What can Y-DNA analysis reveal about the surname Hay?

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Abstract

The family name Hay (plus associated spelling variants) is a prominent Anglo-Norman-in-origin surname that has been well-documented as a Scottish noble lineage since the 12th century CE. Their historical significance, linked to the rise of the Anglo-Norman era (1093-1286 CE) in Scotland, and the historical complexities of surname adoption post-Norman conquest of England, justifies the need for a comprehensive understanding of the genetic history of the Hay noble lineage. This study focuses on examining the patterns of paternal inheritance in lineages with the Hay surname. We conducted a comprehensive analysis of Y-chromosome data that is publicly available on the Family Tree DNA (FTDNA) platform, and specific FTDNA surname projects, as well as looking in more detail at three well-documented male-line descendants of William II HAY, 1st Earl of Erroll, (d. 1201) that have been verified to a high degree of confidence. Our results reveal that all descendants of William II HAY, 1st Earl of Erroll, (d. 1201) derive from the multigenerational Y-SNPs R1a - YP6500 (plus equivalent SNPs BY33394 / FT2017) and R1a - FTT161. Furthermore, subclades of R1a - FTT161 have been identified that confirm direct male-line descent from two of William II HAY's sons. Subclade R1a - BY199342 (plus equivalents) confirms direct

male-line descent from David HAY, 2nd Earl of Erroll, (d. 1241), and subclade R1a - FTA7312 confirms direct male line decent from Robert HAY of Erroll. The result also confirms that the Hay noble lineage shares the Y-SNP R1a - YP4138 (estimated to have occurred 832 CE) with several non-Hay testers that have surnames of Norman origin, therefore, providing further evidence to support the Norman origin hypothesis for these surnames. In addition to the identification of multigenerational Y-SNPs associated to documented Hay noblemen, this study has observed significant Y-DNA haplogroup diversity among males with the surname Hay (plus associated spelling variants: Hays, Haye, Hayes, Hey and Haya). Our results show that only 22% of the men sampled (n=109) with the surname Hay (plus associated spelling variation) are descended from the 12th century progenitor of the noble Hay lineage of Scotland. Therefore, confirming that a significant proportion of males with the surname Hay do not descend from the noble progenitor of the surname.

Introduction

The lands of northern Britain that are now referred to as Scotland have not always been a unified realm. Between the early seventh century until the mid-ninth century, northern Britain was separated into four distinct kingdoms (1). The kingdom of Strathclyde was ruled by the Britons and incorporated the southwest region of modern-day Scotland; however, a large portion of this kingdom was incorporated into the Anglo-Saxon kingdom of Northumbria by the early eighth century which included the Lothians and the southeast border regions (1). The lands that primarily encompassed the northeastern third of Scotland, stretching roughly from the Firth of Forth in the south to Caithness and Orkney in the north was considered the kingdom of Pictavia, and ruled by the Picts (1). The kingdom of Dál Riata was ruled by the Scots, and their kingdom incorporated the western lands north of Loch Lomond and the Hebrides Islands (1).

The four kingdoms remained relatively stable until a significant event took place in 844 CE under the leadership of King Kenneth I (Cináed mac Alpin, died in 858 CE) who successfully unified the kingdom of Dál Riata and Pictavia into a single kingdom often referred to as Alba (2). Although the formation of the kingdom of Alba is generally considered the birth of Scotland, Broun (2015) argues that it is a significant oversight and oversimplification of the historical events that took place (3). Broun (1997) argues that it would not be until the thirteenth century, during the Anglo-Norman era, when the term Scotia (Scotland) was generally used when referring to the whole kingdom (4).

The Anglo-Norman era in Scotland (1093-1286 CE)

The revolutionary change in the governance of Scotland, termed the 'Anglo-Norman era', was mainly facilitated by King David I of Scotland during his reign (c. 1124-1153 CE) (5). However, the start of Norman influence in Scotland started with the Treaty of Abernethy, where King Malcolm III of Scotland swore fealty to King William I of England in 1072 CE (6). King William I of England died on 9 September 1087 CE, succeeded by his son William II (commonly referred to as William Rufus). Malcolm III of Scotland went on to break the terms of the Treaty of Abernethy by invading northern England several times in the early 1090s CE (6). On the 13 November 1093 CE, King Malcolm III of Scotland invaded Berwick in northern England with his son Edward (6). King Malcolm III of Scotland advanced to Alnwick and was ambushed by English forces lead by Robert de Mowbray, Earl of Northumbria. Both King Malcolm III of Scotland and his son Edward were killed, leaving the Scottish forces without leadership, forcing their withdrawal back to the safety of Scotland, and facilitating the start of the Anglo-Norman era (c. 1093-1286 CE) (6).

King David I of Scotland (1084-1153 CE) had a new vision for Scotland, an aspiration to replicate the Norman feudal system imposed in England by King William I of England (c. 1066 CE) (5). To achieve his goal of adopting feudal tenure during his reign (c. 1124-1154 CE), King David I of Scotland attracted Anglo-Normans (people of higher social status of

Anglo-Norman, French, and Flemish origin) to Scotland by offering Scottish lands, royal official appointments, noble titles, and knighthoods in return for feudal services (5). This invitation radically changed the governance of Scotland and impacted on the demographics of the Scottish population to an unknown degree (7).

The documented origins of the Hay surname and the earliest Hay progenitor in Scotland

Among the foreign Anglo-Norman settlers of Scotland was the progenitor of the Scottish noble lineage Hay of Erroll, described as William de la Haya II (c. 1172-1201 CE) (8). William de la Haya II was a Norman knight who is documented as cupbearer (butler) of King William the Lion of Scotland who succeeded King Malcolm IV on 9 December 1165 CE (9). William de la Haya II is believed to be the son of William de la Haya I (born in Cotentin, Normandy) and Julianna de Soulis; sister of Ranulf de Soulis, Lord Liddesdale (9), butler of King Malcolm IV, (c. 1153-1164 CE) (9-11). Black (1946) argues that there are several village names starting with 'La Haye [haie/haia]' in Normandy so one of these villages would be a good candidate for the origins of the surname Haya (12) (e.g., La Haye-du-Puits or La Haye Bellefond, both in the Soules region). Ritchie (1953) also supports La Haye-du-Puits as a possible origin of the Hay noble lineage of Scotland; however, he offers La Haye-de-Herce and La Haye Malherbe as potential alternatives (13). Moncrieffe (2010) argues that there is no doubt that their origins were from Haye-Hue, (Haia-Hugonis, now La Haye-Bellefond) because the La Haye-Hue of Normandy bear the same three escutcheons coat of arms used by the Hays of Erroll, and they also marched with de Soules [Soulis] near St Lo in the Cotentin peninsular of Normandy (14). Barrow (1973) also supports Haye-Hue (La Haye-Bellefond) as the place of origin of the Hay noble lineage (15). The documented links between La Haye-Hue of Normandy, de Soulis (Normandy and Liddesdale), and Hay of Erroll are not likely to be coincidental. The Hay noble lineage firmly established their presence in Scotland, taking control of significant lands located in the Scottish Lowlands (16), and playing a substantial role in Scottish history thereafter. For example, Sir Gilbert de

la Hay was the fifth feudal Baron of Errol, Lord High Constable of Scotland, and companion of King Robert the Bruce of Scotland. Sir Gilbert de la Hay was one of the Scottish noblemen that signed the Declaration of Arbroath on 6 April 1320 CE (17).

The evidence that links William de la Haya I to Normandy is that 'la Haya' is likely a Norman toponymic name, deriving its origin from a place called 'la Haye/Haie' in Normandy. McClure (2015, 2020) argue the case that surnames such as 'de la Haye' and 'de la Mare' often denote high ranking people from estates in Normandy (e.g., a notable individual from la Haie 'the enclosure' or la Mare 'the pool') (18, 19). However, McClure is also appropriately cautious in linking these locations to one specific origin or family (19). There are several villages in Normandy that have such place names, and Norman placenames were also introduced to Britain via the linguistic legacy of the Norman Conquest of 1066 CE. When William the Conqueror and his followers introduced Norman French culture, governance, and language to Britain, placenames often reflected the new Norman elite's language, ownership, heritage, or religious affiliations, and were either imposed on new settlements or modified from existing Anglo-Saxon placenames. A good example is the placename Bernard Castle in County Durham, a place deriving its name from Bernard Baliol I (died before 1167 CE), a baron of Norman descent (20). Other examples include Norman French placename derived from descriptive words such as Belvoir (bel voir) in Leicestershire, meaning 'beautiful view' (21) and Richmond in North Yorkshire that is derived from 'riche mont', meaning 'strong hill' (21, 22). Therefore, there is a strong possibility that many unrelated people adopted these surnames independently. Durie (2022) also highlights the complexities involved In identifying surname origins in his essay on clans, families and kinship structures in Scotland (23). He refers to the Hay noble lineage as being among the most influential families in Scotland; however, he does not discuss their potential origins prior to Scotland (23). Durie also highlights that having a surname that is specifically associated to nobility does not guarantee direct paternal descent from that noble lineage (23).

Surname changes

Surname changes did historically take place with no documentational evidence to explain why/how the change occurred. Instances of surname changes were often the result of adoptions, divorce, out-of-wedlock conceptions, and extra-marital conceptions, so these situations would often remain undocumented (24). The genealogical term for these occurrences is a ‘non-paternity event’ (NPE) or a ‘false paternal event’ (FPE) (24), while Larmuseau et al (2017) uses the term ‘extra pair paternity’ (EPP) (25). Avni et al, (2023) suggested that the chances of a EPP taking place was between 1-5% in each generation, with the chances of discovering a EPP increasing with each successive generation (e.g., there is a 10-50% chance of discovering a EPP over ten-generations) (24). Moreover, King et al, (2014) revealed multiple instances of non-paternity in King Richard III’s family tree through the DNA analysis of material collected from his skeletal remains (26).

Traditional genealogical research heavily relies on documentary evidence to prove genealogies (27, 28). The documentary evidence strongly suggests that William de la Haya II has direct paternal descendants surviving to the present (8, 29). However, traditional genealogical evidence alone is limited because it cannot identify EPP occurring in any of the intervening generations of a pedigree (23) unless they were documented. Based on the evidence provided by Avni et al (2023), there is a good chance that someone with the surname Hay does not descend from William de la Haya II (24). Furthermore, to the best of the authors’ knowledge, William de la Haya I’s proposed link to Normandy is only supported by limited toponymic evidence so the pursuit of further evidence to explore his origins is well justified.

Genetic Genealogy

The advancements in DNA sequencing technology, and the development of haplotype-based methods to detect population substructure have proven to provide insight into the degree of shared ancestry between populations (30-33). A recent study by Morez et al (2023) implemented FineSTRUCTURE clustering analysis and Identity-By-Descent (IBD) on

imputed diploid dataset of ancient Pictish and present-day Scottish genomes, revealing partial population replacement taking place in eastern Scotland during the Anglo-Norman era (34). Morez et al. (2023) demonstrated that there was less genetic affinity between present-day eastern Scottish samples and the ancient Pictish genomes they sequenced, while present-day western Scottish samples shared significantly more genetic affinity with the ancient Pictish genomes (34). Furthermore, Morez et al. (2023) observed a clear genetic signature that differentiated the eastern Scottish population (showing a greater genetic affinity with populations with Anglo-Norman ancestry) from the western Scottish population (showing a greater genetic affinity with ancient samples of Iron-Age-British and Pictish ancestry) (34). Moreover, Gretzinger et al. (2022) observed a noticeable increase in Iron-Age-French ancestry among the present-day English population when compared to the ancient Iron-Age-British samples that have been sequenced (35). Gretzinger et al. (2022) concluded that Iron- Age-French-like ancestry was likely introduced to England during the early Medieval Age by people of Frankish-like origins and this continued through to the late Medieval Age with the Normans (35).

King and Jobling, (2009) argued that because of the correlation between surnames being traditionally inherited paternally, and Y-DNA being biologically passed on from father to son virtually unchanged, the study of Y-DNA has been of great value to genealogical studies investigating direct paternal ancestry (36). The consensus among researchers is that the comparison of mutations found within the Y-chromosome's short tandem repeat markers (Y-STRs) and single nucleotide polymorphisms (Y-SNPs) between two or more males can accurately predict the degree of their patrilineal relationship, show how lineages evolved over time, and predict when lineages arose and diverged (37-41). Specific Y-SNP mutations on the Y-chromosome are also referred to as Y-DNA haplogroups and these define genetic population groupings (42). For example, the Y-SNP M417 is a mutation that defines the haplogroup R1a1a1, a major subclade (branch) of the haplogroup R1a (43, 44). The R-M417 haplogroup is especially significant because it represents the progenitor of a major

183 expansion within the haplogroup R1a, and it is one of the main Y-DNA haplogroups
184 associated with the spread of Indo-European languages (45). Genetic genealogical studies
185 by Holton and Macdonald (2020), Stead (2023), Holton (2023), and DePew et al. (2024)
186 have identified Y-SNPs that occurred in a specific individual or a narrow lineal group of
187 patrilineal related individuals that lived within a known genealogical timeframe (46-49). A Y-
188 SNP that can be specifically designated to an individual is termed a SNP-Progenitor (SNP-
189 Progen) while Y-SNP(s) that can be identified as occurring in a lineal group of patrilineal
190 related individuals are known as Multigenerational-SNPs (Multigen-SNPs) (46-48). The
191 identification of these Y-SNPs is useful to genetic genealogists because they can confirm or
192 reject hypotheses based on ambiguous documented evidence. Furthermore, once these Y-
193 SNPs have been positively confirmed, they can be used to identify descendants that are not
194 fortunate enough to be able to prove their descent with documentational evidence.

195 This study aimed to analyse Y-SNP data from FTDNA's BigY700 tests to investigate whether
196 the Y-DNA testing of proposed well-documented living patrilineal descendants of William de
197 la Haya II supports the genealogical consensus that his direct paternal lineage has survived
198 to the present. The Y-SNP data from testing the BigY700 allows genetic genealogists to
199 estimate a time to the most recent common ancestor (TMRCA) when two or more individuals
200 share a specific Y-SNP, but their common ancestor is unknown. The mutation rates provide
201 a date range for the occurrence of all Y-SNPs that are shared between two or more testers
202 and if the common ancestor between two or more matching testers is known, their shared Y-
203 SNPs can be assigned to specific individuals. Another aim is to identify SNP-Progens or
204 Multigen-SNPs associated to the Hay noble lineage so EPP events can be identified using
205 Y-DNA testing. Furthermore, the study aims to use the data for SNP-Progens or Multigen-
206 SNPs to help identify Hay males of direct paternal descent who cannot prove their lineage
207 due to gaps in the documentary records. The data from this study also have the potential to
208 provide evidence to help reach a reliable conclusion on the proposed Norman origins of
209 William de la Haya (c. 1159-1201 CE). Furthermore, the analysis of Y-DNA haplogroups

found among Family Tree DNA testers with the surname Hay (plus associated spelling variants: Hays, Haye, Hayes, Hey and Haya) will be assessed to reach conclusions on the level of haplogroup diversity. An analysis into Y-DNA haplogroup diversity will provide data to evaluate the hypothesis made by Durie (2022) [20], who suggested that surnames in Scotland were largely adopted for many reasons, and that a surname of noble origin does not mean an individual is descended from the noble progenitors of that surname. Finally, this study will provide further insight into Y-SNP mutation rates using the BigY700 test results of three well-documented Hay patrilineal descendants who can trace their ancestral pedigree back to the 12th century.

Methodology

Holton and Macdonald (2020) highlight the significant challenges faced when researching well-documented living descendants of medieval noble lineages (46). However, they confirmed that there are many examples of individuals of various ancestries who have the good fortune of being well documented, having extant lines of descent to the present day (46). Research by Larmuseau et al. (2014), Stead (2023), and DePew et al (2024) also demonstrates the existence of well-documented lineages back to the high to late Middle Ages (c. 1000-1500 CE) (47, 49, 50).

Traditional genealogical documentary research

The methodology implemented in this study utilised a mixed disciplinary approach that combined traditional genealogical research, genetic genealogical research and archaeogenetic research methods. Holton and Macdonald (2020) demonstrated that authoritative documentary sources can be used to identify living descendants of noble lineages (46). Therefore, a range of publicly available authoritative documentation, primary and secondary sources (Table 1) were used to identify three potential test takers with proven patrilineal descent from William de la Haya II.

235 **Table 1. Examples of the sources consulted to prove the ancestries of the three test**

236 **takers used for this study.**

Document/source information	Access to document physically or online
Register of the Great Seal of Scotland.	Medieval and Early Modern Sources Online (MENSO). vols 1-3, or via Archive.org (search on Register of the Great Seal of Scotland or Registrum Magni Sigilli for volumes 2-7).
Vol. v. 1590-91 #1830. Rex confirmavit Willelmo Domino Hay de Yester.	Thomson, John Maitland (1984) The register of the Great Seal of Scotland. Registrum Magni Sigilli Regum Scotorum. A.D. 1306-1424. New Edition. Vols. I-XI. Edinburgh: The Scottish Record Society. Vol. iii.
Registrum S. Marie de Newbotle, Vol 1. Confirmation of William de Haya, page 12-13. William de Haya, son of John de Haya, knight and Lord of Lochquerwerd.	Innes, Cosmo, ed. (1849) Registrum S. Marie de Neubotle. Vol. 1 (1140-1528). Edinburgh: Bannatyne Club. Medieval and Early Modern Sources Online (MENSO).
Exchequer Rolls of Scotland and Appendix, 1437-1487 p. 679. Sasine Johannis Hay Locherwart, Yester, Duncanlaw, Morhame, Ugstoun, Blankis1479.	Exchequer Rolls of Scotland and Appendix, 1437-1487. Medieval and Early Modern Sources Online (MENSO).
The Scots peerage – Sir John de Haya, page, 417. Abt 1238.	Paul, Sir James Balfour. (1911) The Scots peerage: founded on Wood's ed. Of Sir Robert Douglas's Peerage of Scotland. Vol VIII. Edinburgh: David Douglas. P. 417.
Hay of Yester Papers MSS.14401-14820 The 1st Marquess was known as Lord Yester from 1646 until he succeeded his father, the 1st Earl, in 1654. (ii) Midlothian: barony of Loquhariot (Borthwick), 1652-63 (f. 116).	National Library of Scotland catalogue: GB233/Ch.12446-12539 Yester Documents: Minor Estates 1541-1715. Ch.122446-62 Barony of Loquhariot (Borthwick), 1541-1673. GB233/MS.14402-14412 Correspondence: 1st Marquess of Tweeddale 1652-1696.
The Peerage – William de la Haya	The Peerage website - https://www.thepeerage.com/p27848.htm#i278473
Hay charters.	People of Medieval Scotland (POMS) https://poms.ac.uk/search/?index_type
Hay Births, Marriages, Deaths, Wills and Heraldry. E.g., Baptism of Alexander Hay of Mordington, 15/04/1731, Edinburgh. 685 / 1 170 / 498.	ScotlandsPeople https://www.scotlandspeople.gov.uk

237

238 Based on the outcome of the traditional genealogy research, it was hypothesised that all
239 three potential testers should share a Y-SNP dated to have occurred between 1000-1150
240 CE because their genealogies suggest that they descend from William de la Haya II (c.
241 1172-1201 CE). However, the genealogies of two of the potential testers suggested that they
242 shared a more recent ancestor (John Hay, 1st of Tweeddale, 1595-1653 CE) when
243 compared to the third tester; therefore, likely sharing at least one more Y-SNP in common
244 that occurred between 1150-1595 CE. Furthermore, it is important to highlight that the two
245 well-documented testers that descend from John Hay, 1st of Tweeddale can be confidently
246 documented back to Sir John Hay (1200-1262 CE) and he is hypothesised to be the
247 grandson of William de la Haya II (c. 1172-1201 CE) via his son Robert (8, 51).

248 To confirm that the well-documented individuals were the direct paternal descendants of the
249 noble Hay lineage of Scotland, Y-DNA testing was required to investigate whether the
250 individuals shared Y-SNPs that could be dated to around the time-period of their proposed
251 common noble Hay ancestor. The identified living descendants were invited to participate in
252 this study after the receipt of signed consent with the recruitment period staring on the 6th of
253 February 2024 and ending on the 7th of October 2024. Ethical approval for this research was
254 obtained from the University of Strathclyde's Ethics Committee, reference number:
255 UEC23/94. After signed consent was received, a non-invasive BigY700 test kit was posted
256 out to each participant for cheek cell sample collection using the cotton mouth swabs
257 provided in the test kit. Once received, each participant completed the DNA sample
258 collection and then posted the sample back to the FTDNA laboratory for sequencing. The
259 BigY700 test by Family Tree DNA (FTDNA) was the test of choice for this project for several
260 reasons (52). Firstly, FTDNA was chosen due to their large Y-haplotree, currently consisting
261 of 81,000 branches, 716,000 variants, and 566,000 SNP-tested users in their Y-DNA
262 database (53). Secondly, FTDNA has strict policies that ensure tester privacy and security of
263 data (54); they also provide a 'closed project' option for researchers that ensures a secure
264 platform to carry out data analysis.

265 **Y-DNA testing strategy**

266 This research opted to use FTDNA's BigY700 test which is a next-generation sequencing
267 (NGS) test that covers an approximate 23 Mb of the total 57.2 Mb of the GRCh38 (HG38)
268 reference Y-chromosome (less than 1 % of the whole human genome) (55). The BigY700
269 targets all the Y-SNPs present in the SNP rich regions most relevant for genetic
270 genealogical research with up to 70 reads per position covered; however, any Y-SNP that
271 returns a minimum of 10 derived (positive) reads is reported (52). FTDNA's age estimates
272 for SNPs that feature within their Y-DNA phylogenetic tree are calculated using the
273 methodology developed by McDonald (2021) (56). McDonald's approach calculates
274 coalescence ages (times to most recent common ancestor, or TMRCAs) using a new,
275 probabilistic statistical model that includes Y-SNP, Y-STR and ancillary historical data (56).
276 McDonald demonstrated that this methodology provided highly accurate estimates by using
277 the Y-DNA data of well-documented direct patrilineal Royal Stewart testers (56).

278 In this study, the Y-SNP data of the three documented testers were compared against their
279 specific genealogies to identify SNP-Progens or Multigen-SNPs. FTDNA's age estimates for
280 specific Y-SNPs were accepted as the most accurate estimates since they were calculated
281 using McDonald's methodology (52, 56). The example in Figure 1 demonstrates how a SNP-
282 Progen and Multigen-SNPs are identified by combining the documented genealogical
283 information with the Y-SNP data of four fictitious testers. When two or more Y-DNA testers
284 have well-documented ancestry that triangulates back to a direct paternal ancestor living
285 during the medieval era, Multigen-SNPs and SNP-Progens can also be identified with a high
286 degree of confidence.

287 **Fig 1. Diagram demonstrating how SNP-Progen and Multigen-SNPs are identified.**

288 Figure 1 shows how three BigY700 testers are related to demonstrate how SNP-Progens
289 and Multigen-SNPs are identified. Tester of Lineage_1* is the 3rd cousins of Tester of
290 Lineage_2 via the same direct patrilineal line of descent, sharing the same 2nd great

291 grandfather. Tester of Lineage_1 is the 2nd cousin, once removed of Tester of Lineage_3
292 and Tester of Lineage_3 is the uncle of Tester of Lineage_2. Since Tester of Lineage_1* is
293 the only individual from his immediate patrilineal line, the Y-SNP FT1001 cannot be assigned
294 to a specific individual; therefore, it is termed a Multigen-SNP as it could have occurred
295 between Tester of Lineage_1*, his father, grandfather or great grandfather. Tester of
296 Lineage_2 and Tester of Lineage_3 are more closely related, and they are derived (positive)
297 for the Y-SNP FT1002; however, no new Y-SNPs have occurred in the father of Tester of
298 Lineage_2 because Tester of Lineage_2 remains FT1002 which either occurred in his
299 grandfather of great grandfather (another example of a Multigen-SNP). Furthermore, Figure
300 1 shows that Tester of Lineage_3 can be identified as the SNP-Progen because he is the
301 brother of Tester of Lineage_2's father and Lineage_3 carry an additional Y-SNP called
302 FT1003; therefore, this Y-SNP must have occurred in Tester of Lineage_3, making him the
303 SNP-Progen for FT1003. Based on the information shown in Figure 1, everyone in the
304 phylogenetic tree will have their Y-SNP ancestral path written as shown in Table 2.

305 **Table 2. Y-SNP ancestral path for the individuals shown in Figure 1.**

Individuals shown in Figure 1	Y-SNP ancestral path
Common Direct Paternal Ancestor to all three lineages	FT1000
Great Grandfather, Grandfather, Father and Tester of Lineage_1*	FT1000 > FT1001
Great Grandfather, Grandfather and Father of Tester of Lineage_2*	FT1000 > FT1002
Tester of Lineage_3* and his Son	FT1000 > FT1002 > FT1003

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307

308 To investigate the degree of Y-DNA haplogroup diversity among individuals with the
309 surname Hay, this study utilised the Y-DNA data of 109 testers that is publicly available on
310 the Hay surname FTDNA project (57). In situations where a tester has not carried out any
311 specific Y-SNP testing and they have only tested Y-STR markers, FTDNA only provide a

312 very general Y-DNA haplogroup prediction. The STR data of the testers that had tested
313 between 67-111 STR markers were inputted into the NEVGEN tool (n=29) (58) to predict a
314 more refined Y-DNA haplogroup as implemented by Zhabagin et al (2024) (59). For
315 example, Tester: 398281 was only assigned R-M512 by FTDNA; however, NEVGEN was
316 able to predict a more refined Y-DNA haplogroup for tester using their 67 STR markers.
317 NEVGEN accurately predicted kit number: 398281 as being positive for R -YP287 (58), a
318 SNP several mutations further downstream of R-M512 as illustrated below:

319 R1a - M207 > M173 > M420 > M459 > M512 > M417 > CTS4385 > Y2894 >L664 >
320 FGC41399 > S2894 > YP287.

321 Once all the data were collated, testers were grouped based on the closest major Y-DNA
322 haplogroup they were associated with. For example, kit number: 398281 was grouped in the
323 R1a > L664 grouping.

324 **Results**

325 **Y-DNA Haplogroup diversity among testers with the surname Hay (plus spelling**
326 **variants)**

327 The first set of results demonstrate the Y-DNA haplogroup diversity observed among the
328 testers with the surname Hay (plus spelling variants) that are participating in the Hay FTDNA
329 project. Figure 2 shows that Y-DNA haplogroups R1a, R1b, I1, I2, J1 and Q were all
330 represented.

331 **Fig 2. Y-DNA haplogroup diversity among testers with the surname HAY (plus**
332 **associated spelling variants) within the Hay FTDNA project.**

333 The evidence also demonstrates significant diversity within specific haplogroups (e.g., R1a >
334 YP4141; R1a > L448 & R1a > L664) with haplogroup R1b proving to be the most diverse
335 haplogroup represented. The Y-DNA diversity observed in this study is similar to previous
336 research completed on Clan Forbes (47).

337 **The Y-DNA results of the three well-documented noble Hay descendants**

338 The BigY700 test results of the three well-documented noble Hay descendants showed that
339 they all shared the following Y-SNP ancestral path (see Table 3): R1a-M420 > YP4141 >
340 YP4132 > YP4169 > YP4208 > YP4131 > YP4138 > YP6500 > FTT161.

341 **Table 3. Basic Y-SNP ancestral path and specific Y-SNP details**

Y-SNP name	Location	Ancestral allele	Derived allele	FTDNA TMRCA estimate ranges (Earliest < Median > Latest; 95% probability)
FTT161	CP086569.2: 12101060	A	G	877 CE < **1081 CE** > 1251 CE
YP6500	CM000686.2: 7696598	C	G	687 CE < **930 CE** > 1131 CE
YP4138	CM000686.2: 6863798	G	T	582 CE < **824 CE** > 1027 CE
YP4131	CM000686.2: 2862540	A	G	129 BCE < **219 CE** > 513 CE
YP4208	CM000686.2: 19384185	C	A	3795 BCE < **2945 BCE** > 2218 BCE
YP4169	CM000686.2: 12489924	T	C	4193 BCE < **3291 BCE** > 2581 BCE
YP4132	CM000686.2: 2880609	C	G	5481 BCE < **4406 BCE** > 3483 BCE
YP4141	CM000686.2: 7404757	C	T	13078 BCE < **11025 BCE** > 9250 BCE
M420	CM000686.2: 21311315	T	A	17707 BCE < **15272 BCE** > 13137 BCE

342

343 Bonito et al (2021) suggested that the palindromic regions of the Y-chromosome are highly
344 prone to gene conversion events; therefore, the identification of SNPs may be complex when
345 performing short-read targeted NGS (60). Hallast et al (2023) identifies the four
346 heterochromatic subregions in the human Y-chromosome: the (peri-)centromeric region,
347 DYZ18, DYZ19 and Yq12 as highly repetitive (61); therefore, these regions are less suitable
348 for the identification of reliable Y-SNPs using NGS. Figure 3 is a map of the Y-chromosome
349 that identifies the positions of the Y-SNPs shown in Table 3. These Y-SNPs are located
350 within the non-recombining portion of the Y-chromosome (NRY), where Y-SNPs occur at a
351 relatively slow rate and without the instability caused by gene conversion, deletions, and

duplications. Furthermore, these Y-SNPs are not located in any of the regions that are deemed unreliable for Y-SNP calling; therefore, these Y-SNPs are regarded to be highly stable over generations, making them reliable for phylogenetic studies.

Fig 3. Y-Chromosome map adapted from Jobling and Tyler-Smith (2003) showing Y-SNPs associated with the noble Hay lineage (62)

The sequences in Table 4 show the bases surrounding the Y-SNPs associated to the ancestral path for the noble Hay lineage. It can be observed that each derived Y-SNP is surrounded by non-repetitive sequences; therefore, increasing the likelihood that these Y-SNPs are stable and phylogenetically relevant.

Table 4. Sequencing data of the bases surrounding the Y-SNPs identified in the Y-SNP pathway for the Hay noble lineage

	Seventeen bases either side of the Y-SNP (No reverse reads shown)
Reference FTT161	G A A T A C A A T G T T A T G G A [A] T C C G A T T G A A C A G A A T G G A A T A C A A T G T T A T G G A [G] T C C G A T T G A A C A G A A T G
Reference YP6500	T C A T T T T T T A A A T G C C A [C] T C T T C A A A A T T A A C A A G T C A T T T T T T A A A T G C C A [G] T C T T C A A A A T T A A C A A G
Reference YP4138	G G C G G G G A A A C A G C A A A [G] A T G G G T G G T T G C T C C T T G G C G G G G A A A C A G C A A A [T] A T G G G T G G T T G C T C C T T
Reference YP4131	C G C T A G G T T A C T C T G C A [A] A G G T G G G C T T C T T G T T G C G C T A G G T T A C T C T G C A [G] A G G T G G G C T T C T T G T T G
Reference YP4208	G A G G A G T A T T T T A C T T T [C] A A T T A T G T T G T T G A T C T G A G G A G T A T T T T A C T T T [A] A A T T A T G T T G T T G A T C T
Reference YP4169	C A G G C A T G C T T T A T A G C [T] C C T T G T G G A G G C A A T T A C A G G C A T G C T T T A T A G C [C] C C T T G T G G A G G C A A T T A
Reference YP4132	G G A A G G T C A G A A A T G G C [C] C T T G C T G A T G C C A G C T G G G A A G G T C A G A A A T G G C [G] C T T G C T G A T G C C A G C T G

Reference YP4141	A T G T G T C G T A A G A G G G A [C] G C A G T G G G A G G T A A T T G A T G T G T C G T A A G A G G G A [T] G C A G T G G G A G G T A A T T G
Reference M420	T T C A T T G C T G G C C T C C A [T] T T A G A A A C C A A T G A A A A T T C A T T G C T G G C C T C C A [A] T T A G A A A C C A A T G A A A A

The first line in each row of Table 4 shows the 17 bases of sequence surrounding either side of each Y-SNP found in the Y-SNP pathway for the Hay noble lineage. The sequences are in the Genome Reference Consortium Human Build 38 (GRCh38) format. The 18th base in each sequence is coloured brown and boxed using square brackets to indicate the location of the specific SNP (e.g., FTT161 = [A] ancestral allele; [G] derived allele).

The Y-SNP FTT162 is phylogentically positioned downstream of FTT161 and it defines a noble Hay branch that has a significant number of descendants; n=47 testers at the YFull database (63). This Y-SNP is located in the highly repeatitive heterochromatic region of the Y-chromosome (see Figure 4). This region is regarded as having large portions of noncoding DNA that is typically prone to mutations caused by repilication slippage (64-66); therefore, Y-SNPs occrring within this region of the Y-chromsome need to be treated with caution as they may not be phylogenetically relevant (67).

Since FTT162 is located in a less stable region of the Y-chromosome, we analysed the surrounding sequence either side of this SNP to assess its stability and reliability of being phylogenetically relevant. Figure 4 highlights the repetitive sequences across a 600 bp region with FTT162 in the middle of the sequence and annotated in yellow. The way that FTT162 likely formed is by a change from the TGGAG repeat to TAGAG (TGGAG --> TAGAG; G>A**;** annotated in red), and this terminated the TGGAG repeated sequence that resulted in stabilising this section of sequence. After the TAGAG section had changed, the resulting stability provided a unique background for the FTT162 SNP (A>T; annotated in yellow) to occur. When FTT162 occurred, it changed the dynamics of the surrounding

385 repeats so that two out of five bases were different to the left and to the right of the repeat
386 units either side of FTT162. Therefore, these changes would have increased the stability at
387 FTT162, making it an unlikely place for the DNA polymerase to slip, thus, resticting any
388 converstion to either of the neighbouring repeats; TGGAG or TGGAA, respectively. For the
389 reason discussed above, we have no concerns on the stability and reliability of this Y-SNP.

390 **Figure 4. Y-SNP FTT162 location: CP086569.2:27682309: A > T and surrounding**
391 **Sequence (68, 69)**

392 The three well-documented Hay testers also match a significant number of testers (n=24/109
393 at the HAY FTDNA project) with the surname Hay (plus associated spelling variations) who
394 also test positive for at least FTT161(70). At this point, it is unclear whether YP6500 (plus
395 equivalent SNPs BY33394 / FT2017) are Y-SNPs specific to the Hay noble lineage or
396 whether they occurred in an ancestor that predates William Hay I Normandy, d. 1170 CE.
397 Furthermore, the Y-SNPs BY33394 and FT2017 are assumed to be equivalent to YP6500 as
398 it is unclear whether they appeared simultaneously in the evolutionary timeline, or whether
399 their occurrence was totally independent of each other. New data often changes the status
400 of assumed equivalent Y-SNPs by proving that they occurred independently of other Y-
401 SNPs. Therefore, it is never a guarantee that any Y-SNP is equivalent to other Y-SNPs.
402 Once new data provides enough evidence to show that assumed equivalent Y-SNPs did
403 occur independently, their position within the phylogenetic tree changes accordingly to
404 represent their correct chronological order. The results show that there are some non-Hay
405 surnames among the testers (n=12) who are positive for FTT161 and downstream SNPs,
406 these non-Hay surnames are likely the result of EPP taking place. The results strongly
407 suggest that FTT161 is a Y-SNP that defines the noble Hay lineage with the downstream Y-
408 SNPs of FTT161 identifying descent from William II HAY, 1st Earl of Erroll, (Butler), d. 1201,
409 m. Eve. Most testers with the surname Hay on the Hay FTDNA project (n=85/109) are not
410 direct paternal descendants of the Hay noble progenitor (70). Figure 5 shows the
411 phylogenetic block-tree of R1a-YP4138 which splits to form the subclades YP6500 (ancestor

412 of the Hay noble lineage) and three parallel subclades, CTS11317, BY190800 and
413 BY234056, respectively. The subclades CTS11317, BY190800 and BY234056 have several
414 testers with surnames of Norman origin (Allen, Kilvert, Manwarren/Manering, Merrell,
415 Travers and Vess) (71), and several testers with surnames of English origin. The non-Hay
416 surnames associated to the parallel subclades of YP6500 is expected since the age
417 estimate for R1a > YP4138 is 582 < 800 > 1027 CE (95% probability) (72); a timeframe
418 generally accepted as being before the earliest known adoption of surnames in Europe (73).

419 **Fig 5. R1a > YP4138 Phylogenetic Block-Tree showing the Y-SNPs associated to the**
420 **descendants of the Hay noble progenitor YP6500.**

421 Figure 6 was produced by combining the Y-SNP data with the ancestral pedigrees of the
422 three well-documented Hay testers.

423 **Fig 6. Original Hay Noble phylogenetic tree using the pedigrees of the three well-**
424 **documented noble Hay descendants.**

425 The phylogenetic tree identifies several Multigen-SNPs associated to the noble Hay lineage.
426 Testers HAY_1, HAY_2 and HAY_3 are the three well documented individuals who were
427 identified during the traditional genealogical research phase of the study. The other testers
428 that match the three well-documented Hay individuals can also be placed in approximate
429 positions within the Hay noble phylogenetic tree based on their Y-SNPs; however, further
430 documentational evidence or the testing of more well-documented descendants will be
431 required for a more accurate positioning. Three clear subclades that are phylogenetically
432 downstream of the Y-SNP FTT161 were identified in this study (BY199342, FTA7312 &
433 FTT162). The combined Y-SNP and ancestral documentation data suggests lines of descent
434 from three of the six sons of William II HAY, 1st Earl of Erroll. The Y-SNP BY199342 (plus
435 equivalents) that were found in tester HAY_1 can confidently be assigned to the
436 descendants of David HAY, 2nd Earl of Erroll, first son of William II HAY, 1st Earl of Erroll.
437 However, it is uncertain whether BY199342 occurred in David HAY, 2nd Earl of Erroll or in

438 one of his immediate direct descendants. Furthermore, HAY_2 and HAY_3 are negative for
439 BY199342 (plus, equivalents) and positive for FTA7312 (plus equivalents) while likely
440 descending from Robert HAY of Erroll (the younger brother of David HAY, 2nd Earl of Erroll).
441 The Y-SNP data and the pedigrees of the well-documented testers show a clear genetic
442 divergence that was previously hypothesised. Moreover, the results support the
443 documentary evidence that suggests that HAY_1, HAY_2 and HAY_3 are descendant of
444 William II HAY, 1st Earl of Erroll, d. 1201 CE with a high degree of certainty.

445 **Analysis of the mutation rates observed among the well-documented Hay testers**

446 The results in Table 5 suggest that the Y-SNP mutation rate observed in the Hay noble
447 lineage does not fit the standard average mutation rate proposed by McDonald, (2021);
448 however, the mutation rates do fall within the accepted mutation rate ranges. For example,
449 FTD73694 is dated to 1700 CE with a date ranging from 1428 to 1844 CE with 95 %
450 probability; however, the TMRCA has been identified to 1595 CE with 100% confidence (56).
451 McDonald proposes that the standard molecular clock for Y-SNP mutation rate average is 83
452 years/Y-SNP mutation (56). The data from the three well-documented HAY testers show an
453 average mutation rate of 67.8 years/Y-SNP between 1140-1950 CE. The results for HAY_2
454 and HAY_3 also show an average mutation rate of 41.4 years/Y-SNP between 1140-1595
455 CE.

456 **Table 5. Y-SNP analysis of the three well-document HAY testers.**

457

Participant cohort	Total number of Y-SNPs downstream of FTT161	Number of generations since William HAY, 1st Earl of Erroll, b. 1140 CE	Average years per generation	Average Y-SNP mutation rate (yrs)
HAY_1	11	25	32.4	73.6
HAY_2	12	26	31.2	67.5
HAY_3	13	24	33.75	63.3
Total average from HAY_1, HAY_2 & HAY_3 bet. 1140 – 1950 CE	**12**	**25**	**32.45**	**67.8**
HAY_2 & HAY_3 bet. 1140-1595 CE	**11**	**16**	**28.4**	**41.4**

458

459 Additionally, only one private variant (unique Y-SNP) occurred in HAY_2, and only two
460 private variants occurred in HAY_3 since their common ancestor John HAY, 1st Earl of
461 Tweeddale (1595-1653). Figure 7 illustrates the average mutation rates observed between
462 HAY_2 and HAY_3.

463 **Fig 7. Diagram showing average mutation rate of Y-SNPs for HAY_2 and HAY_3.**

464 The observation of variation in mutation rates during specific time periods could explain a
465 proposed documented pedigree for an existing FTDNA tester with the surname HAY, who is
466 positive for the subclade FTT162 (referred to as HAY_4 in this report). The documentary
467 evidence for HAY_4 suggests possible descent from Robert HAY of Erroll, younger brother
468 of David HAY, 2nd Earl of Erroll. This proposed ancestry would need to span approximately
469 two hundred years, totalling eight generations between William HAY II, 1st Earl of Erroll and
470 Sir William HAY of Locherworth and Yester, Sheriff of Peebles, (1350-1421 CE) which can
471 be seen in Figure 8.

472 **Fig 8. Alternative Hay Noble phylogenetic tree when HAY-4's proposed pedigree is**
473 **considered.**

474 If HAY_4's pedigree is correct, the eleven Y-SNPs shared between HAY_2 and HAY_3
475 would have to have occurred during a period between 1350-1595 CE (245 years). In
476 addition, Hay_4's pedigree would require an average Y-SNP mutation rate of 1 x Y-
477 SNP/22.3 years with an average generation rate of 30.6 years (Figure 9).

478 **Fig 9. Diagram showing the average Y-SNP mutation rate if HAY_4's proposed**
479 **pedigree is considered.**

480 The average mutation rate of 22.3 years/Y-SNP that is associated to HAY_4's proposed
481 pedigree falls within the possible mutation rate range since FTT162 is estimated to have
482 occurred in 1107 CE, with a range between 898 CE and 1280 CE with 95% probability(74).

Therefore, this ancestral pedigree of HAY_4 is possible on a genetic level. However, there are alternative ancestral pedigrees for HAY_4, but these cannot be documented back to William II HAY, 1st Earl of Erroll, (d.1201) due to a lack of records. To validate HAY_4's true line of descent back to William II HAY, 1st Earl of Erroll, (d. 1201), the Y-DNA testing of a well-documented direct paternal descendant of the four remaining sons of William II HAY (William, Malcolm, Thomas and John HAY I of Naughton) would be required.

Discussion

The Y-DNA haplogroup diversity observed among the Hay FTDNA project testers demonstrate a lack of homogeneity among the FTDNA testers with the surname Hay (plus associated spelling variabts). Only 22% of the FTDNA testers with the surname Hay descend from a Hay nobleman, defined by the Y-SNPs YP6500 and FTT161 (plus, subclades). A similar percentage of Y-DNA haplogroup diversity was also observed in a Clan Forbes genetic study where Stead (2023) reported 27% of FTDNA testers within the Clan Forbes project were shown to be direct paternal descendants of the noble lineage (47). Furthermore, the results also support the hypothesis made by Durie (2022) who suggested that surnames in Scotland were largely adopted for many reasons, and that a surname of noble origin does not mean an individual is descended from the noble progenitors of that surname (23). More research needs to be conducted on other surnames associated to Scottish nobility for comparison to this study and the Clan Forbes genetic study(47). With further data, more specific questions can be asked; for example, are there specific historical events that facilitated surname changes, and can this be evident in Y-DNA data?

The Y-SNP YP4138, plus equivalents, are directly upstream of YP6500 in the phylogenetic tree. Subclades of YP4138 are found among several testers with the Norman-in-origin surnames Manwarren, Kilvert and Travers. therefore, strongly supporting the Norman origins of YP4138 and its subclades. The age estimate for YP4138 is 582 < 800 > 1027 CE (95% probability) (72), therefore, also aligning with the Norman origin hypothesis. Some testers

with the surname Travers have well-documented ancestry from the Travers noble lineage of Horton, Cheshire (75) and Cork, Ireland (76). Although the Travers lineage of Horton and Cork can only be confidently documented back to the mid-15th century, they are probably descended from the Norman ancestor of Ralph Travers of Berney, c. 1197 (75, 76). Further testing of well-documented individuals with surnames of Norman origin that match the noble Hay and Travers testers could provide important Y-SNP data to help shed further light on their ancestral connections.

The research conducted in this study has provided strong evidence that the Multigen-SNPs YP6500 (plus equivalents) and FTT161 are key Y-SNPs that identify descent from the Hay noble lineage. Furthermore, two subclades of FTT161 (BY199342 & FTA7312) are Multigen-SNPs that indicate direct paternal descent from David HAY, 2nd Earl of Erroll and his younger brother Robert HAY of Erroll. Any individual that matches these key Y-SNPs can be confirmed as a direct paternal descendent of the Hay noble lineage with a high degree of confidence, even if documentary evidence is absent. Furthermore, the Y-SNP data can also provide more specific ancestral designations (e.g., descent from David HAY, 2nd Earl of Erroll or his younger brother Robert). This dataset will become more refined when additional well-documented Hay testers complete BigY700 testing, leading to more Multigen_SNPs being assigned to specific Hay noblemen, and potentially identifying specific SNP-Progens. Invariant mutation rates across the human Y-chromosome have generally been accepted among researchers such as Xue et al, (2009), Helgason et al, (2015) and Kutanan et al, (2019) (77-79). The consensus among these authors were that the Y-SNP mutation rate in human Y lineages remained homogeneous; however, this was not supported by the research conducted by Ding et al, (2021) (80). Ding et al, (2021) suggests variable mutation rates across the human Y-chromosome haplogroups; however, it is not clear whether this heterogeneity is caused by interhaplogroup mutation rate variation (80). The Y-SNP data in this study supports the theory of variable mutation rates across the human Y-chromosome

535 haplogroups (mean Y-SNP mutation rate of 67.8 years/SNP as opposed to the standard 83
536 years/SNP rate) (56).

537 This study is the first to observe the Y-SNP mutation rates of well-documented testers with
538 ancestry tracing back to a common ancestor living in the 12th century. Although the data
539 clearly demonstrate varying mutations rates during different time periods, it is unclear what
540 causes this phenomenon. One explanation for this phenomenon could be that greater
541 numbers of male offspring were born during the period where more Y-SNPs mutations are
542 being observed. Furthermore, factors such as higher than average conception age of the Y-
543 SNP progenitors could result in more Y-SNPs occurring, limitations with NGS, and specific
544 haplogroup genetic mechanisms could also be at play.

545 The technological and methodological advances made by the telomere-to-telomere (T2T)
546 consortium has already had a huge impact on identifying new Y-SNPs that were not reported
547 with NGS technology (81). Although the BigY700 has identified several T2T Y-SNPs (e.g.,
548 FTT161 and FTT162) within the noble Hay phylogenetic tree (82), these Y-SNPs did not get
549 recognised until T2T research was made available to researchers. Therefore, it is
550 recommended that several noble Hay testers are eventually sequenced using the longread
551 sequencing methodology implemented by the T2T consortium as the current research
552 suggests that a higher resolution of the Y-chromosome can be achieved (81, 83, 84).
553 Furthermore, longread sequencing will likely develop the noble Hay phylogenetic tree by
554 identifying new Y-SNPs, resulting in more accurate Y-SNP dating.

555 To the best of our knowledge, this study is the first to suggest variation in Y-SNP mutation
556 rates using well-documented testers with proven pedigrees dating back to the 12th century.
557 To explore patterns in the variation of average Y-SNP mutation rates further, investigations
558 into a wider range of well-documented lineages is recommended for future research. If
559 similar variation of average Y-SNP mutation rates can be observed in other well-documented
560 lineages, further research could focus on investigating possible causes for such variation,

561 and the potential implications on Y-SNP dating. The dating estimates for Y-SNPs are very
562 ambiguous due to the very large date ranges currently available. However, the identification
563 of Multigen-SNPs and SNP-Progens provides far more precise dating of Y-SNPs, but the
564 methodology is limited to well-documented lineages that can be traced back to the high
565 Middle Ages era. Those lineages of noble descent are the only realistic candidates that can
566 be reliably investigated to identify Multigen-SNPs and SNP-Progens back to the medieval
567 era. Further limitations occur when a noble lineage has died out or researchers fail to recruit
568 a well-documented individual for Y-DNA testing. Furthermore, investigating other noble
569 lineages will provide more comparative data to permit conclusions on whether Y-DNA
570 haplogroup diversity can be observed in other surnames associated to nobility. Y-DNA
571 haplogroup diversity is likely facilitated by several mechanisms; however, specific historical
572 events could be a key factor that facilitate the adoption of certain surnames. The impact of
573 wars and migrations could be two key facilitators to explore in future research.

574 **Conclusions**

575 The identification of Multigen-SNPs and SNP-Progens are of huge value to genealogical
576 researchers. As demonstrated in this research and in other studies, Y-DNA testing has been
577 proven to bridge significant gaps that exist in the documentary evidence when researching
578 ancestral pedigrees (46-49). Furthermore, direct paternal descent that is proven by
579 documentation is never a guarantee of true descent due to the probability of EPP taking
580 place. In reverse, not having a noble surname does not mean that an individual is not a
581 direct paternal descendant of a noble lineage. The Hay testers had genetic matches with 24
582 individuals who have the surname Hay (plus asscoiated spelling variants) and 12 individuals
583 who did not have the surname Hay. Our genetic data proves that the 12 non-Hay testers are
584 descendants of a noble Hay ancestor, and a surname change has occurred at some point in
585 their ancestry, likely the result of an illegitimate conception sometime in the past. It is likely
586 that several of the testers with the surname Hay are descendanded from a younger son of a
587 noble lineage and these lineages eventually disappeared from the records as their

descendants were landless. Research that focuses on Multigen-SNPs and SNP-Progen identification adds another dimension for validating pedigrees with a high degree of certainty. Furthermore, this type of research provides reliable data that can be used by researchers to challenge poorly researched pedigrees that make erroneous conclusions.

By comparing the Y-SNPs and ancestries of the three well-documented Hay noble descendants, we have managed to confidently identify several Multigen-SNPs associated to the noble Hay lineage. The genetic data for this study also provides further evidence that the Hay noble lineage originated in Normandy as they share the Y-SNP R1a-YP3148 with several individuals who have a surname of Norman origin. One specific tester that matches the Hay noble lineage is proven to be a well-documented descendant of the noble Travers of Horton lineage. This research demonstrates that significant Y-DNA haplogroup diversity exists among FTDNA testers with the surname Hay. The Y-DNA haplogroup diversity observed in this study is strong evidence that supports Durie (2022) who suggested that most men with a surname associated to nobility will not be a direct paternal descendant of the noble progenitor (23).

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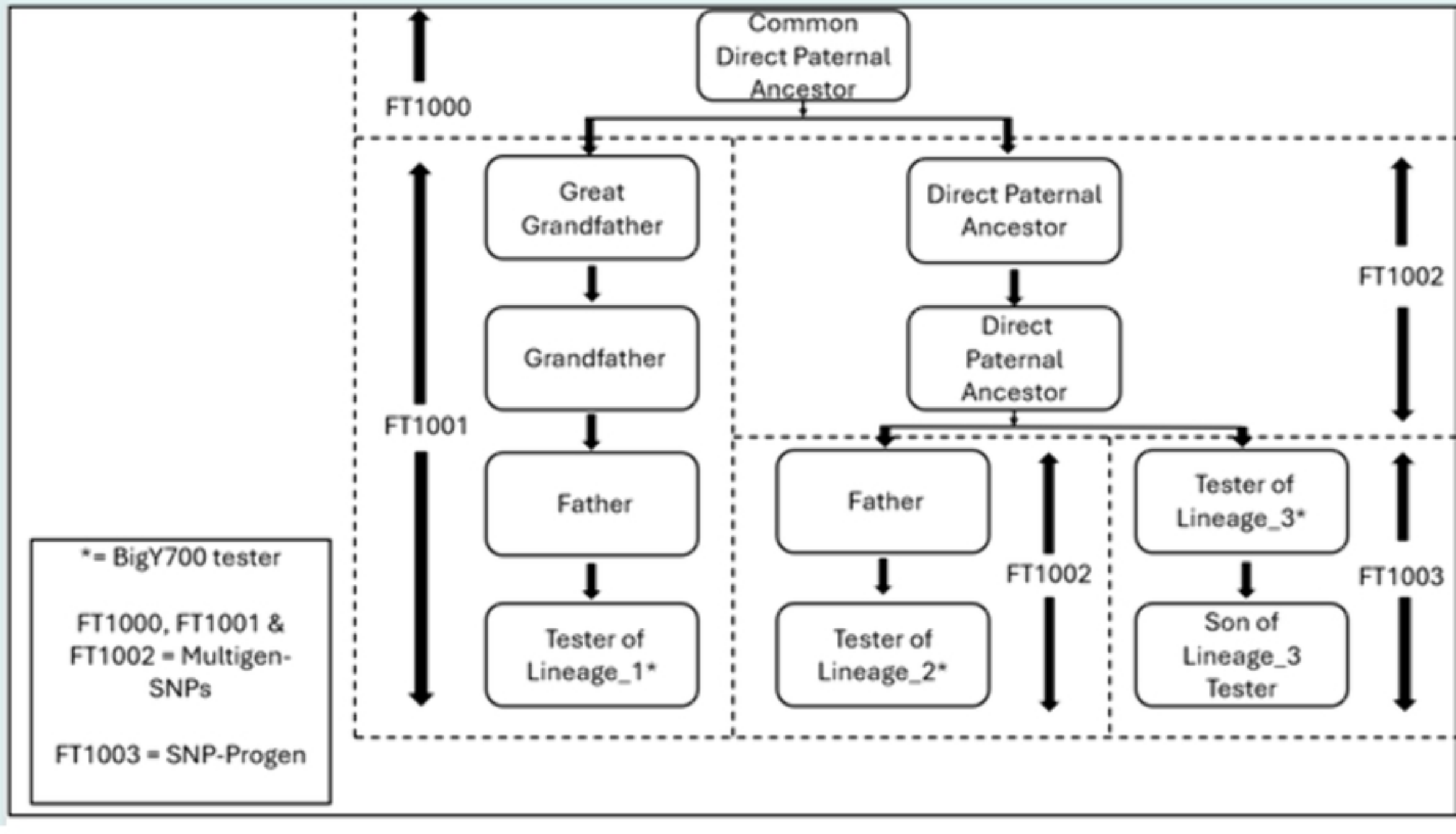

Common Direct Paternal Ancestor
FT1000
Great Grandfather
Grandfather
Father
Tester of Lineage_1*
FT1001
Direct Paternal Ancestor
Direct Paternal Ancestor
FT1002
Father
Tester of Lineage_2*
FT1002
Tester of Lineage_3*
Son of Lineage_3 Tester
FT1003
*= BigY700 tester
FT1000, FT1001 & FT1002 = Multigen-SNPs
FT1003 = SNP-Progen

Figure 1

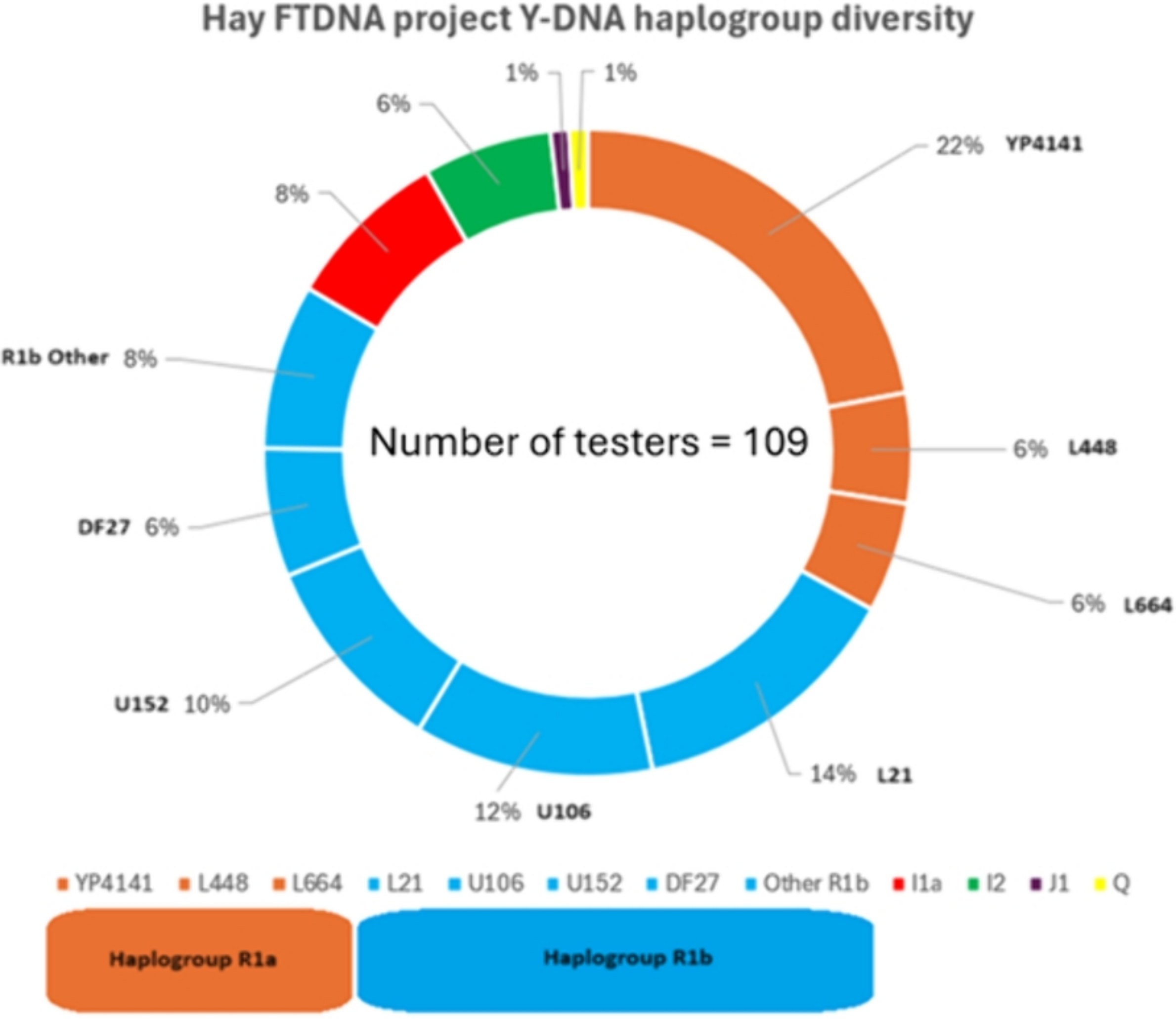

Hay FTDNA project Y-DNA haplogroup diversity
1%
1%
6%
8%
22% YP4141
R1b Other 8%
Number of testers = 109
6% L448
DF27 6%
6% L664
U152 10%
14% L21
12% U106
YP4141
L448
L664
L21
U106
U152
DF27
Other R1b
I1a
I2
J1
Q
Haplogroup R1a
Haplogroup R1b

Figure 2

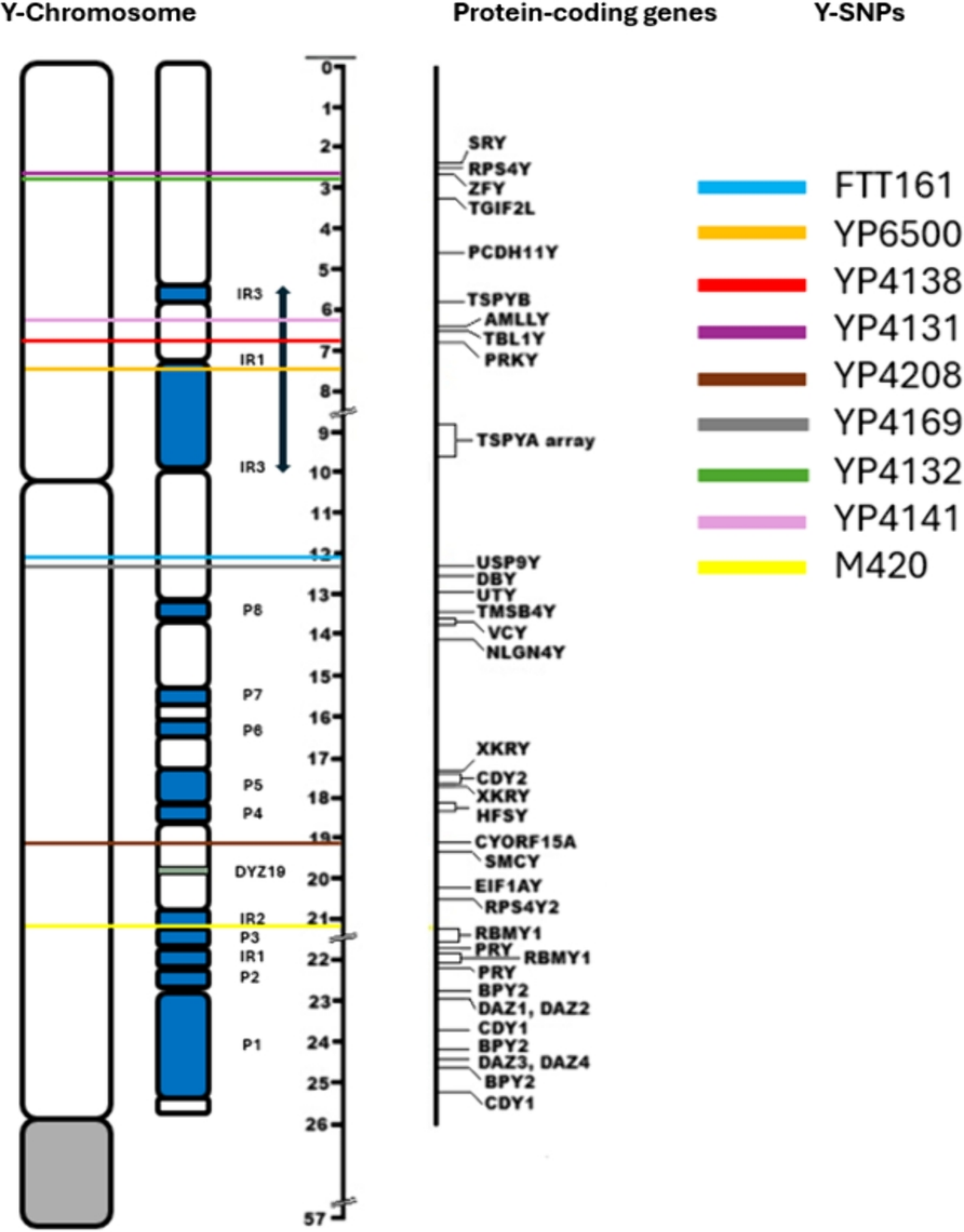
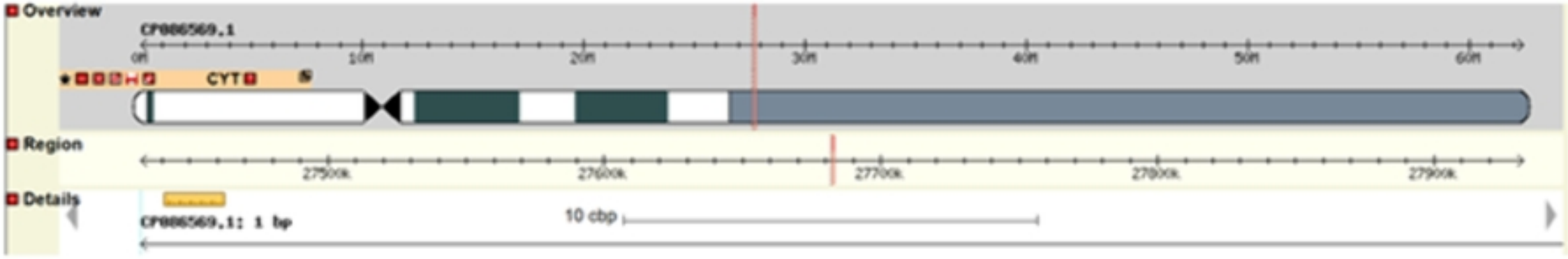

Y-Chromosome
Protein-coding genes
Y-SNPs
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
57
IR3
IR1
IR3
P8
P7
P6
P5
P4
DYZ19
IR2
P3
IR1
P2
P1
SRY
RPS4Y
ZFY
TGIF2L
PCDH11Y
TSPYB
AMLLY
TBL1Y
PRKY
TSPYA array
USP9Y
DBY
UTY
TMSB4Y
VCY
NLGN4Y
XKRY
CDY2
XKRY
HFSY
CYORF15A
SMCY
EIF1AY
RPS4Y2
RBMY1
PRY
RBMY1
PRY
BPY2
DAZ1, DAZ2
CDY1
BPY2
DAZ3, DAZ4
BPY2
CDY1
FTT161
YP6500
YP4138
YP4131
YP4208
YP4169
YP4132
YP4141
M420

Figure 3



FASTA

Showing 601 bp region from base 27682000 to 27682600.

Homo sapiens isolate NA24385 chromosome Y

GenBank: CP086569.2

GenBank Graphics

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>CP086569.2:27682000-27682600 Homo sapiens isolate NA24385 chromosome Y
GAGTGCGGTGGAATGGAATGGAATGGCATCAAATCGCATGGTAATGAATCAAATGGAATCAAATGGAATG
AAATAATGGAATCGAAGGCAAACGAATGGAATCGAATTGCACTGATTCTACTGACTTCGAACAAAATGAA
ATGAAATGCGGTGAAGTGGAGTGGAGTGGAATGTATTAGGGTGGAATGGAATTGAATGGTGTGGAGTGGA
GTGGAGTGTCCAGGAGTGGAATGGGAAGAAATGGAATTGAACGGAGTGGAGTGGAGTGGAATGGAGGGTA
ATGGAGTGGAATGGAGTGGAGTGGAGTAGAGTGGAATGGGTTGGAGTGGAATGCAGAGGACAGGAGTGGA
GTGTGGTGGACTGGAGTGGAGTGGAGTGGAGTGAAGTGGATTGGATTGAAATAGAGCGGAGCAGAGTGGA
ATGCAATTGAATCACATGGTACTGAATCAAATCGAATGGAATTAAATCGAATGAAAAAACGGAATCAAAA
GCAAACGAATGGAGTCAAACCACATTGGTTAGACTGATATCGAATAATATCAAAAGAAATGTGGTGAAGT
GGAGTGGAGTGTAATGAAATGGGGTGGAATGAAATTGAATG
```

FTT162 at CP086569.2:27682309 A>T

TGGAG(repeat) → TAGAG (ref) → TAGTG (FTT162)

Figure 4

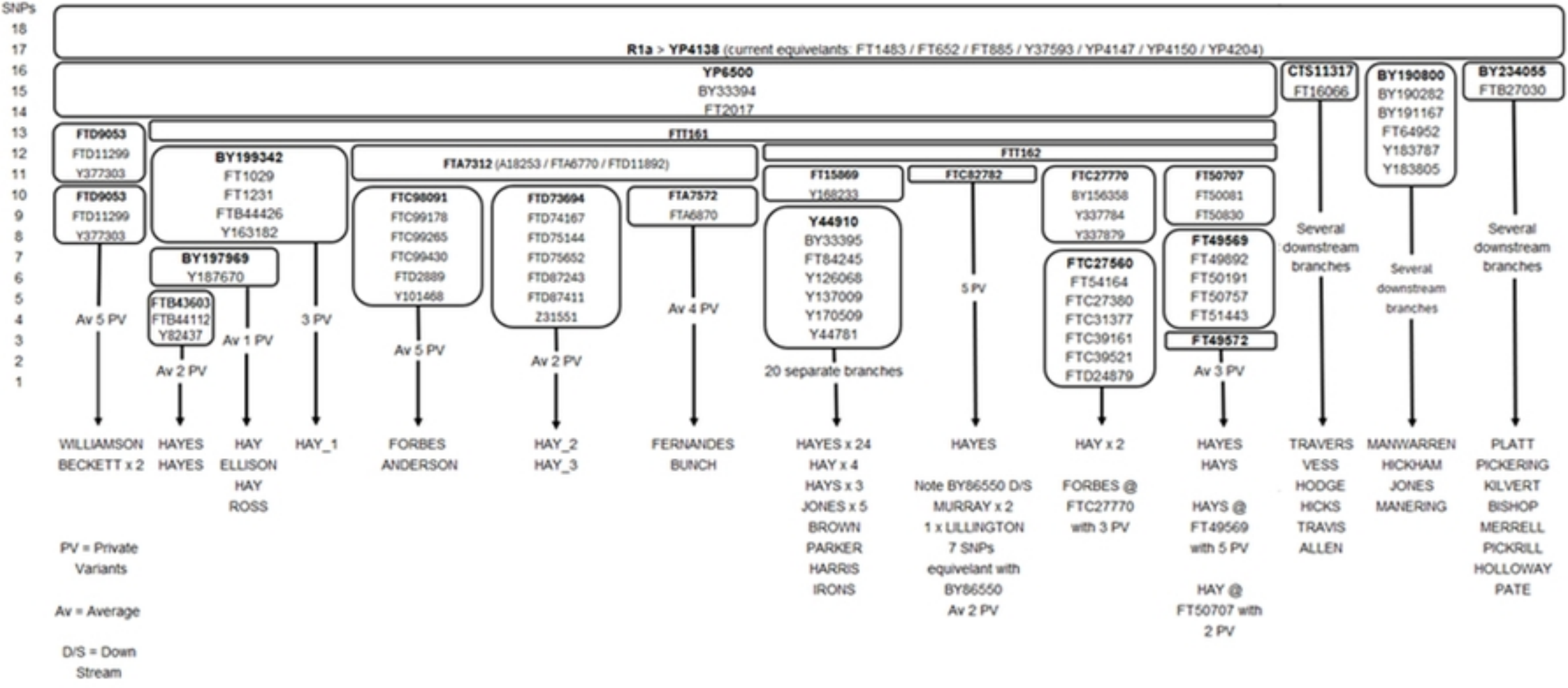
SNPs
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
R1a > YP4138 (current equivelants: FT1483 / FT652 / FT885 / Y37593 / YP4147 / YP4150 / YP4204)
YP6500
BY33394
FT2017
CTS11317
FT16066
BY190800
BY190282
BY191167
FT64952
Y183787
Y183805
BY234055
FTB27030
FTD9053
FTD11299
Y377303
FTD9053
FTD11299
Y377303
FTT161
BY199342
FT1029
FT1231
FTB44426
Y163182
BY197969
Y187670
FTB43603
FTB44112
Y82437
FTA7312 (A18253 / FTA6770 / FTD11892)
FTC98091
FTC99178
FTC99265
FTC99430
FTD2889
Y101468
FTD73694
FTD74167
FTD75144
FTD75652
FTD87243
FTD87411
Z31551
FTA7572
FTA6870
FTT162
FT15869
Y168233
Y44910
BY33395
FT84245
Y126068
Y137009
Y170509
Y44781
FTC82782
FTC27770
BY156358
Y337784
Y337879
FTC27560
FT54164
FTC27380
FTC31377
FTC39161
FTC39521
FTD24879
FT50707
FT50081
FT50830
FT49569
FT49692
FT50191
FT50757
FT51443
FT49572
Av 5 PV
Av 2 PV
Av 1 PV
3 PV
Av 5 PV
Av 2 PV
Av 4 PV
20 separate branches
5 PV
Av 3 PV
Several downstream branches
Several downstream branches
Several downstream branches
WILLIAMSON
BECKETT x 2
HAYES
HAYES
HAY
ELLISON
HAY
ROSS
HAY_1
FORBES
ANDERSON
HAY_2
HAY_3
FERNANDES
BUNCH
HAYES x 24
HAY x 4
HAYS x 3
JONES x 5
BROWN
PARKER
HARRIS
IRONS
HAYES
Note BY86550 D/S
MURRAY x 2
1 x LILLINGTON
7 SNPs
equivelant with
BY86550
Av 2 PV
HAY x 2
FORBES @
FTC27770
with 3 PV
HAYES
HAYS
HAYS @
FT49569
with 5 PV
HAY @
FT50707 with
2 PV
TRAVERS
VESS
HODGE
HICKS
TRAVIS
ALLEN
MANWARREN
HICKHAM
JONES
MANERING
PLATT
PICKERING
KILVERT
BISHOP
MERRELL
PICKRILL
HOLLOWAY
PATE
PV = Private
Variants
Av = Average
D/S = Down
Stream

Figure 5

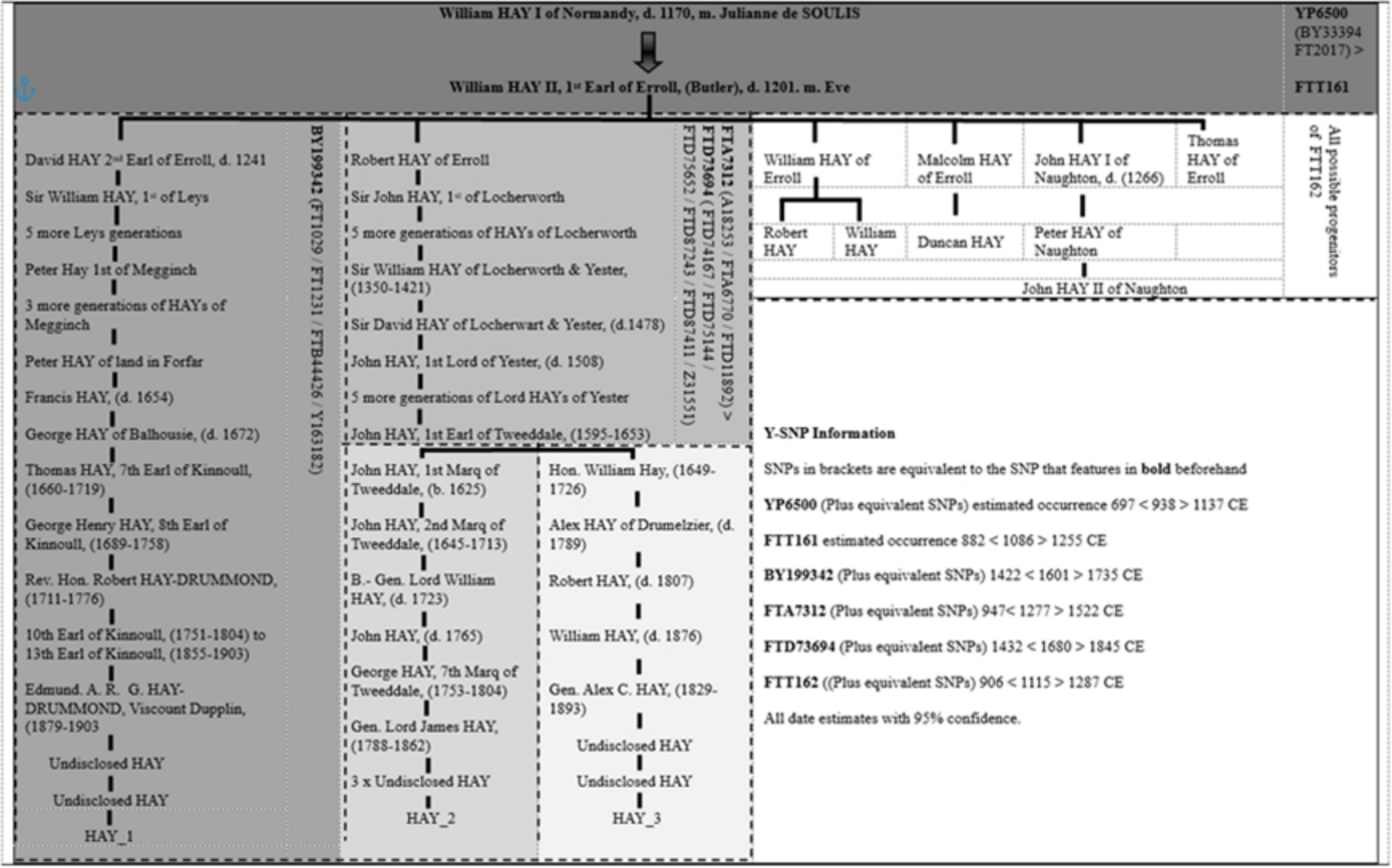
William HAY I of Normandy, d. 1170, m. Julianne de SOULIS
YP6500 (BY33394 FT2017) >
FTT161
William HAY II, 1st Earl of Erroll, (Butler), d. 1201. m. Eve
David HAY 2nd Earl of Erroll, d. 1241
Sir William HAY, 1st of Leys
5 more Leys generations
Peter Hay 1st of Megginch
3 more generations of HAYs of Megginch
Peter HAY of land in Forfar
Francis HAY, (d. 1654)
George HAY of Balhousie, (d. 1672)
Thomas HAY, 7th Earl of Kinnoull, (1660-1719)
George Henry HAY, 8th Earl of Kinnoull, (1689-1758)
Rev. Hon. Robert HAY-DRUMMOND, (1711-1776)
10th Earl of Kinnoull, (1751-1804) to 13th Earl of Kinnoull, (1855-1903)
Edmund. A. R. G. HAY-DRUMMOND, Viscount Dupplin, (1879-1903
Undisclosed HAY
Undisclosed HAY
HAY_1
BY199342 (FT1029 / FT1231 / FTB44426 / Y163182)
Robert HAY of Erroll
Sir John HAY, 1st of Locherworth
5 more generations of HAYs of Locherworth
Sir William HAY of Locherworth & Yester, (1350-1421)
Sir David HAY of Locherwart & Yester, (d.1478)
John HAY, 1st Lord of Yester, (d. 1508)
5 more generations of Lord HAYs of Yester
John HAY, 1st Earl of Tweeddale, (1595-1653)
FTA7312 (A18253 / FTA6770 / FTD11892) > FTD73694 (FTD74167 / FTD75144 / FTD75652 / FTD87243 / FTD87411 / Z31551)
John HAY, 1st Marq of Tweeddale, (b. 1625)
John HAY, 2nd Marq of Tweeddale, (1645-1713)
B.- Gen. Lord William HAY, (d. 1723)
John HAY, (d. 1765)
George HAY, 7th Marq of Tweeddale, (1753-1804)
Gen. Lord James HAY, (1788-1862)
3 x Undisclosed HAY
HAY_2
Hon. William Hay, (1649-1726)
Alex HAY of Drumelzier, (d. 1789)
Robert HAY, (d. 1807)
William HAY, (d. 1876)
Gen. Alex C. HAY, (1829-1893)
Undisclosed HAY
Undisclosed HAY
HAY_3
William HAY of Erroll
Malcolm HAY of Erroll
John HAY I of Naughton, d. (1266)
Thomas HAY of Erroll
Robert HAY
William HAY
Duncan HAY
Peter HAY of Naughton
John HAY II of Naughton
All possible progenitors of FTT162
Y-SNP Information
SNPs in brackets are equivalent to the SNP that features in bold beforehand
YP6500 (Plus equivalent SNPs) estimated occurrence 697 < 938 > 1137 CE
FTT161 estimated occurrence 882 < 1086 > 1255 CE
BY199342 (Plus equivalent SNPs) 1422 < 1601 > 1735 CE
FTA7312 (Plus equivalent SNPs) 947< 1277 > 1522 CE
FTD73694 (Plus equivalent SNPs) 1432 < 1680 > 1845 CE
FTT162 ((Plus equivalent SNPs) 906 < 1115 > 1287 CE
All date estimates with 95% confidence.

Figure 6

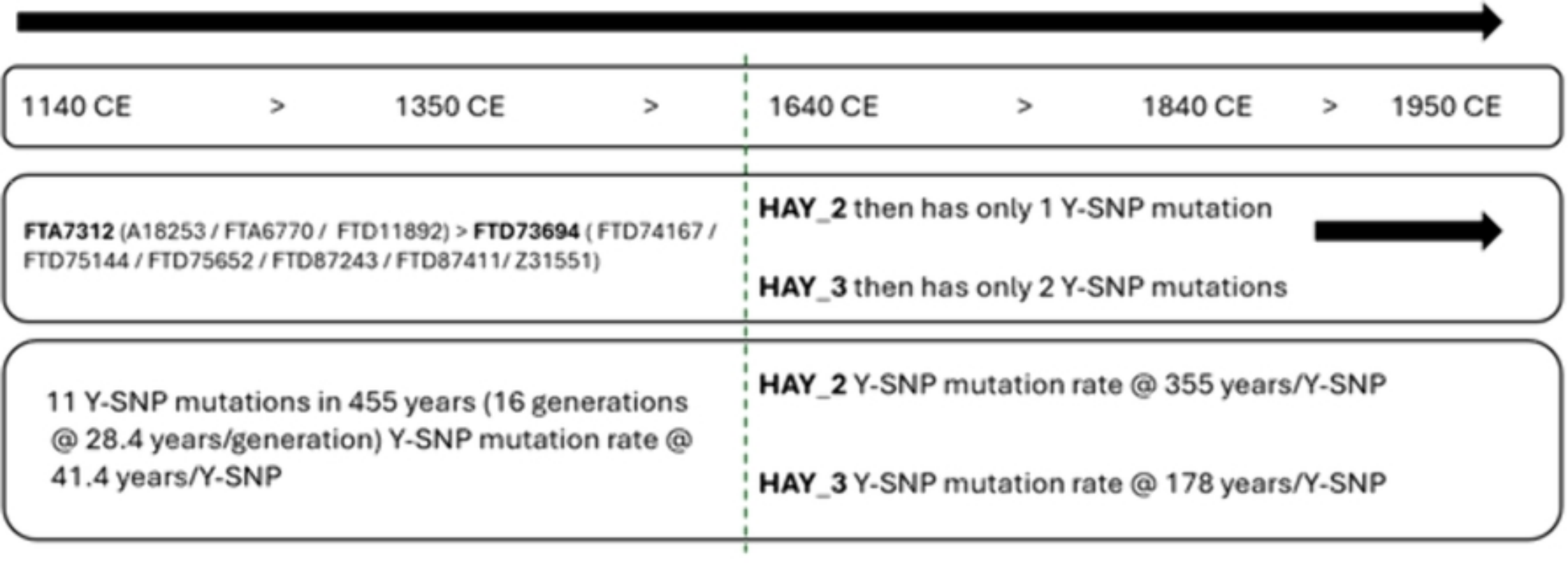
1140 CE > 1350 CE > 1640 CE > 1840 CE > 1950 CE
FTA7312 (A18253 / FTA6770 / FTD11892) > FTD73694 (FTD74167 / FTD75144 / FTD75652 / FTD87243 / FTD87411/ Z31551)
HAY_2 then has only 1 Y-SNP mutation
HAY_3 then has only 2 Y-SNP mutations
11 Y-SNP mutations in 455 years (16 generations @ 28.4 years/generation) Y-SNP mutation rate @ 41.4 years/Y-SNP
HAY_2 Y-SNP mutation rate @ 355 years/Y-SNP
HAY_3 Y-SNP mutation rate @ 178 years/Y-SNP

Figure 7

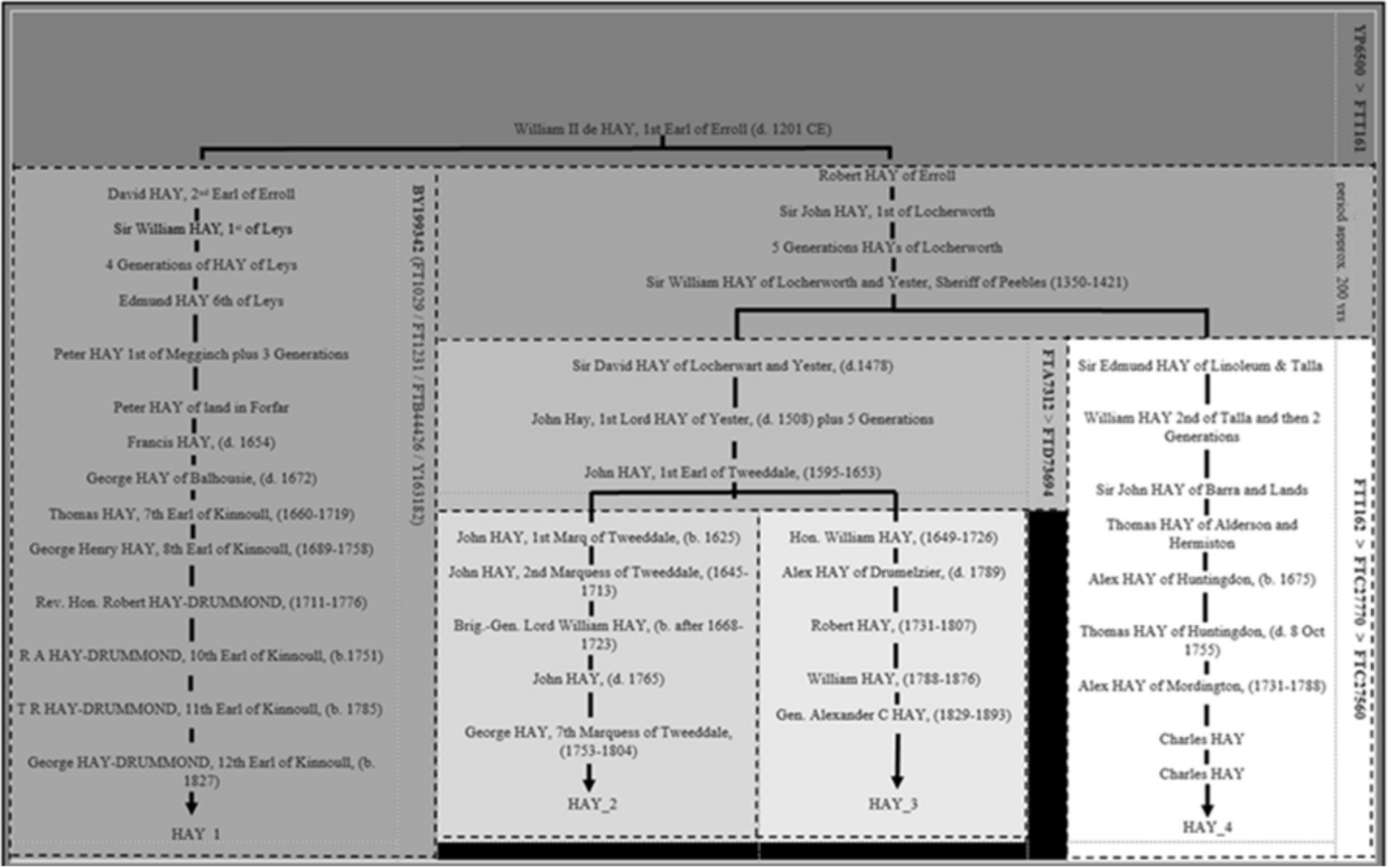
YP6500 > FTT161
William II de HAY, 1st Earl of Erroll (d. 1201 CE)
BY169842 (FT1029 / FT1231 / FTB44426 / Y169182)
David HAY, 2nd Earl of Erroll
Sir William HAY, 1st of Leys
4 Generations of HAY of Leys
Edmund HAY 6th of Leys
Peter HAY 1st of Megginch plus 3 Generations
Peter HAY of land in Forfar
Francis HAY, (d. 1654)
George HAY of Balhousie, (d. 1672)
Thomas HAY, 7th Earl of Kinnoull, (1660-1719)
George Henry HAY, 8th Earl of Kinnoull, (1689-1758)
Rev. Hon. Robert HAY-DRUMMOND, (1711-1776)
R A HAY-DRUMMOND, 10th Earl of Kinnoull, (b.1751)
T R HAY-DRUMMOND, 11th Earl of Kinnoull, (b. 1785)
George HAY-DRUMMOND, 12th Earl of Kinnoull, (b. 1827)
HAY_1
Robert HAY of Erroll
Sir John HAY, 1st of Locherworth
5 Generations HAYs of Locherworth
Sir William HAY of Locherworth and Yester, Sheriff of Peebles (1350-1421)
period approx. 200 yrs
Sir David HAY of Locherwart and Yester, (d.1478)
John Hay, 1st Lord HAY of Yester, (d. 1508) plus 5 Generations
John HAY, 1st Earl of Tweeddale, (1595-1653)
FTA7312 > FTD73694
John HAY, 1st Marq of Tweeddale, (b. 1625)
John HAY, 2nd Marquess of Tweeddale, (1645-1713)
Brig.-Gen. Lord William HAY, (b. after 1668-1723)
John HAY, (d. 1765)
George HAY, 7th Marquess of Tweeddale, (1753-1804)
HAY_2
Hon. William HAY, (1649-1726)
Alex HAY of Drumelzier, (d. 1789)
Robert HAY, (1731-1807)
William HAY, (1788-1876)
Gen. Alexander C HAY, (1829-1893)
HAY_3
Sir Edmund HAY of Linoleum & Talla
William HAY 2nd of Talla and then 2 Generations
Sir John HAY of Barra and Lands
Thomas HAY of Alderson and Hermiston
Alex HAY of Huntingdon, (b. 1675)
Thomas HAY of Huntingdon, (d. 8 Oct 1755)
Alex HAY of Mordington, (1731-1788)
Charles HAY
Charles HAY
HAY_4
FTT162 > FTC27770 > FTC27560

Figure 8

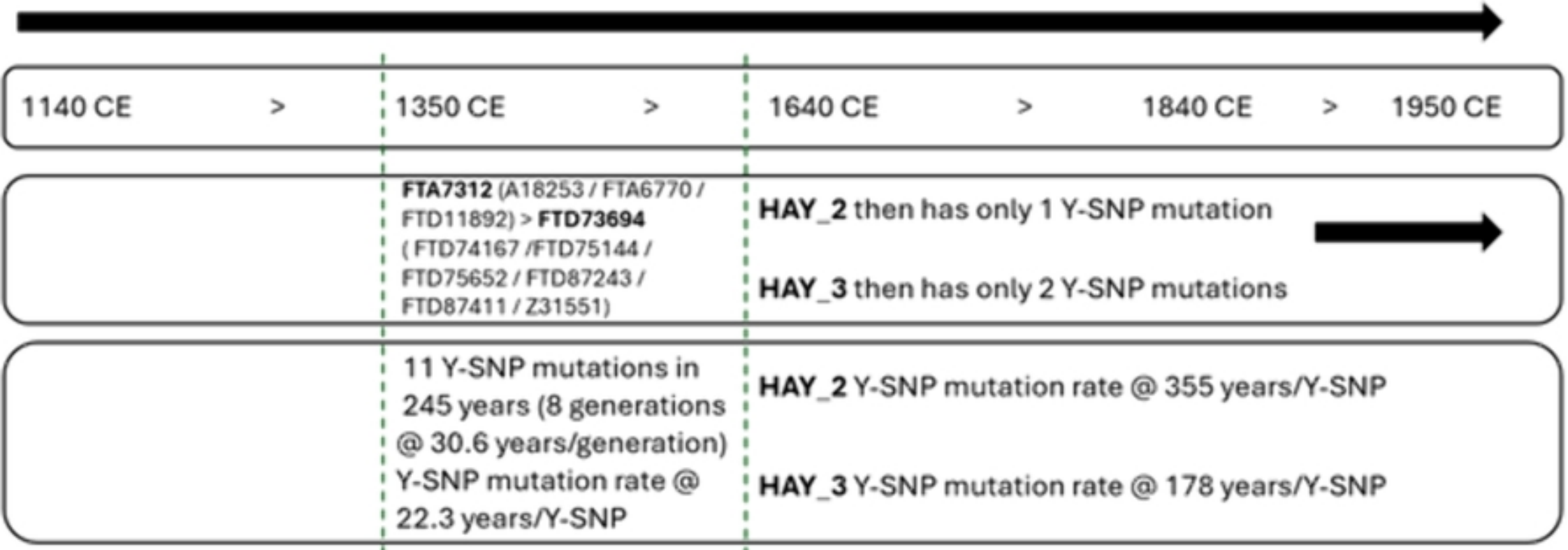
1140 CE > 1350 CE > 1640 CE > 1840 CE > 1950 CE
FTA7312 (A18253 / FTA6770 / FTD11892) > FTD73694 (FTD74167 /FTD75144 / FTD75652 / FTD87243 / FTD87411 / Z31551)
HAY_2 then has only 1 Y-SNP mutation
HAY_3 then has only 2 Y-SNP mutations
11 Y-SNP mutations in 245 years (8 generations @ 30.6 years/generation) Y-SNP mutation rate @ 22.3 years/Y-SNP
HAY_2 Y-SNP mutation rate @ 355 years/Y-SNP
HAY_3 Y-SNP mutation rate @ 178 years/Y-SNP

Figure 9