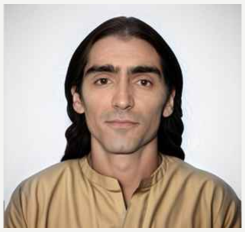
RAJKO ANCESTRY REPORT

Yours Simulated G25 Explore Your DNA coordinates are :
Rajko_scaled,0.129758,0.131003,0.041106,0.020672,0.035699,0.002231,0.00329,0.005077,0.00225,0.000911,-0.005521,-0.000899,0.002973,0.012937,-0.014386,0.007027,0.019818,0.0026,-0.004022,0.002626,-0.00262,-0.005688,0.008134,-0.007109,-0.006107
NB : please remember yours reals coordinates are the ones that will provide the most accurate results. To order your reals coordinates, please contact teepean47 (partner of Daviski), the cost is $15 if you use Wise directly with the link and transfer unless you are using USD or CAD with Swift/wire payments in which case you have to add the transfer costs to the amount. For credit card payments you can use Stripe. The price of 15€ covers the costs from Stripe : https://buy.stripe.com/bIYaFJ2qocAK4Rq9AB

Your ancient break down is :

TUR_Barcin_N :

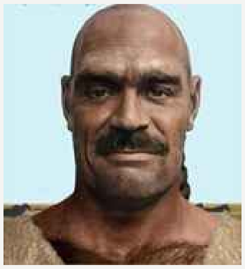


The DNA sample referred to as TUR_Barcin_N comes from the Barcın Höyük archaeological site in Turkey. This sample is associated with the Neolithic period, dating back to approximately 6500–6200 BCE. It represents the genetic profile of early Anatolian farmers, who played a significant role in the spread of agriculture into Europe.

The genetic makeup of this sample shows a strong connection to the Anatolian Neolithic population, with some links to early European farmers. The Y-DNA haplogroup is often associated with G2a, and the mtDNA haplogroups vary but are typically linked to early farming communities.

46.83 %

Yamnaya_RUS_Samara:



The Yamnaya culture, which thrived on the Pontic-Caspian steppe from around 3300 to 2600 BCE, has been extensively studied through ancient DNA analysis. The genetic makeup of the Yamnaya people is particularly significant because it has had a lasting impact on the genetic landscape of Europe and parts of Asia.

Genetic studies have shown that the Yamnaya people were a mix of Eastern European Hunter-Gatherers (EHG) and Caucasus Hunter-Gatherers (CHG) in roughly equal proportions

- This blend is often referred to as 'Steppe ancestry'. The Yamnaya also had some genetic contributions from Anatolian farmers, which they likely acquired through interactions with neighboring populations

- Y-chromosome haplogroups commonly found in Yamnaya individuals include R1b and I2, which are prevalent in modern European populations

- Mitochondrial DNA (mtDNA) haplogroups such as U5, H, and T have also been identified, indicating diverse maternal lineages

- The Yamnaya culture is closely linked to the spread of Indo-European languages and had a significant influence on subsequent cultures, such as the Corded Ware and Bell Beaker cultures

- Their migrations and interactions with other groups played a crucial role in shaping the genetic and cultural landscape of prehistoric Europe.

41.80 %

WHG:

Western Hunter-Gatherers (WHG) were a group of Mesolithic hunter-gatherers who lived in Europe from around 15,000 to 5,000 years ago. Their genetic ancestry is a significant component of modern European populations1

.Genetic studies have shown that WHGs had a distinct genetic profile, with Y-chromosome haplogroups such as I2 and mitochondrial DNA (mtDNA) haplogroups like U5 and U41

. These haplogroups are still present in modern European populations, indicating the lasting genetic legacy of WHGs.

WHGs were part of a broader network of hunter-gatherer groups in Europe, including Eastern Hunter-Gatherers (EHG) and Scandinavian Hunter-Gatherers (SHG). The interactions and migrations of these groups contributed to the complex genetic landscape of ancient Europe

10.25 %

Han:  The Han Chinese, the largest ethnic group in the world, have a rich and complex genetic history. Studies show that their genetic structure can be divided into two main groups: Northern Han and Southern Han. These groups reflect historical migrations, environmental adaptations, and interactions with neighboring populations The Han Chinese primarily belong to the Y-DNA haplogroup O, which is common among East Asian populations. Their mitochondrial DNA (mtDNA) also shows diversity, with haplogroups such as D, B, and F being prevalent. These genetic markers trace back to ancient East Asian populations and highlight the deep ancestry of the Han people	**0.80 %**
Levant PPNB:  The Pre-Pottery Neolithic B (PPNB) period, dating from around 8800 to 6500 BCE, is a significant era in the Levant region's prehistory. Genetic studies of ancient DNA from this period have provided valuable insights into the early agricultural communities and their genetic makeup. Ancient DNA analysis from PPNB sites, such as 'Ain Ghazal in Jordan, has revealed a mix of genetic ancestries. These populations show a blend of local Levantine hunter-gatherer ancestry and genetic contributions from Anatolia and the Zagros Mountains . This genetic mixture reflects the movement and interaction of different groups during the Neolithic period, likely associated with the spread of agriculture .The Y-chromosome haplogroups identified in PPNB individuals include E1b1b, G2a, and J, which are common in the Near East and surrounding regions . Mitochondrial DNA (mtDNA) haplogroups such as H, K, N, and T have also been found, indicating diverse maternal lineages .These genetic findings help us understand the complex demographic processes that shaped the early farming communities in the Levant and their connections with neighbouring regions.	**0.32 %**

All the reports below are based on Euclidian distance, please use the legend below to evaluate if your genetic distance is good. Remember that most ethnic reports are based on "genetic similarity" and not "direct ancestry".

GREAT	GOOD	AVERAGE	DISTANT	🟨	VERY DISTANT	🟧	🟧	🟥	🟥

Your modern break down is :

How to interpret ? This report is trying to break your ancestry using modern references, if you are mixed, you may see your differents ancestries appearing on this report, else it may show something more ancient.

Fit :	0.016080009519595578
Lithuanian_RA :	33.49 %
Greek_Cyclades_Kea :	16.57 %
Sardinian :	14.17 %
Pomak_Tikves_Plain :	13.54 %
Cossack_Kuban :	11.67 %
Abkhasian_Gudauta :	5.28 %
Spanish_Soria :	4.71 %

Your modern Breakdown Interpretation (by OpenAI) :

Your Y-DNA haplogroup **FT36856** is a subclade of **I2**, which is one of the most common paternal lineages in the Balkans, particularly among South Slavs, including Serbs. This haplogroup has deep roots in Southeastern Europe and is often associated with the spread of Slavic populations during the early medieval period.

Now, let's analyze your **modern population breakdown**:

1. Lithuanian_RA (33.49%) - "RA" likely refers to "Reference Ancient" or a proxy for Baltic/Slavic ancestry. - This high percentage suggests a strong **Balto-Slavic genetic component**, which aligns with the spread of Slavic peoples from Eastern Europe into the Balkans. - Many Serbs, Croats, and Bosnians carry significant Eastern European ancestry due to the Slavic migrations.

2. Greek_Cyclades_Kea (16.57%) - The Cyclades (including Kea) are islands in the Aegean Sea, part of Greece. - This indicates **a Mediterranean or Aegean genetic influence**, possibly linked to ancient Greek or pre-Slavic Balkan populations. - This could reflect historical interactions between Slavic settlers and native Balkan populations.

3. Sardinian (14.17%) - Sardinians are often used as a genetic proxy for **Neolithic European ancestry**. - This suggests a strong **pre-Indo-European substrate**, possibly linked to early farmers who settled the Balkans before the arrival of Indo-Europeans.

4. Pomak_Tikves_Plain (13.54%) - Pomaks are Slavic-speaking Muslims in Bulgaria and Greece, with a mix of Slavic and indigenous Balkan ancestry. - The **Tikves Plain** is in North Macedonia, an area historically inhabited by Slavs, Greeks, and Thracians. - This component likely reflects **regional Balkan ancestry**, shared with other South Slavs.

5. Cossack_Kuban (11.67%) - The Kuban Cossacks are a group from southern Russia and Ukraine, with strong East Slavic and steppe ancestry. - This suggests **a possible Eastern European or steppe influence**, aligning with the early Slavic migrations.

6. Abkhasian_Gudauta (5.28%) - The Abkhazians are a Caucasian ethnic group from the Black Sea region. - This could indicate **a minor Caucasus genetic signal**, possibly from historical interactions between the Balkans and the eastern Black Sea region.

7. Spanish_Soria (4.71%) - Soria is a region in Spain, and this signal likely represents **shared ancient European ancestry** rather than a direct Spanish connection. - It could reflect **Neolithic or Roman-era migration patterns**.

Summary Interpretation Your genetic breakdown suggests a mix of: 1. **Slavic (Balto-Slavic) ancestry** – Strong Lithuanian_RA and Cossack_Kuban signals. 2. **Native Balkan/Mediterranean ancestry** – Greek_Cyclades_Kea and Pomak_Tikves_Plain components. 3. **Pre-Indo-European (Neolithic Farmer) ancestry** – Sardinian influence. 4. **Minor Caucasus/Black Sea influence** – Abkhasian signal. 5. **Ancient Western European signal** – Spanish_Soria, likely reflecting deep European ancestry rather than direct Iberian connections.

What does this mean for your Serbian heritage? - Your Y-DNA (FT36856) suggests deep paternal roots in the Balkans, likely linked to early Slavic migrations. - Your autosomal DNA shows a strong **Balto-Slavic component**, but also significant **pre-Slavic Balkan and Mediterranean ancestry**. - The **Greek and Sardinian influences** suggest admixture with pre-Slavic populations in the Balkans. - The **Cossack/Kuban and Abkhasian signals** might indicate historical interactions with East Slavic or Caucasus groups.

This is a typical South Slavic genetic profile, showing a mix of **Slavic, Balkan, and Mediterranean influences**. Your ancestry is deeply connected to the broader history of the Balkans, reflecting migrations and cultural exchanges over thousands of years.

Would you like a deeper historical context on any specific component?

Your ancient break down is :

How to interpret ? This report is trying to break your ancestry using ancient references.

Fit :	0.010335817480814006
Slavic*(AD*540-1270) :	25.55 %
Sardinian*(AD*770-1000) :	17.84 %
Baltic*(AD*900-1050) :	15.62 %
Baltic*(AD*260-540) :	12.56 %
Byzantine*Anatolia*(AD*500-1100) :	9.31 %
Roman*Anatolia*(100*BC-AD*700) :	9.31 %
Roman*Italy*(20*BC-AD*600) :	4.01 %
Kartvelian :	1.70 %
Lazica :	1.70 %

Your Ancient Breakdown Interpretation (by OpenAI) :

Your Y-DNA haplogroup **FT36856** is a subclade of **I2-PH908**, which is common among South Slavs, particularly Serbs, Croats, and Bosniaks. This haplogroup is strongly associated with the Slavic migrations into the Balkans during the early medieval period (6th-7th centuries AD).

Now, let's interpret your **modern breakdown**:

1. Slavic (AD 540-1270) – 25.55% - This component represents your **early medieval Slavic ancestry**, which arrived in the Balkans during the migration period (6th-7th centuries AD). - It reflects genetic similarities with populations from **Poland, Ukraine, Belarus, and western Russia**. - The date range (AD 540-1270) corresponds to the expansion of Slavic tribes and the formation of early Slavic states.

2. Sardinian (AD 770-1000) – 17.84% - This may indicate **ancient Mediterranean or pre-Slavic Balkan ancestry**. - Sardinians are often used as a reference for **Neolithic farmer ancestry**, which was widespread in Europe before the Indo-European migrations. - This could reflect remnants of **Illyrian, Thracian, or even Roman-era populations** in the Balkans.

3. Baltic (AD 900-1050) – 15.62% - This suggests genetic links to **Baltic peoples (Lithuanians, Latvians, Estonians, or early Balto-Slavic groups)**. - It might be connected to the **early medieval movements of Slavic and Balto-Slavic tribes**.

4. Baltic (AD 260-540) – 12.56% - This represents an **earlier phase of Baltic or Balto-Slavic ancestry**, likely from the migration period. - It could be linked to the **Proto-Slavic homeland** in Eastern Europe before their expansion.

5. Byzantine Anatolia (AD 500-1100) – 9.31% - This reflects **genetic influence from the Eastern Roman (Byzantine) Empire**, which ruled the Balkans for centuries. - It could be linked to **Greek, Anatolian, or other Eastern Mediterranean populations** that mixed with Balkan peoples.

6. Roman Anatolia (100 BC - AD 700) – 9.31% - Similar to the Byzantine component, this suggests **Roman-era Anatolian influence**, possibly from Greek or Roman settlers in the Balkans. - It could also be linked

to **Thracian or Phrygian populations**, who had genetic similarities with Anatolians.

7. Roman Italy (20 BC - AD 600) – 4.01% - This may indicate **genetic input from Roman colonists or soldiers** who settled in the Balkans during the Roman Empire. - It could also reflect **Italic influence on pre-Slavic Balkan populations**.

8. Kartvelian (1.70%) & Lazica (1.70%) - These refer to **Caucasian genetic influence**, possibly from **Georgians or Laz people**. - This could be due to **Byzantine or Roman-era connections** between the Balkans and the Caucasus.

Overall Interpretation: Your genetic breakdown suggests a **strong South Slavic identity** with a mix of **early medieval Slavic, Baltic, and indigenous Balkan (Illyrian/Thracian/Roman) influences**. The presence of **Byzantine, Roman, and even minor Caucasian components** reflects the complex history of the Balkans, which was influenced by migrations, conquests, and cultural exchanges over centuries.

Your **Y-DNA (FT36856 - I2-PH908)** confirms your paternal lineage as part of the **early Slavic expansion**, while your autosomal DNA shows a blend of **Slavic, pre-Slavic Balkan, and Mediterranean influences**.

Would you like me to compare this to other Serbian genetic profiles?

Your 50 closests modern populations are :

How to interpret ? if you obtain a good distance with your first population (e.g bright green), you could very likely be from that ethnicity or a close ethnicity, else you are most probably mixed or your ethnicity is not referenced on Davidski datasheet.

Bosniak_Croatia	0.0194259965800955
Croat_Herzegovina	0.0228100326786263
Serb_Croatia	0.0238321910649141
Croat_Dalmatia	0.0243705511820624
Serb_Serbia_Macva	0.0246467500650822
Bosnian	0.0248262248841825
Bosniak	0.0253575325930551
Serbian	0.0254725372509297
Montenegrin	0.0256412388351265
Serb_Serbia_Belgrade	0.0259828804402839
Serb_Serbia_Toplica	0.026028372341543
Croat_Bosnia	0.026096932867293
Serb	0.0270629918748185
Serb_Serbia_Sumadija	0.0275381527731472

Serb_Bosnia	0.0278531675625055
Serb_Serbia_Nisava	0.028007499106687
Bosniak_Sandzak	0.028058729417141
Moldovan	0.0281860124529881
Serb_Serbia_Pomoravlje	0.0299160445747763
Romanian	0.0302038096603723
Serb_Serbia_Jablanica	0.0312798925695086
Croatian	0.0321058465547943
Serb_Serbia_Pcinja	0.0321790106435857
Serb_Serbia_Backa	0.0322274442595127
Croat	0.0328819929016719
Serb_Serbia_Central_Banat	0.0335069250901959
Bulgarian	0.034205849017383
Serb_Serbia_Moravica	0.0342130262911658
Macedonian	0.0342289858891554
Pomak_Bulgaria	0.0343210618892561
Pomak_Rhodope_Mountains	0.0348266097546115
Serb_Herzegovina	0.0363228260189099
Slovene	0.036421239566958
Slovenian	0.0373609326703711
Austrian	0.038075222415634
Hungarian	0.0380962488704597
Serb_Serbia_Rasina	0.0387798008504427
Pomak_Greece	0.0389106061479295
Rusyn_Ukraine	0.0392620624012545
Moldovan_Stefan_Voda	0.0393888388004775
Pomak_Danubian_Plain	0.0408671698555209
Croat_Slavonia	0.0408942477495307
Ukrainian_Zakarpattia	0.0415101383037927
Italian_Südtyrol	0.0431061585871439

Italian_Northeast	0.0443409727904114
Pomak_North_Macedonia	0.0445404950157719
Pomak_Tikves_Plain	0.0445407079871885
Italian_Friuli_Sappada_(Bavarian)	0.0447286653562868
Gagauz	0.0453568838986983
Italian_Friuli_Timau_(Bavarian)	0.0453681266876778

Your 50 closests modern 2-Ways are :

The 2Ways compares your coordinates to the ones of all referenced populations within the modern datasheet of Davidski. It measures how closely your admixture percentages are aligned with each population. It's important to understand that 2Ways aren't measuring shared DNA between your kit and referenced samples.

If you are from one ethnicity you should only concentrate on yours closests populations, else if you are mixed (e.g parents from differents ethnicities), yours closests 2Ways should be close to "50% Parent 1 Ethnicity - 50% Parent 2 Ethnicity". if you are more mixed (for example from latina America), your 2Ways is not going to be accurate.

62% Bulgarian + 38% Slovakian	0.0208602310236766
64% Slovakian + 36% Greek_Laconia	0.0213185899402851
55% Slovakian + 45% Greek_Central_Macedonia	0.0219057320573829
74% Bulgarian + 26% Cossack_Kuban	0.0219193316731867
79% Romanian + 21% Cossack_Kuban	0.021925905050325
86% Bosnian + 14% Spanish_Soria	0.0219497237670946
70% Romanian + 30% Slovakian	0.0221072648965761
55% Slovakian + 45% Rumelia_East	0.0221137227464483
76% Bulgarian + 24% Lithuanian_VA	0.0222473521131241
62% Slovakian + 38% Greek_Peloponnese	0.0224156112660869
56% Slovakian + 44% Albanian	0.0224281069583072
93% Bosnian + 7% Sardinian	0.0224554893470653
74% Macedonian + 26% Cossack_Kuban	0.0225319134442146
86% Montenegrin + 14% Cossack_Kuban	0.0226579701290512
65% Slovakian + 35% Greek_Izmir	0.0226890778502774
82% Romanian + 18% Lithuanian_VA	0.022717330787805
69% Bulgarian + 31% Sorb_Niederlausitz	0.0228668054788424

73% Bosnian + 27% Bulgarian	0.022891820698937
76% Bulgarian + 24% Lithuanian_PA	0.0228923152294632
78% Bulgarian + 22% Lithuanian_RA	0.0229310612477919
84% Romanian + 16% Lithuanian_RA	0.0230266824434554
66% Bosnian + 34% Romanian	0.0230731540576167
80% Bulgarian + 20% Lithuanian_SZ	0.023100604905131
72% Slovakian + 28% Greek_Kos	0.0231385800634621
68% Slovakian + 32% Italian_Basilicata	0.0231398191596584
88% Bosnian + 12% Spanish_Castello	0.023148222039909
80% Bulgarian + 20% Latvian	0.023152447783588
85% Romanian + 15% Lithuanian_SZ	0.0231602709111151
86% Serbian + 14% Cossack_Kuban	0.0231871631241894
56% Ukrainian_Rivne + 44% Greek_Laconia	0.0231978768912883
82% Romanian + 18% Lithuanian_PA	0.02320549343033
86% Romanian + 14% Latvian	0.0232210800801937
68% Slovakian + 32% Italian_Apulia	0.0232397323118832
71% Bulgarian + 29% Ukrainian_Rivne	0.0232619168737998
88% Bosnian + 12% Spanish_Murcia	0.0232931601536704
72% Romanian + 28% Moldovan_o	0.0233089092057334
78% Romanian + 22% Russian_Belgorod	0.0233093690694074
55% Italian_Umbria + 45% Lithuanian_RA	0.0233101904449563
90% Bosnian + 10% Greek_Laconia	0.0233166861791951
58% Greek_Central_Macedonia + 42% Cossack_Kuban	0.023320647419709
88% Bosnian + 12% Spanish_Baleares	0.0233207807480749
88% Bosnian + 12% Spanish_Pirineu	0.0233330297900417
77% Bulgarian + 23% Russian_Pskov	0.0233559240628192
89% Bosnian + 11% Spanish_La_Rioja	0.0233649833765405
89% Bosnian + 11% Spanish_Cantabria	0.0233738497181531
51% Greek_Laconia + 49% Lithuanian_PA	0.0233944976500429
88% Bosnian + 12% Spanish_Menorca	0.023397825385932

79% Romanian + 21% Ukrainian_Chernihiv	0.0234032398031459
53% Italian_Umbria + 47% Lithuanian_VA	0.0234078873873991
83% Romanian + 17% Russian_Pskov	0.0234370708027622
72% Bulgarian + 28% Ukrainian_Chernihiv	0.0234400753916736

Your ancient map :

How to interpret ? This map is trying to break your ancient ancestry and display on a map.

Your modern similitud map :

How to interpret ? This similitud Map is based on the modern Davidski G25 sheet + the French averages of the Explore Your DNA Project !. It's only going to be accurate for people that belong to ONE ethnicity, else it's going to show midpoints, which are the populations closest to your genetic composition. This map is a snapshot of you similitud with pre colonial period populations, means for example that people from Latin America are going to show ancestry in both Americas & Europe, same for North Americans, Australians & South Africans...Nomadic tribes and diasporas (Ashkenazis, Romas...) are not going to appear on the map so it's also going to show their ancient ancestry (e.g Ashkenazis are going to appear in both the Levant and Europe).

GREAT	GOOD	AVERAGE	DISTANT	VERY DISTANT