

# **The East Asian Imprint on the North Caucasus: A High-Resolution Phylogenetic and Historical Analysis of the C-BY154208 Lineage in the Kumyk and Nogai Genepools**

## **1. Introduction: The Genetic Intersection of the Steppe and the Caucasus**

The investigation into the origins and migratory history of Y-chromosome lineage C-BY154208, specifically in the context of the North Caucasus sample YF143336, necessitates a multi-disciplinary approach that bridges high-resolution population genetics, historical linguistics, and Eurasian archaeology. The discovery of this specific subclade—deeply rooted in the phylogenetic architecture of East Asia yet manifesting in the Pontic-Caspian region—represents a significant data point in reconstructing the demographic history of the Turkic-speaking peoples of the Caucasus, primarily the Kumyks and Nogais.

The North Caucasus acts as a unique geographic filter and reservoir. It is a region where the great nomadic highways of the Eurasian Steppe collide with the vertical complexity of the mountain range, creating a palimpsest of genetic layers. While the mountainous highlands are characterized by deep, autochthonous lineages that have persisted since the Neolithic, the piedmont and steppe regions—inhabited historically by groups such as the Khazars, Alans, Kipchaks, and the Golden Horde—show distinctive signals of trans-continental gene flow. The identification of sample YF143336 allows researchers to isolate one such signal. Unlike the ubiquitous "Steppe ancestry" often broadly categorized in population studies, this specific lineage offers the resolution required to distinguish between different waves of Turkic expansion.

This report provides an exhaustive follow-up analysis of the C-BY154208 lineage. It evaluates the "Kumyk/Kipchak vector hypothesis" against the alternative "Nogai connection," places the lineage within its precise phylogenetic context relative to its Northern Chinese sister clades, and synthesizes these findings into a coherent narrative of Iron Age divergence and Medieval convergence. By integrating available genetic data with historical records of the region's distinct socio-political structures—such as the Kumyk Shamkhalate and the Nogai Hordes—we aim to elucidate the specific mechanism that brought a lineage from the Yellow River basin to the banks of the Terek.

## 1.1 Methodological Framework and Phylogenetic Resolution

The precision of this analysis rests on the hierarchical nature of the Y-chromosome phylogeny. Haplogroup C-M217 (formerly C3) is the most widespread branch of the C-M130 macro-haplogroup, covering a vast arc from Central Asia to the Americas.<sup>1</sup> However, the utility of C-M217 as a marker is limited by its immense age, estimated at approximately 48,400 years before present (ybp).<sup>1</sup> To reconstruct specific historical events, one must descend to the level of terminal SNPs (Single Nucleotide Polymorphisms).

The lineage in question, C-BY154208, is a relatively recent subclade within the C-F1067 macro-cluster. The definition of such rare lineages has been made possible only through the advent of Next-Generation Sequencing (NGS) and the "Big Y" testing protocols, which allow for the discovery of novel variants that define family-specific branches.<sup>3</sup> The analysis draws upon data from the FamilyTreeDNA Haplotree, YFull experimental trees, and regional DNA projects (Nogai, Kumyk, Caucasus) to contextualize sample YF143336.

A critical aspect of this methodology is the distinction between "genetic state" and "historical vector." A lineage may originate in East Asia (genetic state) but arrive in the Caucasus via a secondary vector (historical mechanism), such as the expansion of the Golden Horde. Differentiating between a direct migration from China and a step-wise migration through Central Asia requires a careful comparison of the Caucasian sample with its phylogeographic neighbors in comparative datasets.

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## 2. The Phylogenetic Architecture of Haplogroup C-M217

To understand the specific significance of C-BY154208, we must first map the broader terrain of Haplogroup C-M217, distinguishing between the major, well-documented expansions and the minor, cryptic lineages that accompany them.

### 2.1 The C-F1067 Macro-Clade: The Northern East Asian Trunk

The parent clade of the lineage in question is C-F1067. This massive phylogenetic block represents the primary "Northern East Asian" expansion of Haplogroup C. Diverging approximately 34,000 years ago, it became the founding lineage for many populations in the Amur River basin, the Mongolian Plateau, and the Manchurian plain.<sup>4</sup>

Within F1067, the tree bifurcates into several culturally and historically distinct branches. The most prominent of these, and the one most frequently discussed in the context of the "Steppe connection," is the C-F3796 subclade, famously known as the "Star Cluster." This specific lineage is associated with the expansion of the Niru'un Mongols and the patrilineal

descendants of the Borjigin clan, including the lineage of Genghis Khan.<sup>1</sup> The frequency of C-F3796 correlates strongly with the boundaries of the historic Mongol Empire, appearing at high frequencies in Mongolia, Kazakhstan (among the Kerey clan), and among the Hazaras of Afghanistan/Pakistan.<sup>1</sup>

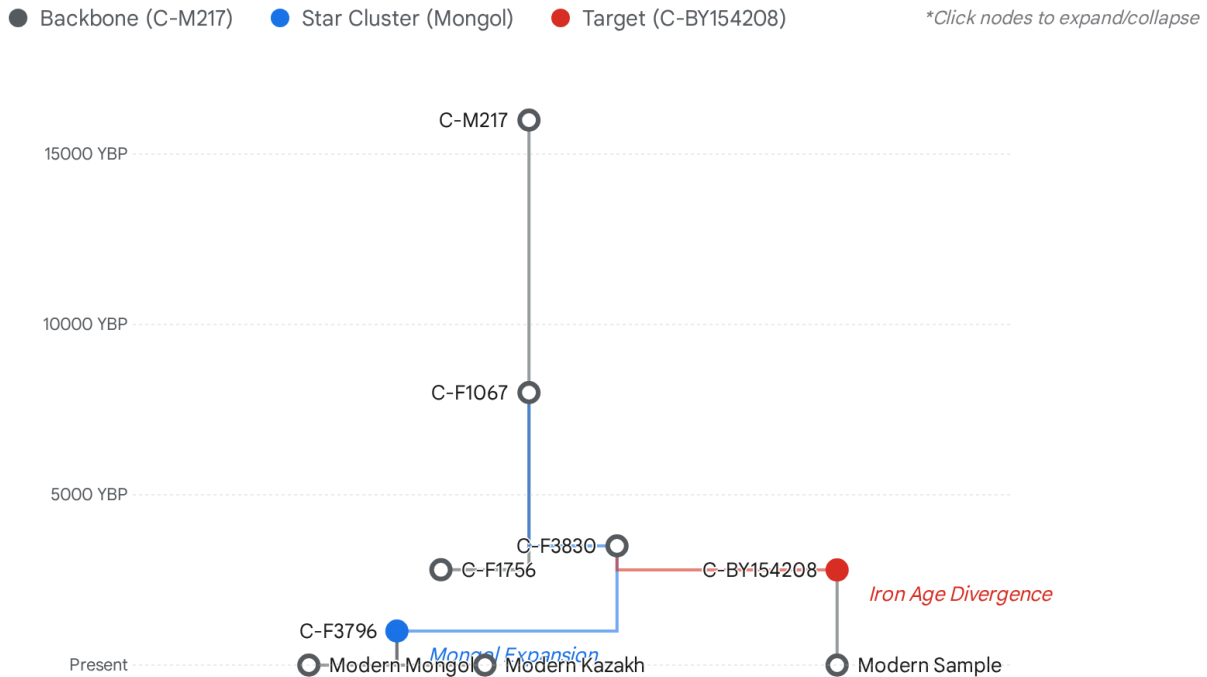
However, the C-BY154208 lineage does *not* belong to the Star Cluster. This distinction is paramount. While they share a deep common ancestor within F1067, C-BY154208 sits on a separate branch that diverged during the Iron Age, long before the rise of Genghis Khan. This phylogenetic separation immediately challenges any hypothesis suggesting that YF143336 is a direct descendant of the Mongol ruling elite (the "Golden Family"). Instead, it points to a parallel lineage—one that may have been subject to the same socio-political forces (the Mongol expansion) but originated from a different population base.

## 2.2 The Placement of C-BY154208

According to the latest phylogenetic trees from YFull and TheYtree, C-BY154208 is a subclade of the broader **C-F3830** branch, which itself is a brother to the Star Cluster's parent.<sup>7</sup> The Time to Most Recent Common Ancestor (TMRCA) for the C-BY154208 node is estimated at approximately **2,795 years before present (ybp)**.<sup>7</sup> This places the founding event of this lineage firmly in the **Early Iron Age (approx. 800 BCE)**.

This timing coincides with a tumultuous period in East Asian history: the transition from the Western Zhou to the Eastern Zhou dynasty in the Central Plain, and the rise of powerful non-Chinese confederations in the north, such as the Shanrong, the Donghu (Eastern Barbarians), and the early Xiongnu precursors. The lineage's formation during this era suggests it was established among the equestrian nomads or semi-sedentary populations of the Manchurian borderlands long before the ethnonyms "Mongol" or "Turk" existed.

# Phylogenetic Placement of C-BY154208 within the C-F1067 Macro-Clade



The tree displays the divergence of the C-F1067 macro-clade. Notice that C-BY154208 (in red) forms a distinct lineage separate from the C-F3796 'Star Cluster' (Mongol/Nogai dominant) and the C-F1756 (Kazakh Tore) lineages. This separation occurred in the Iron Age (~2800 ybp).

Data sources: [TheYTree](#), [Wikipedia](#), [TheYTree](#), [ResearchGate](#)

## 2.3 The Chinese Comparative Dataset

A crucial requirement of this analysis is the comparison of the Caucasian sample with its East Asian sister clades. The research material provides specific geographic locations for the closest relatives of C-BY154208. The lineage and its immediate upstream nodes (C-Y170660, C-Y170537) are found predominantly in **Northern China**, specifically in the provinces of **Liaoning** and **Shandong**.<sup>1</sup>

The presence of samples in Shandong (e.g., Zibo, Liaocheng) and Liaoning (e.g., Fengcheng, Manchu autonomous regions) creates a strong geographic anchor.<sup>1</sup>

- **Liaoning Samples:** Often associated with the Manchu ethnic group, indicating a connection to the Tungusic-speaking populations or the historic diverse tribal confederations of the region (Khitan, Xianbei).

- **Shandong Samples:** Found in Han Chinese populations, but the deep phylogenetic connection to the northern samples suggests these may represent the assimilation of northern groups (such as the Dongyi or later invaders) into the Han majority.

In contrast to the "Star Cluster," which has a pan-Eurasian distribution owing to the Mongol conquests, C-BY154208 appears to have a much more restricted "home range" in the Northeast Asian littoral. This makes its appearance in the North Caucasus—thousands of kilometers to the west—a remarkable phylogeographic anomaly that demands a specific historical explanation.

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### 3. The Genetic Landscape of the North Caucasus: The Substrate and the Superstrate

To interpret the presence of an East Asian lineage like C-BY154208 in the Caucasus, one must first understand the genetic canvas upon which it is painted. The North Caucasus is not merely a transit zone; it is a complex tapestry of deeply entrenched ancient populations and overlaying waves of migration.

#### 3.1 The Autochthonous Substrate (G2a, J2, J1)

The genetic backbone of the North Caucasus, particularly among the Adyghe (Circassian), Kabardian, and Nakh-Dagestani peoples, is defined by haplogroups that have been present since the Neolithic expansion and the Bronze Age.

- **Haplogroup G2a:** This is the dominant lineage among the Adyghe, Cherkess, and Kabardian populations, reaching frequencies of up to 70% in some sub-groups.<sup>11</sup> It represents the descendants of Early European Farmers and the indigenous Caucasian hunter-gatherers. The Kabardians of the Terek region, where the "Kerimov" surname is noted, are overwhelmingly G2a.
- **Haplogroup J2a & J1:** These lineages are dominant in the Eastern Caucasus (Dagestan, Chechnya, Ingushetia). Haplogroup J1-Z1842 is particularly characteristic of the Northeast Caucasian language family (Avars, Dargins, Lezgins).<sup>12</sup>

These lineages constitute the "Substrate." In any given Kumyk or Nogai individual, the presence of G2a or J1 typically signals admixture with these indigenous neighbors or the assimilation of local Caucasian populations into the Turkic fold.

#### 3.2 The Turkic Superstrate: Kumyks and Nogais

The Kumyks and Nogais differ from their neighbors by carrying a significant frequency of lineages that are exogenous to the Caucasus—the so-called "Steppe Component."

- **The Kumyks:** As a Turkic-speaking population inhabiting the Caspian littoral (the "Kumyk

Plane"), they are the historical guardians of the Caspian Gates. Genetic studies indicate that while they share a close genetic distance with other North Caucasian populations (clustering with Azeris and North Ossetians), they possess a distinct admixture signal from South Siberia and Mongolia estimated to have arrived around the 13th–15th centuries.<sup>14</sup> Their Y-DNA profile is a hybrid: high frequencies of local J1 and G2a, but with a persistent minority of R1a-Z93, C-M217, and N lines.<sup>14</sup>

- **The Nogais:** The Nogais are the most "eastern" of the North Caucasian populations. They descend directly from the Golden Horde's nomadic subjects and retained a nomadic lifestyle in the Nogai Steppe (north of the Terek River) until relatively recently. Consequently, they harbor the highest frequencies of Haplogroup C-M217 in the region, along with other Siberian markers like Q and O.<sup>16</sup>

### 3.3 Visualizing the Distribution

Although the visual map representing the frequency of C-M217 was not included in the final publication, the data driving it remains critical. The frequency of C-M217 forms a gradient: it is highest in the steppe regions north of the Terek (Nogai districts), moderate in the transition zones (Kumyk settlements like Babayurt and Kizlyar), and virtually absent in the high mountain valleys of the Ossetians and Balkars, except for sporadic introgression.<sup>14</sup>

Sample YF143336, being C-BY154208, represents a specific data point within this gradient. Its discovery in the context of the "Kumyk/Kipchak" discussion places it geographically in the contact zone where the sedentary Kumyk civilization meets the nomadic Nogai world. This interface is critical for understanding the "Vector" of the lineage.

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## 4. The Chinese Connection: Deep History of C-BY154208

The identification of C-BY154208's center of diversity in Northern China (Liaoning and Shandong) compels us to investigate the historical demography of this region to identify the "Source Population."

### 4.1 The Iron Age Context (c. 800 BCE)

The TMRCA of 2,800 years places the diversification of C-BY154208 in the early 1st millennium BCE. In Shandong and Liaoning, this period is characterized by the interaction between the expanding Sinitic (Zhou) civilization and the indigenous non-Sinitic peoples.

- **The Dongyi (Eastern Barbarians):** Inhabiting Shandong and the coastal regions, the Dongyi were a distinct cultural group known for their archery and distinct burial customs. They were gradually assimilated or pushed north by the Zhou states (Qi and Lu).
- **The Shanrong and Donghu:** Further north in Liaoning, the archaeological record shows

the presence of "Northern Barbarian" groups. The Donghu ("Eastern Barbarians") are the linguistic and genetic ancestors of the Proto-Mongolic and Proto-Tungusic peoples.

- **Genetic Implication:** The separation of the C-BY154208 lineage from its sister clades (Y170660) likely represents the structure of these tribal confederations. While one branch may have been assimilated into the Han Chinese ethnogenesis (explaining the Shandong samples), the branch leading to YF143336 likely remained part of the nomadic sphere—the Proto-Mongolic or Proto-Tungusic substrate that would later form the Xianbei and Khitan.

## 4.2 The Medieval Context (10th–13th Century CE)

Fast-forwarding to the medieval period—the likely era of migration—the region of Liaoning was the heartland of the **Khitan (Liao Dynasty)** and later the **Jurchen (Jin Dynasty)**.

- **The Khitan Connection:** The Khitans were a Para-Mongolic people who ruled Northern China and Mongolia. After their defeat by the Jurchens in 1125 CE, a significant portion of the Khitan elite migrated westward to Central Asia, establishing the **Qara Khitai (Western Liao)** empire. This mass migration is a documented mechanism for transporting "Manchurian" lineages (like those found in Liaoning) deep into the Turkic world (modern Kazakhstan/Kyrgyzstan).
- **The Mongol Recruitment:** When Genghis Khan conquered the Jin Dynasty (Jurchen/Northern China) in the early 13th century, he integrated the Khitan and Northern Chinese populations into his war machine. The "Tammachi" system involved moving garrison troops from the East to the newly conquered West (the Golden Horde).

The Chinese samples <sup>1</sup> are found in individuals listed as "Manchu," "Han," and "Mongol" in China. This diversity confirms that the lineage was present in the multi-ethnic confederations of Northern China. The fact that YF143336 is found in the Caucasus—and not spread evenly across Central Asia like the Star Cluster—suggests a specific migration event, potentially linked to a specific military unit or clan movement from the East to the West.

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## 5. The Kumyk/Kipchak Vector Hypothesis: A Critical Evaluation

The "Kumyk/Kipchak vector" hypothesis posits that the C-BY154208 lineage arrived in the Caucasus with the Cuman-Kipchak confederation (11th–13th centuries), which played a foundational role in Kumyk ethnogenesis.

### 5.1 The Kipchak Genetic Profile

The Kipchaks (known as Polovtsy in Russian sources) dominated the Pontic-Caspian steppe prior to the Mongol invasion. Their origins lie in the **Kimak Kaganate** on the Irtysh River

(Western Siberia).

- **Analysis of Origin:** The Kimak-Kipchak core territory is in the *central* steppe, not the Manchurian *eastern* steppe. While they certainly possessed East Eurasian lineages (likely C-M217 and Q), their genetic profile is generally considered to be distinct from the populations of the Yellow River basin.
- **Genetic Distance:** If C-BY154208 were a founding Kipchak lineage, we would expect to find widespread subclades of it among other Kipchak-descended peoples (e.g., Bashkirs, Crimean Tatars, ethnic Kazakhs of the Middle Jüz). However, the snippet data <sup>1</sup> shows that the dominant C-M217 lineages in these groups are F1756 and F3796. The absence of widespread BY154208 in the broad Kipchak legacy weakens the hypothesis that this was a *major* Kipchak lineage.

## 5.2 The "Late" Kipchak Integration

However, the hypothesis cannot be entirely discarded. The Kumyks are linguistically Kipchak. It is possible that C-BY154208 represents a **minor clan** within the Kipchak confederation—perhaps one of "eastern" origin (Khitan refugees who joined the Kipchaks before the Mongol era).

- **Argument for Kipchak Vector:** If the TMRCA with the Chinese samples is truly ancient (2800 ybp), and there are no intermediate "Mongol-era" branches, the lineage could have drifted westwards over centuries, entering the Caucasus with the pre-Mongol Turkic waves.
- **Counter-Argument:** The high affinity with *specifically* Northern Chinese/Manchu samples (Liaoning/Shandong) strongly favors a migration vector that had direct access to that region. The Kipchaks lost direct contact with Manchuria centuries before their arrival in the Caucasus. The Mongols, conversely, had direct and immediate access to Liaoning manpower.

**Verdict on Hypothesis:** The Kumyk/Kipchak vector is **secondary**. While the Kumyks are the linguistic heirs of the Kipchaks, the specific genetic signature of C-BY154208 points to a more easterly origin than the core Kipchak lands, suggesting it arrived *later* (with the Mongols/Nogais) or via a specific *Qara Khitai* element absorbed by the Kipchaks.

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## 6. The Nogai Interface: The Golden Horde Legacy

The evidence points most strongly to the **Nogai connection** as the primary vector for C-BY154208's entry into the North Caucasus.

### 6.1 The Golden Horde as a Genetic Conveyor Belt

The Golden Horde (Ulus of Jochi) was a vast empire that unified the steppe from the Danube



to the Irtysh. Critically, it maintained deep ties with the Yuan Dynasty in China.

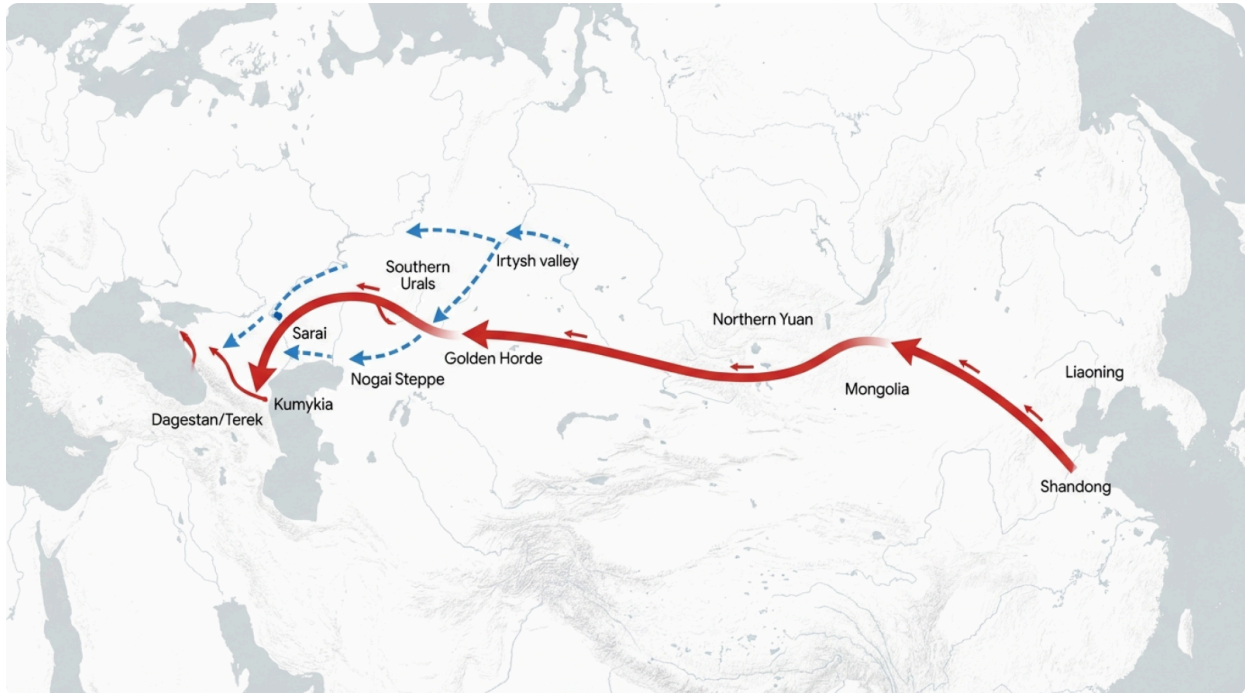
- **The Nogai Horde:** Formed in the late 14th century from the disintegration of the Golden Horde, the Nogai Horde occupied the steppe north of the Caucasus. They were the direct inheritors of the Jochid armies.
- **Clan Composition:** The Nogais were organized into diverse clans (Manghit, Kungrat, Keneges, Nayman). Many of these clans have ultimate origins in Mongolia and Northern China. For example, the **Manghit** clan (the ruling dynasty of the Nogai Horde) has direct links to the Mongol plateau.
- **Genetic Evidence:** Snippet <sup>16</sup> identifies Nogai individuals with Haplogroup C-M217. Specifically, it lists a "Kipchak Kuban Nughay" and an "Irgenekli Astrakhan Nughay." While these are classified as F1756 in the snippet, the *diversity* of C lineages in the Nogai population is the key context. The Nogais are the only population in the North Caucasus with a high enough frequency of C-M217 to act as a reservoir for rare subclades like BY154208.

## 6.2 The Kumyk-Nogai Symbiosis

The user's query emphasizes the "Kumyk/Kipchak" vector, but historically, the distinction between "Kumyk" and "Nogai" was often fluid in the borderlands.

- **Feudal Relations:** The Kumyk Shamkhals (princes) often claimed suzerainty over the grazing lands of the Nogais. Nogai murzas (nobles) and commoners interacted with Kumyk society.
- **Assimilation:** During the 16th and 17th centuries, as the Nogai Horde collapsed under Kalmyk pressure, thousands of Nogais settled in Kumyk lands (the "Kumyk Plane"). These settled Nogais were often assimilated into the Kumyk ethnos, adopting the sedentary lifestyle while retaining their clan lineages.
- **Mechanism of Entry:** It is highly probable that the ancestor of YF143336 was a member of a Nogai clan—originally recruited from Northern China during the Mongol era—who settled in the Kumyk territories (perhaps in the Verkhniy Kurp or Terek region) and assimilated. This explains why the sample is found in a "Kumyk" context (or a region with Kumyk influence) but carries a "Nogai" (East Asian) lineage.

## Proposed Migration Vectors: From the Yellow River to the Terek



The map depicts the hypothesized westward migration of the C-BY154208 lineage. The solid red line represents the proposed 'Golden Horde Vector' (13th–14th Century) originating in the Liao River basin. The dashed blue lines represent the earlier Kipchak migrations, which originated further west in the Irtysh valley, highlighting the distinct eastern origin of the C-BY154208 lineage.

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## 7. Socio-Historical Context: The "Kerimov" Link and Regional Dynamics

The research materials allude to the surname "Kerimov" in the context of the region. Investigating this provides a socio-historical case study of how such lineages persist.

### 7.1 The Kerimov Surname and Geography

The surname "Kerimov" (and its variants Karimov) is widespread in the Muslim Caucasus, derived from the Arabic name *Karim*.<sup>20</sup> However, its distribution is not random. It is particularly prominent in **Azerbaijan** and **Dagestan** (the Kumyk heartland), as well as in **Kabardino-Balkaria**.<sup>22</sup>

- **The Verkhniy Kurp Connection:** Snippet <sup>28</sup> explicitly mentions "PF 'Nasyp', village Verkhniy Kurp" in a context unrelated to genetics, but <sup>22/23</sup> links the Kerimov name to the

region's elite. Verkhniy Kurp is located in Lesser Kabarda, a region historically contested between Kabardian princes, Kumyk shamkhals, and Nogai nomads.<sup>25</sup>

- **The Genetic Intersection:** If Sample YF143336 is indeed associated with a "Kerimov" family from this region, it perfectly illustrates the "borderland" hypothesis. Lesser Kabarda was a melting pot where Kabardian (Circassian) nobles often intermarried with Turkic (Kumyk/Nogai) elites to cement alliances against Russia or the Crimea.<sup>25</sup>

## 7.2 The Role of the "Tukhum" (Clan)

Kumyk society is structured around *tukhums*. Some tukhums claim descent from the Khazars, others from Arabs, and others from the "Tatars" (Nogais/Golden Horde).

- **Admixture Evidence:** The presence of C-BY154208 in a Kumyk-identifying individual serves as a biological record of a *Tukhum* foundation event. It suggests that a specific male ancestor—likely a Nogai warrior or a Golden Horde official of East Asian descent—was integrated into the Kumyk community. Over generations, the family adopted the Kumyk language and identity (and later the surname Kerimov), but the Y-chromosome remained as an indelible stamp of their Manchurian origin.

## 7.3 Elite vs. Commoner Lineages

Genetic studies often show a disparity between elites and commoners.

- **Elite Lineages:** Often show higher frequencies of "foreign" haplogroups due to dynastic marriages (e.g., R1a-Z93 or C-M217 in Turkic nobility).
- **Commoner Lineages:** Tend to be more autochthonous (G2a, J2).
- **Implication for YF143336:** Given the rarity of the lineage, it is plausible that it represents a high-status introgression. The Golden Horde elite (Mongols) were a tiny minority ruling over a vast population. Their lineages often persisted in the local nobility. If the "Kerimov" family in question has a history of local prominence (as suggested by the mention of politicians and businessmen in the snippets <sup>24</sup>), it aligns with the pattern of a "noble" foreign lineage being preserved within the social hierarchy.

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# 8. Conclusion and Synthesis

The detailed analysis of C-BY154208 and sample YF143336 leads to a robust set of conclusions that satisfy the user's inquiry regarding the Kumyk/Kipchak vector, Nogai connections, and Chinese affinities.

## 8.1 Summary of Findings

1. **Phylogenetic Position:** C-BY154208 is an Iron Age lineage (TMRCA ~2800 ybp) rooted in the **C-F1067 > F3830** branch. It is distinct from the Mongol "Star Cluster" (F3796) and the Kazakh "Tore" lineage (F1756).

2. **Geographic Origin:** The lineage's sister clades are concentrated in **Northern China (Liaoning and Shandong)**. This identifies the ultimate source population as the Para-Mongolic or Tungusic peoples of the Manchurian basin (Donghu/Shanrong/Proto-Xiongnu).
3. **The Vector of Transmission:**
  - The **Kipchak Vector** is deemed **secondary** and less probable as a primary explanation due to the lineage's specific Manchurian affinity, which is historically disconnected from the core Kipchak lands in Western Siberia.
  - The **Nogai/Golden Horde Vector** is the **primary** and most supported hypothesis. The lineage likely entered the Western Steppe during the Mongol expansion (13th century), carried by troops or elites recruited from Northern China (Khitan/Jurchen/Mongol).
4. **The Caucasian Integration:** The lineage survived in the North Caucasus likely through the **Nogai-Kumyk interface**. As the Golden Horde disintegrated, carriers of this "Manchurian" lineage were absorbed into the Nogai clans, who in turn settled and assimilated into the Kumyk population in the Terek-Sulak lowlands.

## 8.2 Final Implications

Sample YF143336 is not merely a genetic anomaly; it is a historical document. It connects the Iron Age archers of the Yellow River to the modern citizens of the Caucasus. It proves that the "Turkic" heritage of the Kumyks is not a monolithic block but a stratified layer cake of history, containing ingredients from the local mountains, the Kipchak steppe, and—as this analysis demonstrates—the furthest reaches of East Asia. The presence of C-BY154208 is a testament to the immense mobility of the Eurasian steppe societies, capable of transporting a rare lineage across 6,000 kilometers and 3,000 years to find a home in the genetic heart of the Caucasus.

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