A Chromosome 19 Case Study: Genetic Evidence for Relationships Among Ralston-Variant Lineages

A DNA Time Capsule?

Prepared for the

Ralston Surname Project

July 2026

Author

J. Edwin Ralston

Administrator, FamilyTreeDNA Ralston Surname Project

Version 1.0

Table of Contents

Abstract iv
Introduction 1
Study Scope and Methodology 1
PART 1 - Shared Match Analysis 2
1. Initial Discovery 2
2. Initial Shared Match Observations 2
3. Significance of Matches from Different Wives 3
4. Significance of Matches from Different Children 3
5. Collateral Family Lines 3
6. Additional Ralston-Variant Families 4
7. Criteria for Identifying the Shared-Match Cluster 4
8. Shared-Match Cluster Table 7
9. Descendancy Trees 8
10. Evaluating the Evidence: Genuine Relationships or Coincidental Matches? 9
PART 2 - Chromosome 19 Analysis 10
1. Extending the Analysis Beyond AncestryDNA 10
2. Segment Mapping 10
GEDmatch 10
FamilyTreeDNA 11
MyHeritage 12
3. Chromosome 19: Characteristics and Precautions 13
Implications for the Depth of the Shared Ancestry 15
4. Triangulation 15
Triangulation terminology 15
GEDmatch Triangulation 15
Identifying Potential Matches 16
GEDmatch Chromosome 19 Triangulation Results 17
DR.John.70.rt vs. DR.Joan.41 Match Triangulation 17
5. Consolidated Chromosome 19 Segment Map 18
OT.Wend.61.an and the Donegal Connection 18
The OT.Jole.07.mh Match 18
PART 3: Discussion 20
1. Sticky Segments 20
2. Most Likely Interpretation 21
3. Important Limitations 21
PART 4 – Supporting Evidence and Future Research 22
1. Y-DNA Evidence 22

2. Future Research..... 23
Additional Y-DNA Testing..... 23
Conclusions..... 23
References.....24
Appendices.....25

List of Figures

Figure 1. Ancestry Shared-Match Cluster Table..... 7
Figure 2. Descendancy Trees..... 8
Figure 3. GEDmatch Compact Segment Mapper..... 11
Figure 4. FamilyTreeDNA Chromosome Browser..... 11
Figure 5. MyHeritage Chromosome Browser..... 13
Figure 6. Consolidated Chromosome 19 Segment Map..... 19

About the Author

J. Edwin Ralston has researched family history and genetic genealogy for more than 15 years, with a primary focus since his retirement in 2016. He is a volunteer administrator of the Ralston Surname Project at FamilyTreeDNA, where he helps coordinate Y-DNA and autosomal DNA research involving Ralston and related surname lineages. The Ralston Surname Project includes approximately 170 participants worldwide. His research emphasizes the integration of traditional genealogy with chromosome segment analysis, triangulation, and Y-DNA evidence to investigate historical family relationships. He is also the author of the websites **davidralston.info** and **ralstonproject.com**.

This report presents an independent genealogical DNA study prepared for the Ralston Surname Project. Its conclusions are based on the genetic and genealogical evidence available at the time of publication and may be revised as additional evidence becomes available.

Abstract

This study analyzes a large, multi-lineage autosomal **DNA cluster** centered on a shared Chromosome 19 segment found among descendants of numerous Ralston-variant families—Ralston, Roleston, Raulston, and Roulston—as well as two collateral lineages, Powers / Leece and Carpenter / Caraway. Using shared-match clustering, chromosome segment overlap, triangulation, and cross-platform validation (AncestryDNA, GEDmatch, FamilyTreeDNA, and MyHeritage), the analysis identifies a single, durable segment inherited by descendants of at least **seven independent 18th-century families**.

Although Chromosome 19 contains known pile-up regions, the segment examined here is unusually large, consistently triangulated, and inherited by descendants of multiple children within each family group. These patterns are difficult to reconcile with random population-level matching and are more consistent with **inheritance from a genuine shared ancestor.** Y-DNA evidence further supports a connection to northwest Ireland, particularly County Tyrone and County Donegal, where the I-BY194140 haplogroup is concentrated.

Taken together, the autosomal, triangulation, and Y-DNA evidence strongly suggest that these families—traditionally treated as unrelated—descend from an ancestor who lived prior to the earliest documented Ralston-variant families. The Chromosome 19 segment therefore **functions as a genetic** "**time capsule**," preserving evidence of a shared ancestral lineage that predates surviving genealogical records.

Introduction

Autosomal DNA is inherited from all ancestral lines through recombination, a process that shuffles genetic material in every generation. As a result, the amount of DNA inherited from **any particular ancestor decreases over time** and varies considerably among descendants.[1] While close relatives almost always share detectable autosomal DNA, more distant relatives may inherit little or none from a specific ancestral line. **Consequently, autosomal DNA alone rarely identifies relationships beyond approximately five to eight generations.**[2]

Because of these limitations, studies of **more distant relationships** must rely on the combined weight of multiple forms of evidence rather than any single DNA match. Shared-match clustering, chromosome segment overlap, triangulation, documented genealogies, and Y-DNA evidence each contribute independent information. When these independent observations **converge upon the same conclusion**, they can provide evidence for relationships that would not be apparent from any one source alone.[3]

Study Scope and Methodology

This study examines patterns of autosomal DNA sharing among descendants of the following ancestral families. While any individual DNA match may be ambiguous, repeated patterns of matching across multiple independent descendant groups may provide evidence of shared ancestry that would not be apparent from isolated comparisons.

- **David Ralston** (1741–1831), probably from Tyrone, and both his wives
- **Rachel Roleston** (1755–1807) and **Andrew Hayes** (1740–1805) Some researchers identify Rachel as a daughter of Robert Rolston (1715–1774) of County Tyrone.
- **William Rolstone** (c1708–1767) and his wife **Eleanor**, represented primarily through descendants of their son Matthew, together with one descendant of their son David.
- **Thomas Ralston** (1812–1895), born in Ireland, and **Sarah Fox** (1807–1869)
- **John Tate Ralston** (1774–1827) - son of Robert Ralston - and **Lettie Harris** (1776–1828)
- **John Powers** (1804–1885) and **Sarah Vicey Leece** (1810-1866)[4]
- **Wiley Carpenter** (1813–1859) and **Laney Caraway** (1822–1878)[5]
- Other **Ralston** or **Roulston** predecessors

---

[1] ISOGG, *Autosomal DNA Statistic*s.
[2] ISOGG, *Cousin Statistics.*
[3] ISOGG, *Autosomal DNA.*
[4] Sarah descends from a Dougherty family from Ireland (by most sources from either Tyrone or Donegal)
[5] Laney's mother, Margaret Clemmons (1791–1884), was born in Newberry County, South Carolina, to a mother whose identity has not been determined. Newberry County was also home to the family of Robert Ralston, father of John Tate Ralston.

The analysis combines:

1. Ancestry shared match clustering
2. GEDmatch segment analysis
3. GEDmatch triangulation analysis
4. MyHeritage match data
5. FTDNA match data
6. Y-DNA haplogroup evidence

The purpose of this study is not to identify the precise common ancestor of these families. Rather, it evaluates whether the combined genetic evidence supports the existence of a shared ancestral relationship among these lineages.

To protect the privacy of living individuals, all DNA testers are identified throughout this report by **coded identifiers**. Public usernames, kit numbers, and other personally identifying information have been omitted.

PART 1 - Shared Match Analysis

1. Initial Discovery

This investigation originated during routine examination of the AncestryDNA results of two cousins, designated **DR.Joan.41.rt** and **DR.John.70.rt**. Both are descendants of David Ralston (1741–1831) through his grandson Andrew Ralston (1798–1863), but through different wives. **DR.John.70.rt** descends through Andrew's first wife, Loveagh Wauchop, while **DR.Joan.41.rt** descends through his second wife, Mary Ann "Polly" Woods.

Despite their equal genealogical distance from Andrew Ralston, **DR.Joan.41.rt shared substantially more identifiable DNA matches with descendants of David Ralston** than did DR.John.70.rt. Further examination revealed that DR.Joan.41.rt also shared DNA with **descendants of other Ralston-variant families**—an **unexpected finding** that prompted further investigation.

---

2. Initial Shared Match Observations

Analysis revealed a large group of DNA matches to **DR.Joan.41.rt** (later identified as occurring on chromosome 19). **There were more than one hundred AncestryDNA matches that formed a large shared-match cluster.** AncestryDNA's SideView analysis assigned all of these matches to **DR.Joan.41.rt**'s paternal side, which is the side that would

have passed down her DNA from Andrew Ralston. These matches were not isolated occurrences. Among these matches were descendants of a few other David and Andrew Ralston descendants, but primarily descendants of **several other Ralston, Raulston, Roleston, etc. lines.** Additionally, included are large groups descending from the Leece/Powers family and the Caraway/Carpenter family. A few other Ralston/Rouston matches were part of the cluster, though not tying to a larger distinct family group.

---

3. Significance of Matches from Different Wives

The majority of matches to this large cluster by the David Ralston line are to **DR.Joan.41.rt**, a descendant of Andrew Ralston through his second wife. However, other Andrew Ralston descendants also shared many of these matches, primarily **DR.dano.48.an** who descends from Andrew Ralston through his first wife.

Their descent through different wives is significant because Andrew Ralston is their most recent common ancestor, whereas neither wife is shared between the two lines. Consequently, any DNA segment inherited by both descendants must have originated with Andrew Ralston or one of his ancestors, rather than with either of his wives.

---

4. Significance of Matches from Different Children

A family group or sub-cluster was included in this analysis **only when the shared matches descended from different children of the ancestral couple being evaluated.** This criterion was intended to reduce the likelihood that a shared DNA segment originated through a spouse or another line introduced in a later generation.

When descendants of multiple children of the same ancestral couple share the segment, the most parsimonious explanation is that the segment was inherited through that couple or their ancestors rather than through a descendant-specific connection. While this does not prove that the ancestral couple was the ultimate source of the segment, it strengthens the case that the connection predates the separation of their children into distinct family branches.

---

5. Collateral Family Lines

In addition to the sub-clusters representing Ralston and variant-surname families, two prominent collateral family groups were identified:

- Descendants of **John Powers (1804–1885) and Sarah Vicey Leece (1810–1866) –** represented by **23 DNA matches** descending from multiple children**.**
- Descendants of **Wiley Carpenter (1813–1859) and Laney Caraway (1822–1878) – r**epresented by **17 DNA matches** descending from multiple children**.**

These collateral family groups satisfy the same inclusion criteria applied to the Ralston surname groups, with representatives from multiple independent descendant branches. Although no documented genealogical relationship has been established between these families and the Ralston-variant lineages represented within the Chromosome 19 cluster, they are included because of their consistent genetic association with the cluster. The possible significance of these collateral relationships is discussed later in this report.

---

6. Additional Ralston-Variant Families

The **"Other" category** consists of lineages that satisfy the criteria for inclusion in the Chromosome 19 cluster but do not meet the additional requirements for recognition as independent family groups. Each includes a documented Ralston or Roulston ancestor but lacks representative DNA matches descending from multiple children of the ancestral couple.

One such lineage is represented by **OT.Gilb.01.an**, together with two children and two grandchildren, who descend from Eliza Ann Ralston, born about 1815 in Kentucky, whose parents are unknown.

Another is **OT.Wend.61.an** of County Donegal, Ireland. Her genealogy includes multiple documented Roulston lines from County Donegal. OT.Wend.61.an is noteworthy because evidence places the Y-DNA haplogroup I-BY194140, shared by several paternal lines represented in this study, in northwest Ireland. Her DNA matches further associate the Chromosome 19 cluster with the same geographic region as the documented origins of the I-BY194140 lineage.

The final "Other" lineage is represented by **OT.Debr.06.an**, a descendant of James Jeremiah Ralston (1798–1883) of Ireland.

---

7. Criteria for Identifying the Shared-Match Cluster

To illustrate how this chromosome 19 cluster was identified, four representative members of the emerging cluster were selected for detailed analysis of their shared matches with

DR.Joan.41.rt at AncestryDNA. Each was subsequently shown to share a triangulated chromosome 19 segment with **DR.Joan.41.rt.**

- From the Rachel Roleston group - **RR.Darr.60.an**,
- From the Thomas Ralston group - **TR.R. R.88.an**,
- From the Powers / Leece group - **PL.leah.61.an**, and
- From the “Other” group - **OT.Wend.61.an**.

In each case the total shared matches between **DR.Joan.41.rt** and the representative members were listed and analyzed. This process involved first eliminating unrelated matches - those which could not be assigned as part of this cluster.

- **Cluster matches.** Matches whose documented genealogy and shared-match pattern met the criteria for inclusion in the proposed chromosome 19 network. To be included, a match was required to share DNA with multiple individuals from multiple independent family groups within the cluster. Matches limited to a single family group, or to only one individual from multiple family groups, were not considered sufficient evidence for inclusion because such relationships could result from unrelated ancestral connections.
- **Not in the cluster**. Matches who do not meet the above criteria or who were from **DR.Joan.41.rt**’s maternal side were excluded from being part of the cluster. Several matches exhibited shared-match patterns suggestive of possible membership, often matching one representative from two different family groups. To minimize false-positive assignments resulting from unrelated ancestral connections, these individuals were conservatively classified as "Not in Cluster" unless additional corroborating shared matches were present.

Next, the remaining shared matches on the list were examined to determine if there was sufficient genealogical information provided to make an evaluation. The following were eliminated:

- **Private Trees**. Matches whose trees were entirely private and therefore unavailable for genealogical analysis.
- **No Trees**. Matches with no family tree attached to the DNA test.
- **Insufficient Trees**. The available genealogy is inadequate for analysis because one or more ancestral lines cannot be reconstructed due to missing or private individuals, conflicting or erroneous relationships, or because an unlinked account contains multiple trees and the tree associated with the DNA match cannot be determined.

The remaining shared matches comprised those considered part of the defined cluster for which sufficient genealogical information was available. These matches were then classified either:

- **Family Group** - Assigned by documented genealogy[6] to a family group identified in this study, or
- **Unknown Connection.**

Identification Results

The results of this evaluation are found in the following table. These results should not be taken to imply that individuals in the “unknown connection” category are unrelated. Rather, the underlying biological relationship may remain undocumented because of incomplete historical records, errors in existing pedigrees, or ancestral relationships that have not yet been identified through traditional genealogy.

	RR.Darr.60.an	TR.R. R.88.an	PL.leah.61.an	OT.Wend.61.an
Total Matches shared with DR.Joan.41.rt	**209**	**234**	**292**	**174**
Less Maternal Side	29	1	70	5
Less Not in Cluster	13	12	18	5
Remaining matches (in cluster)	**167**	**221**	**204**	**164**
Less No trees	33	36	28	22
Less Private trees	8	12	8	8
Less Insufficient Trees	46	74	59	48
Traceable matches	**80**	**99**	**109**	**86**
Assigned to Family Group	62	62	77	58
Unknown Connection	18	37	32	28
Percentage in a Family Group	**77.50%**	**62.63%**	**70.64%**	**67.44%**

[6] An exception was made for DNA matches with insufficient genealogical information when DNA evidence established the individual as the parent, child, or full sibling of a match already assigned to an identified family group. In these cases, the individual was assigned to the same family group because the immediate biological relationship was established directly by the DNA evidence. Half-siblings and more distant relationships were not assigned under this exception.

8. Shared-Match Cluster Table

Figure 1. Ancestry Shared-Match Cluster Table

Ancestry.com "Ralston" Cluster

To Ralston-variant, Powers / Leece and Carpenter / Caraway Lines

Numbers represent average identifiable shared DNA matches in common between the specified ancestral clusters.

		Average Number of Descendants Matched of						
Lineage	Avg cM	David Ralston	Rachel Roleston	William Rolstone	Thomas Ralston	John Tate Ralston	Powers / Leece	Carpenter / Caraway
DR.Joan.41.rt			31	27	7	8	23	17
David Ralston (7)			7	5	2	2	3	5
Rachel Roleston (31)	18	2	22	6	2	3	4	9
William Rolstone (27)	18	1	7	9	1	2	2	5
Thomas Ralston (7)	20	2	7	4	5	2	2	7
John Tate Ralston (8)	19	2	12	5	2	5	3	8
Powers / Leece (23)	15	1	5	3	1	1	13	4
Carpenter / Caraway (17)	22	2	17	8	2	4	6	13

A more complete version of the AncestryDNA shared-match table appears in Appendix One.

This table is a summary showing the number of shared matches each of these groups have in common with each other and with DR.Joan.41.rt, providing an illustration of how all these matches form a large cluster, with each family group forming a sub-cluster within the larger cluster. For each family group it shows the average number of matches for each group to itself and other groups.

Only two descendants of David Ralston and his second wife, Mary Reid, were identified among the Ancestry chromosome 19 matches. Their apparent representation within the cluster is likely understated, as Ancestry reports only matches exceeding approximately 20 cM. Additional relationships to other cluster members may exist below that threshold and therefore are not visible in the available data. Given the generational distance involved, shared DNA among descendants of David Ralston would often be expected to fall below this reporting threshold. The same limitation may also affect identification of other Andrew Ralston

descendants. In addition, Ancestry's Timber filtering may suppress some legitimate matches in regions prone to excess matching, including portions of chromosome 19.

---

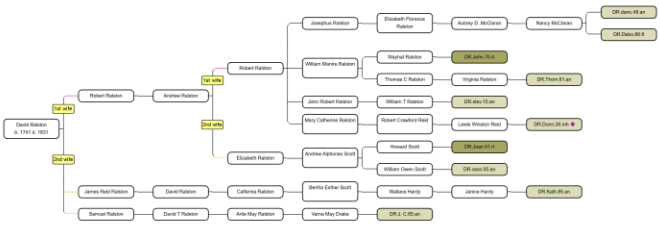
9. Descendancy Trees

As a way to visualize the different lines, descendancy trees were constructed showing the shared ancestral lineage of each group of shared matches. The 140 people shown on these trees are DNA matches to DR.Joan.41 (or DR.John.70.rt from segment matches) and are part of this shared match cluster. Although the majority of the matches in these trees are from AncestryDNA, a few were added from other platforms. The shared matches in these clusters are shown in tan/gold on the trees.

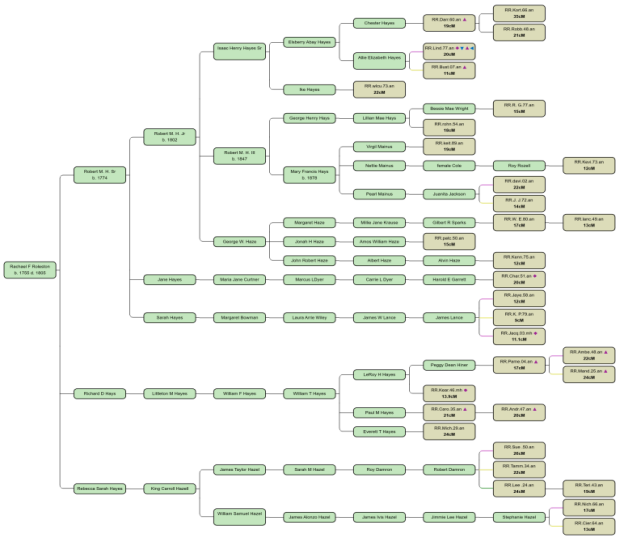
Note that each line descends from two or more children of the ancestral couple. These trees may be found in Appendix Two or click any thumbnail to view the full-size tree:

Figure 2. Descendancy Trees

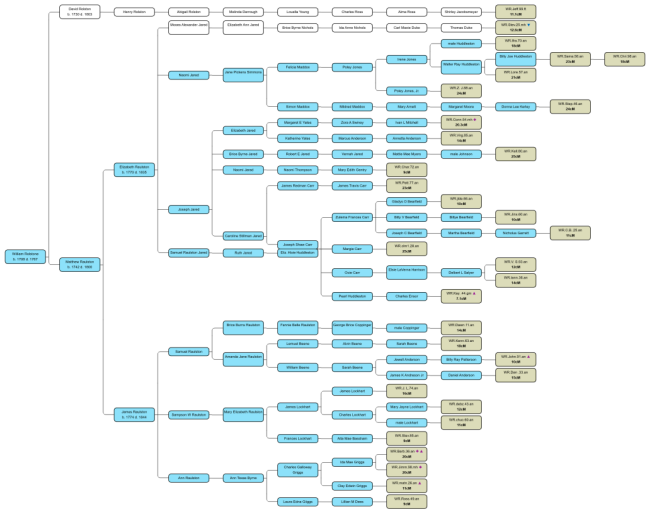
David Ralston:



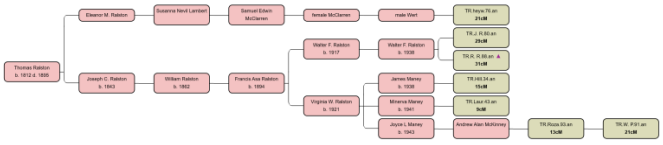
Rachel Roleston:



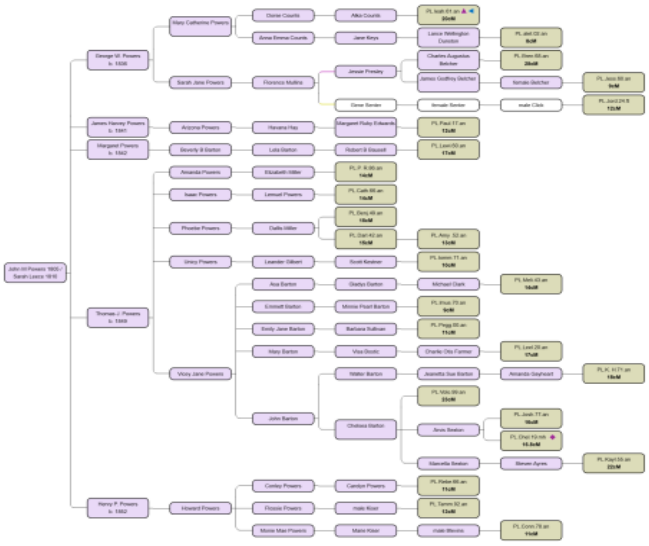
William Rolstone:



Thomas Ralston:



Powers / Leece:



John Tate Ralston:



Carpenter / Caraway:



---

10. Evaluating the Evidence: Genuine Relationships or Coincidental Matches?

At first glance, these findings appeared difficult to reconcile. For the matches to represent legitimate relationships among these paternal Ralston-variant lines, the shared historical origin would likely have been generations ago. Among the families represented in this study, the earliest documented ancestor is William Rolstone of Virginia, believed to have been born in the **early 1700s**. Any common origin shared by all of these lines would therefore have to **predate the earliest surviving genealogical records**. Detectable autosomal DNA inherited from such a **distant ancestor would ordinarily be expected to be rare**. However, the repeated appearance of matching descendants across multiple independent branches argues against simple random coincidence.

In genetic genealogy, it is not unusual to identify an occasional DNA match to a descendant of a distant common ancestral family, supported by a small number of shared matches to other descendants of that same individual. What appeared unusual in this case was the presence of **multiple matches** connecting descendants of several distinct Ralston, Roleston, Raulston, and Roulston lines that, if related, would have to converge on a shared ancestral source predating documented genealogy. This raised two competing possibilities: either the observed pattern reflected an artifact of the data, or it represented evidence of a genuine historical relationship among these families. The probability of numerous unrelated Ralston-variant

descendants repeatedly appearing within the same match clusters seemed **difficult to dismiss as mere coincidence**.

PART 2 - Chromosome 19 Analysis

1. Extending the Analysis Beyond AncestryDNA

The questions raised by the shared-match analysis prompted a broader investigation using platforms that provide chromosome segment data. Unlike AncestryDNA, these platforms allow direct comparison of shared chromosome segments, triangulation analysis, and cross-platform validation of the observed match patterns. Together, these methods provide stronger evidence for evaluating whether the observed DNA cluster is consistent with inheritance from a shared ancestral source.

This phase of the study involved locating the same individuals identified in the AncestryDNA cluster, together with additional descendants of the same ancestral family groups, within the **MyHeritage DNA**, **FamilyTreeDNA**, and **GEDmatch** databases. Because autosomal DNA is inherited randomly through recombination, not every documented descendant would be expected to inherit the chromosome 19 segment examined in this study. Additional descendants were included only when chromosome segment analysis demonstrated that they shared the chromosome 19 segment with members of the established cluster.

---

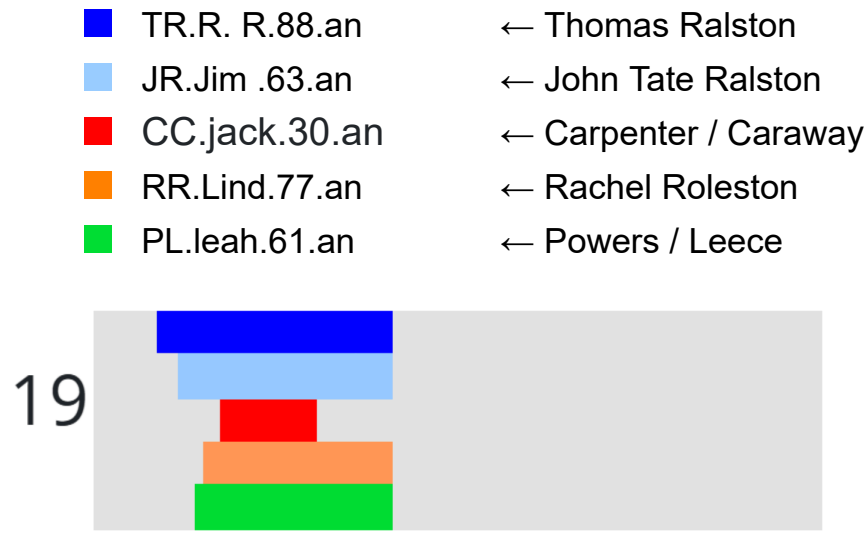
2. Segment Mapping

Chromosome browsers display the genomic locations of shared DNA segments, allowing direct comparison of segment overlap among multiple individuals. Such overlaps may indicate inheritance from a common ancestral source; however, chromosome overlap alone cannot distinguish genuine inheritance from population-level matching, identical-by-state segments, or chromosome 19 pile-up effects. Consequently, additional analyses—including triangulation and cross-platform validation—were necessary before drawing conclusions.

GEDmatch

The following is a representative chromosome compact map from GEDmatch showing how a few representatives from this cluster match DR.Joan.41.rt on Chromosome 19:

Figure 3. GEDmatch Compact Segment Mapper

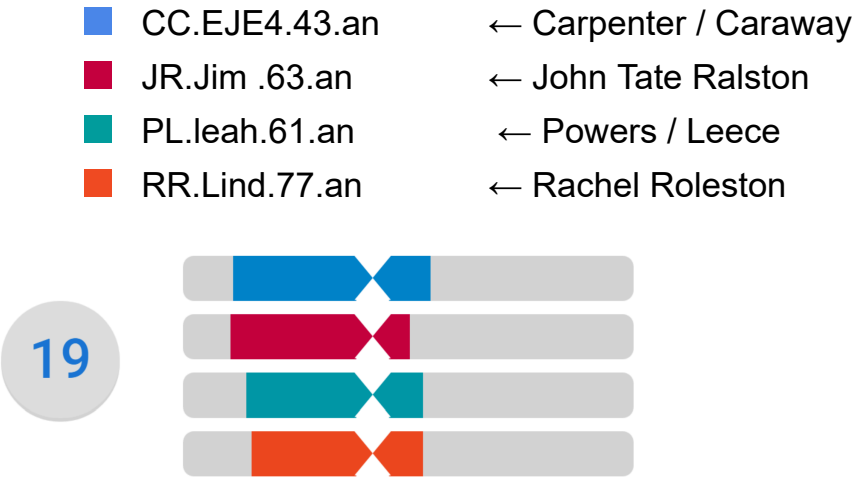


This shared overlap on chromosome 19 is consistent with inheritance from a common ancestral source. Although chromosome overlap alone cannot establish shared ancestry, it provides the foundation for the triangulation and cross-platform analyses that follow.

FamilyTreeDNA

Below is an example of a chromosome browser at FamilyTreeDNA comparing DR.Joan.41.rt to four members of the Ancestry cluster:

Figure 4. FamilyTreeDNA Chromosome Browser



However, overlapping chromosome segments alone are not sufficient to establish shared ancestry. Such overlaps may occur coincidentally, may represent segments that are **identical**

by state (IBS)[7] rather than **identical by descent (IBD)**[8], or may derive from different parental chromosomes[9]. Consequently, additional analysis is required to determine whether the shared segments represent genuine inheritance from a common ancestral source. One of the most powerful methods for making that determination is triangulation, discussed in the following section.

A standard chromosome browser, however, does not by itself establish triangulation. Humans possess two copies of each autosomal chromosome—one inherited from the mother and one from the father. Chromosome browsers compare each match only to the test subject and cannot determine whether two matching individuals share the segment on the same parental chromosome. Thus, even if Person A and Person B both overlap the test subject at the same location, one match could derive from the maternal chromosome and the other from the paternal chromosome.

In this study, AncestryDNA assigned all members of this cluster to DR.Joan.41.rt's paternal side. This finding substantially strengthens the evidence that the chromosome 19 segment derives from a common paternal lineage. Nevertheless, parental assignment alone does not constitute triangulation because it does not demonstrate that the matching individuals also share the segment with one another.

True triangulation occurs when three or more individuals all match one another on the same overlapping chromosomal segment. For a valid triangulation group, Person A must match Person B, Person B must match Person C, and Person C must match Person A within the same segment boundaries. Such a result provides strong evidence that all members of the group inherited the segment from a common ancestral source.[10]

MyHeritage

Compare the results for these users on MyHeritage.com:

Figure 5a. MyHeritage Chromosome Browser

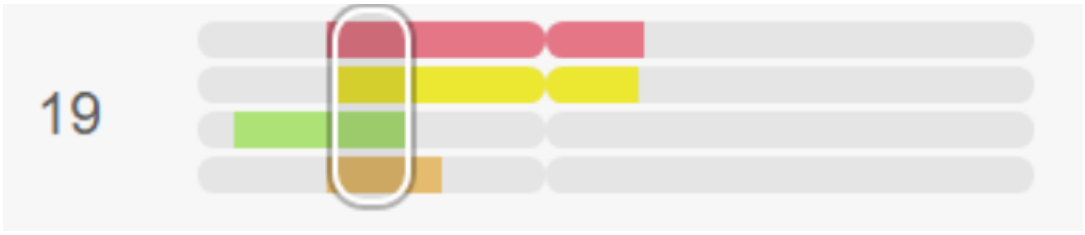
RR.Lind.77.an	← Rachel Roleston
OT.Wend.61.an	← Donegal Roulstons
WR.Conn.54.mh	← William Rolstone
RR.Jacq.03.mh	← Rachel Roleston
PL.Chel.19.mh	← Powers / Leece

[7] ISOGG, *Identical by State.*
[8] ISOGG, *Identical by Descent.*
[9] Estes, Roberta, *Hit a Genetic Genealogy Home Run Using Your Double-Sided, Two-Faced Chromosomes While Avoiding Imposters*.
[10] ISOGG, *Triangulation*.



Figure 5b. MyHeritage Chromosome Browser

RR.Lind.77.an ← Rachel Roleston
OT.Wend.61.an ← Donegal Roulstons
DR.Donn.26.mh ← David Ralston (Andrew Ralston 1st wife)
RR.Kear.46.mh ← Rachel Roleston



The rounded rectangle identifies the chromosomal interval over which all compared kits triangulate, indicating inheritance of the same DNA segment. Note that the DR.Donn.26.mh match confirms another member of the David Ralston family is part of this cluster, matching beyond DR.Joan.41.rt or DR.John.70.rt

---

3. Chromosome 19: Characteristics and Precautions

Autosomal DNA alone cannot definitively prove exact genealogical relationships, as shared segments may simply reflect a deeper, ancient population pool rather than a recent common ancestor. Consequently, small segment matches must be interpreted with caution, and any tentative genetic associations must be cross-examined alongside documented genealogies and historical context.[11]

Chromosome 19 warrants particular caution in genetic genealogy studies. As the most gene-dense chromosome in the human genome,[12] it contains several regions prone to

[11] ISOGG, *Endogamy*.
[12] International Human Genome Sequencing Consortium.

elevated, anomalous matching among unrelated individuals. These **"pile-up regions"** occur due to ancient population histories, structural chromosomal features, or localized reductions in recombination rather than recent genealogical relationships.[13] For this reason, chromosome 19 matches should not be interpreted in isolation; indeed, this structural volatility makes these segments highly susceptible to heavy Timber filtering by AncestryDNA.[14] Therefore, the analysis must account for the likelihood that some chromosome 19 matches described in this report reflect deep **population-level sharing rather than recent inheritance**.

Furthermore, different testing companies apply varying methods to suppress or filter pile-up regions. For example, certain chromosome 19 matches reported by FamilyTreeDNA, GEDmatch, and MyHeritage are completely omitted by AncestryDNA due to differences in segment-filtering algorithms.[15] However, the vulnerability of this chromosome to pile-ups **does not inherently invalidate all matches** within the region, nor does it preclude the presence of legitimate DNA segments passed down from recent ancestors. Categorically disregarding these matches risks discarding valid genealogical evidence alongside the algorithmic background noise—akin to pulling up the **wheat with the tares.**

While Chromosome 19 contains regions prone to elevated background matching, the segment identified in this study exhibits characteristics that distinguish it from typical pile up artifacts.

1. The shared segment is **substantially large**r than the short, low quality segments commonly associated with population level matching.[16]
2. The segment triangulates across descendants of at least **seven independent 18th century lineages**—each represented by multiple children of the ancestral couple—**making random coincidence statistically implausible**.
3. The segment appears consistently **across four testing platforms**, each using different filtering algorithms, which reduces the likelihood that the observed pattern is an artifact of any single company's methodology.

Most importantly, the individuals who share this segment do not merely overlap with the test subject; they also match one another on the same segment, forming a true **triangulation group**. This pattern is incompatible with pile up behavior, which typically produces broad, unstructured clusters lacking genealogical coherence. Instead, the Chromosome 19 segment analyzed here displays a structured, lineage specific inheritance pattern that aligns with documented genealogies and cross platform triangulation.

[13] ISOGG, *Identical by Descent*.
[14] AncestryDNA *Matching White Paper*.
[15] ISOGG, *Autosomal DNA Tools*.
[16] Family History Fanatics, *Small DNA Segments*.

Implications for the Depth of the Shared Ancestry

The breadth of the triangulation group indicates that the shared ancestor must predate the earliest documented Ralston-variant individuals in colonial America. Descendants of David Ralston, Rachel Roleston, William Rolstone, Thomas Ralston, and John Tate Ralston all carry the same segment, despite these lines diverging by the early to mid 1700s. The presence of the same segment among descendants of the Powers / Leece and Carpenter / Caraway families—who have no known genealogical connection to the Ralston-variant lines—further supports a deeper ancestral origin.

---

4. Triangulation

Triangulation terminology

In this report, a match described as “triangulated” means that the individual triangulates with one of the study reference tests, DR.Joan.41.rt or DR.John.70.rt, and at least one additional member of the chromosome 19 cluster belonging to an identified family group. The term does not imply that every individual shown in a figure belongs to the same triangulation group across the entire overlapping interval.

GEDmatch Triangulation

The GEDmatch Triangulation Tool automates the identification of triangulated groups by finding individuals who not only match the test subject on the same chromosomal segment, but also match one another within that interval. The resulting report groups these individuals into triangulation sets, allowing large numbers of potential IBD matches to be evaluated efficiently.

Because the report is subject to practical limits on the number and type of matches included, some legitimate triangulated matches may be omitted. Additional members of the chromosome 19 cluster were therefore identified using Segment Search and Multiple Kit Analysis, described below.

Identifying Potential Matches

Potential matches were initially identified using GEDmatch Tier 1 search tools, including **Segment Search** and **People Who Match Both Kits**, together with shared-match ("In Common With") comparisons on other testing platforms. These searches identified individuals who shared overlapping chromosome segments with the study participants.

Candidate kit numbers were then evaluated using the GEDmatch Tier 1 **Multiple Kit Analysis** tool. By comparing a curated group of kits simultaneously, this analysis determined whether the observed segment overlaps represented true triangulated groups rather than isolated pairwise matches, revealing relationships not apparent from individual comparisons alone.

Based on cross-platform analyses, DR.Joan.41.rt was found to share the core research cluster on chromosome 19, specifically between genomic positions **5,246,717** and **32,682,723**. A GEDmatch Segment Search was performed within this interval to identify all users sharing overlapping DNA segments with DR.Joan.41.rt.

The initial Segment Search identified **127** individuals matching DR.Joan.41.rt within the specified genomic interval. Because each autosomal chromosome consists of one maternal and one paternal copy, and because shared DNA segments vary in length and quality, not every individual identified within the interval would be expected to triangulate.

The resulting matches were evaluated using the same criteria previously applied to the AncestryDNA shared-match cluster.

Category	Number
Total matches to DR.Joan.41.rt	127
Less: Did not triangulate (opposite parental chromosome)	45
Triangulated matches	**82**
Less: Private, incomplete, or no family tree	57
Matches with evaluable lineage	**25**
Assigned to a Family Group	17
Unknown Connection (4 unique lineages)	8

Of the **25 matches** whose genealogies could be evaluated, **17 (68%)** were assigned to one of the established family groups. This unusually high proportion of genealogically connected matches provides additional support that the chromosome 19 segment represents inheritance from a shared ancestral source rather than random population-level matching.

GEDmatch Chromosome 19 Triangulation Results

The following are the 17 matches identified as part of the family groups cluster: (Pseudonyms ending in “.an” are part of the original AncestryDNA cluster.)

- JR.Jim .63.an ← John Tate Ralston
- WR.matn.26.an ← William Rolstone
- WR.Barb.36.an ← William Rolstone
- WR.John.91.an ← William Rolstone
- WR.Kay .44.gm ← William Rolstone
- RR.Ambe.48.an * ← Rachel Roleston
- RR.Caro.35.an ← Rachel Roleston
- RR.Darr.60.an ← Rachel Roleston
- RR.Andr.47.an * ← Rachel Roleston
- RR.Lind.77.an ← Rachel Roleston
- RR.Mand.25.an * ← Rachel Roleston
- RR.Pame.04.an ← Rachel Roleston
- TR.R. R.88.an ← Thomas Ralston
- PL.leah.61.an ← Powers / Leece
- CC.jack.30.an ← Carpenter / Caraway
- CC.T. E.77.an * ← Carpenter / Caraway
- OT.Wend.61.an ← William & Eliza Roulston

* Since RR.Andr.47.an is RR.Caro.35.an's son, RR.Ambe.48.an and RR.Mand.25.an are RR.Pame.04.an's daughters, and CC.T. E.77.an is CC.jack.30.an's brother, these redundant matches were removed from the triangulation report for clarity.

The resultant report (Appendix Three) shows definite triangulation between all these kits.

DR.John.70.rt vs. DR.Joan.41 Match Triangulation

As noted at the beginning of this report, DR.Joan.41.rt appears to match more "Ralston" descendants than DR.John.70.rt. This appears to also be true on Chromosome 19, In an area higher on 19, just beyond the segment where DR.Joan.41 matches the cluster, DR.John.70.rt matches PL.leah.61.an and RR.Lind.77.an of the cluster. His triangulation with these matches is shown at the bottom of the report. Taken by itself, this small triangulation could be dismissed as insignificant, but given the triangulation of these same individuals with DR.Joan.41 on the same chromosome, adds more weight to this.

These findings suggest that this region of chromosome 19 may originally have formed part of a **larger ancestral segment** that was progressively subdivided through recombination over successive generations, with different portions inherited by different descendant lines.

5. Consolidated Chromosome 19 Segment Map

The following table is a **consolidated segment map** of **DR.Joan.41.rt**'s Chromosome 19 segment matches to people in this cluster from FamilyTreeDNA, MyHeritage, and GEDmatch including **DR.John.70.rt**'s matches at a higher location on Chromosome 19. Note that **DR.John.70.rt** matches some of the same people on this higher segment as **DR.Joan.41.rt** on the lower segment.

The lack of a triangulation symbol by any match does not mean they do not triangulate, but rather their DNA was not uploaded to or tested at GEDmatch or MyHeritage.

OT.Wend.61.an and the Donegal Connection

One especially important MyHeritage match involved OT.Wend.61.an, a descendant of a couple of Roulston lines of Donegal.

This connection is significant because OT.Wend.61.an lives in Donegal, Ireland, her Roulston ancestors also lived in Donegal, and the line remained in Ireland rather than emigrating to America. This suggests that at least some of the shared ancestry among these Ralston / Roulston lines predates emigration.

In other words, the relationship may derive from a broader Ulster Ralston / Roulston family network already established in Ireland before migration to America.

The OT.Jole.07.mh Match

Another intriguing MyHeritage match involved OT.Jole.07.mh, apparently from a separate UK-based Roulston line. Although the tree attached to this match was limited, the appearance of another Roulston surname line outside the previously identified American clusters may provide additional evidence that these families were historically related.

Figure 6. Consolidated Chromosome 19 Segment Map

With results from FamilyTreeDNA, MyHeritage, and GEDmatch

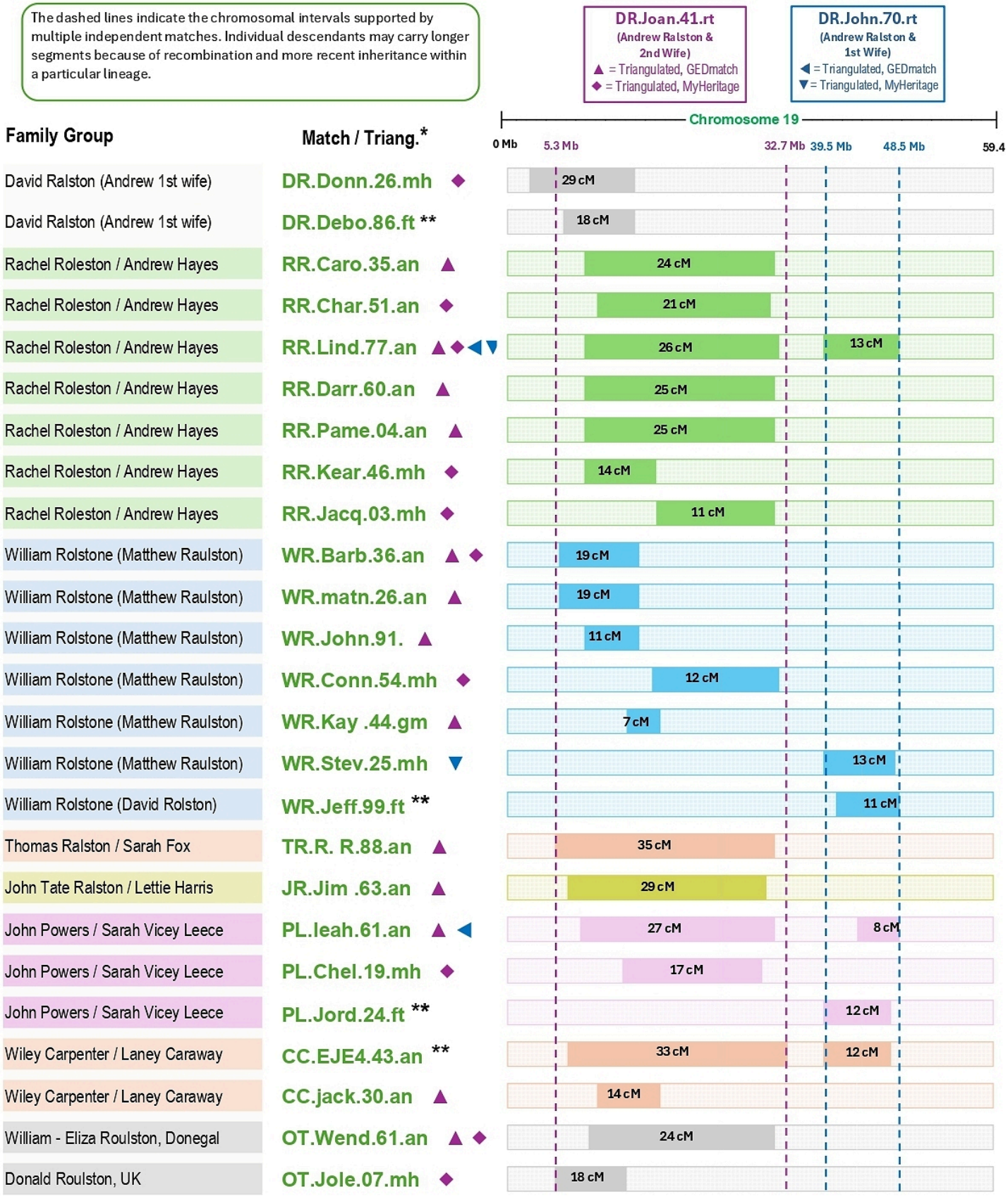


Figure 6 (continued). Notes

* A match is described as "triangulated" if the individual triangulates with one of the study reference tests, **DR.Joan.41.rt** or **DR.John.70.rt**, and at least one additional member of the chromosome 19 cluster belonging to an identified family group.

** Segment identified at FamilyTreeDNA. FamilyTreeDNA does not provide triangulation information.

Note: The following matches, although having triangulated segments, were omitted from this chart due to redundancy, being siblings or children of other triangulated matches.

Descendants of Rachel Roleston: **RR.Ambe.48.an**, **RR.Andr.47.an**, **RR.Bust.07.an**, and **RR.Mand.25.an**

Descendant of Matthew Raulston: **MR.Jimm.98.mh**

Descendant of Caraway / Carpenter: **CC.T. E.77.an**

PART 3: Discussion

1. Sticky Segments

In genetic genealogy, the colloquial term sticky refers to ancestral segments that persist across generations without being disrupted by recombination during meiosis. While autosomal DNA typically subdivides with each generation, these intact fragments escape crossover events, passing down entirely whole. When shared by large cohorts of descendants, they can mimic or exacerbate population-level pile-up regions.[17]

Because some chromosomal segments may persist across multiple generations with relatively little recombination, they can preserve evidence of shared ancestry that would otherwise be lost. When supported by triangulation, documented genealogy, and other independent evidence, such segments may provide insight into relationships extending beyond the reach of traditional records.

*In this sense, such segments can be viewed as genetic **"time capsules,"** preserving evidence of ancestral relationships across many generations.*

Several observations suggest that the chromosome 19 cluster described in this report represents a genuine ancestral segment surviving over centuries, rather than a simple, anomalous pile-up effect. **Usually, matches due to IBS Pile-up are hundreds or thousands of random people on this exact segment who have completely different backgrounds.** But descendants of the David Ralston, Rachel Roleston, William Rolstone, Thomas Ralston, John Tate Ralston, Powers / Leece, and Carpenter / Caraway families recur

[17] Bettinger, Blaine, *Proof of Sticky Segments.*

repeatedly among the identifiable matches. These biological connections cross multiple testing platforms and involve numerous independently reconstructed descendant lines, frequently showcasing overlapping chromosome 19 fragments among disparate lineages within the proposed network.

Critically, the lineages of David Ralston, William Rolstone, and John Tate Ralston are corroborated by Y-DNA testing, which confirms that all three paternal lines belong to the same downstream Y-DNA haplogroup, I-BY194140.[18] [19] While a shared haplogroup does not independently prove that this specific autosomal chromosome 19 segment derives from the same ancestor, it establishes a compelling, independent line of evidence consistent with a shared paternal origin among these families. Accordingly, the most plausible interpretation of the data is that at least a portion of the observed chromosome 19 cluster reflects inheritance from a genuine common ancestor or ancestral family network. The unique structural resilience of chromosome 19 may have actively contributed to the long-term preservation of this segment, permitting modern descendants of multiple related lineages to retain recognizable, overlapping fragments today. Nonetheless, the precise ancestral source of the segment remains tentative, and additional triangulation will be required to fully resolve its origin.

---

2. Most Likely Interpretation

The combined evidence strongly suggests that several Ralston, Roleston, Raulston, and Roulston lines traditionally treated as separate families likely descend from a related paternal family network in Ulster.

The exact relationship remains unknown.

The DNA evidence is particularly consistent with a relationship originating before migration to America.

---

3. Important Limitations

This report does not claim definitive proof of the exact genealogical relationship among these lines.

Several limitations remain:

- Not all lines have documented Y-DNA testers

[18] The Ralston Project, *DNA Results: Group 1 – Ulster*.
[19] FamilyTreeDNA Discover, *Y-DNA Haplogroup I-BY194140.*

- Documentary evidence connecting the lines remains incomplete
- Some autosomal sharing may reflect broader Ulster founder effects or intermarriage
- The precise common historical origin has not yet been identified

Nevertheless, the combined DNA evidence strongly argues against the observed pattern being entirely coincidental.

PART 4 – Supporting Evidence and Future Research

1. Y-DNA Evidence

One of the strongest pieces of corroborating evidence connecting several of these lines is shared Y-DNA. Of the paternal “Ralston” lines of this cluster, only three have been Y-DNA tested.

- David Ralston
- Mathew Raulston
- John Tate Ralston

All three belong to the Y-DNA haplogroup: **I-BY194140.**

This is significant because Y-DNA is inherited through the direct paternal line and changes relatively slowly over time. The presence of the same downstream haplogroup among these lines strongly suggests descent from a shared paternal ancestor within genealogical or near-genealogical timeframe.

The significance of the autosomal shared-match networks discussed later in this report is reinforced by the fact that the known Y-DNA-tested descendants from the David Ralston, Mathew Raulston, and John Tate Ralston lines all belong to haplogroup I-BY194140. If the observed autosomal relationships were entirely unrelated to the Ralston paternal ancestry, the convergence of all tested paternal lines within the same downstream Y-DNA branch would be difficult to explain as mere coincidence.

While no known Y-DNA testers currently exist from several of the other lines discussed in this report, the autosomal evidence suggests those lines may also be related. So, if male line descendants of Thomas Ralston’s and Rachel Roleston’s line were Y-DNA tested, these results would suggest they, too, would be haplogroup I-BY194140.

---

2. Future Research

Additional Y-DNA Testing

Additional Y-DNA testing would likely be the most valuable next step.

Particularly important would be Y-DNA testing from documented male-line descendants of:

- Thomas Ralston
- William Roulston (Donegal)
- Rachel Roleston's paternal line (if male paternal descendants exist)

If these lines also prove to belong to I-BY194140 or nearby downstream branches, the evidence for a shared paternal origin would become substantially stronger.

Conclusions

The combined autosomal, triangulation, and Y-DNA evidence presented in this study strongly supports the conclusion that several Ralston, Roleston, Raulston, and Roulston lineages share a common historical origin.

The principal findings include:

- Shared Y-DNA haplogroup **I-BY194140** among multiple documented paternal lines.
- Repeated autosomal clustering among descendants of multiple independent Ralston family groups.
- Shared chromosome 19 segments inherited through multiple descendants of different children within several family groups.
- Triangulated chromosome 19 segments involving descendants from independent Ralston, Roleston, Raulston, Roulston, and collateral family groups.
- Independent confirmation of the chromosome 19 network across **AncestryDNA, GEDmatch, MyHeritage, and FamilyTreeDNA**.
- Participation of both American and Irish Roulston descendants, including documented County Donegal lineages.

Taken together, these independent lines of evidence are consistent with the existence of a broader Ulster Ralston / Roulston paternal family network that **predates migration to North America**.

Although the precise genealogical relationships among these families remain unresolved, the evidence strongly suggests that they are unlikely to represent unrelated surname families that independently adopted similar surnames. Rather, they are more likely **descendants of a**

common ancestral family whose relationships extend beyond the reach of currently available documentary records.

References

Online resources cited in this report were accessed between July 2025 and July 2026. Because several cited resources are maintained as living documents and may be updated periodically, readers should consult the most recent versions available from the cited websites.

International Society of Genetic Genealogy (ISOGG). *Autosomal DNA Statistics*. https://isogg.org/wiki/Autosomal_DNA_statistics

International Society of Genetic Genealogy (ISOGG). *Cousin Statistics*. https://isogg.org/wiki/Cousin_statistics

International Society of Genetic Genealogy (ISOGG). *Autosomal DNA*. https://isogg.org/wiki/Autosomal_DNA

International Society of Genetic Genealogy (ISOGG). *Chromosome Browser.* https://isogg.org/wiki/Chromosome_browser

International Society of Genetic Genealogy (ISOGG). *Centromere*. https://isogg.org/wiki/Centromere

International Society of Genetic Genealogy (ISOGG). *Identical by State*. https://isogg.org/wiki/Identical_by_state

International Society of Genetic Genealogy (ISOGG). *Identical by Descent*. https://isogg.org/wiki/Identical_by_descent

Estes, Roberta. "*Hit a Genetic Genealogy Home Run Using Your Double-Sided, Two-Faced Chromosomes While Avoiding Imposters.*" DNAeXplained, October 18, 2019. https://dna-explained.com/2019/10/18/hit-a-genetic-genealogy-home-run-using-your-double-sided-two-faced-chromosomes-while-avoiding-imposters/

International Society of Genetic Genealogy (ISOGG). *Triangulation.* https://isogg.org/wiki/Triangulation

International Society of Genetic Genealogy (ISOGG). *Endogamy.* https://isogg.org/wiki/Endogamy

International Human Genome Sequencing Consortium. "*Finishing the Euchromatic Sequence of the Human Genome.*" Nature 431 (2004): 931-945. *https://www.nature.com/articles/nature02399*

Ancestry. *AncestryDNA Matching White Paper (2020)*. *https://www.ancestrycdn.com/support/us/2020/07/2020whitepaper.pdf*

International Society of Genetic Genealogy (ISOGG). *Autosomal DNA Tools*. *https://isogg.org/wiki/Autosomal_DNA_tools*

Family History Fanatics. *Small DNA Segments*. *https://www.familyhistoryfanatics.com/smalldnasegments*

Bettinger, Blaine. "*Proof of Sticky Segments*." The Genetic Genealogist (Segmentology), November 16, 2015. *https://segmentology.org/2015/11/16/proof-of-sticky-segments/*

Ralston, J. E., The Ralston Project. *DNA Results: Group 1 – Ulster.* *https://ralstonproject.com/results/*

FamilyTreeDNA. Discover: *Y-DNA Haplogroup I-BY194140*. *https://discover.familytreedna.com/y-dna/I-BY194140/*

Appendices

1. Shared-match clusters
2. Descendency trees for each line
3. GEDmatch triangulation report