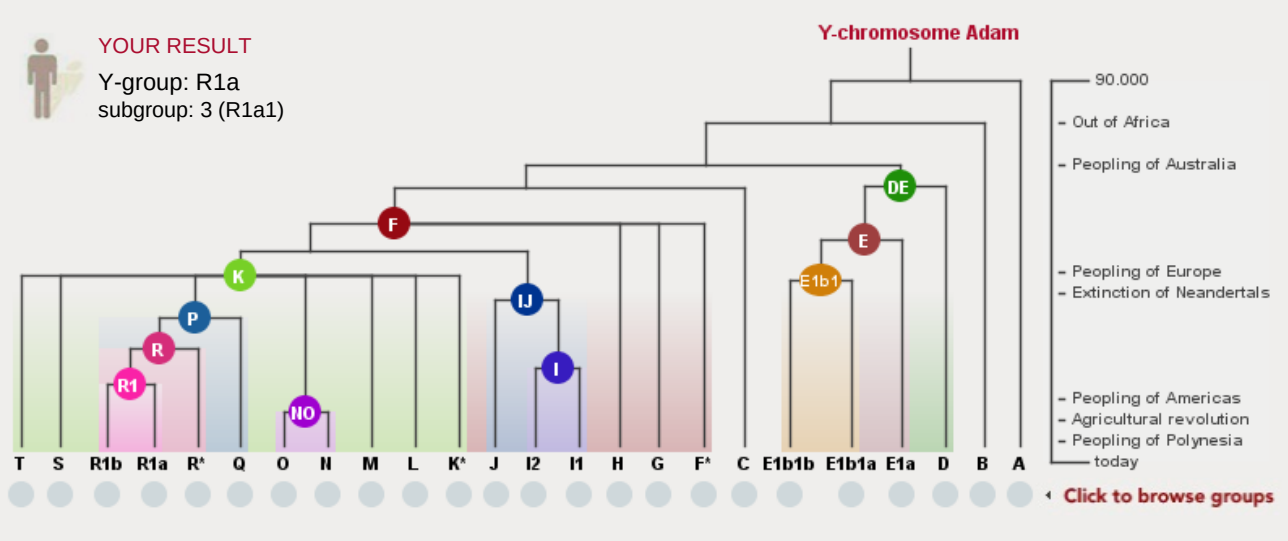
All members of mitogroup U* can trace their mitochondrial DNA to one woman who is thought to have lived about 60 thousand years ago, probably somewhere in the Near East. This woman belonged to a group of hunter-gatherers that colonized Europe and parts of Asia thousands of years before the agricultural revolution that occurred about 10 thousand years ago. This was part of a series of human migrations that are thought to be associated with the spread of the Upper Paleolithic (Stone Age) Aurignacian culture.

Mitogroup U* actually represents a collection of rare mitogroups, called U1, U3, U4, U7 and U9, that today have an extremely broad geographical distribution ranging from Europe to India and northern Africa. They are also found in Arabia, the northern Caucasus Mountains, and throughout the Near East. About 5 percent of people from European populations belong to Mitogroup U*. The sub-mitogroups U1, U3 and U4 are primarily found in European and North African populations. In contrast, the sub-mitogroup U7 is hardly found in European populations, but is found at 4 to 10 percent frequency in the populations of the Near East, Central Asia, Pakistan and India.

For more information about mitogroup U*:

1. en.wikipedia.org (U3)
2. en.wikipedia.org (U4)
3. en.wikipedia.org (U7)

deCODEme



Male line analysis: Your Y-group is R1a

9.1% of deCODEme users are a member of this group.

All members of Y-Group R1a can trace their Y chromosomes back to one man who is thought to have lived about 10 to 15 thousand years ago, probably in Western Asia. This man belonged to a group of hunter-gatherers that may later have made the Eurasian Steppes north of the Black and Caspian Seas their homeland. Some scientists believe that the male-line ancestors of Y-group R1a were among those responsible for the westwards expansion of the so-called Kurgan culture into Eastern and Central Europe about 5 thousand years ago. These peoples had domesticated the horse and may have been responsible for the spread of the first Indo-European languages into Europe.

Today, the greatest concentration of Y-group R1a members is found in the Slavic peoples of Eastern Europe, where 30 to 50 percent of males belong to this Y-group. Members are also found in Central and Western Asia, India, Pakistan, as well as among some populations of Mongolia and southern Siberia.

Notable members of Y-group R1a:

1. Somerled, 12th century founder of Clan Donald

For more information about Y-group R1a:

1. en.wikipedia.org
2. www.isogg.org

Somerled

From Wikipedia, the free encyclopedia

Somerled (Old Norse *Sumarliði*, Scottish Gaelic *Somhairle*, commonly Anglicized from Gaelic as *Sorley*) was a military and political leader of the Scottish Isles in the 12th century who was known in Gaelic as *rí Innse Gall* ("King of the Hebrides"). His father was Gillebride. The name, a common one amongst the Vikings, means *summer traveller* and is a kenning for Viking.[1]

Somerled first appears in historical chronicles in the year 1140[*citation needed*] as the regulus, or King, of Kintyre (Cinn Tìre) when he marries Raghnailt the daughter of Olaf (or Amhlaibh), King of Mann and the Isles. The year 1153 saw the deaths of two kings: David I of Scotland and Olaf of Mann. There was much confusion and discord as a result and Somerled took his chance—making offensive moves against both Scotland and Mann and the Isles, the latter having been inherited from Olaf by Somerled's brother-in-law, Goraidh mac Amhlaibh.

A summoning was sent, from Thorfin the most powerful jarl of the Hebrides, to Somerled Dougal—Somerled's own son by his wife, the daughter of the Manx king—to move so he might be "King over the Isles". In 1156 Goraidh was defeated in battle against 80 ships of Somerled's fleet and the two enemies partitioned the isles between them. Goraidh kept the islands north of Ardnamurchan with Somerled gaining the rest. However, two years following this Somerled returned to the Isle of Man with 53 warships. He defeated Goraidh again and this time forced him to flee to Norway. Somerled's kingdom now stretched from the Isle of Man to the Butt of Lewis.

Thus both Viking and Scot formed one people under a single lord and came to share a single culture, one way of life—they were to become a powerful and noted race known as the Gall-Gaidheal, literally meaning 'Foreign-Gaels'. It was upon the seas their power was situated under the rule of the Kings of the Isles yet new enemies arose in the east. The Stuarts made inroads in the west coast and eventually Somerled assembled a sizeable army to repel them. He advanced to the centre of the Stewarts' own territory, to Renfrew, where a great battle was fought in 1164. Much confusion surrounds the manner of the battle, and indeed whether a battle occurred at all, but what is certain is that Somerled was assassinated, after which his army retreated from the area.

Following the death of Somerled several powerful lords emerged from within his kingdom. The lordship was contested by two main families; that of Somerled and his descendants and that of the descendants of Goraidh mac Amhlaibh. During the 12th and 13th centuries the Scandinavian world saw much change in methods of rule and administration which ultimately resulted in more strongly centralized, unified kingdoms such as Denmark and Norway. However, this did not happen in the Kingdom of the Isles, which was instead absorbed into the greater Kingdom of Scotland, albeit its place in that state and the loyalty of its inhabitants to the King of Scots would remain peripheral and temperamental for centuries to come.

In 2005 an unpublished study by Professor of Human Genetics Bryan Sykes of Oxford led him to the conclusion that Somerled has possibly 500,000 living descendants—making him the second most common currently-known ancestor after Genghis Khan. Sykes's research led him to conclude that Somerled was a member of the Y-DNA R1a1 Haplogroup, sometimes considered the marker of Viking descent among men of deep British or Scottish ancestry.[2] [1] (http://www.undiscoveredscotland.co.uk/usbiography/stu/somerled.html) [2] (http://www.electricscotland.com/history/articles/norse.htm) Sykes' work has not been peer-reviewed.

Contents

Family

Main article: Clann Somhairle

By his first wife, who is unknown, their children were:

- Somhairle Og mac Somhairle
- Gillecallum mac Somhairle b. c 1135, Killed in battle in 1164 during Battle of Renfrew.

He also fathered:

- Gillies mac Somhairle
- Gall mac Somhairle

By his second wife, Ragnhildis Ólafsdóttir, daughter of Olaf I Godredsson, King of Mann and the Isles and Ingeborg Haakonsdottir daughter of Haakon Paulsson, Earl of Orkney, their children were:

- Dugall mac Somhairle (c. 1145 – c. 1192)
- Reginald mac Somhairle (c. 1148–1207)
- Aonghas mac Somhairle (c. 1150–1210)
- Olav mac Somhairle
- Bethag nic Somhairle, St Ronan's first prioress.

In fiction

Somerled is the central character of Nigel Tranter's novel *Lord of the Isles* (1983).

Head of State of the Isle of Man		
Preceded by **Godred V**	**King of Mann and the Isles** 1158–1164	Succeeded by **Ragnald III**

See also

- Lord of the Isles
- Clan Donald
- Clan MacDougall
- Norse-Gaels

- Uí Ímair
- John MacDonald II
- Scotland in the High Middle Ages

References

1. ^ Murray (1973) p.168.
2. ^ "DNA shows Celtic hero Somerled's Viking roots" (http://news.scotsman.com/latestnews/DNA-shows-Celtic-hero-Somerleds.2621296.jp) . *Scotsman*. 2005-04-26. http://news.scotsman.com/latestnews/DNA-shows-Celtic-hero-Somerleds.2621296.jp.

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- Murray, W.H. (1973) *The Islands of Western Scotland.* London. Eyre Methuen.
- Stiùbhart, Domhnall Uilleam *Rìoghachd nan Eilean* (Clò Hallaig, 2005) ISBN 0-9549914-0-0
- Williams, Ronald *The Lords of the Isles* (Chatto & Windus, 1997) ISBN 1-899863-17-6

Notes

Map of kinship

From a genetic point of view we are all unique, but some individuals are more similar than others.

Generally speaking, genetic differences reflect geography. People from the same geographic area tend to be more genetically similar than people from distant parts of the world.

Open Map Of Kinship

How it works

In this tool, you can examine your genetic relationship to people from all over the world at the same time as seeing how they are related to each other. Each small circle on the map represents one person from one of the world populations.

You are represented by a an icon of a person and you can also see the positions of your deCODEme friends.

What you see is like a map. Instead of cities or towns separated by geographical distances, we show the genetic distances between you and over 1000 individuals from 50 different worldwide populations. You will notice that people from the same population tend to form tight clusters on the map of kinship. Likewise, populations from the same regions of the world also tend to cluster together on the map.

Your position on the map tells you how closely related you are to the individuals and populations that are shov Initially, you are shown a map of kinship showing all the 50 world populations. By moving your mouse over the you will see the world regions to which they belong. If you click on one of the individuals on the world map, you map of the region this individual comes from. If you are not shown on one or more regional maps, then this is l closely related to its people.

The map of kinship is based on a statistical method called principal components analysis, sometimes called P method takes the genetic code of many individuals and uncovers hidden genetic patterns or dimensions involv SNPs. The technical term for these dimensions is “principal components” or PCs for short. Each dimension or thread of shared ancestry between individuals and can be used to arrange individuals to show how they are re these relationships in the three-dimensional map of kinship that can be opened by clicking on the “Open Map

By default, we show the three strongest dimensions (1-2-3) found in the set of individuals shown. However, yo to six different dimensions for the world map or the six regional maps.

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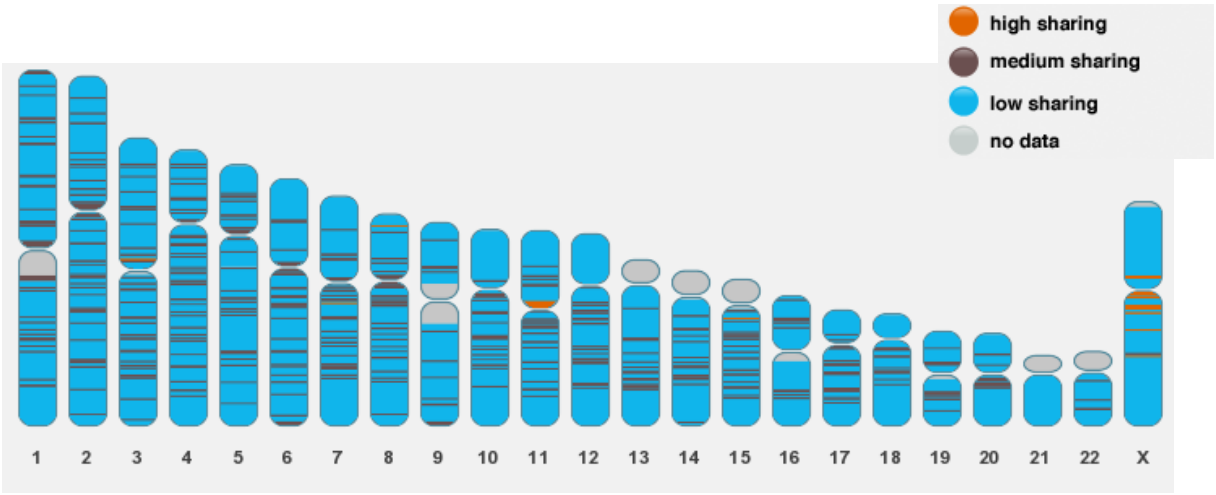

ZOOM
SHOW IN GENOME BROWSER

Fragment size: 1Mb **Update Image**

Your genetic sharing with Tuscan individual

Sharing 18.3% (low: 81.7%, medium: 18.0%, high: 0.3%)

Your genome was created through the fusion of two germ cells. The sperm cell from your father carried 23 chromosomes and the egg cell from your mother contained 23 corresponding chromosomes. In total, then, your genome is composed of 46 chromosomes, which can be arranged into 23 pairs.

When your parents produced the germ cells that gave rise to you, their chromosomes underwent a mixing process called recombination. In other words, the 23 chromosomes you inherited from your mother were a mixture of the chromosomes she inherited from her parents (your maternal grandparents). In the same way, the chromosomes you inherited from your father are a mixture of the chromosomes he inherited from his parents (your paternal grandparents).

Your chromosomes are therefore a mosaic of your parents' chromosomes, whose chromosomes were in turn a mosaic of their parents' chromosomes (your grandparents), whose chromosomes were in turn a mosaic of their parents' chromosomes (your great-grandparents), and so on, as your genealogy is traced back in time. This means that your genome can be viewed as a mosaic or tapestry made up of fragments of chromosomes from your ancestors. Fragments of chromosomes inherited from very recent ancestors, say grandparents, are expected to be large – typically tens of millions of nucleotides in size. As ancestors become more ancient, then the size of the chromosome fragments inherited from them become smaller – down to a few thousand or hundred nucleotides for ancestors born thousands of years ago.

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When we determine the amount of genetic sharing between individuals, we do not examine all the chromosomes at once. Rather, we break the chromosomes down into fragments of a particular size (the default size is 1 million nucleotides or 1Mb) and evaluate sharing for each fragment.

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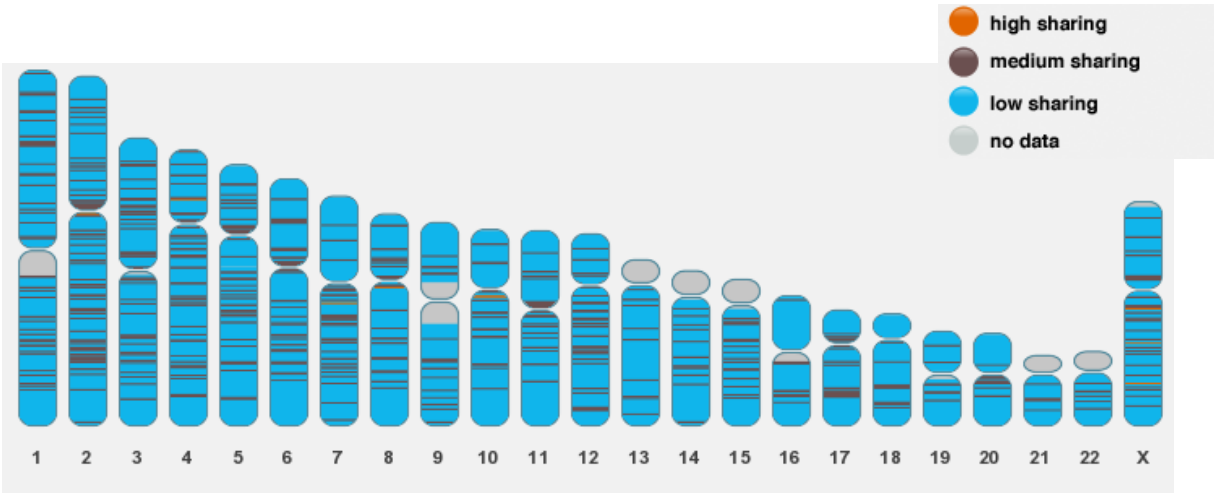

ZOOM
SHOW IN GENOME BROWSER

Fragment size: 1Mb **Update Image**

Your genetic sharing with Basque individual

Sharing 20.0% (low: 80.0%, medium: 19.8%, high: 0.2%)

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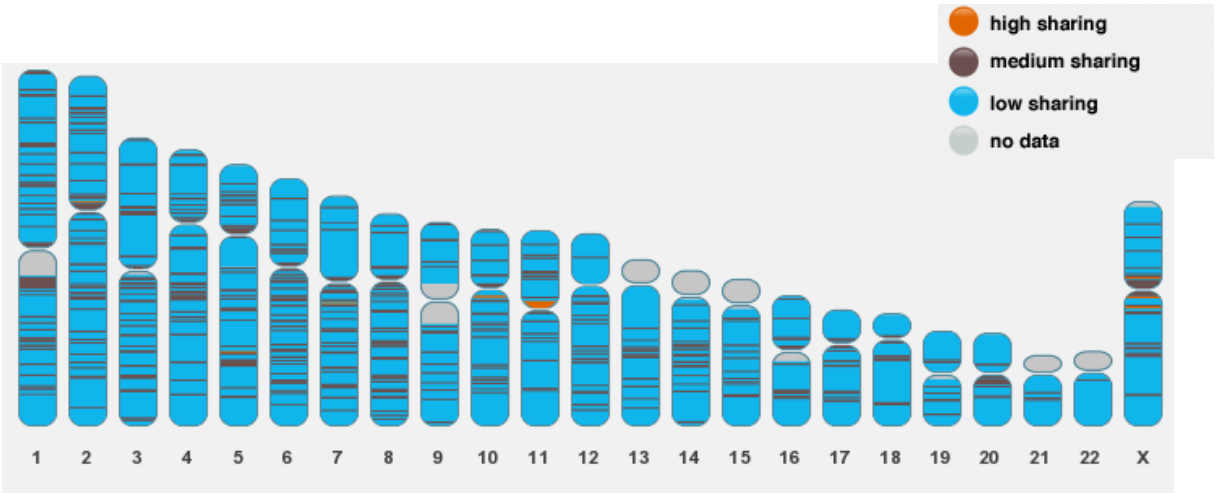

ZOOM
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Fragment size: 1Mb **Update Image**

Your genetic sharing with French individual

Sharing 20.2% (low: 79.8%, medium: 19.9%, high: 0.3%)

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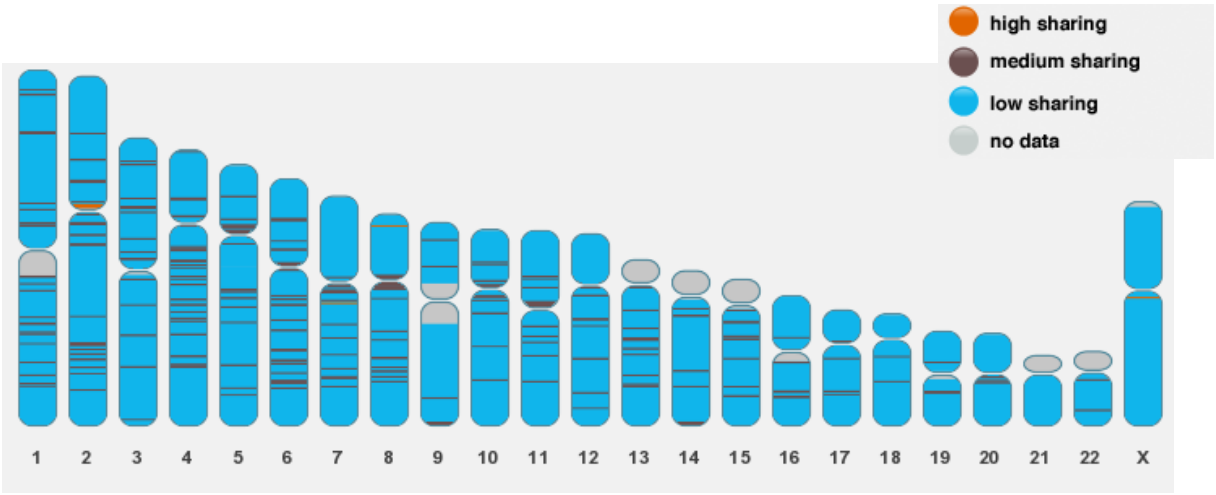

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