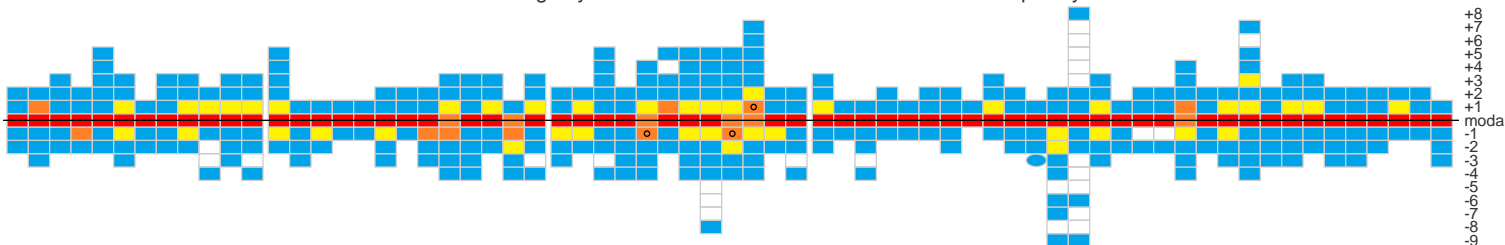


R-L21

This is the modal haplotype for the whole tree including any subtrees.

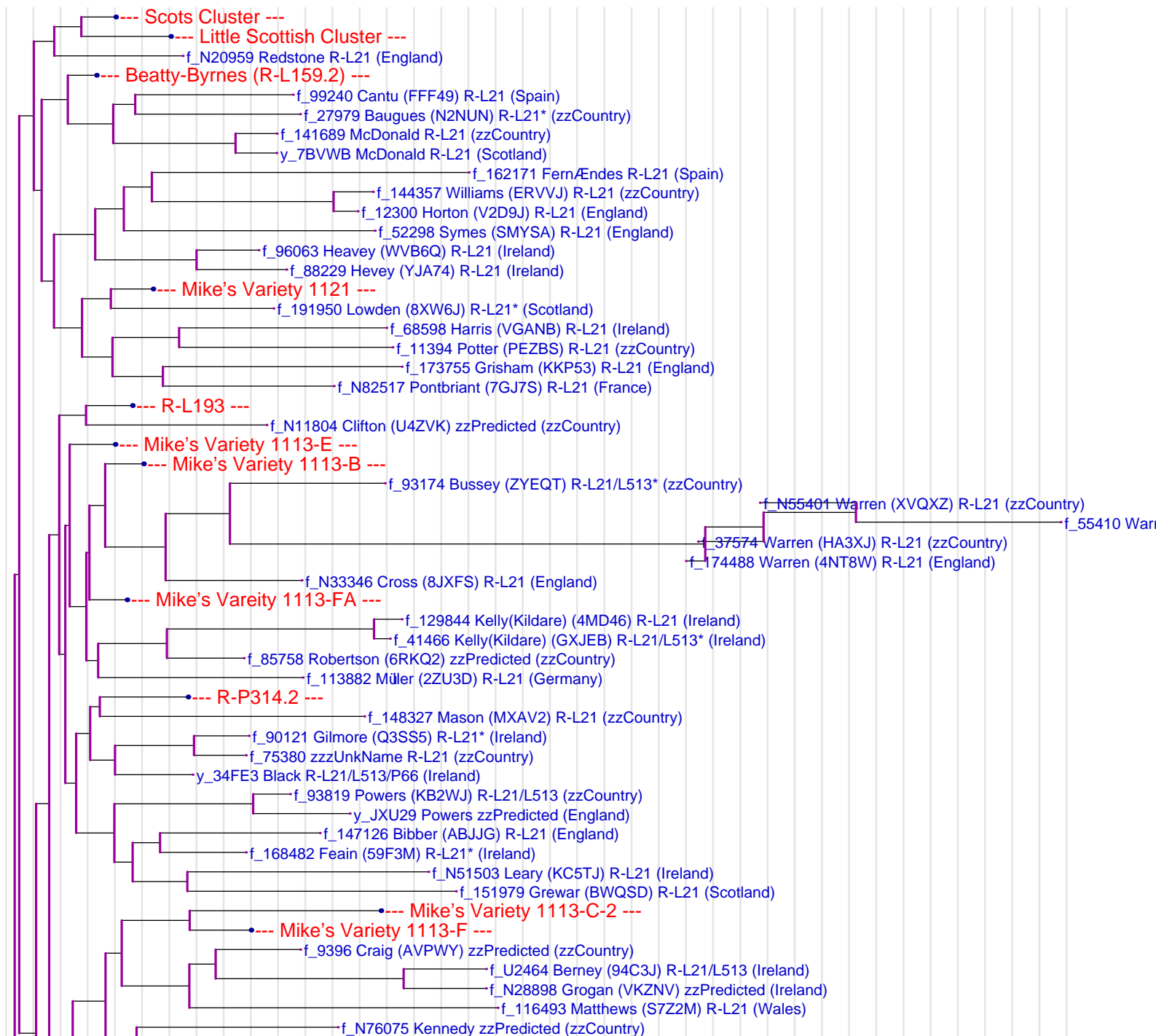
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
-----	-----	----	-----	------	------	-----	-----	-----	------	-----	--------	-----	------	------	-----	-----	-----	-----	-----	-----	------	------	------	------	-----	----	---------	---------	-----	-----	-----	-----	------	------	-----	-----	-----	-----	--------	--------	-----	-----	-----	-----	-------	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

This is the marker distribution for the whole tree including any subtrees. The color indicates the relative frequency of the alleles.

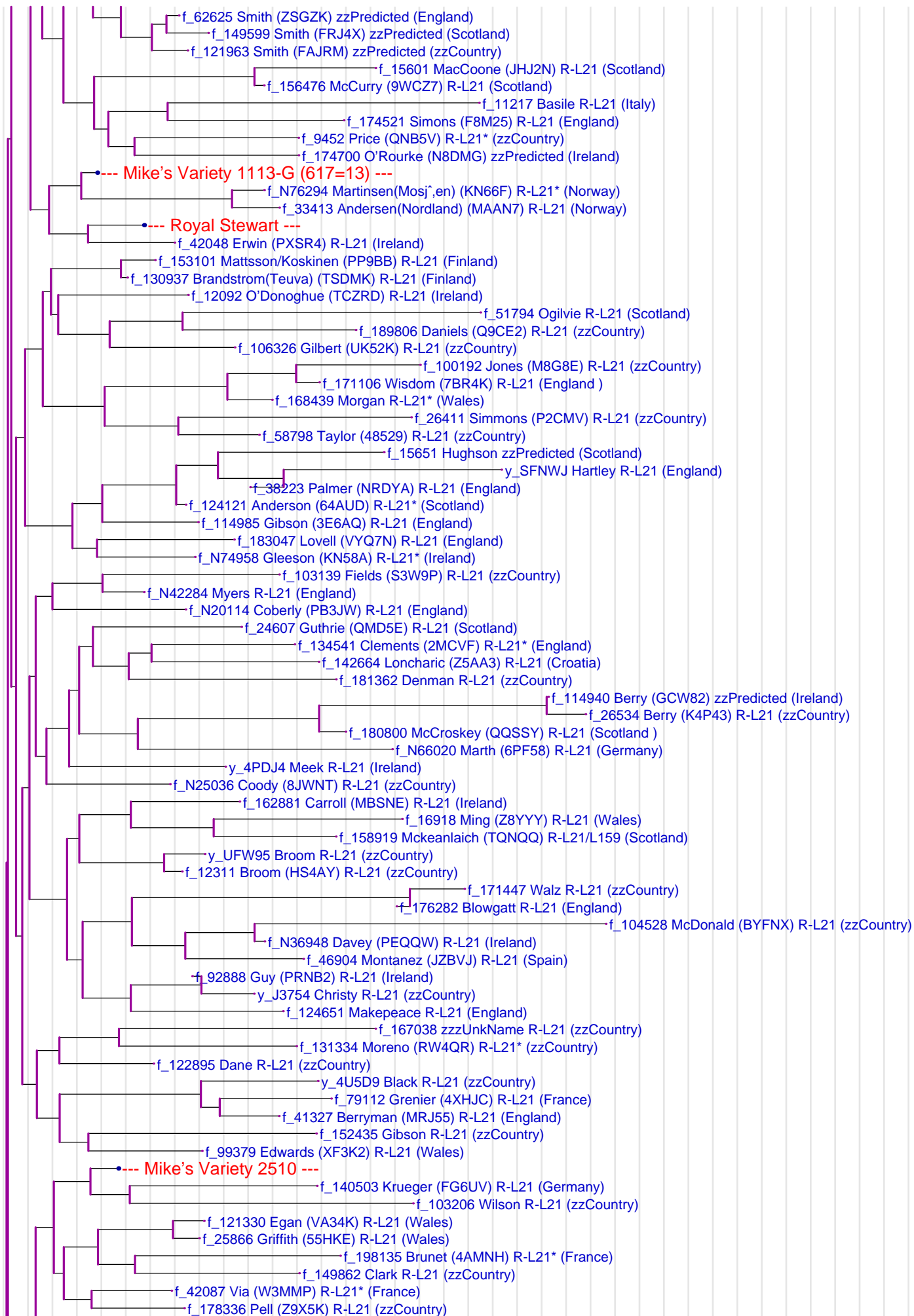


Age Analysis

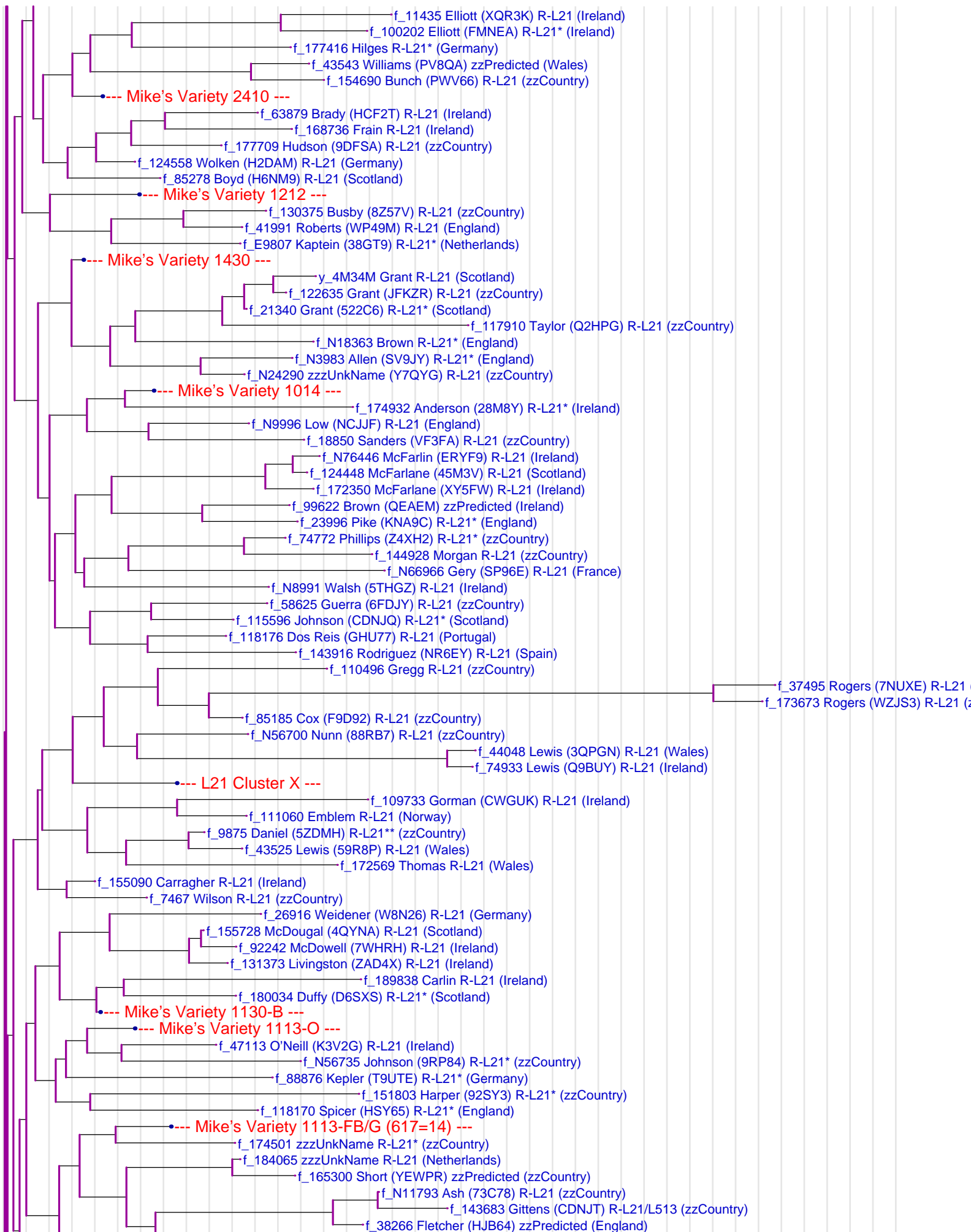
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
2715	181905	43808	24.08%	136.81±13.69	3420.23±483.777



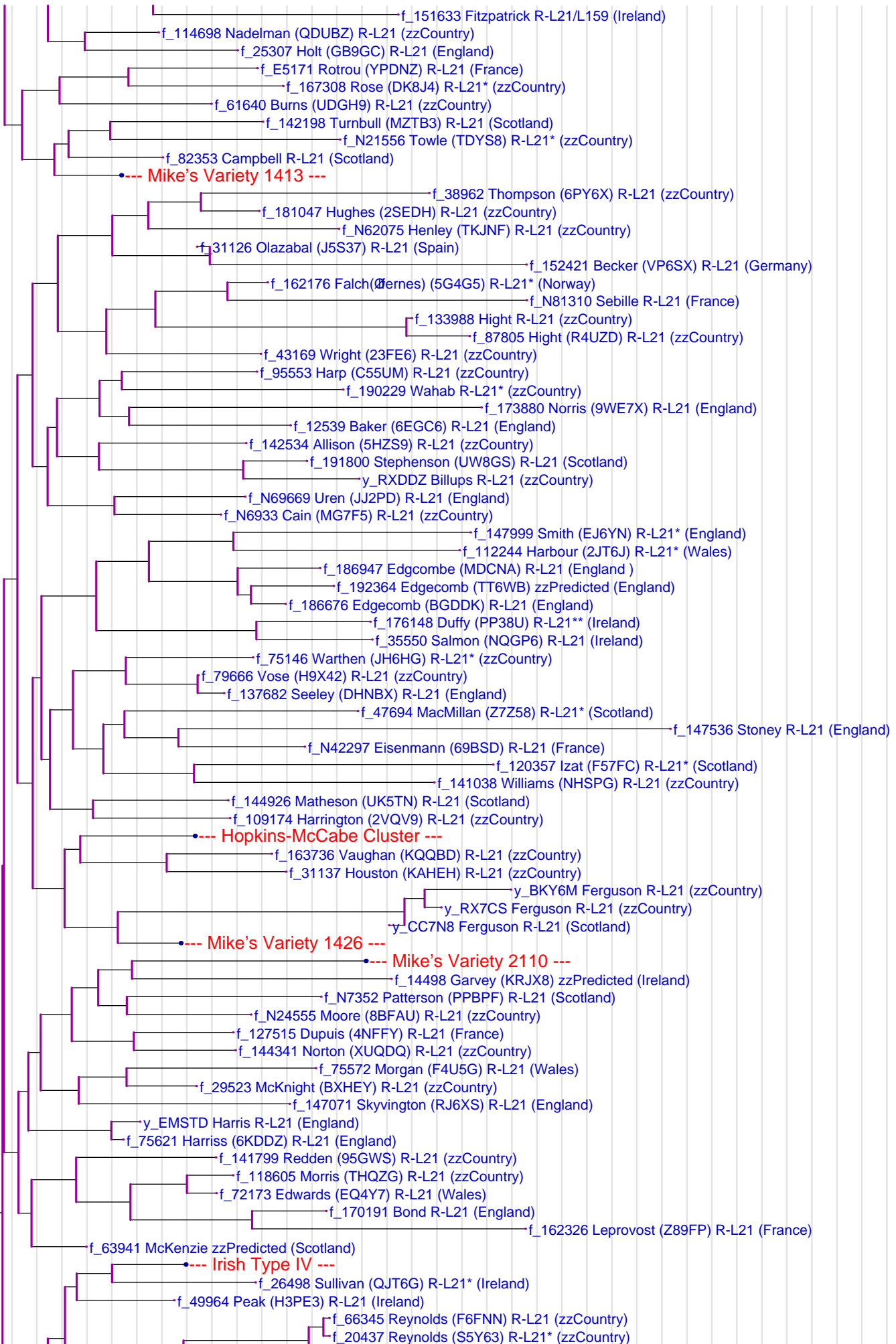
The vertical grey lines are separated 10 generations apart.



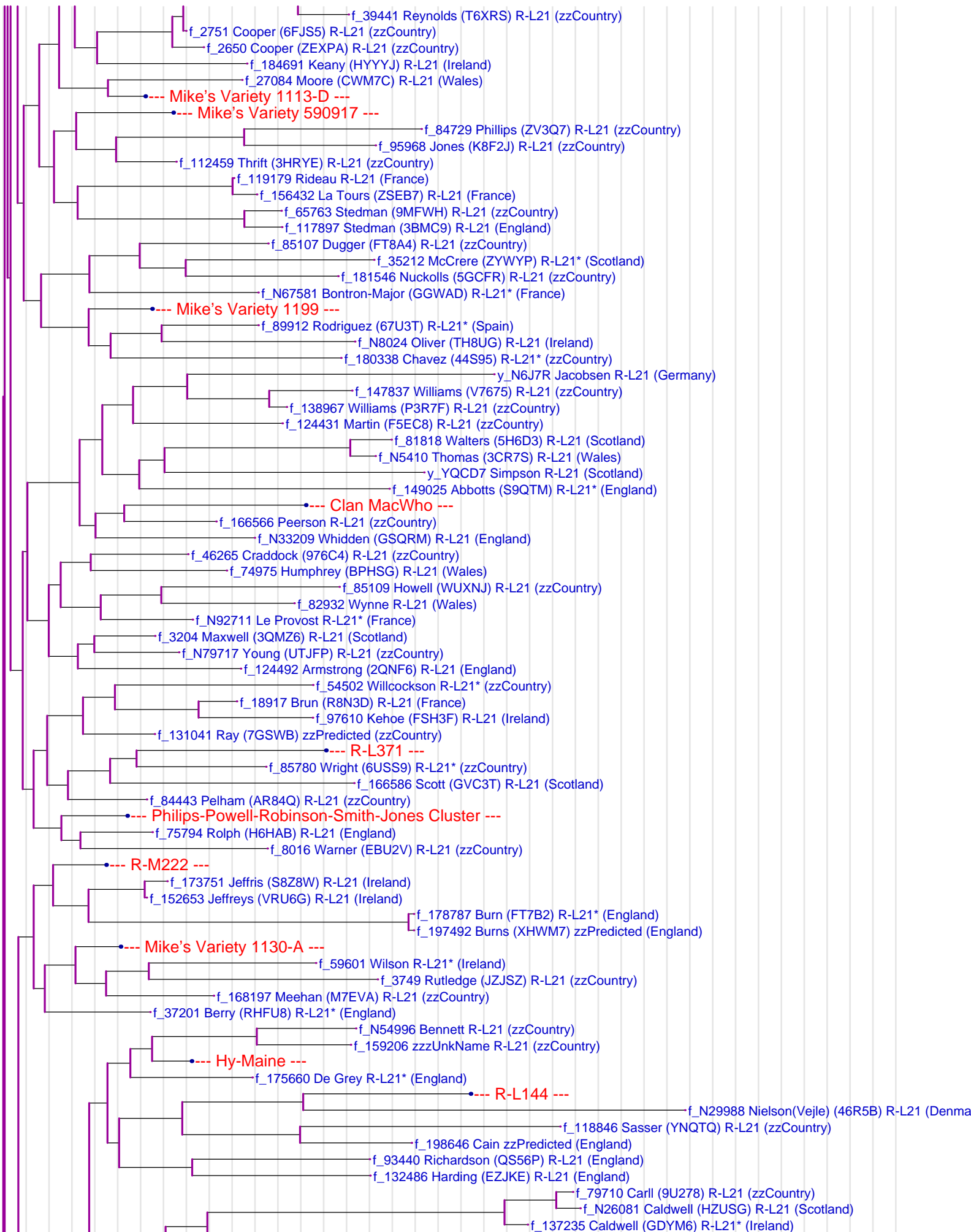
The vertical grey lines are separated 10 generations apart.



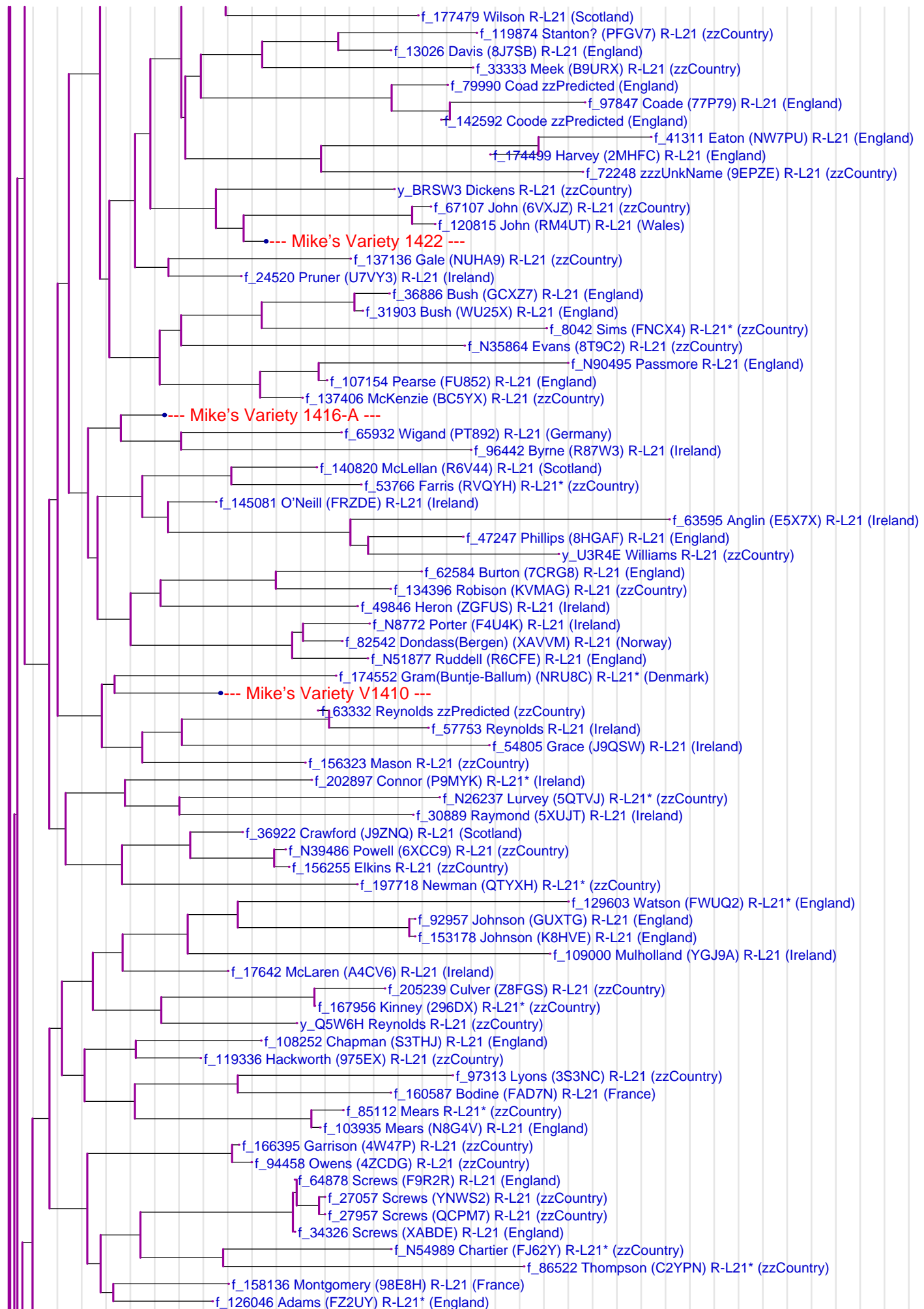
The vertical grey lines are separated 10 generations apart.



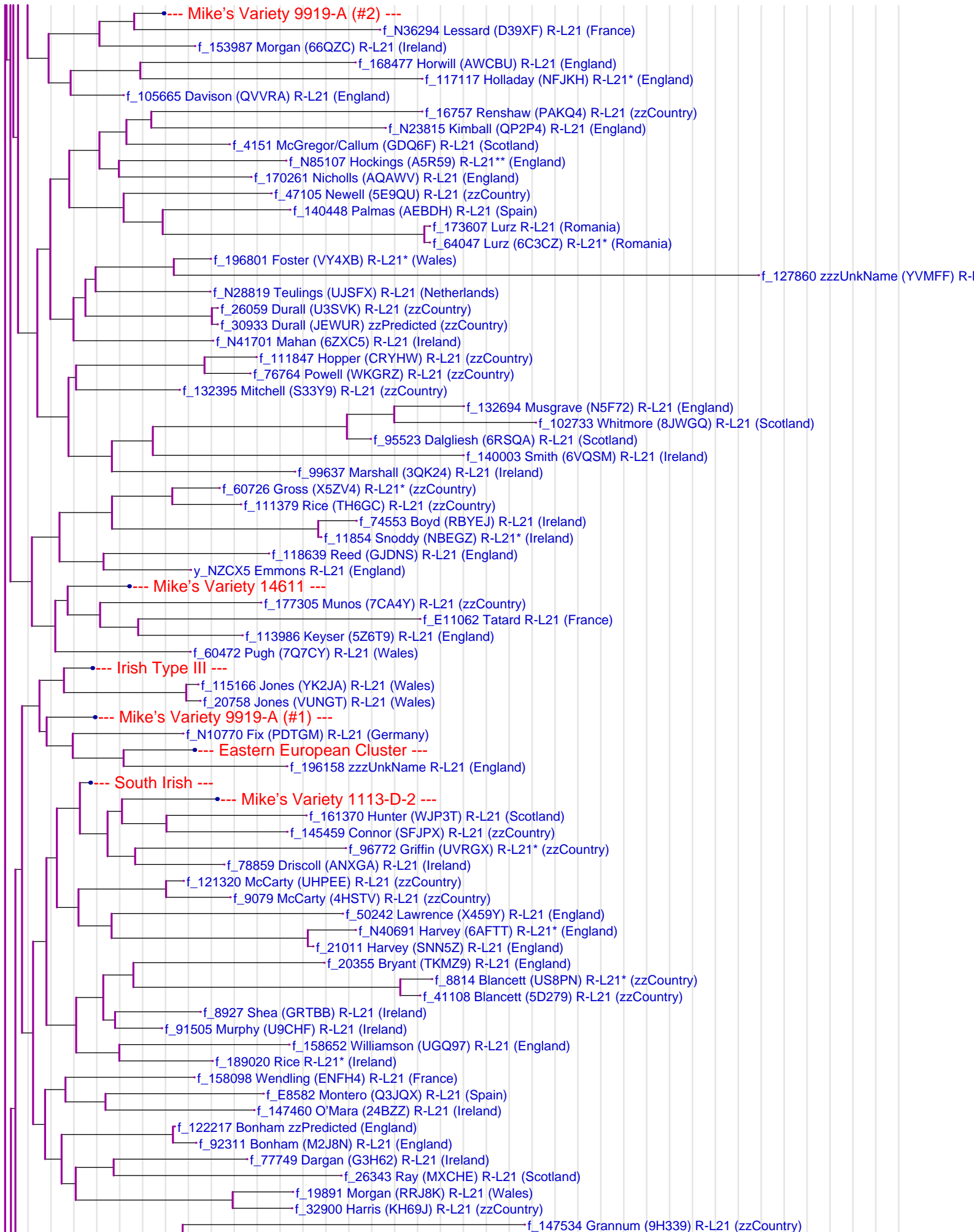
The vertical grey lines are separated 10 generations apart.



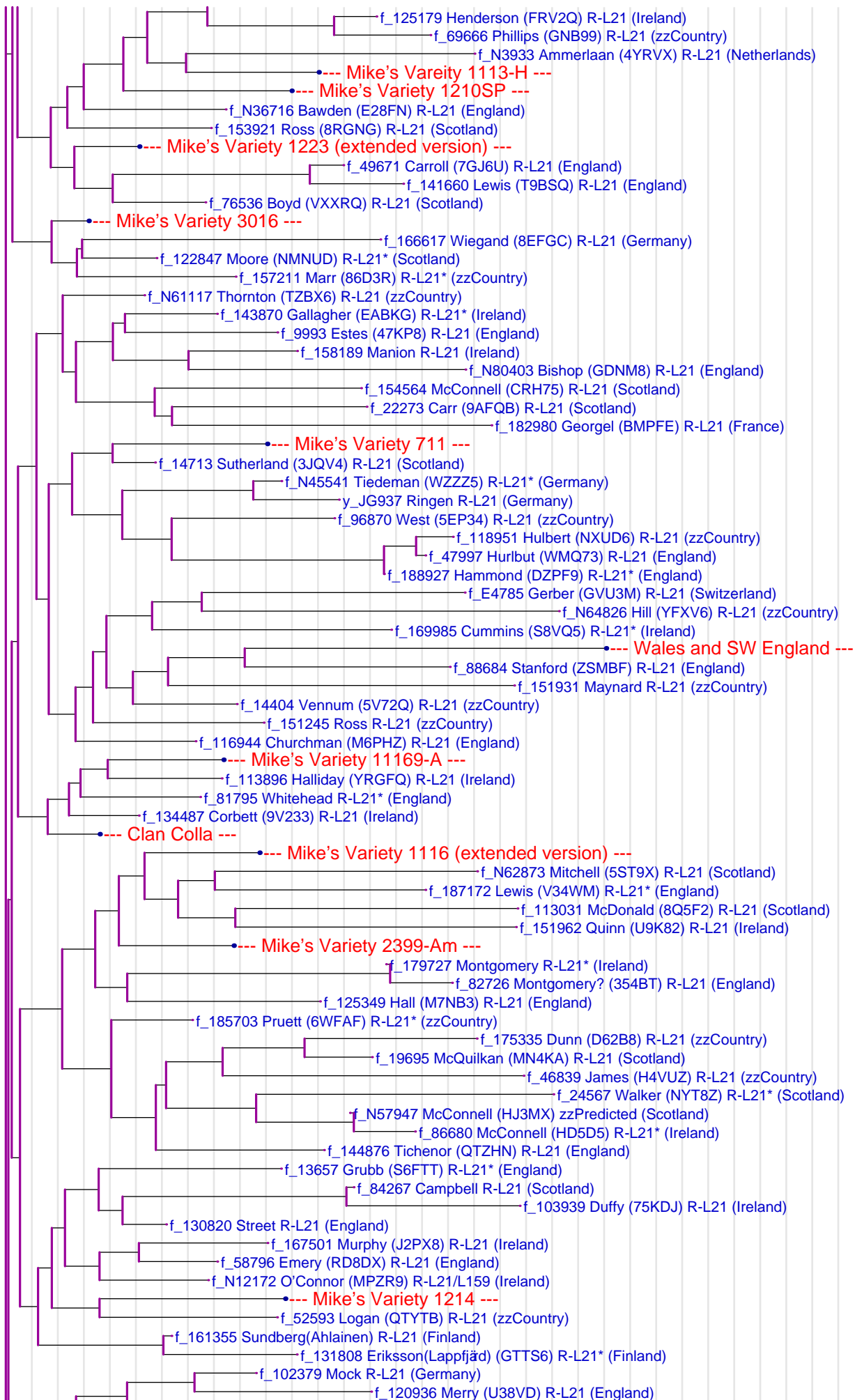
The vertical grey lines are separated 10 generations apart.



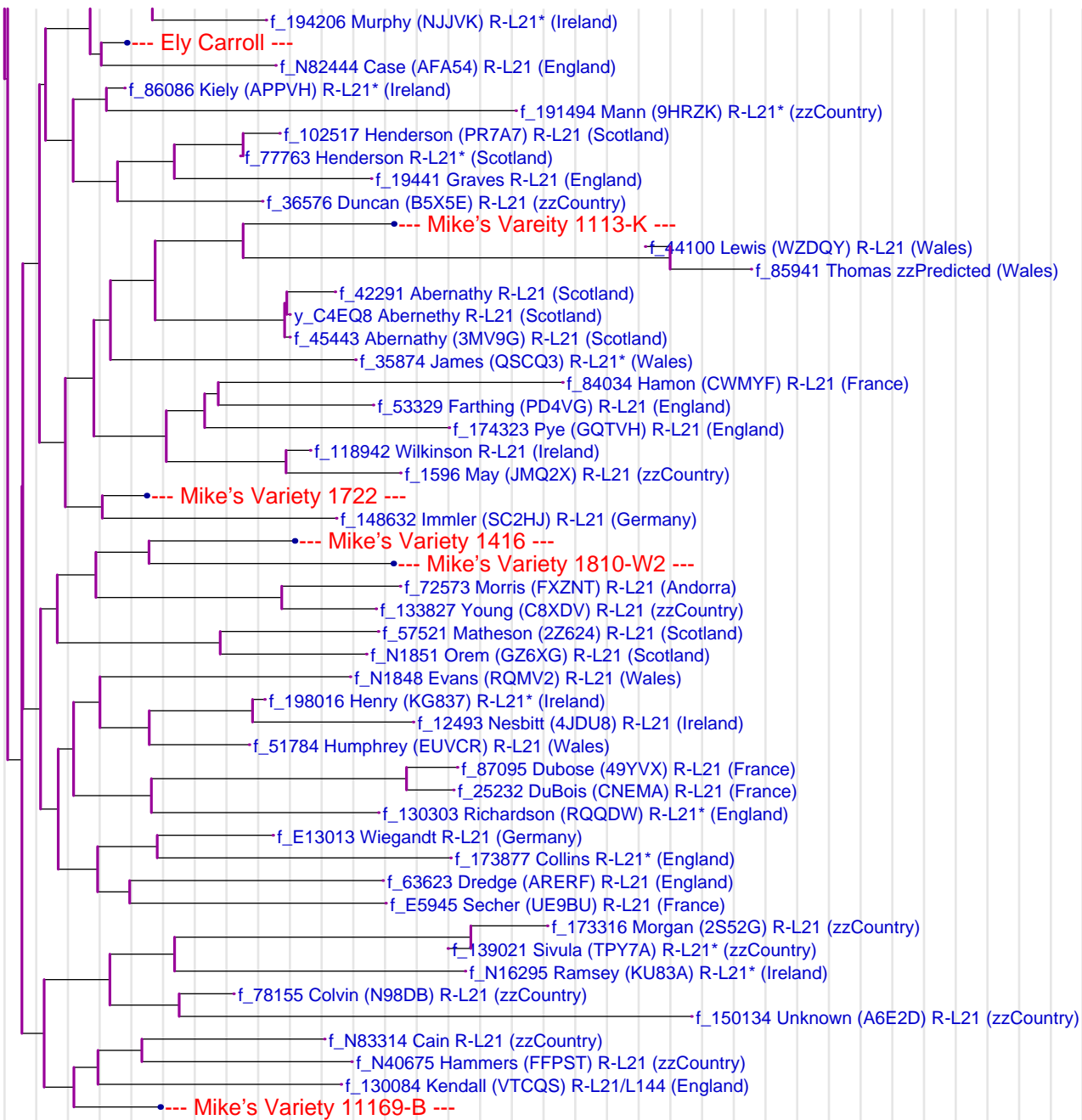
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



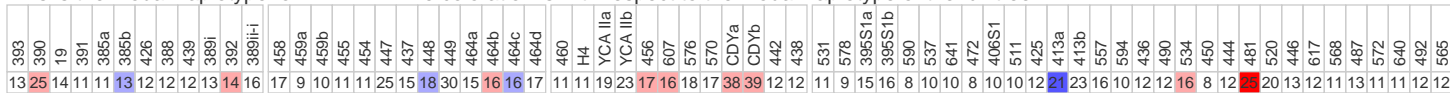
The vertical grey lines are separated 10 generations apart.



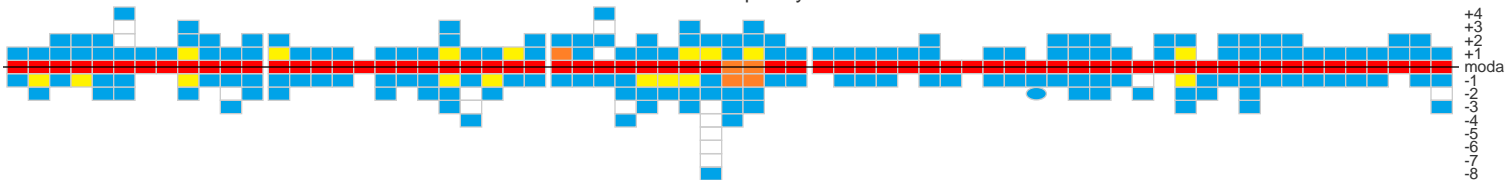
The vertical grey lines are separated 10 generations apart.

R-M222

This is the modal haplotype for R-M222. The coloration is with respect to the modal haplotype of the full tree.



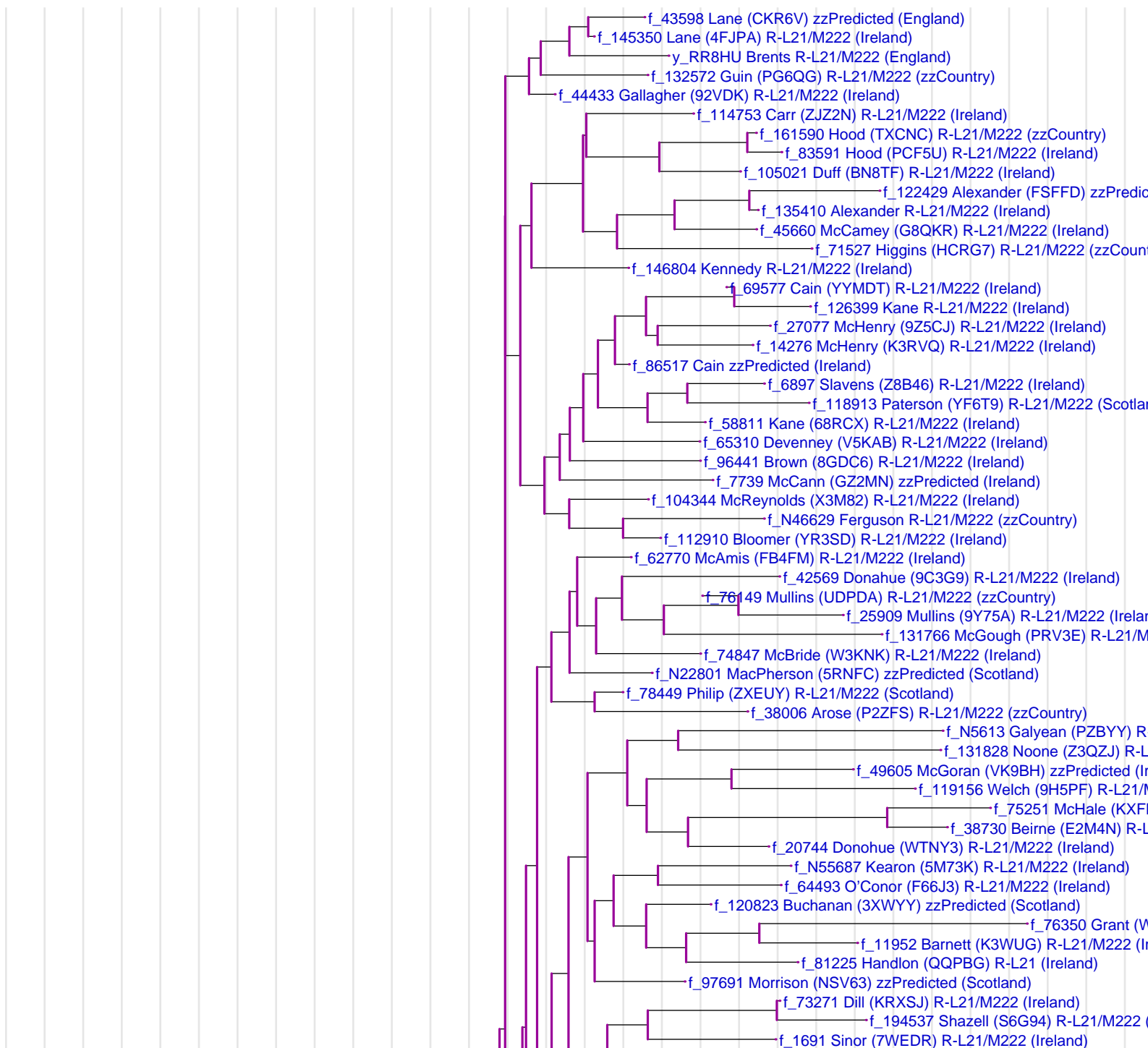
This is the marker distribution for R-M222. The color indicates the relative frequency of the alleles.



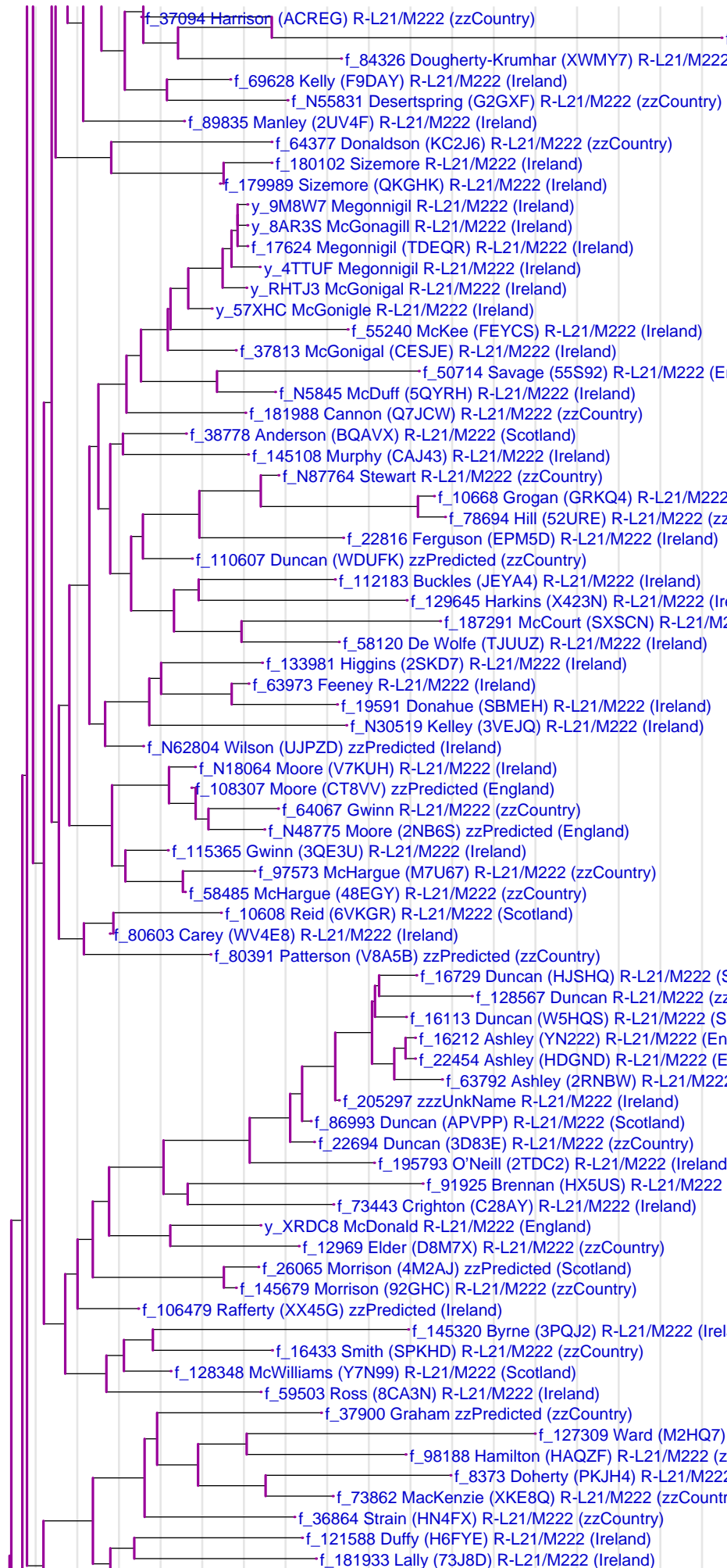
Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
487	32629	3649	11.18%	59.22±5.93	1480.62±209.57

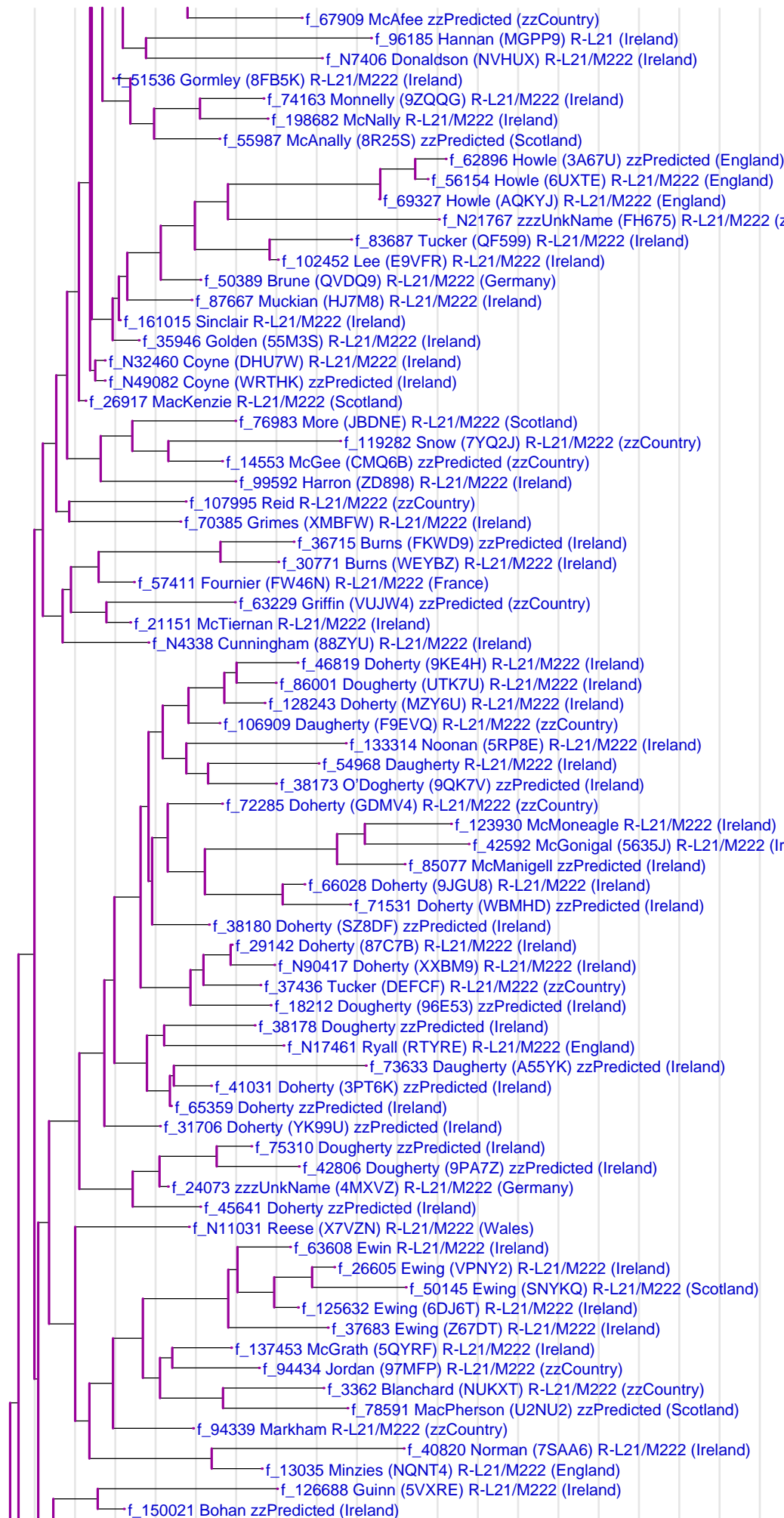
Note: Leister (f_N26284) is in fact M222-, and I'm not sure about Mullins (HN3QQ).



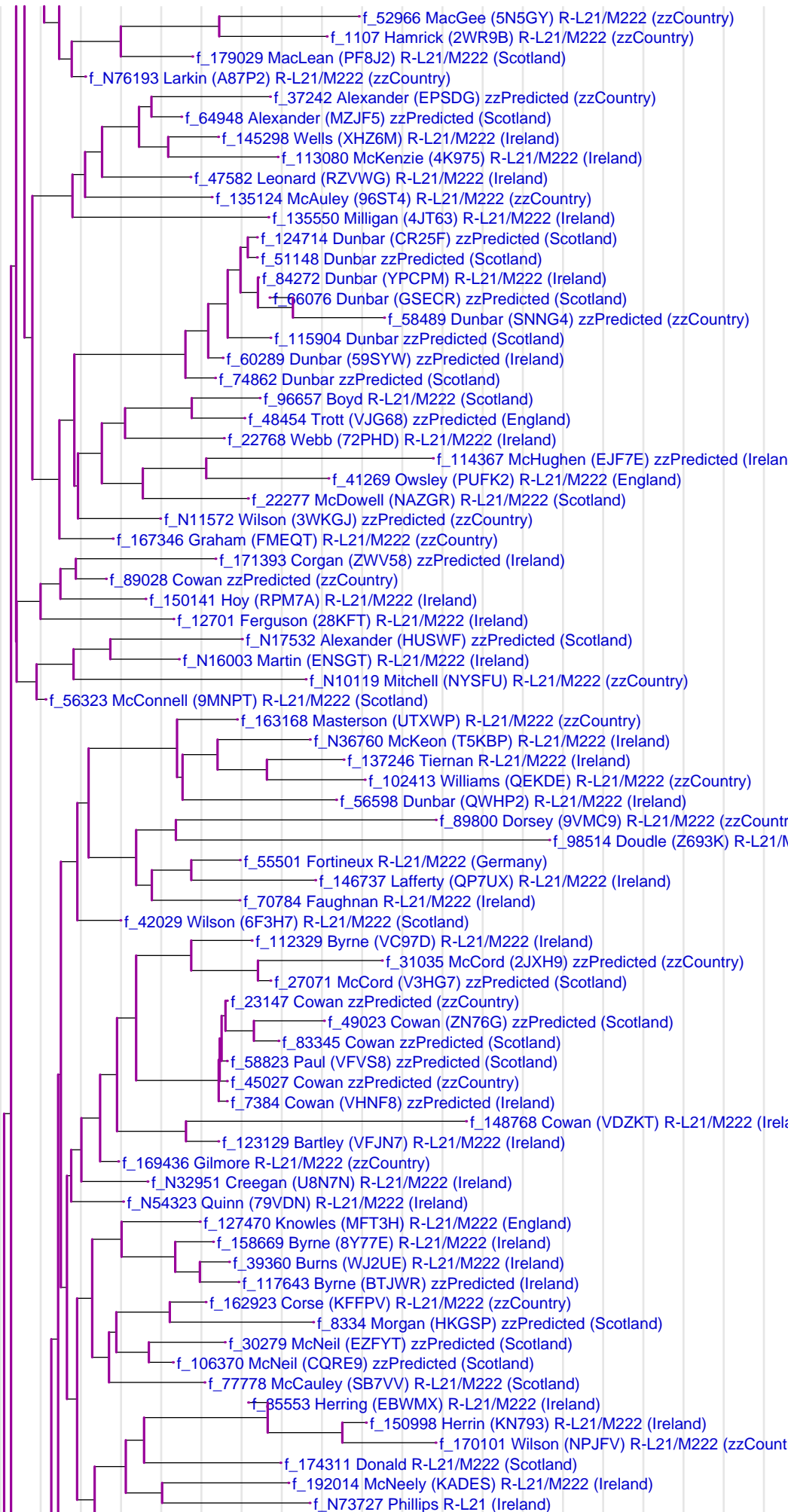
The vertical grey lines are separated 10 generations apart.



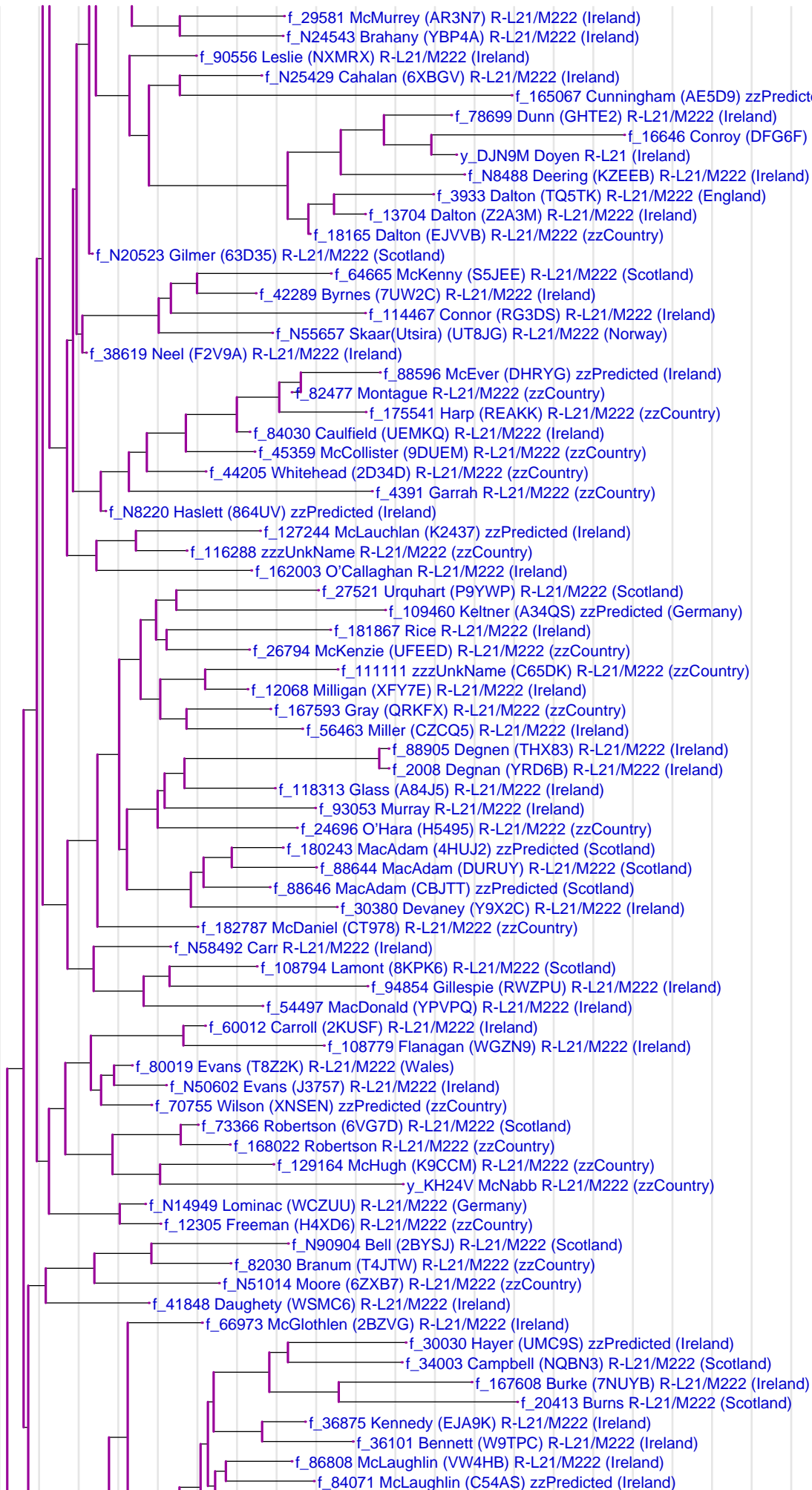
The vertical grey lines are separated 10 generations apart.



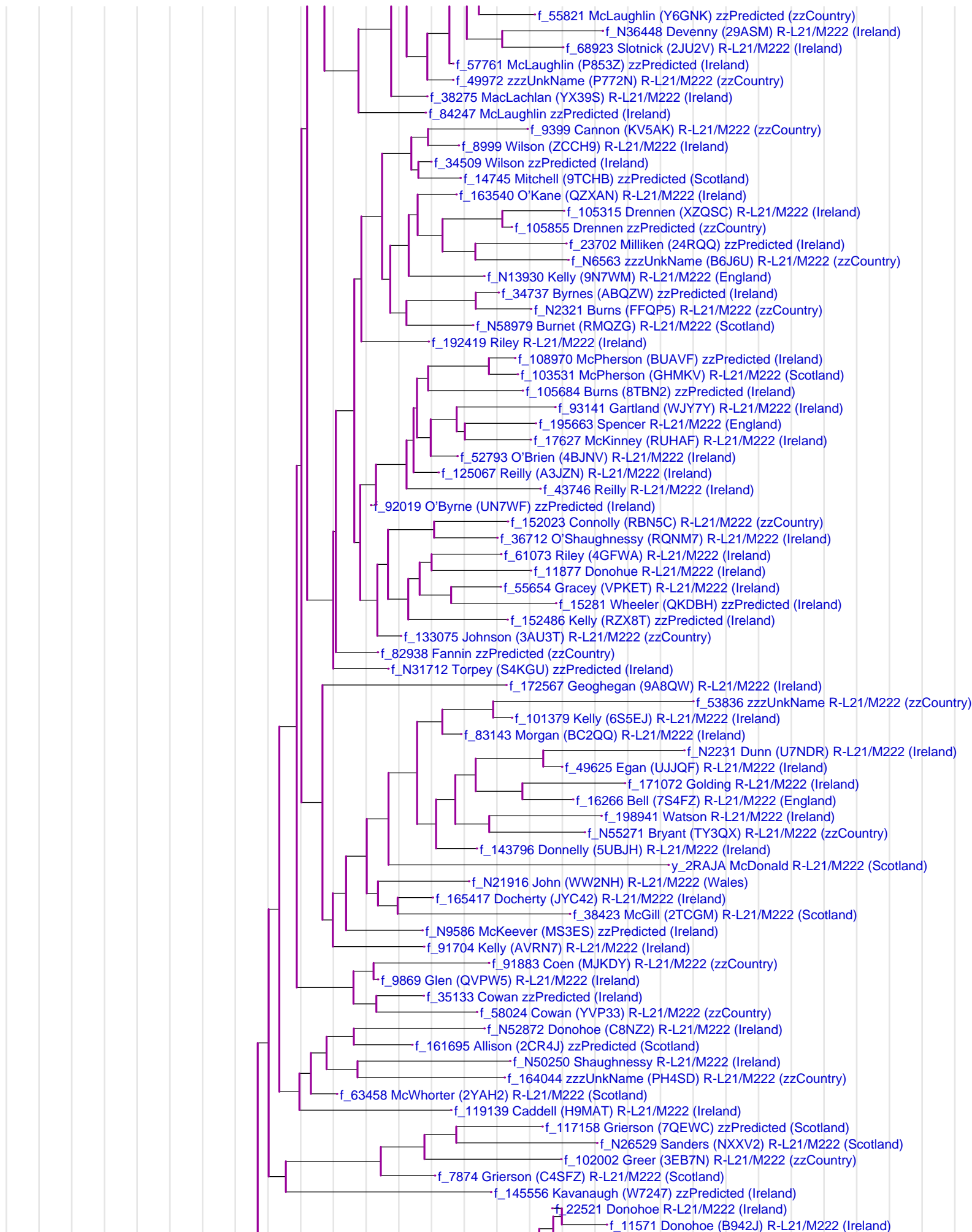
The vertical grey lines are separated 10 generations apart.



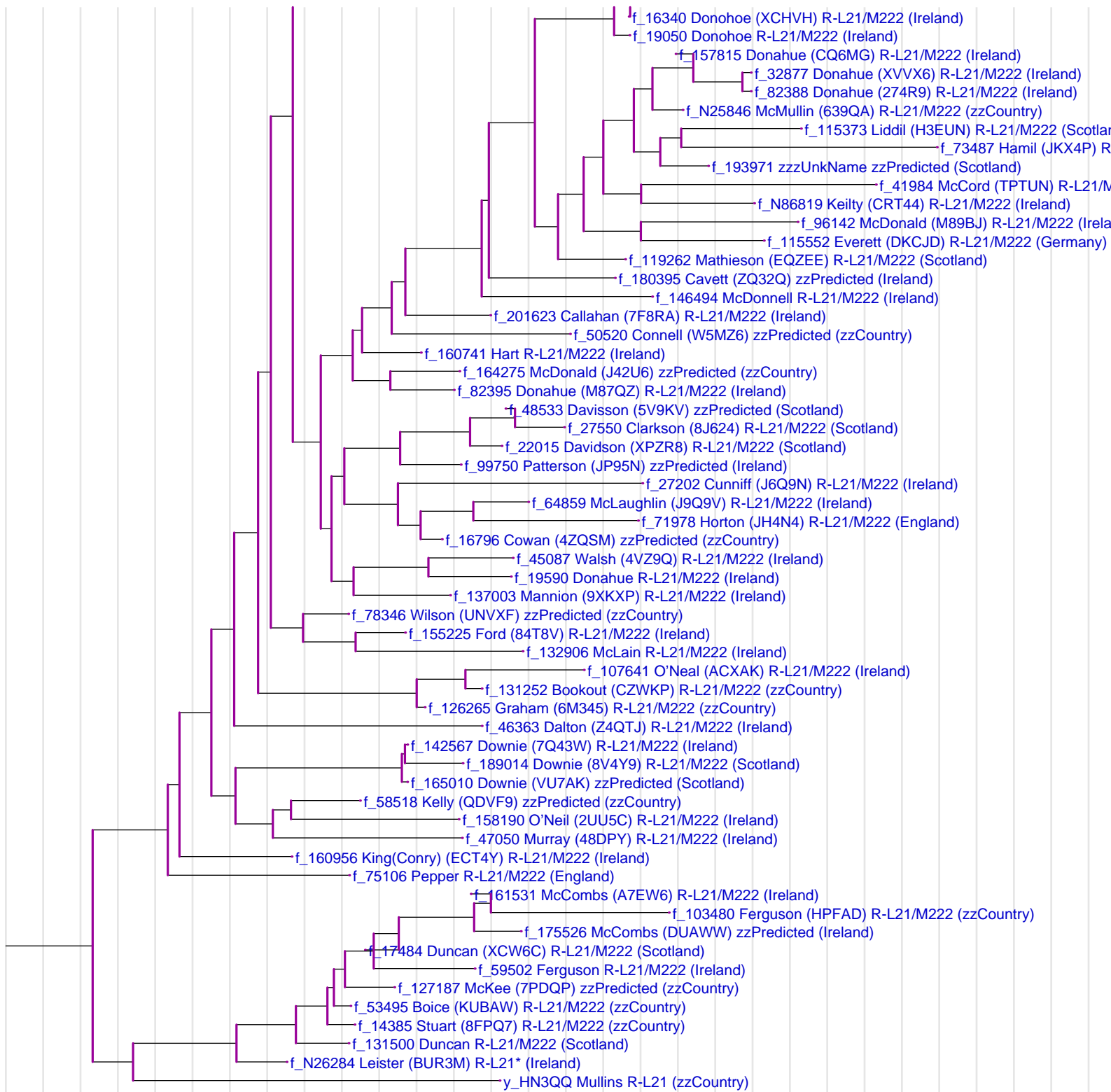
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



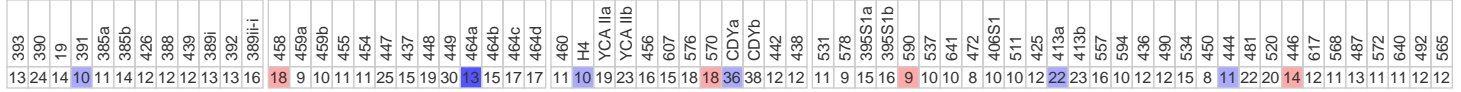
The vertical grey lines are separated 10 generations apart.



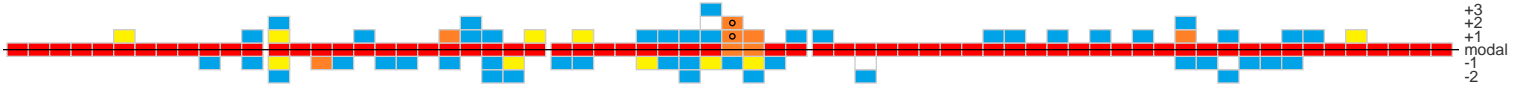
The vertical grey lines are separated 10 generations apart.

Little Scottish Cluster

This is the modal haplotype for Little Scottish Cluster. The coloration is with respect to the modal haplotype of the full tree.

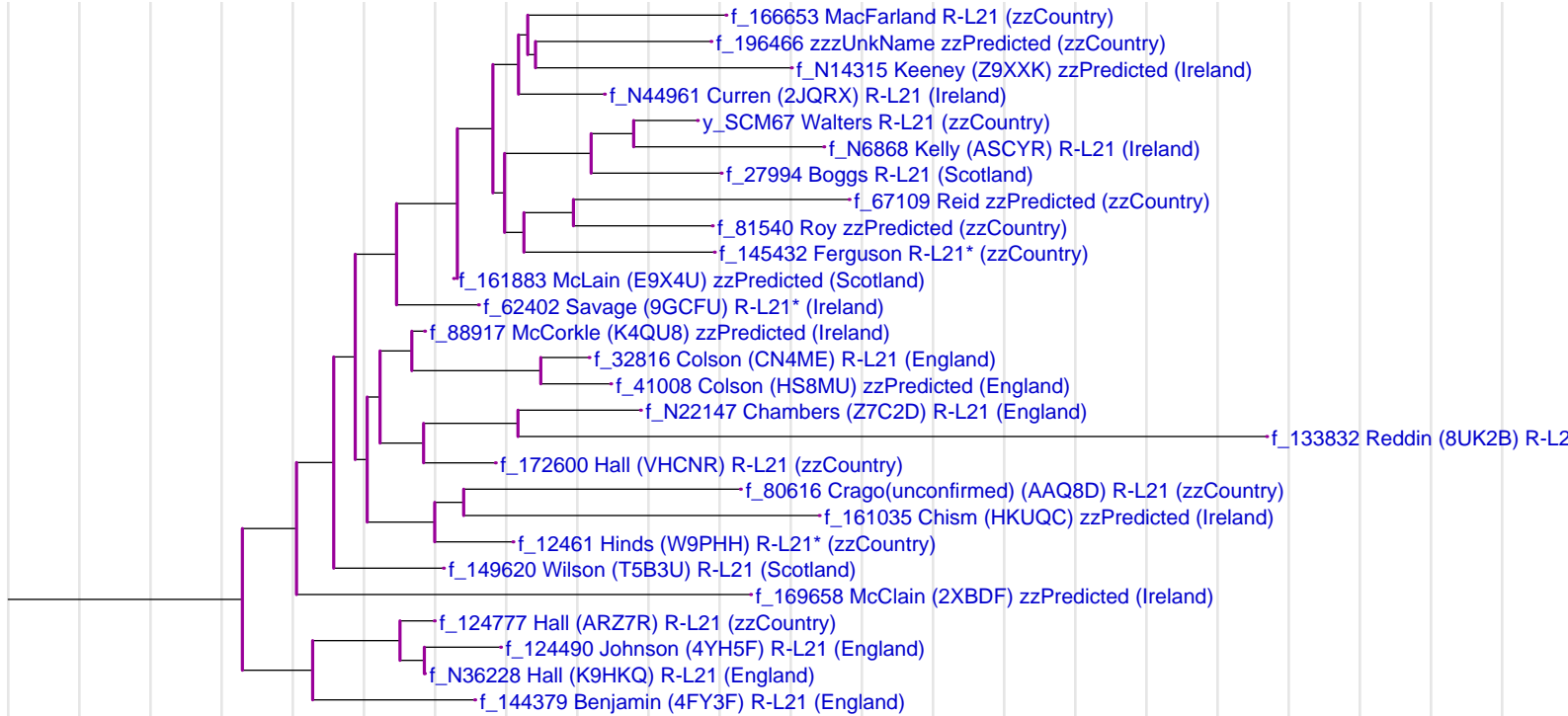


This is the marker distribution for Little Scottish Cluster. The color indicates the relative frequency of the alleles.



Age Analysis

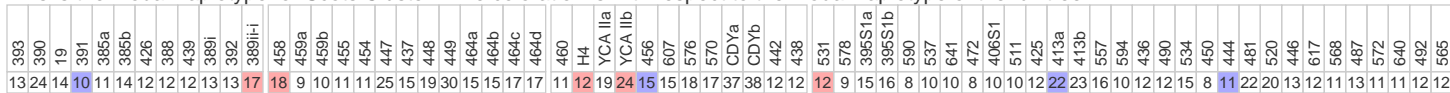
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
27	1809	165	9.12%	47.78±4.92	1194.57±171.472



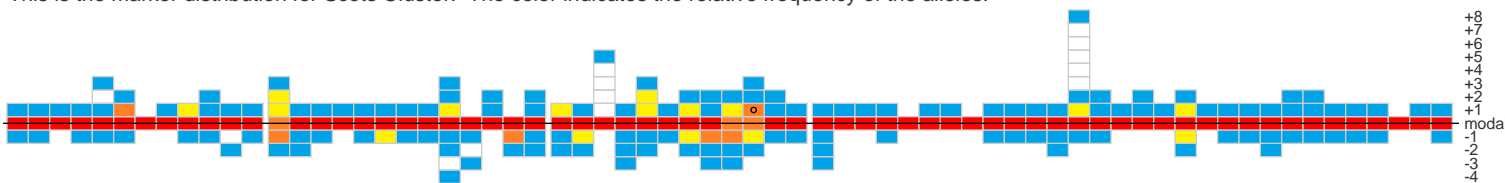
The vertical grey lines are separated 10 generations apart.

Scots Cluster

This is the modal haplotype for Scots Cluster. The coloration is with respect to the modal haplotype of the full tree.

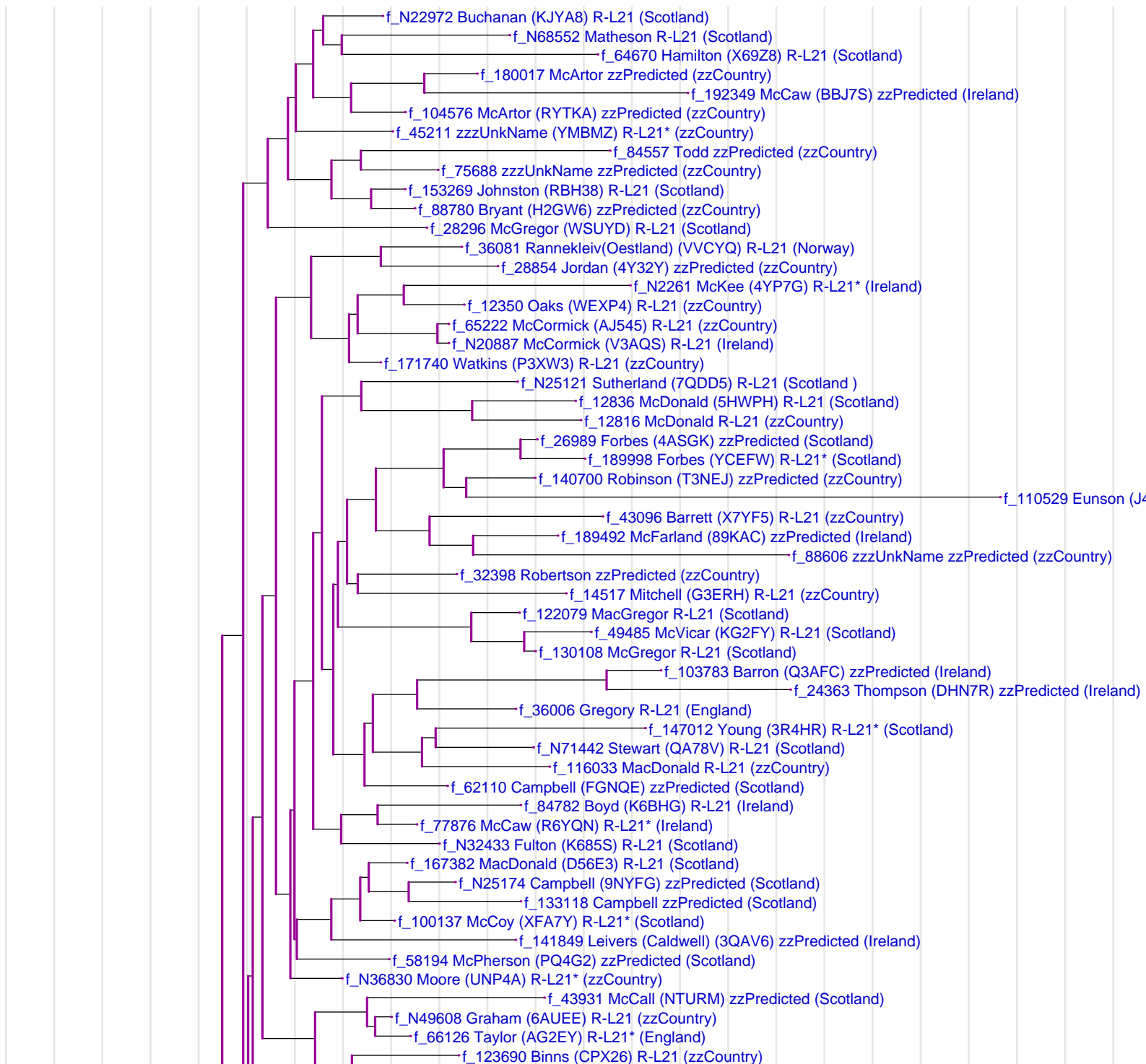


This is the marker distribution for Scots Cluster. The color indicates the relative frequency of the alleles.

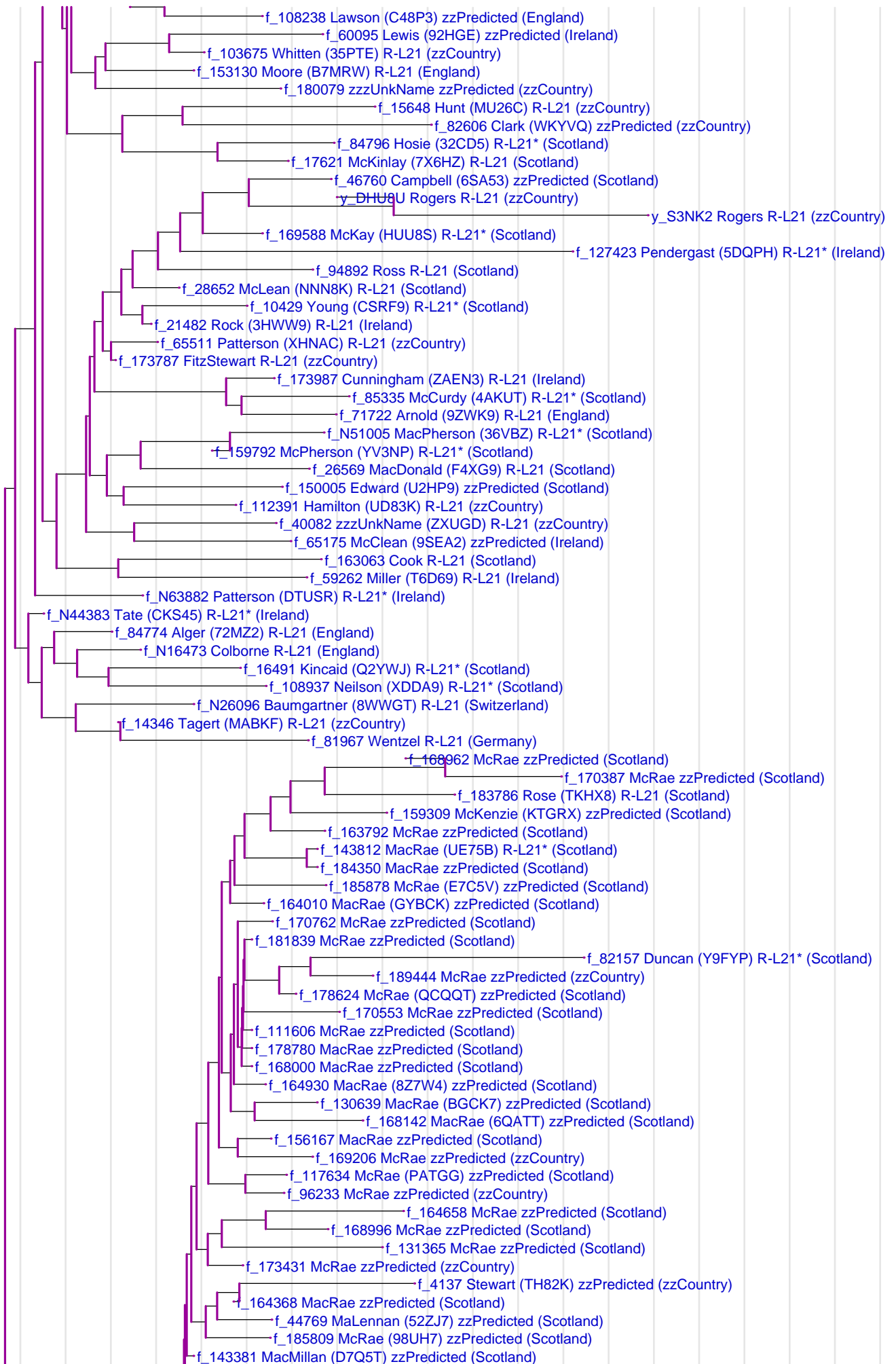


Age Analysis

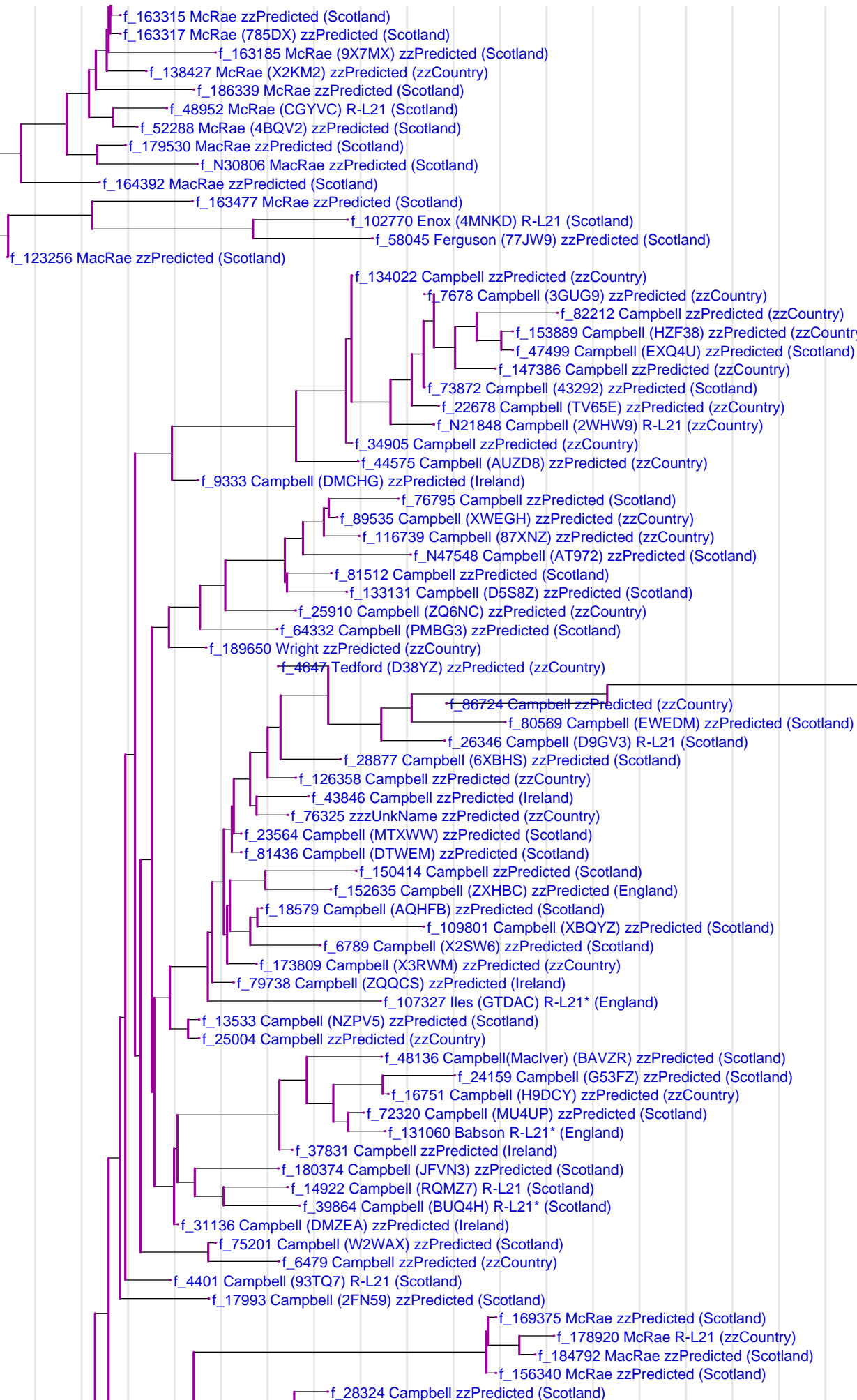
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
274	18358	2100	11.44%	60.66±6.08	1516.54±214.797



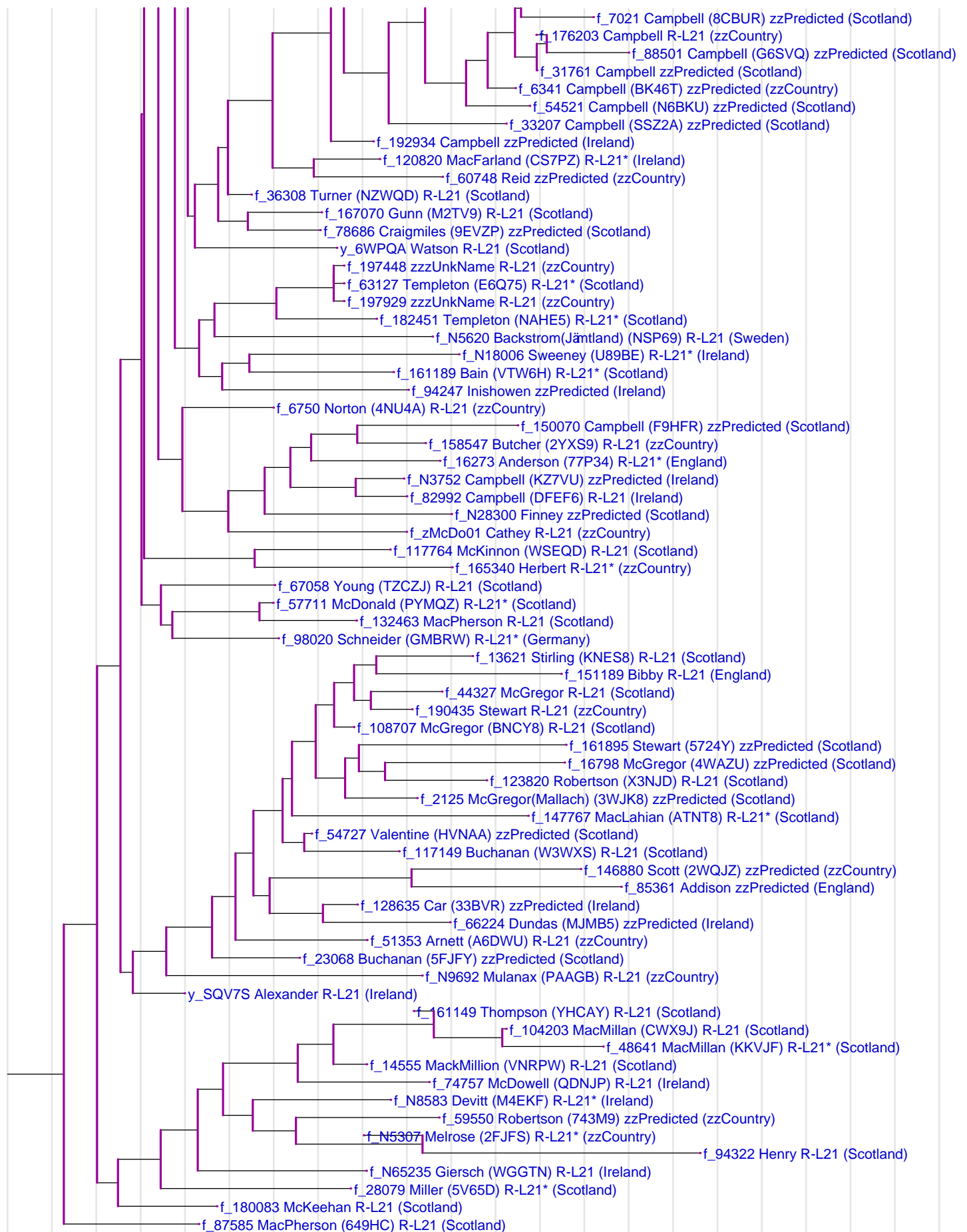
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



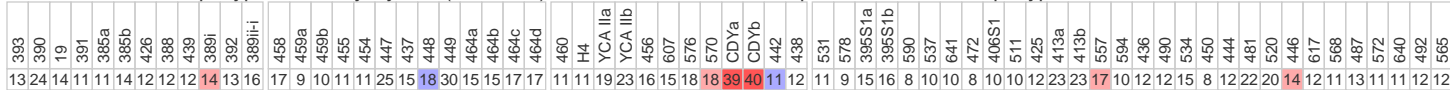
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

Beatty-Byrnes (R-L159.2)

This is the modal haplotype for Beatty-Byrnes (R-L159.2). The coloration is with respect to the modal haplotype of the full tree.



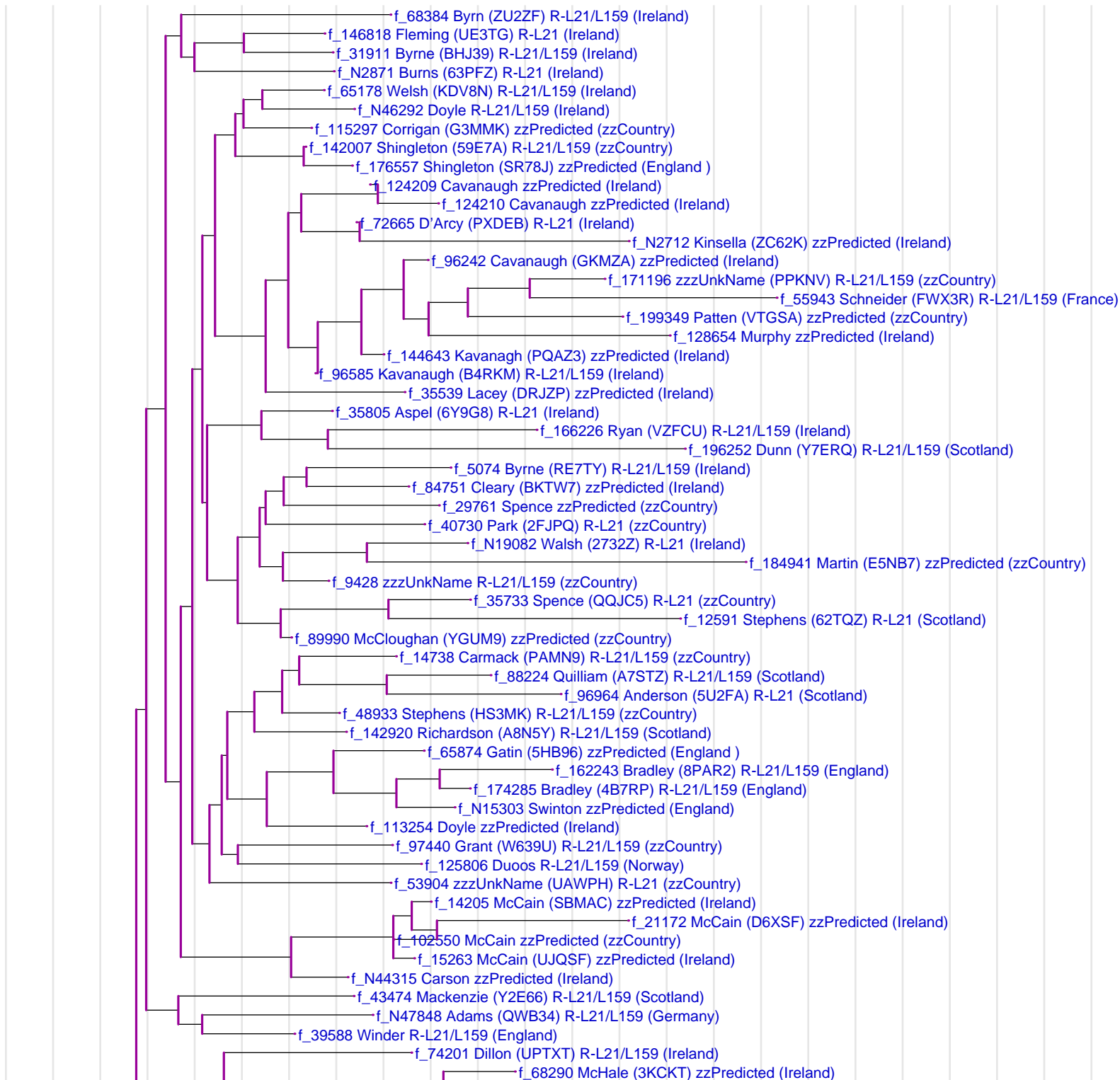
This is the marker distribution for Beatty-Byrnes (R-L159.2). The color indicates the relative frequency of the alleles.



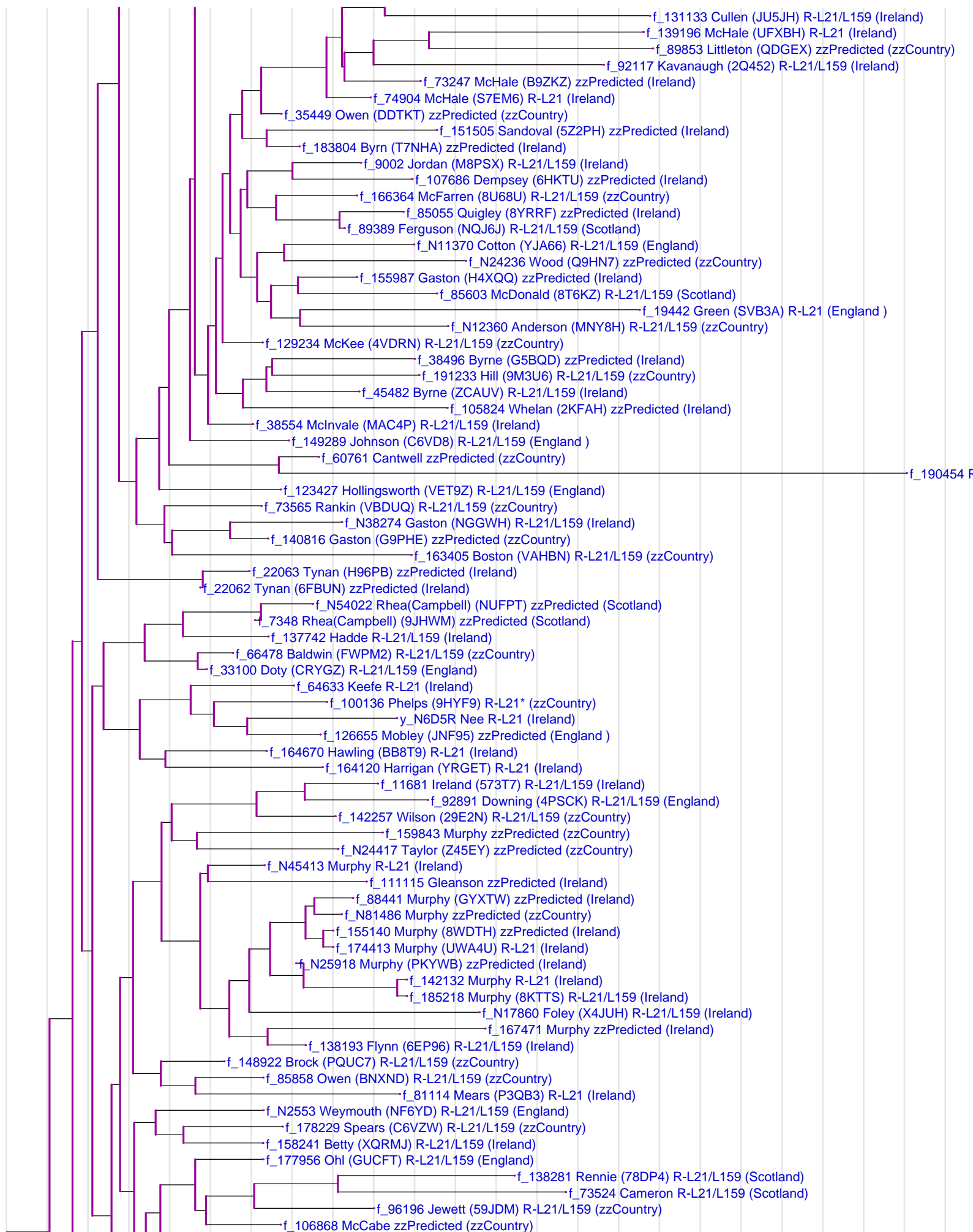
Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
146	9782	1095	11.19%	59.28±5.96	1482.12±210.2

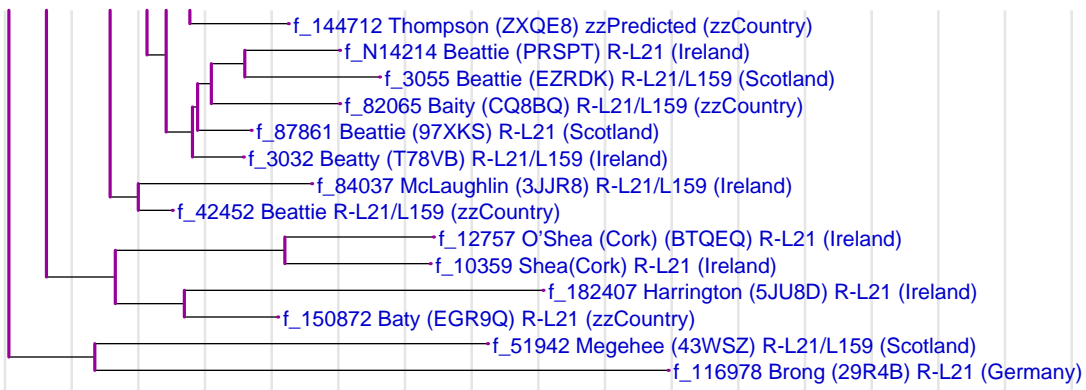
Note: This cluster is also known as the Leinster Cluster.



The vertical grey lines are separated 10 generations apart.



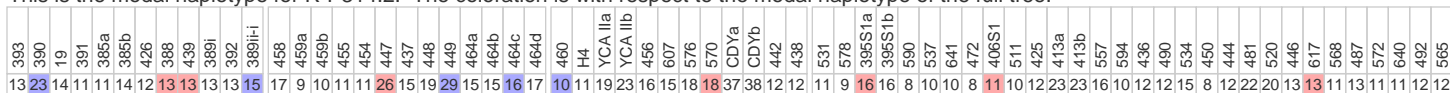
The vertical grey lines are separated 10 generations apart.



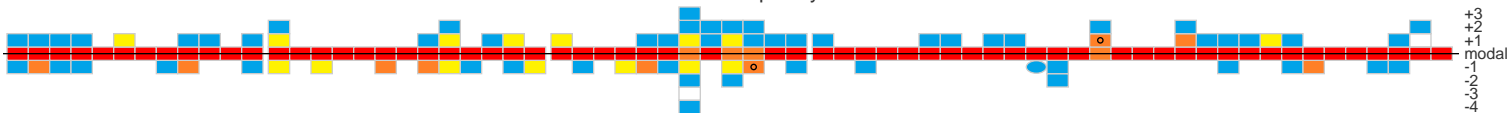
The vertical grey lines are separated 10 generations apart.

R-P314.2

This is the modal haplotype for R-P314.2. The coloration is with respect to the modal haplotype of the full tree.



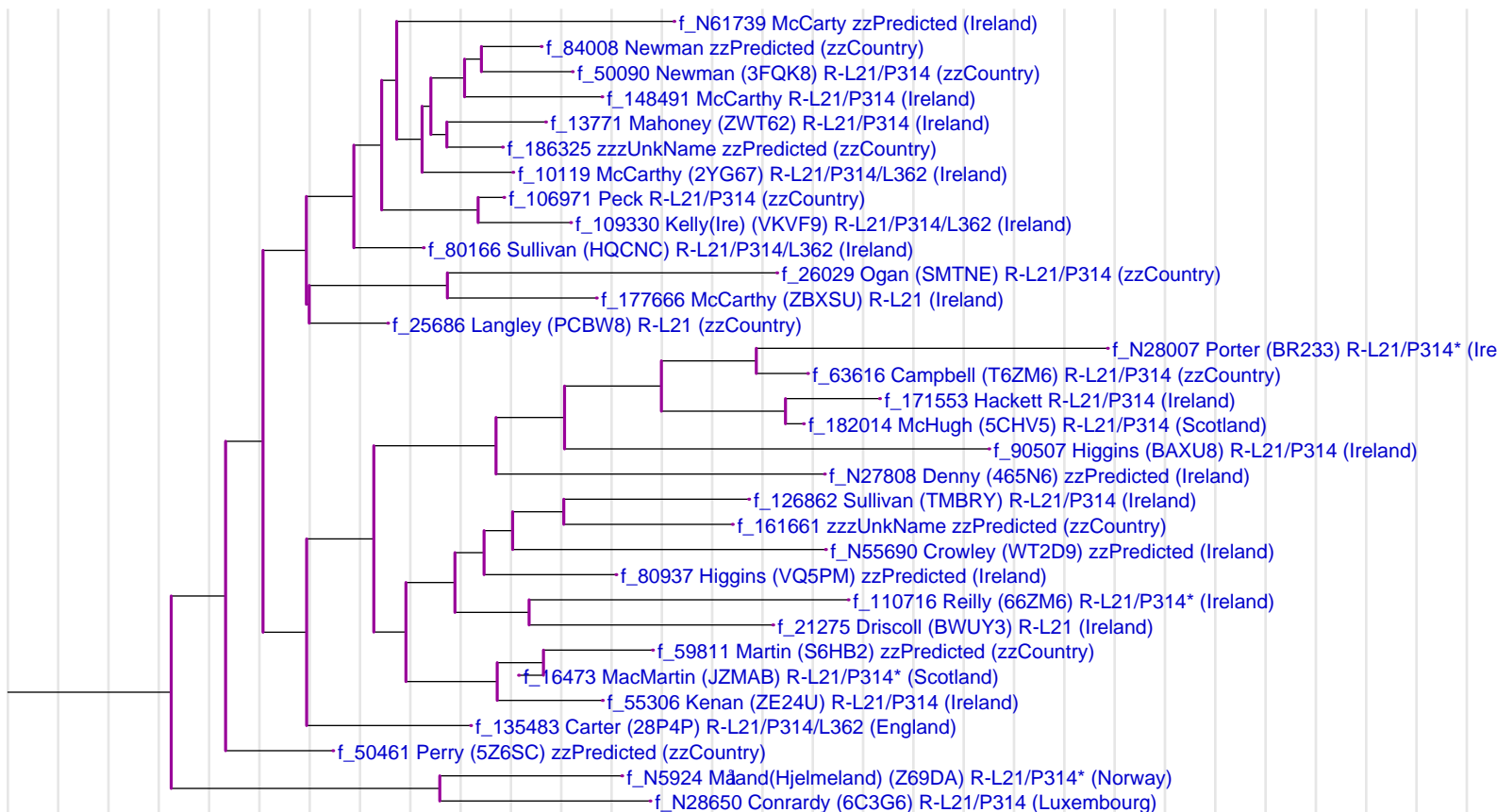
This is the marker distribution for R-P314.2. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
32	2144	291	13.57%	72.80±7.47	1819.91±260.774

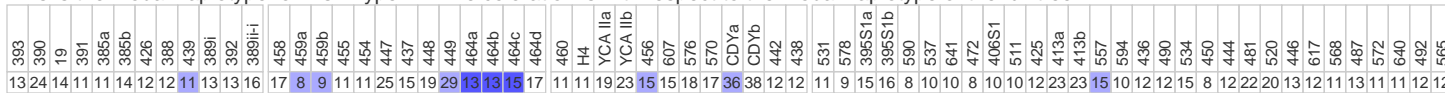
Note: Mike Walsh has divided R-P314.2 into two groups, those with DYS617=12, and those with DYS617=13.



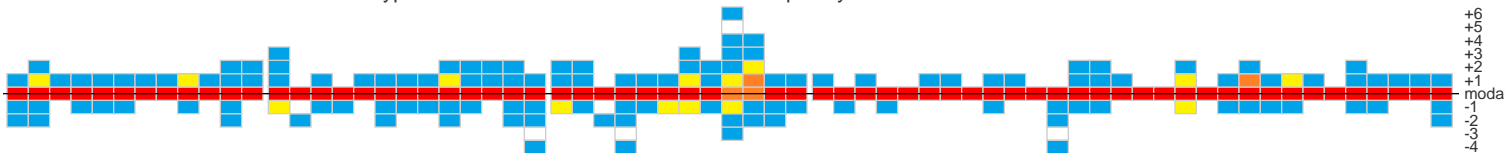
The vertical grey lines are separated 10 generations apart.

Irish Type III

This is the modal haplotype for Irish Type III. The coloration is with respect to the modal haplotype of the full tree.



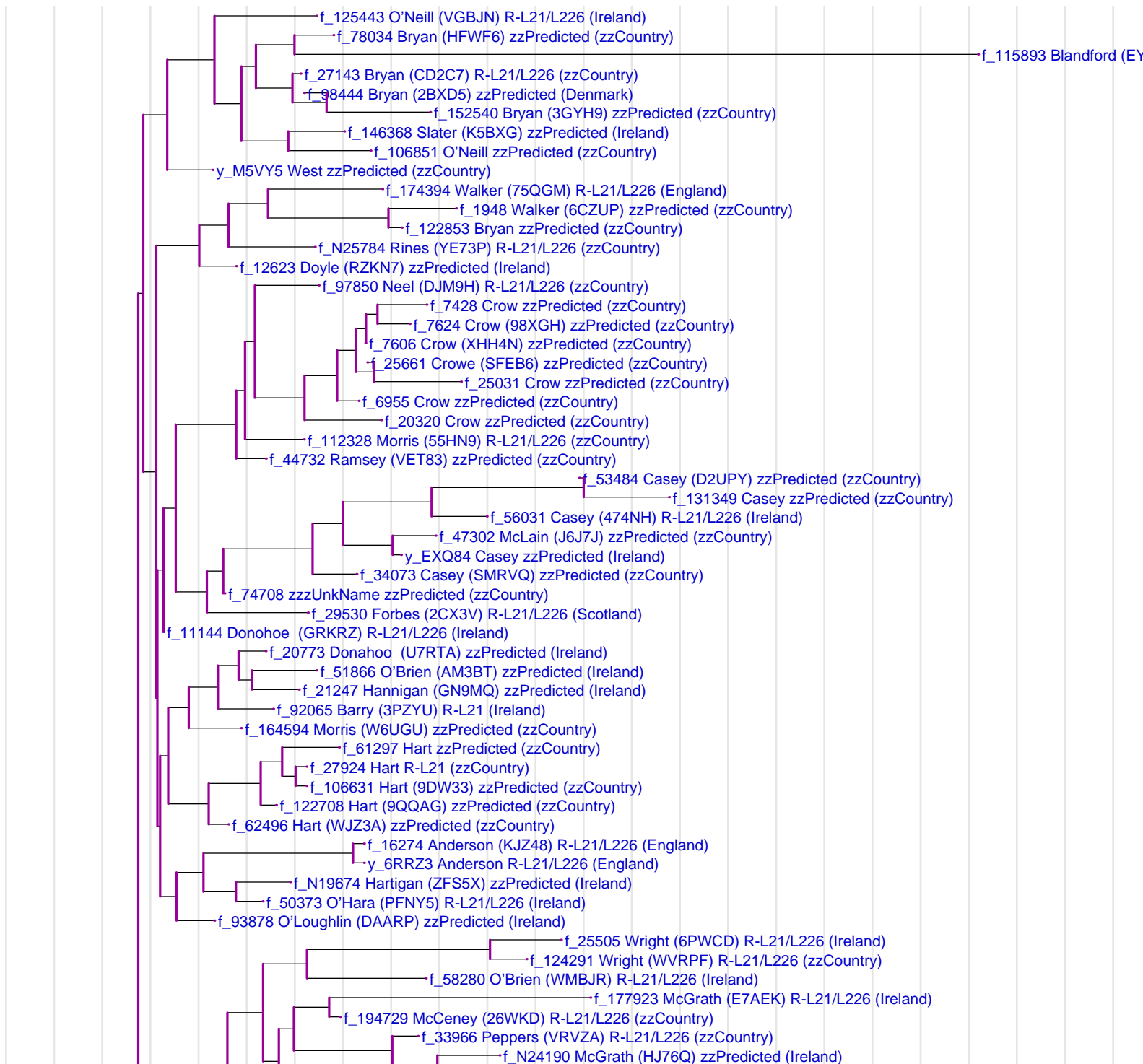
This is the marker distribution for Irish Type III. The color indicates the relative frequency of the alleles.



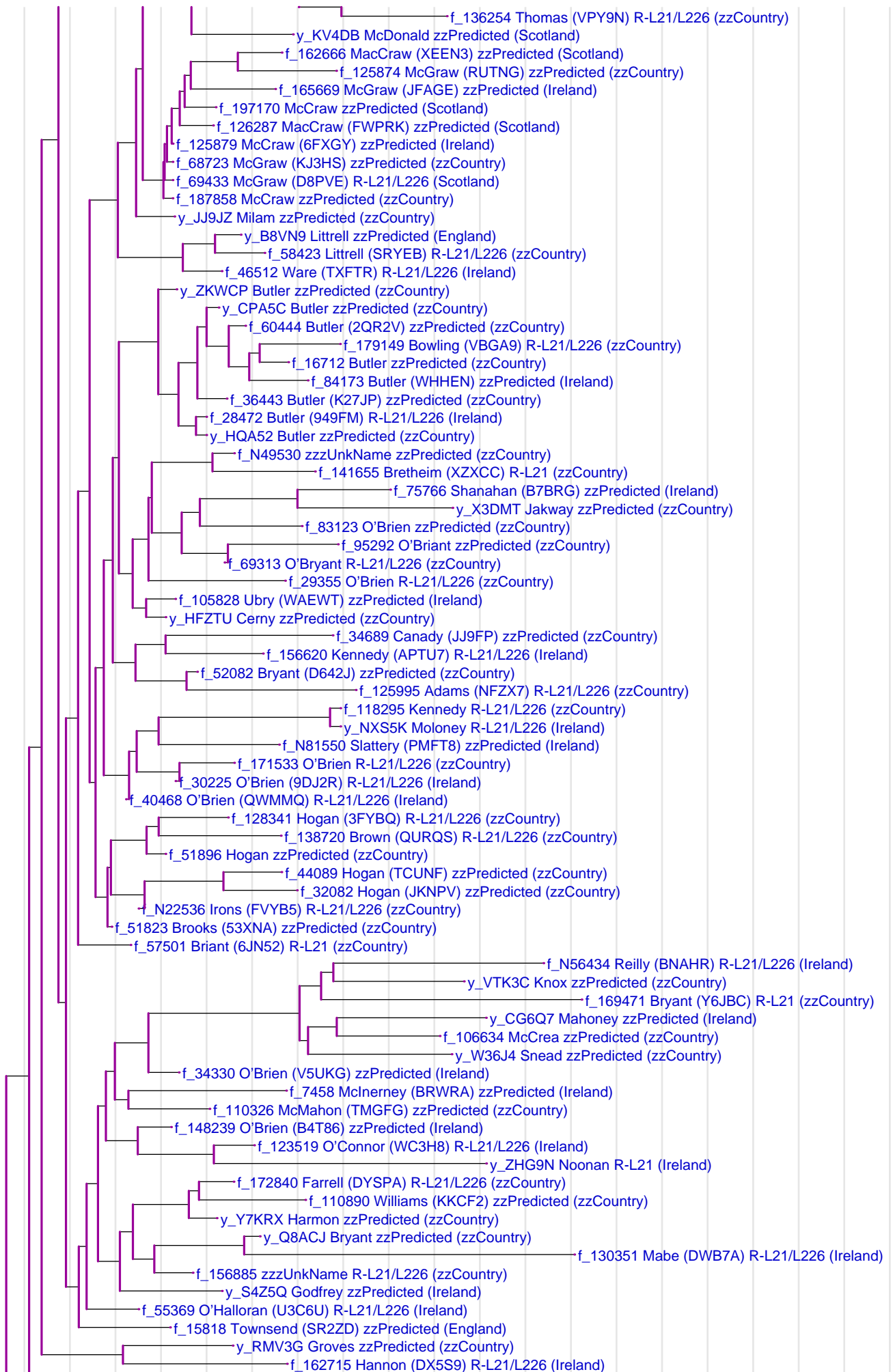
Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
182	12194	1175	9.64%	50.62±5.08	1265.41±179.358

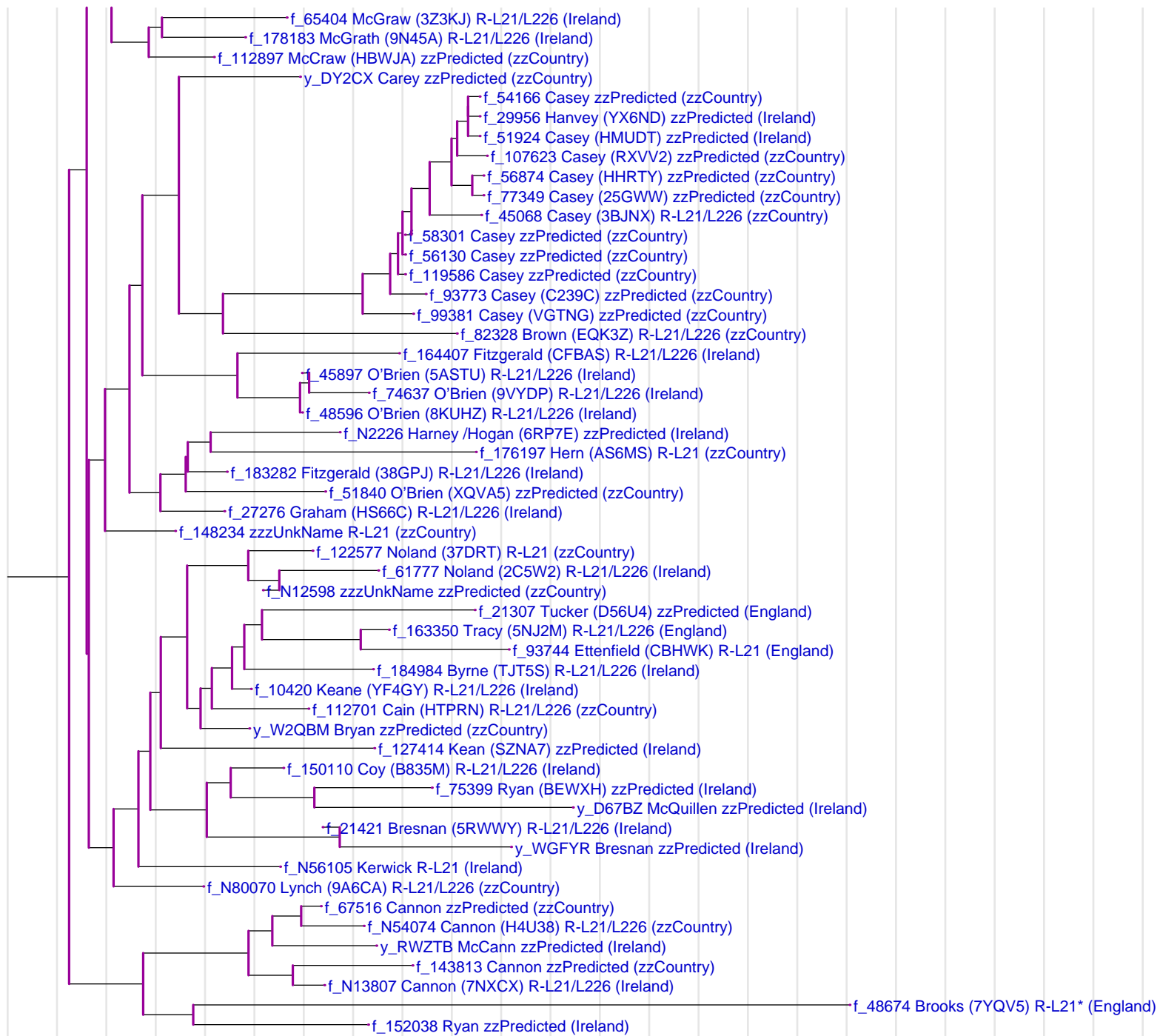
Note: Although Blandford (f_115893) and Brooks (48674) are situated within R-L226, they are L226-.



The vertical grey lines are separated 10 generations apart.



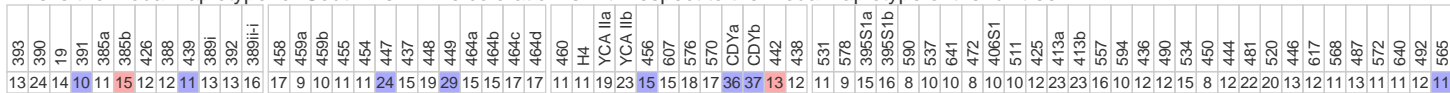
The vertical grey lines are separated 10 generations apart.



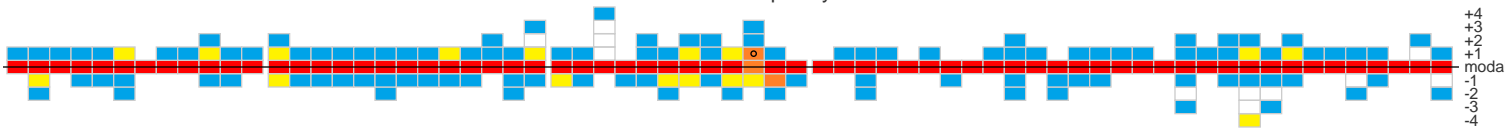
The vertical grey lines are separated 10 generations apart.

South Irish

This is the modal haplotype for South Irish. The coloration is with respect to the modal haplotype of the full tree.



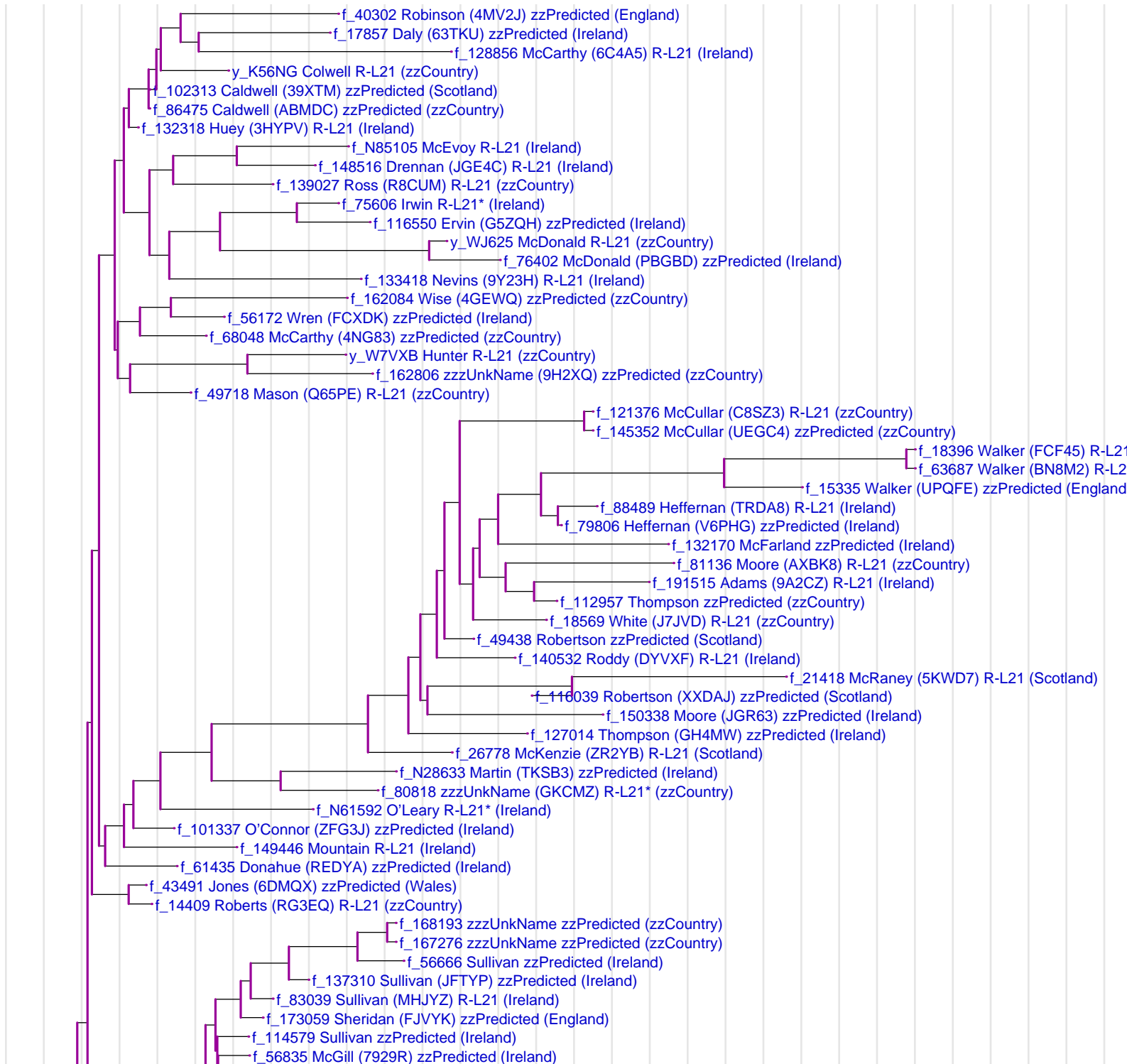
This is the marker distribution for South Irish. The color indicates the relative frequency of the alleles.



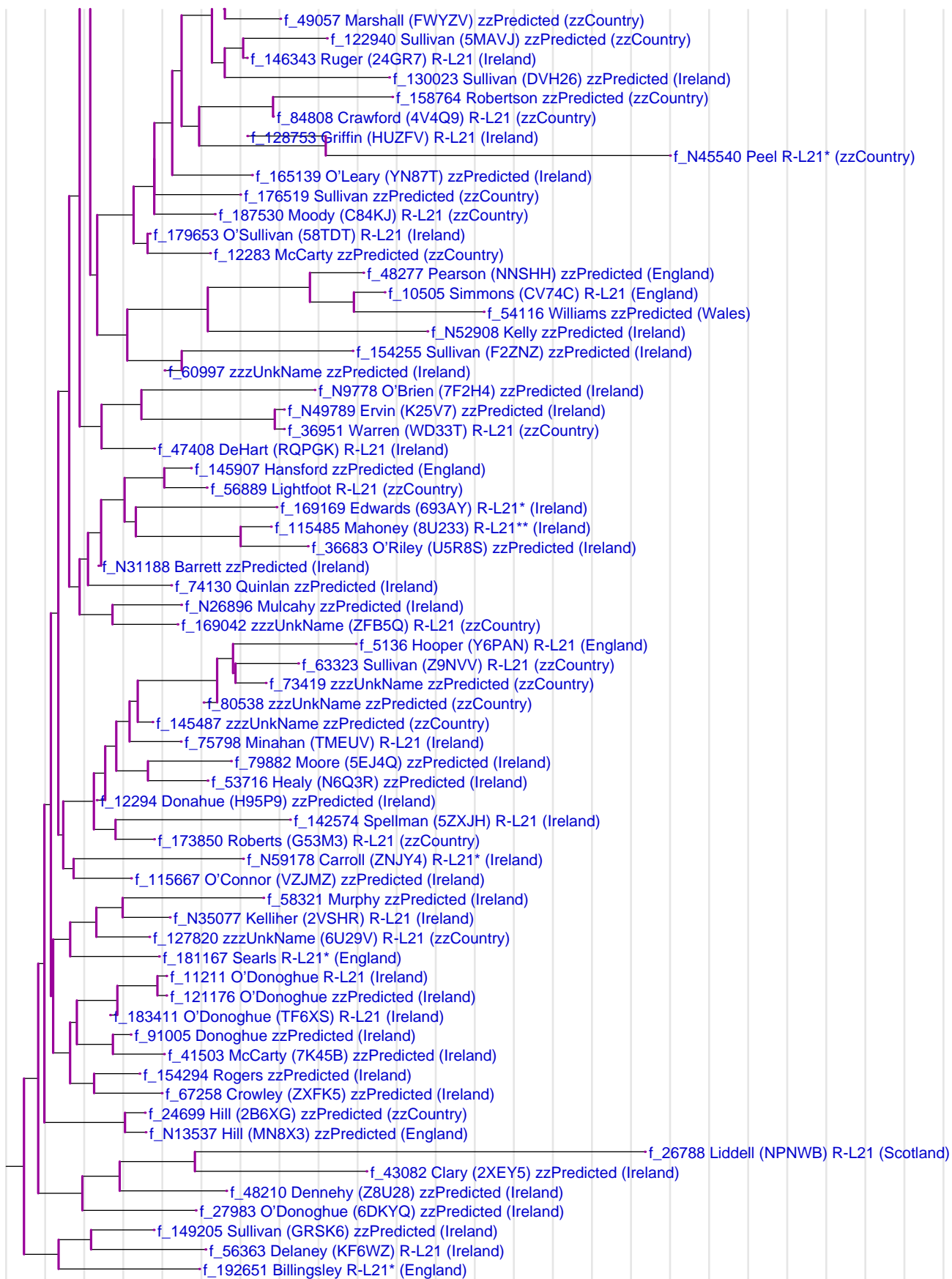
Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
121	8107	876	10.81%	57.11±5.75	1427.75±202.604

Note: AKA Irish Type II, this is Mike's Variety 1511-A-T2. At 67-markers, it's not always clear who should be included in this cluster near to where it connects to rest of



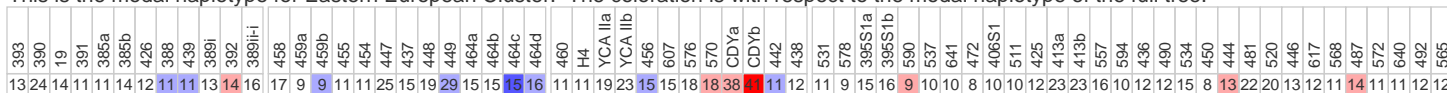
The vertical grey lines are separated 10 generations apart.



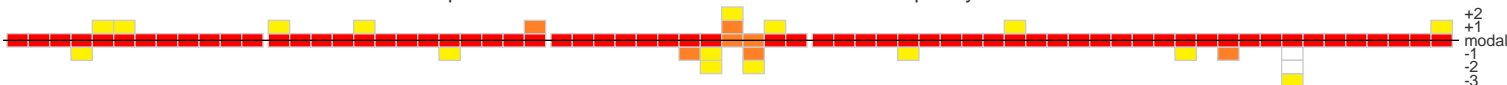
The vertical grey lines are separated 10 generations apart.

Eastern European Cluster

This is the modal haplotype for Eastern European Cluster. The coloration is with respect to the modal haplotype of the full tree.



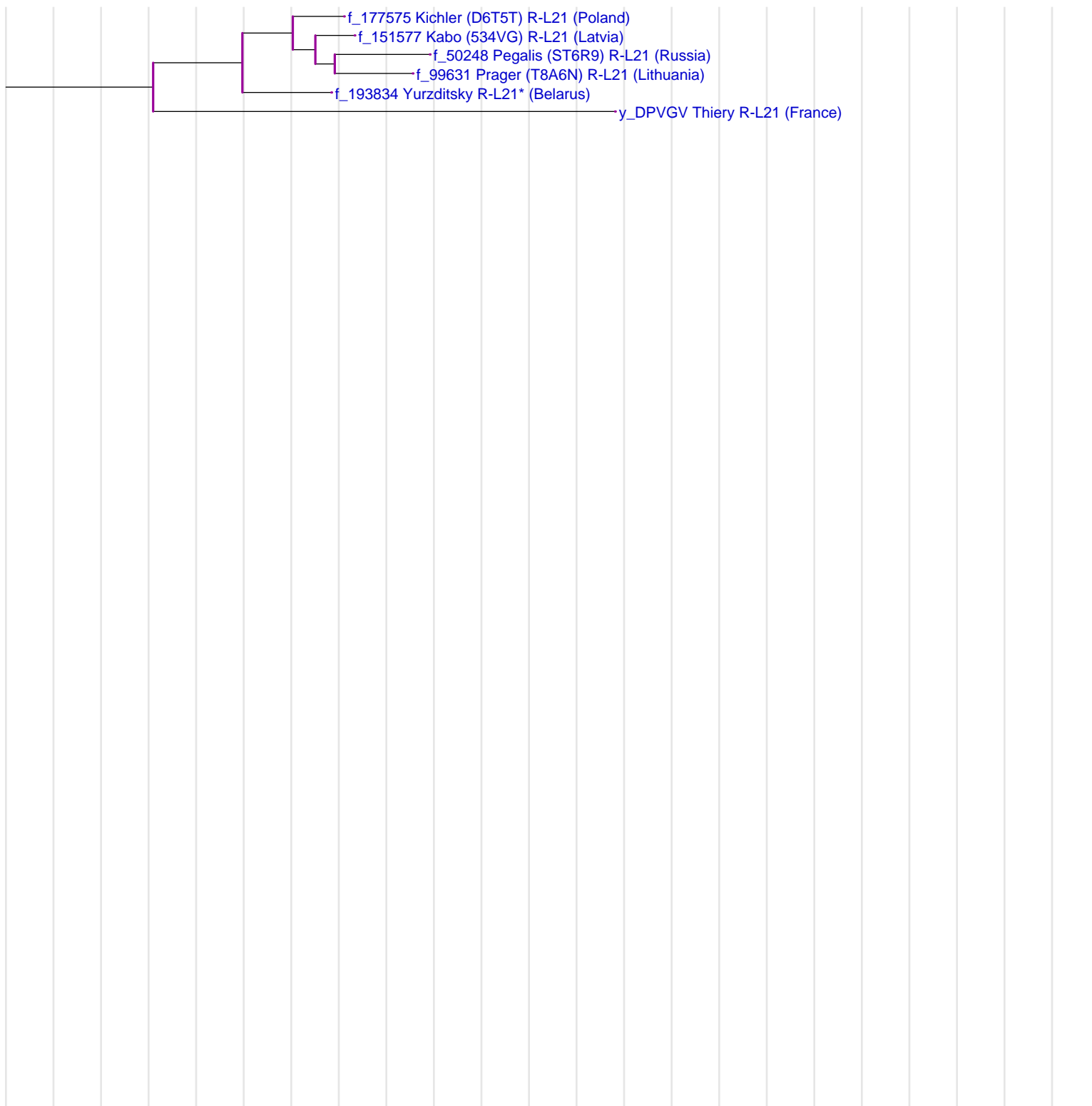
This is the marker distribution for Eastern European Cluster. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	31	7.71%	40.10±4.52	1002.57±150.996

Note: This is Mike Walsh's Variety 1111EE.



The vertical grey lines are separated 10 generations apart.

R-L144

This is the modal haplotype for R-L144. The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565
13	24	14	10	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	30	15	15	16	17	11	11	19	23	16	15	17	18	36	40	12	12	11	10	15	16	8	10	10	8	10	10	12	23	16	10	12	12	15	8	12	22	20	12	10	11	13	11	11	12	12	

This is the marker distribution for R-L144. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
14	938	115	12.26%	65.30±6.91	1632.46±237.695

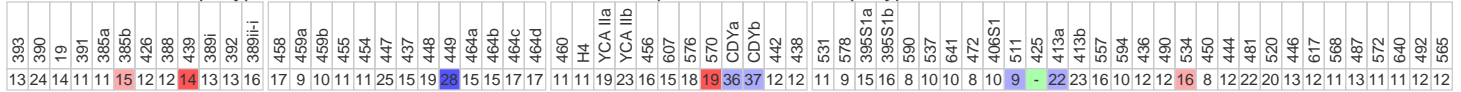
Note: Although Sanchez has an unusually low value for DYS413, he is L144-



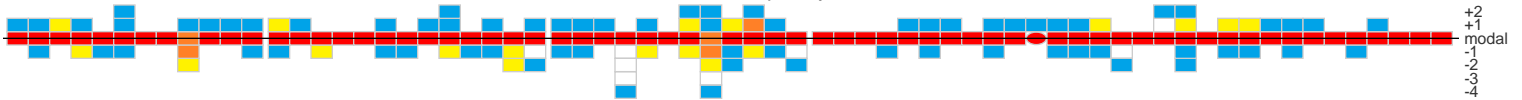
The vertical grey lines are separated 10 generations apart.

Clan Colla

This is the modal haplotype for Clan Colla. The coloration is with respect to the modal haplotype of the full tree.



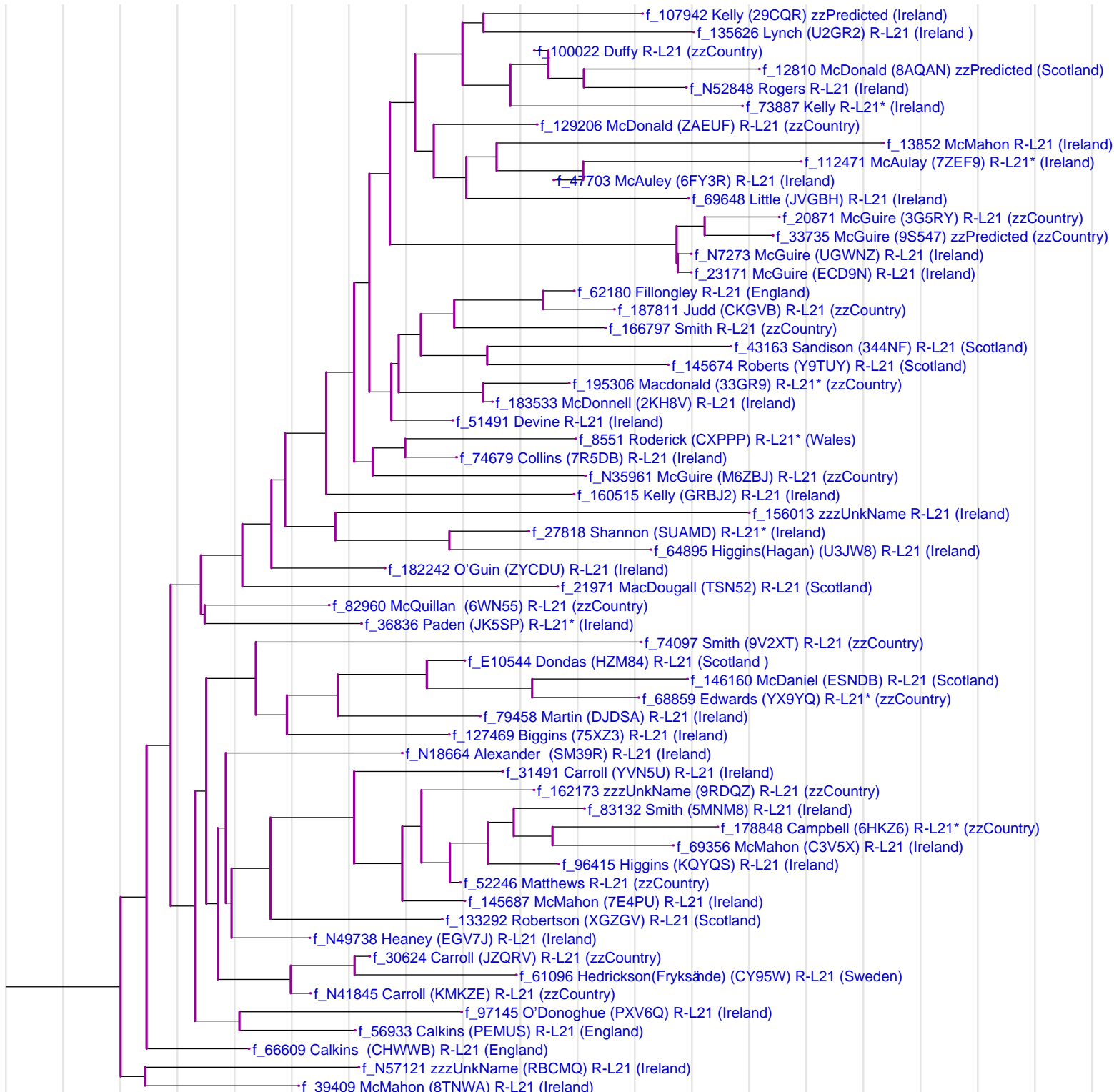
This is the marker distribution for Clan Colla. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
59	3953	394	9.97%	52.45±5.32	1311.18±186.717

Note: Jones (f100192) and Wisdom (171106) have DYS 425 = 12, and so perhaps shouldn't be considered a part of this cluster.



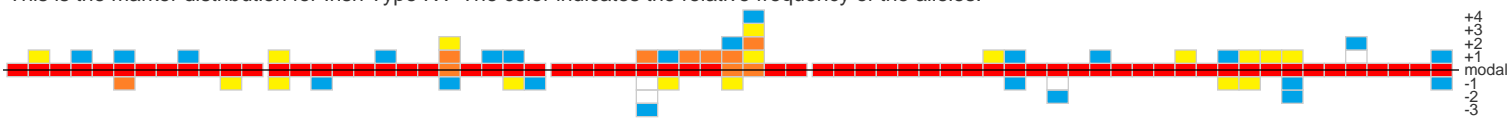
The vertical grey lines are separated 10 generations apart.

Irish Type IV

This is the modal haplotype for Irish Type IV. The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	10	12	15	13	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	16	18	10	10	19	23	15	15	17	17	36	37	12	12	11	9	15	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	21	13	12	11	13	11	11	12	12

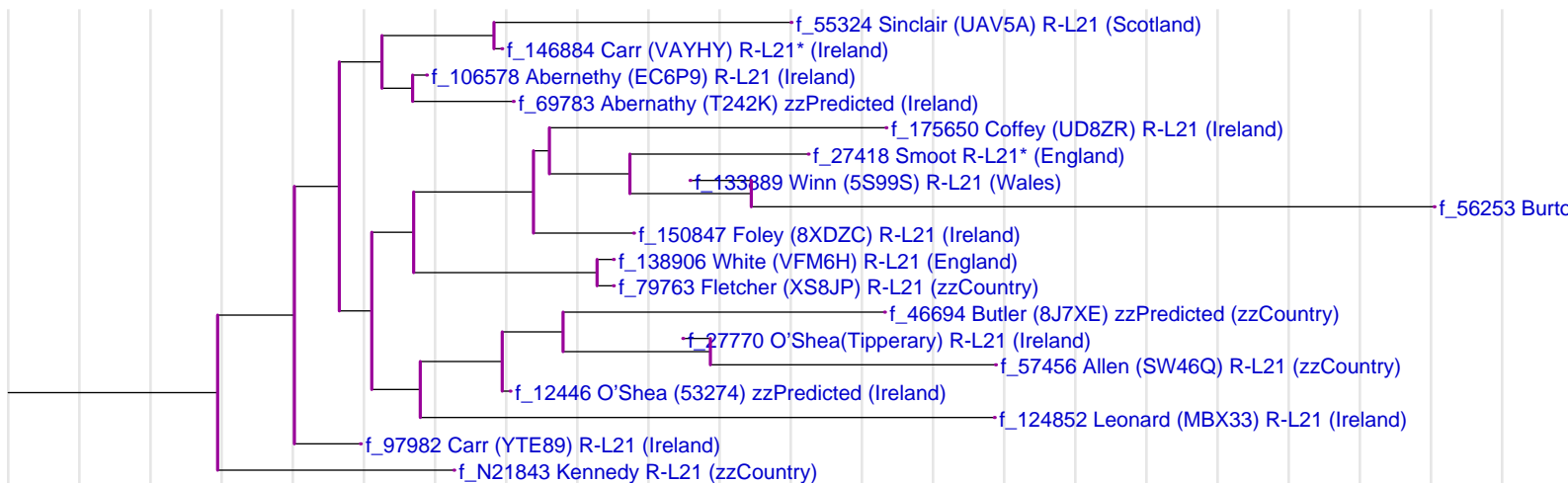
This is the marker distribution for Irish Type IV. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
18	1206	131	10.86%	57.43±6.00	1435.69±207.663

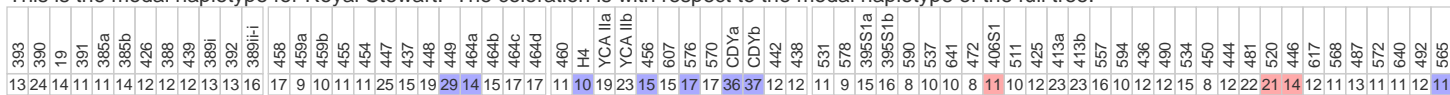
Note: This is Mike's Variety 1310-T4



The vertical grey lines are separated 10 generations apart.

Royal Stewart

This is the modal haplotype for Royal Stewart. The coloration is with respect to the modal haplotype of the full tree.



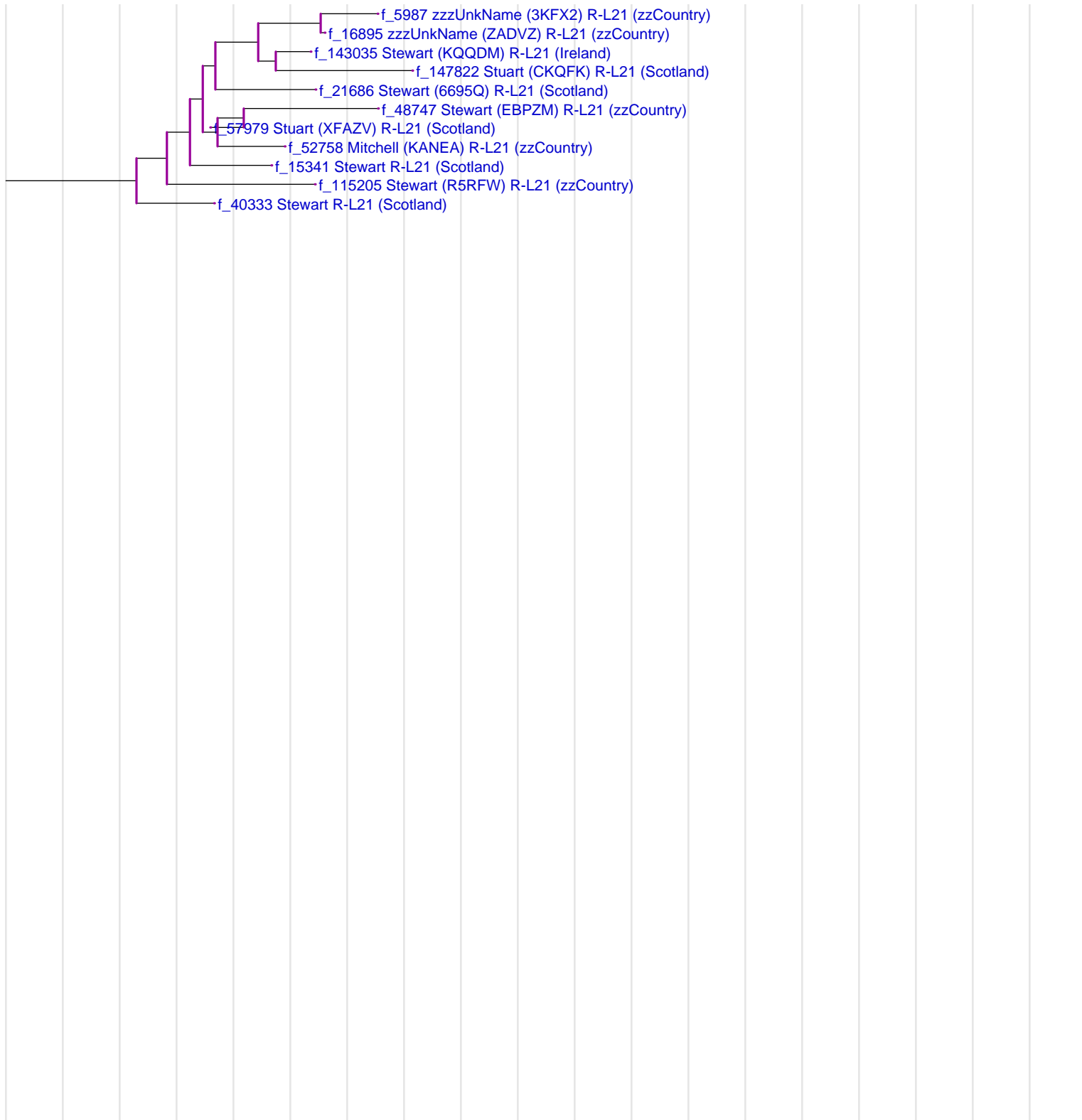
This is the marker distribution for Royal Stewart. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
11	737	34	4.61%	23.61±2.52	590.275±86.3905

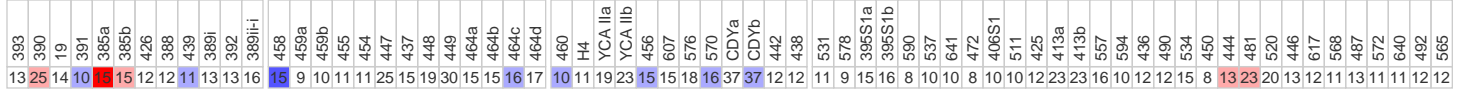
Note: This is essentially Mike's Variety 1011-STU



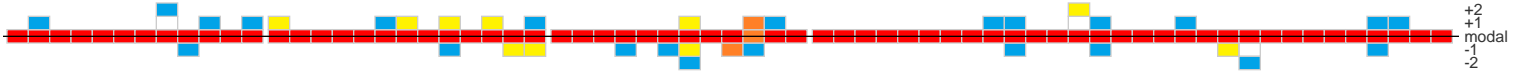
The vertical grey lines are separated 10 generations apart.

Clan MacWho

This is the modal haplotype for Clan MacWho. The coloration is with respect to the modal haplotype of the full tree.



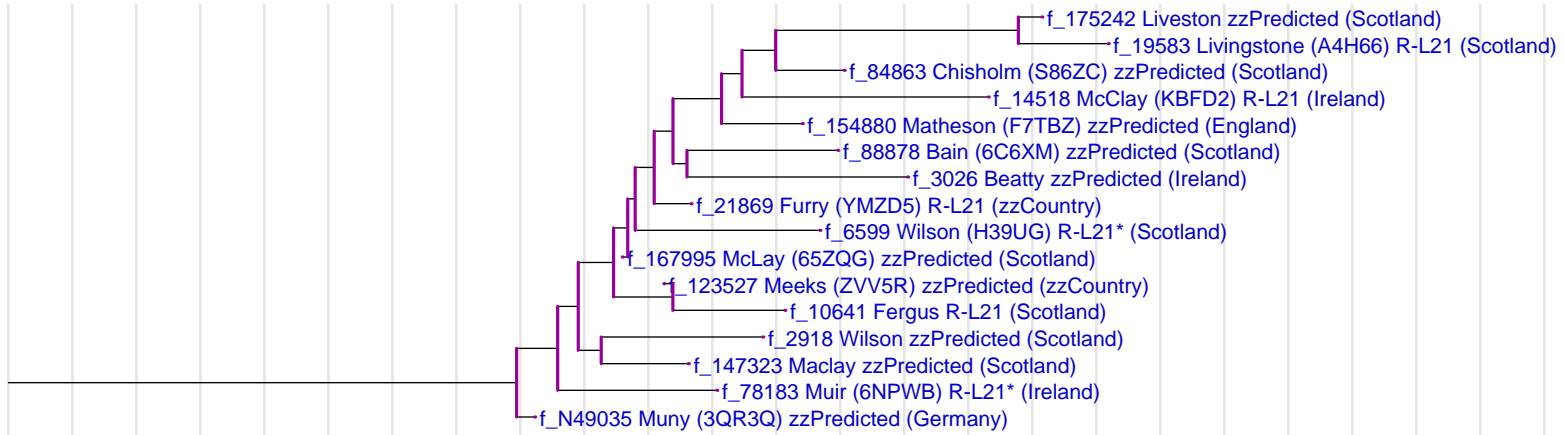
This is the marker distribution for Clan MacWho. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
16	1072	59	5.50%	28.30±2.97	707.429±102.479

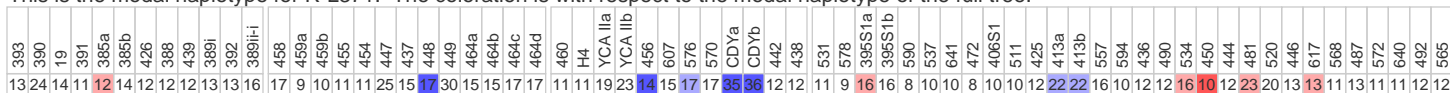
Note: This is Mike's Variety 1515-Who



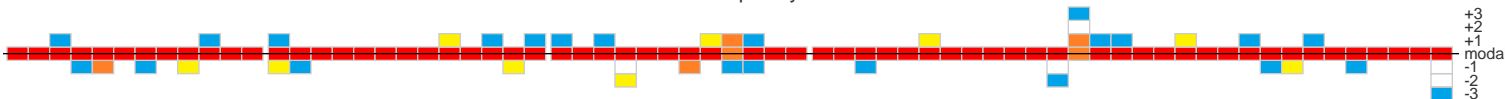
The vertical grey lines are separated 10 generations apart.

R-L371

This is the modal haplotype for R-L371. The coloration is with respect to the modal haplotype of the full tree.



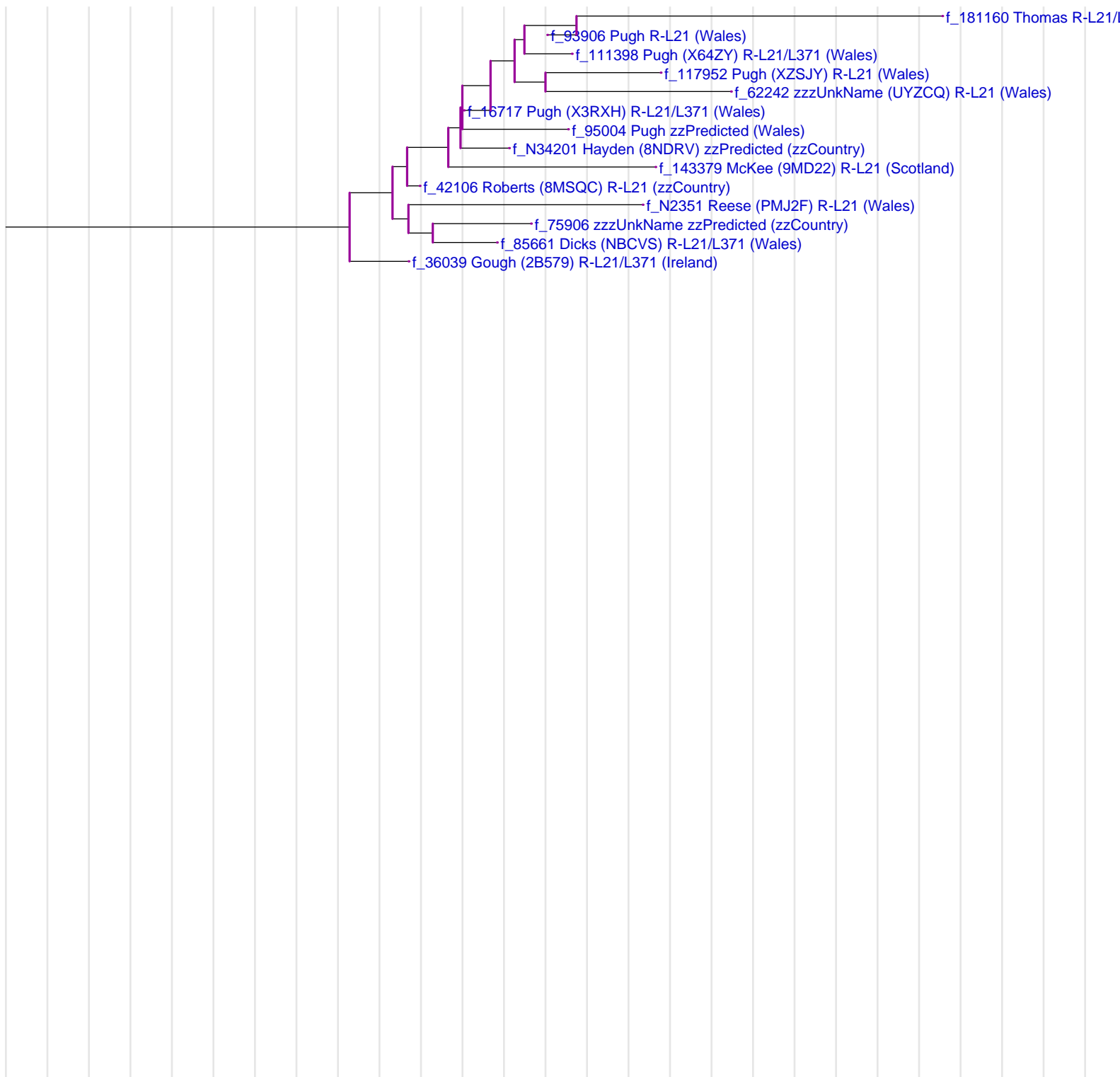
This is the marker distribution for R-L371. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
14	938	69	7.36%	38.18±4.03	954.604±138.815

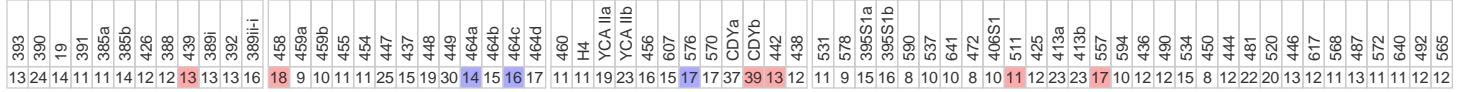
Note: AKA Wales I. This is Mike's Variety 1830-W1(-A) or the 17-14-10 cluster by Robert Hughes.



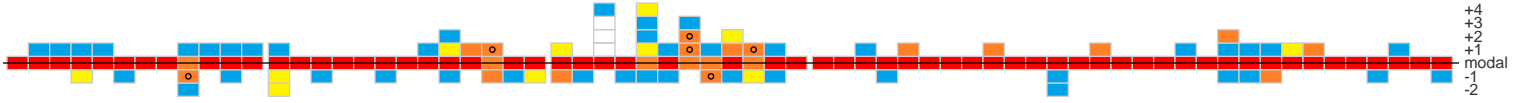
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1130-B

This is the modal haplotype for Mike's Variety 1130-B. The coloration is with respect to the modal haplotype of the full tree.



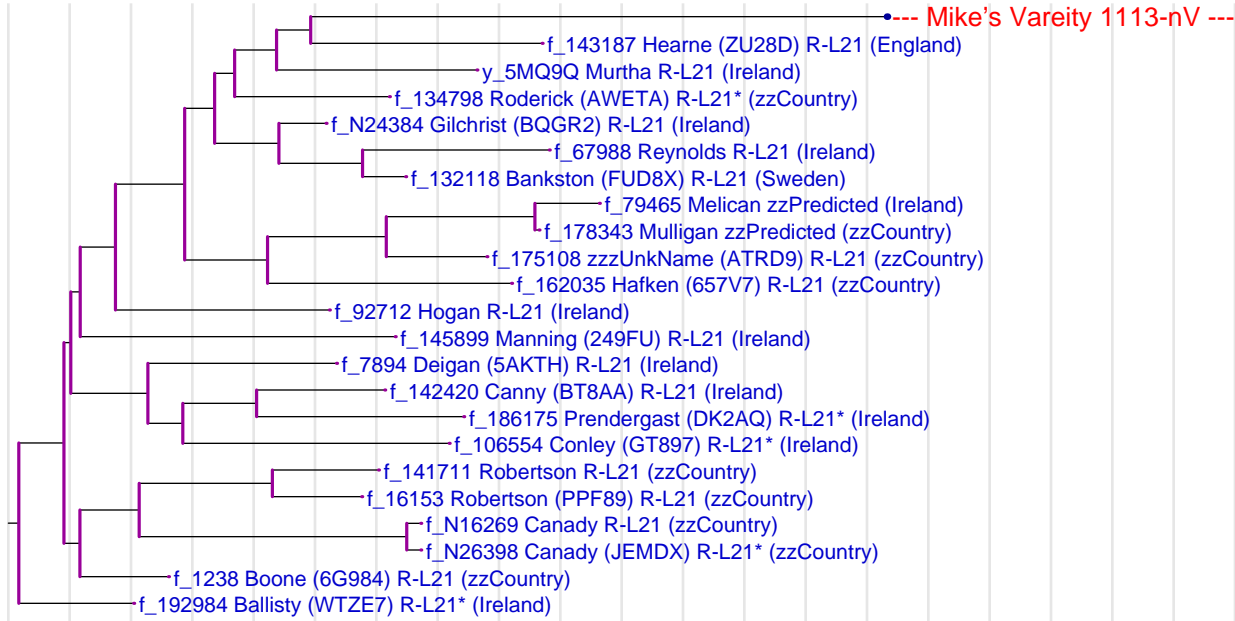
This is the marker distribution for Mike's Variety 1130-B. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
31	2077	329	15.84%	86.00±8.84	2149.94±308.28

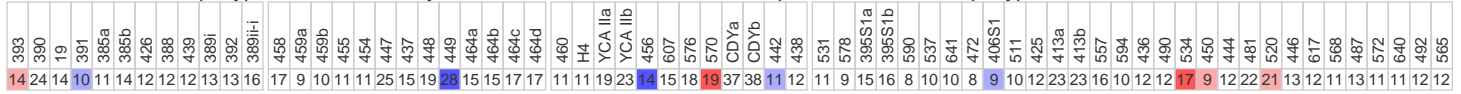
Note: The age of this cluster is exaggerated by the inclusion of 1113-nV.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 11169-A

This is the modal haplotype for Mike's Variety 11169-A. The coloration is with respect to the modal haplotype of the full tree.

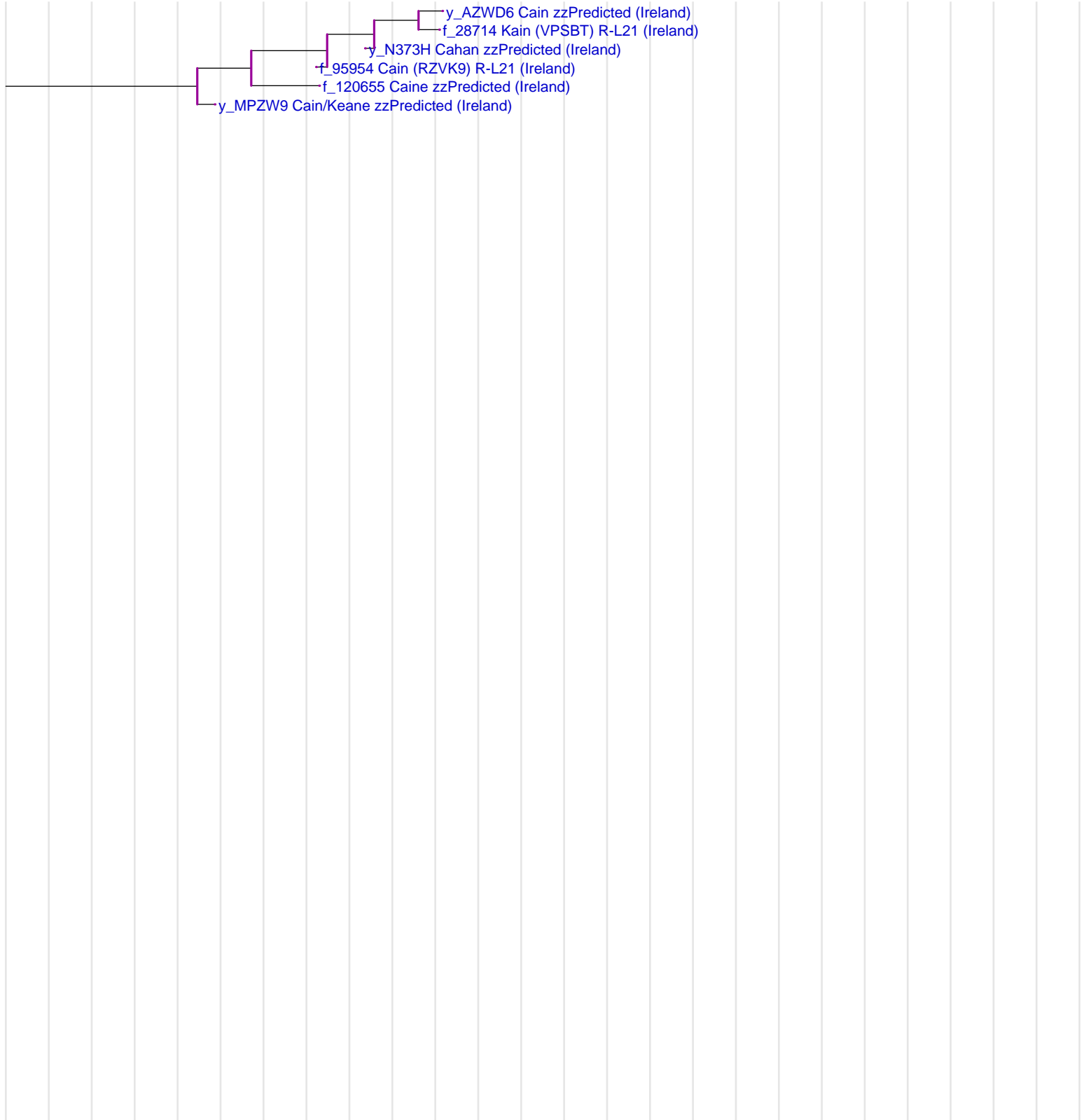


This is the marker distribution for Mike's Variety 11169-A. The color indicates the relative frequency of the alleles.



Age Analysis

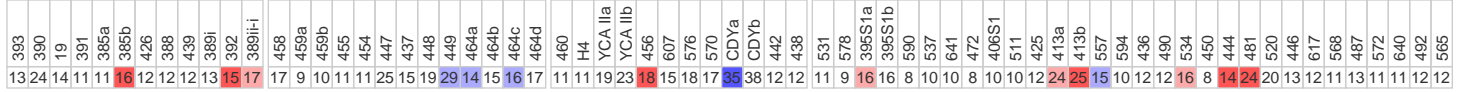
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	13	3.23%	16.43±1.84	410.872±61.7247



The vertical grey lines are separated 10 generations apart.

Wales and SW England

This is the modal haplotype for Wales and SW England. The coloration is with respect to the modal haplotype of the full tree.



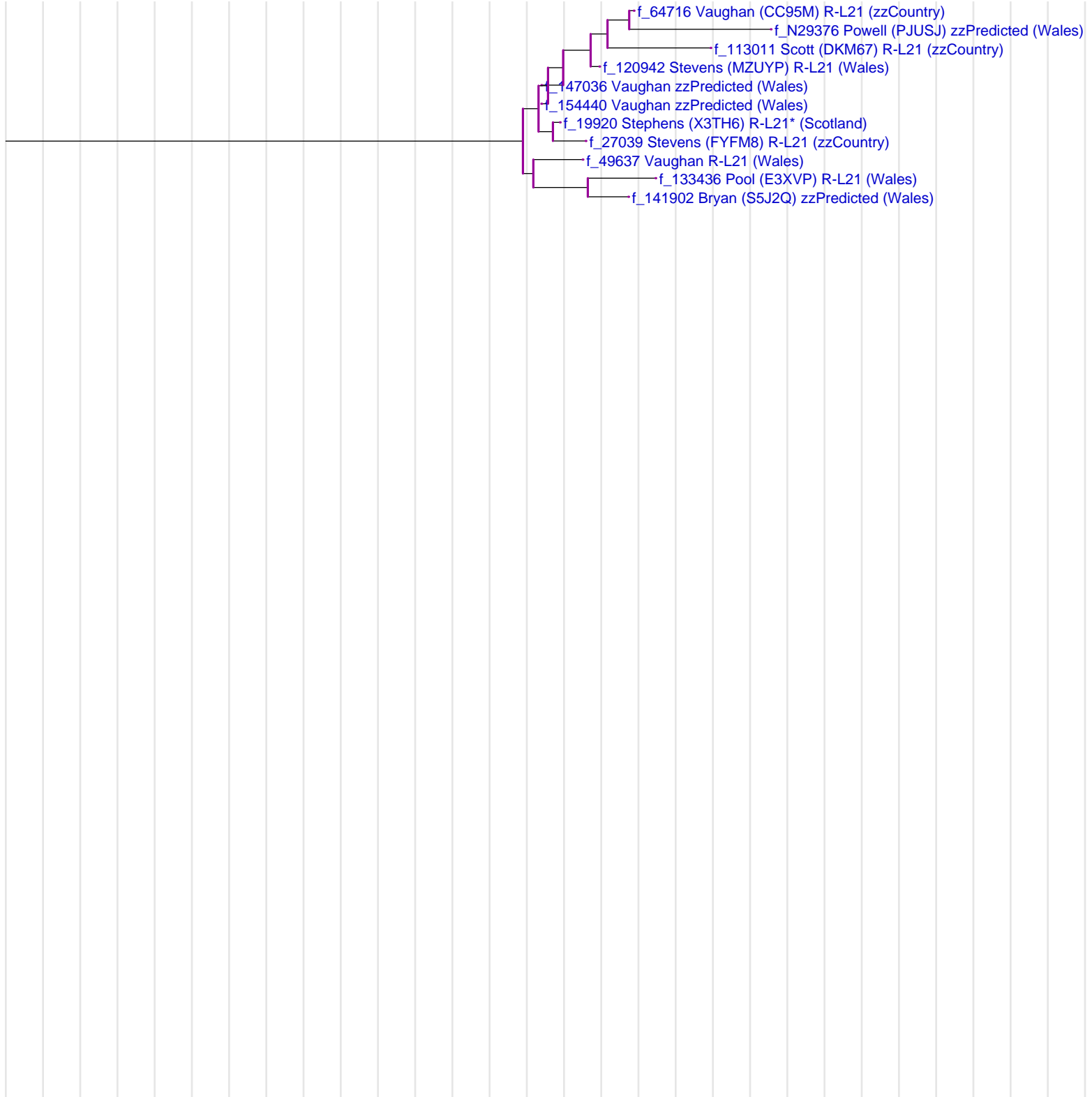
This is the marker distribution for Wales and SW England. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
11	737	26	3.53%	17.96±1.92	448.894±65.6755

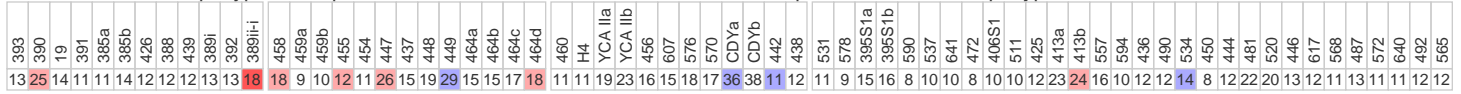
Note: This is Mike's Variety 1416-B-WSW



The vertical grey lines are separated 10 generations apart.

Hopkins-McCabe Cluster

This is the modal haplotype for Hopkins-McCabe Cluster. The coloration is with respect to the modal haplotype of the full tree.



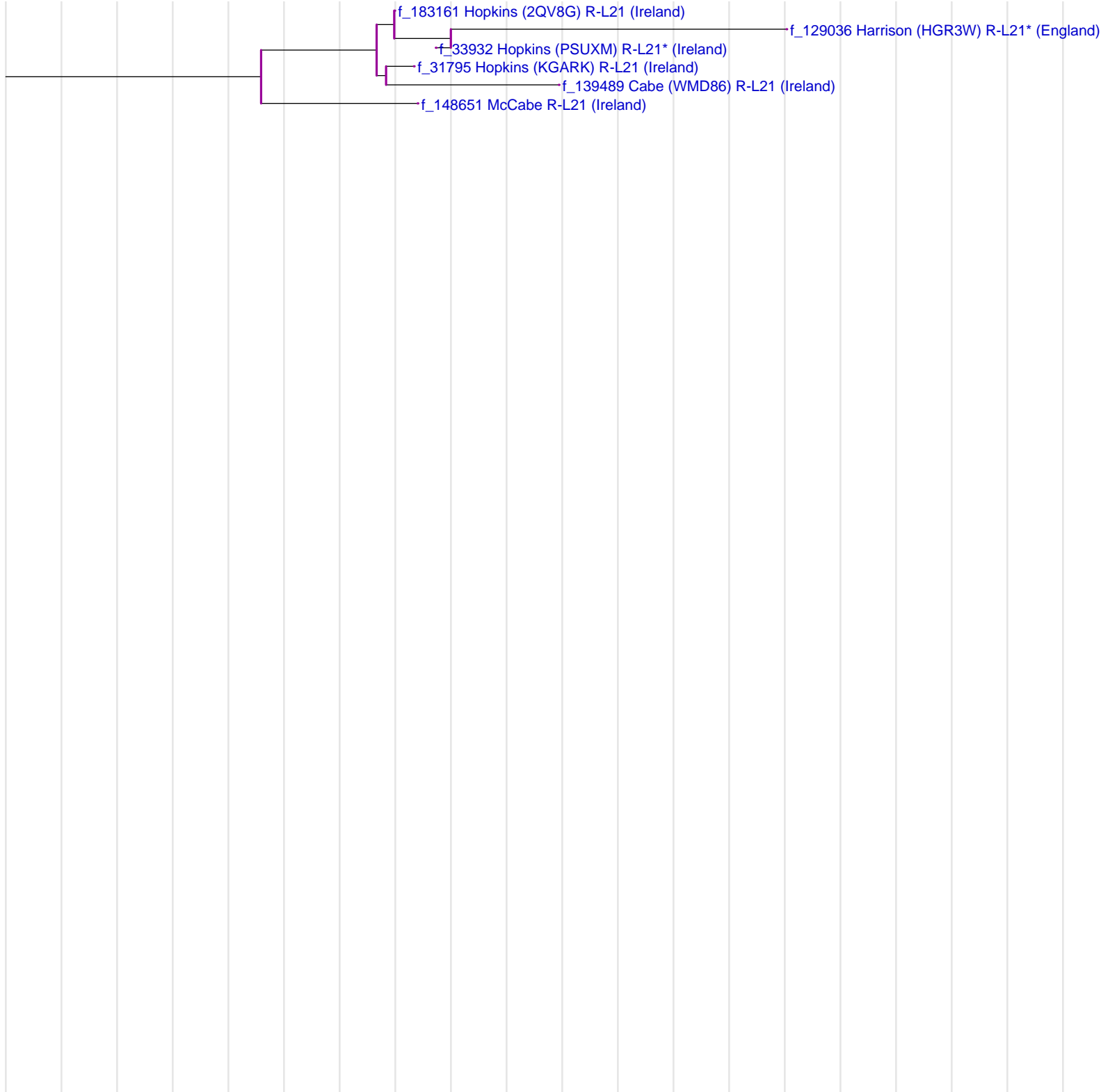
This is the marker distribution for Hopkins-McCabe Cluster. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	24	5.97%	30.77±3.46	769.224±115.738

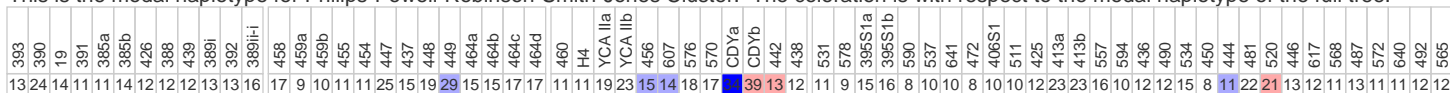
Note: This is Mike's Variety 1226.



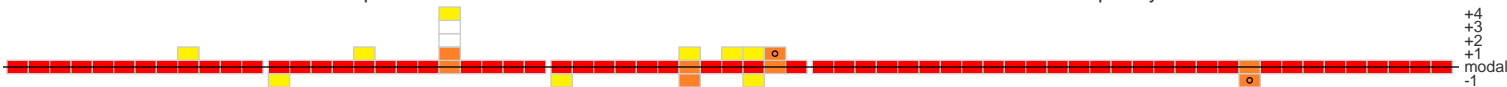
The vertical grey lines are separated 10 generations apart.

Philips-Powell-Robinson-Smith-Jones Cluster

This is the modal haplotype for Philips-Powell-Robinson-Smith-Jones Cluster. The coloration is with respect to the modal haplotype of the full tree.



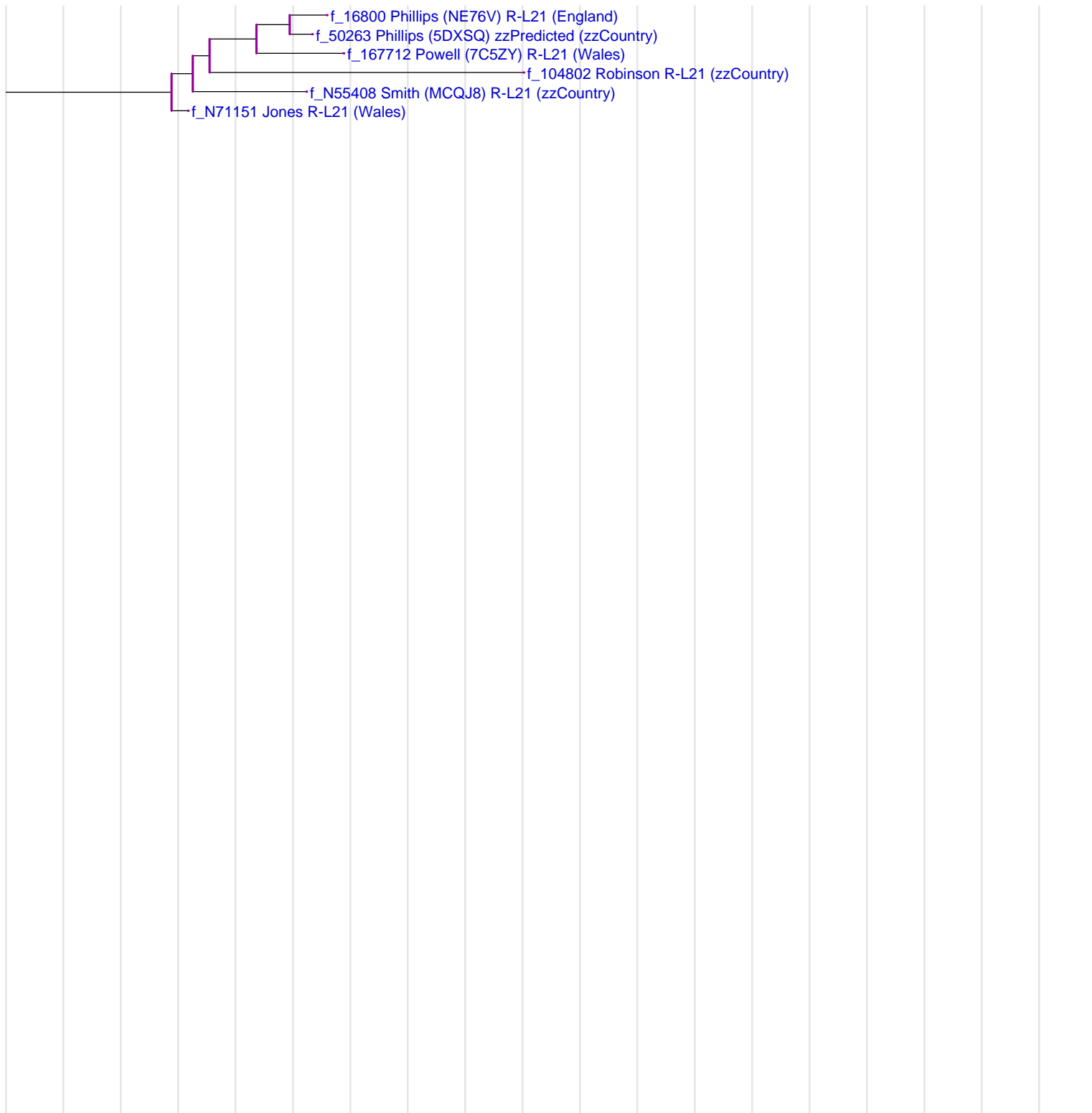
This is the marker distribution for Philips-Powell-Robinson-Smith-Jones Cluster. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	22	5.47%	28.13±3.16	703.32±105.792

Note: This is Mike's Variety 1114



The vertical grey lines are separated 10 generations apart.

Mike's Variety 2410

This is the modal haplotype for Mike's Variety 2410. The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	11	11	15	12	12	12	13	13	16	17	9	10	11	11	25	15	20	30	15	16	17	17	11	10	19	24	15	15	18	16	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12

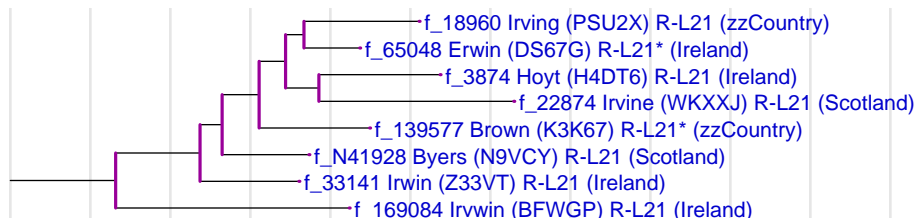
This is the marker distribution for Mike's Variety 2410. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
8	536	24	4.48%	22.90±2.50	572.517±84.8217

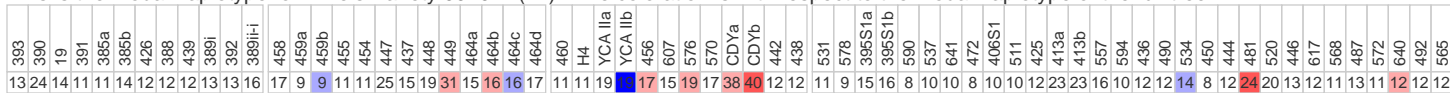
Note: This cluster does not include Lewis (f44100), although Mike has him classified as 2410 also.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 9919-A (#1)

This is the modal haplotype for Mike's Variety 9919-A (#1). The coloration is with respect to the modal haplotype of the full tree.



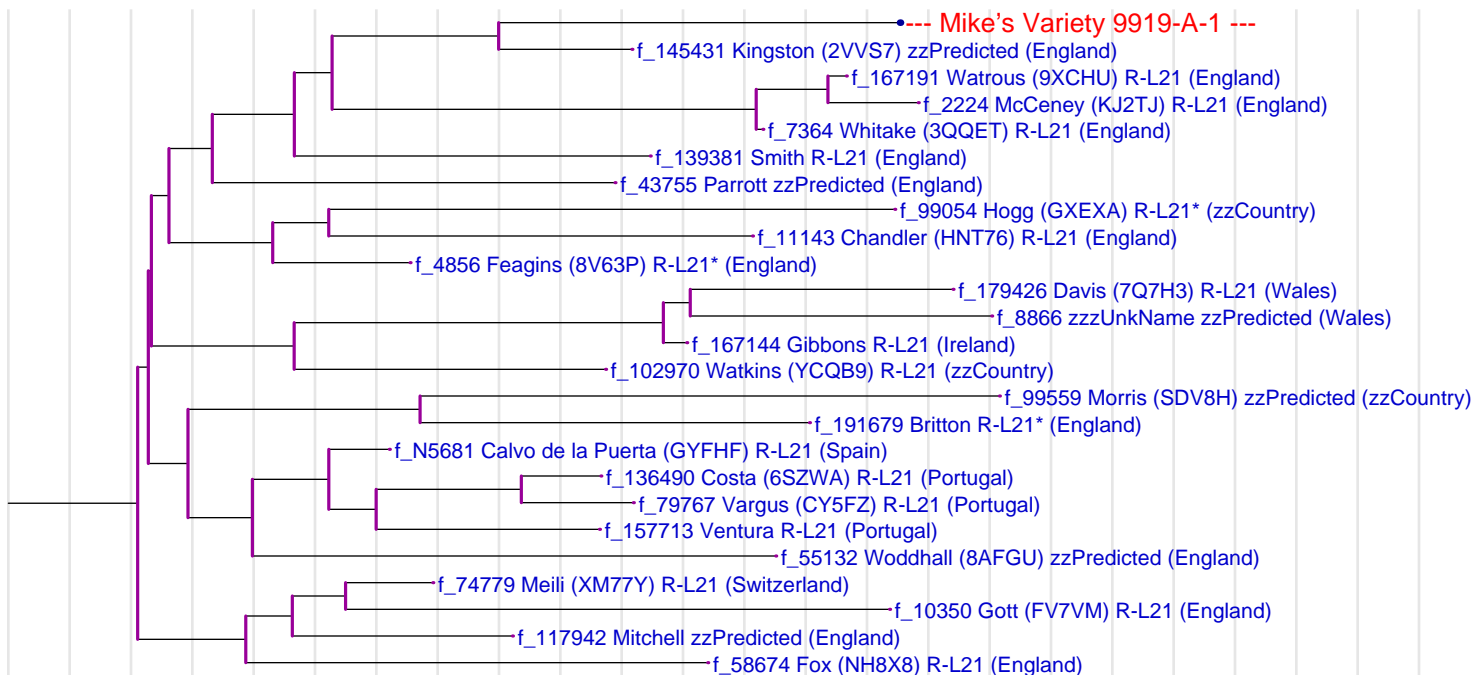
This is the marker distribution for Mike's Variety 9919-A (#1). The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
43	2881	607	21.07%	117.70±12.02	2942.47±420.516

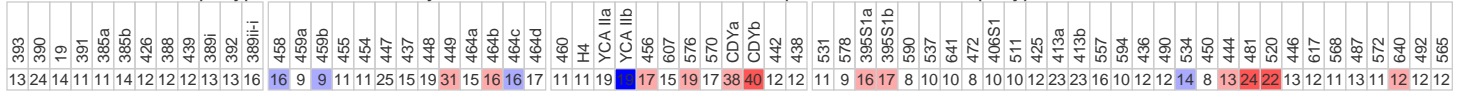
Note: This is a part of the 9919 Cluster.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 9919-A-1

This is the modal haplotype for Mike's Variety 9919-A-1. The coloration is with respect to the modal haplotype of the full tree.

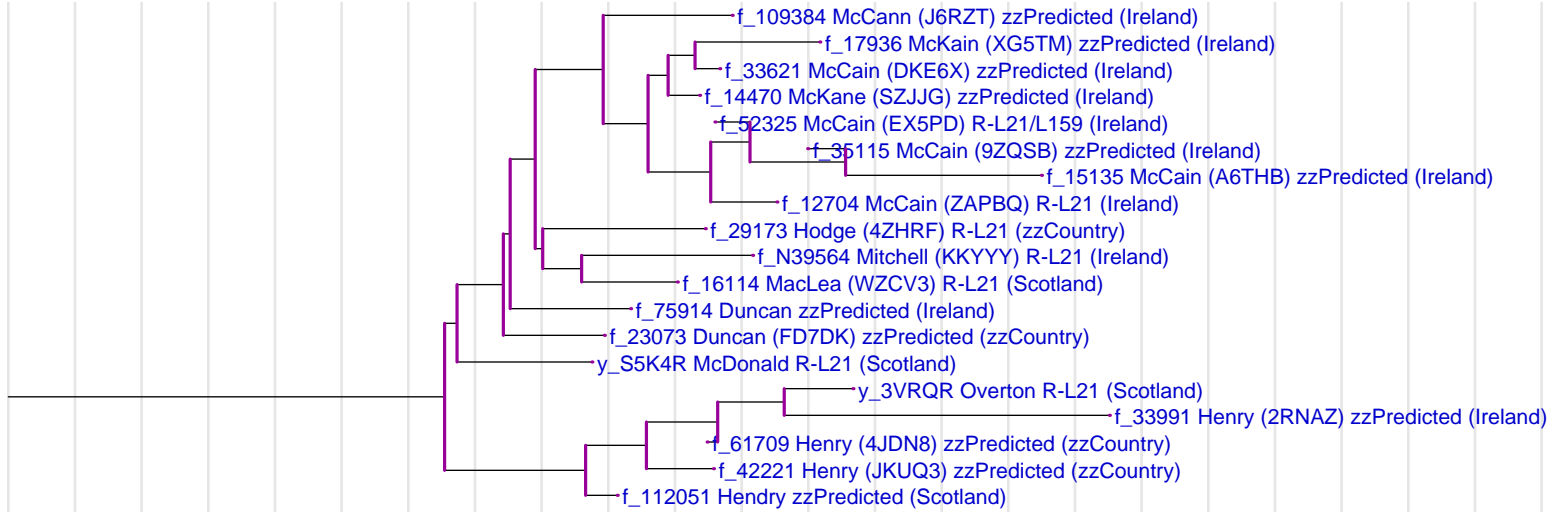


This is the marker distribution for Mike's Variety 9919-A-1. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
19	1273	88	6.91%	35.80±3.73	895.024±129.209



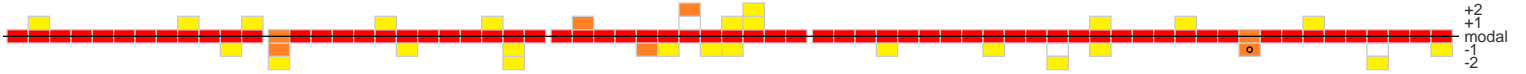
The vertical grey lines are separated 10 generations apart.

Mike's Variety 9919-A (#2)

This is the modal haplotype for Mike's Variety 9919-A (#2). The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	11	14	14	12	12	11	13	13	16	19	9	9	11	11	25	15	19	30	15	15	17	17	10	10	19	16	15	18	18	18	36	38	13	12	11	9	15	16	8	10	10	8	10	10	12	23	23	17	10	10	12	12	15	8	12	22	20	13	12	11	13	11	12	12	12

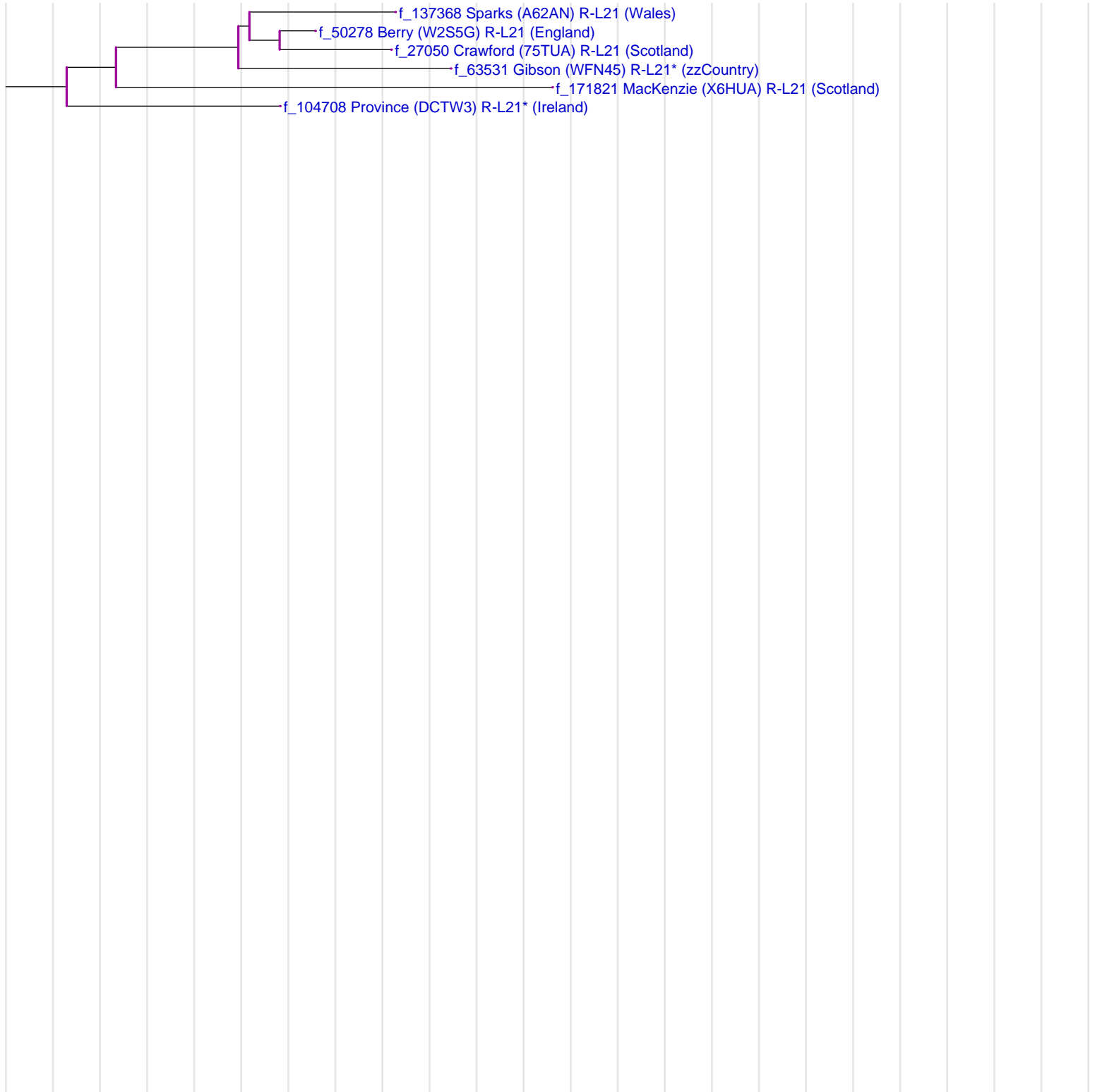
This is the marker distribution for Mike's Variety 9919-A (#2). The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	42	10.45%	55.12±6.22	1377.88±207.847

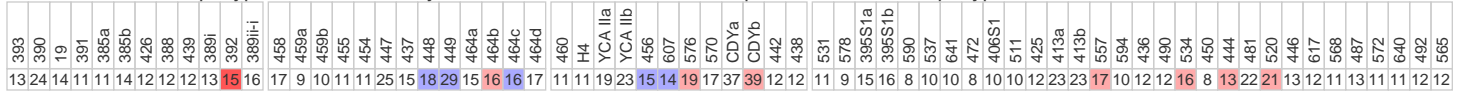
Note: This is a part of the 9919 Cluster.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1416

This is the modal haplotype for Mike's Variety 1416. The coloration is with respect to the modal haplotype of the full tree.

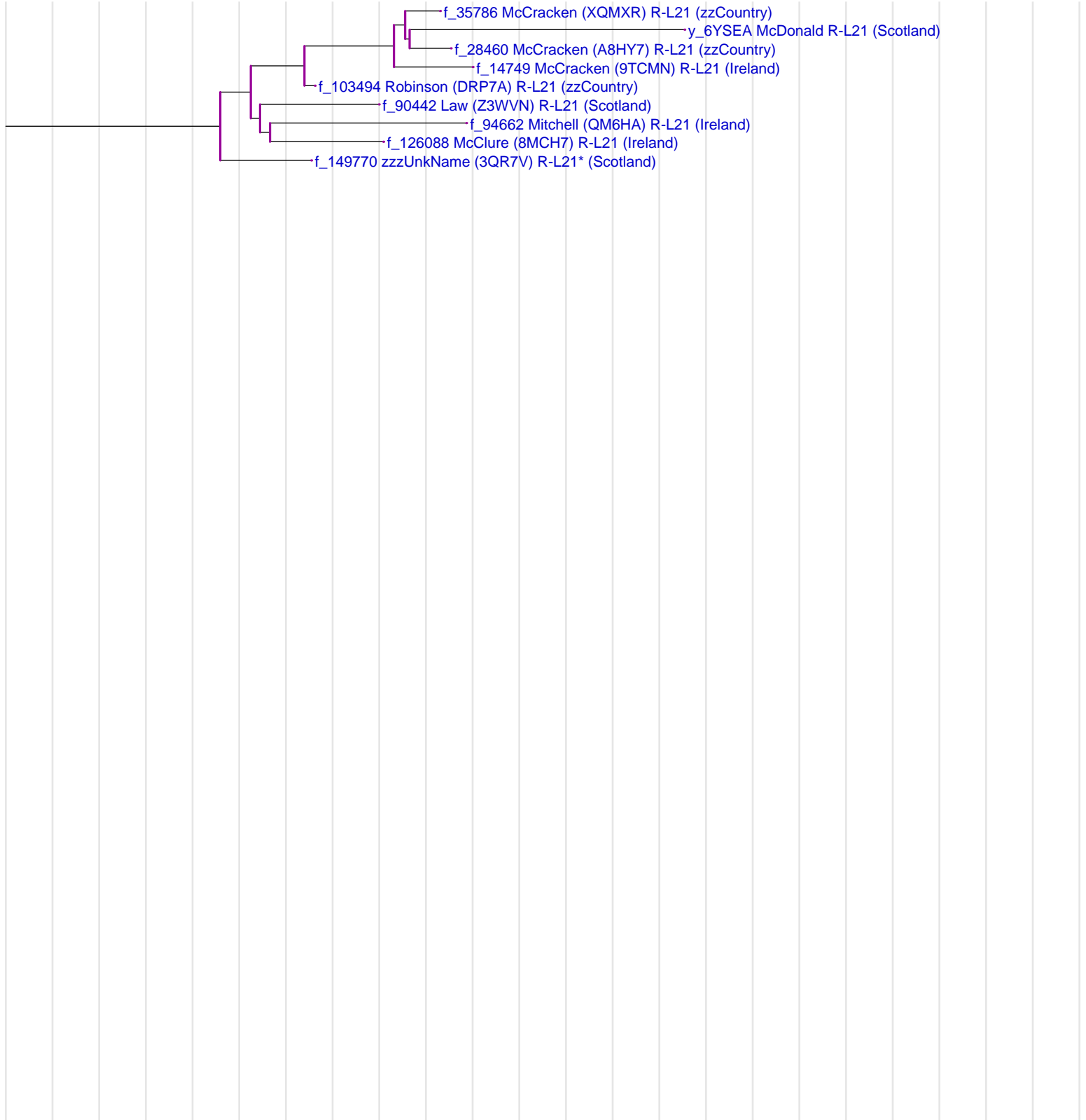


This is the marker distribution for Mike's Variety 1416. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
9	603	47	7.79%	40.55±4.40	1013.78±149.65



The vertical grey lines are separated 10 generations apart.

Mike's Variety V1410

This is the modal haplotype for Mike's Variety V1410. The coloration is with respect to the modal haplotype of the full tree.

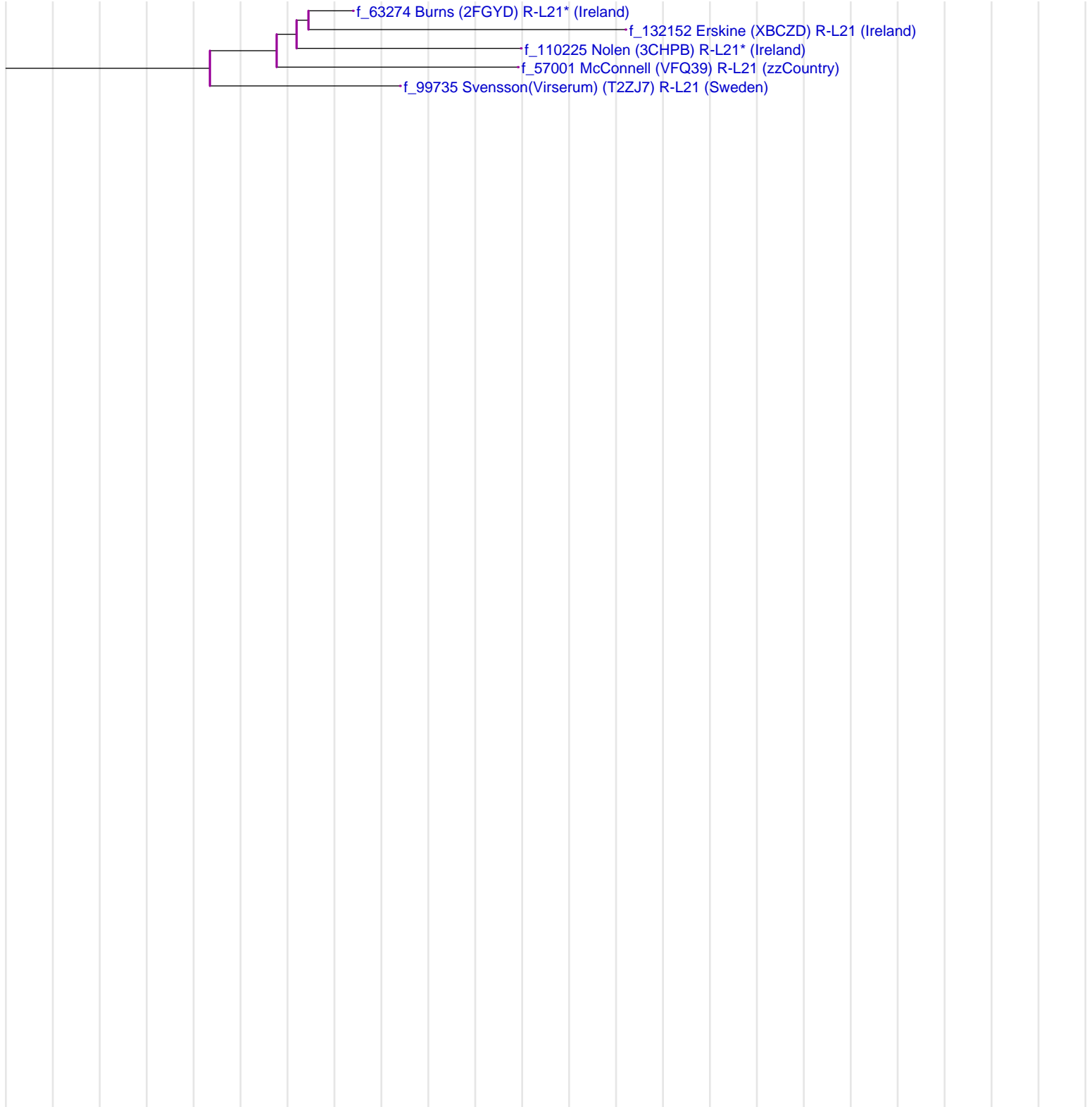
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
14	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	16	17	11	11	19	23	15	17	18	17	37	40	13	12	11	10	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	12	14	8	12	22	20	13	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety V1410. The color indicates the relative frequency of the alleles.



Age Analysis

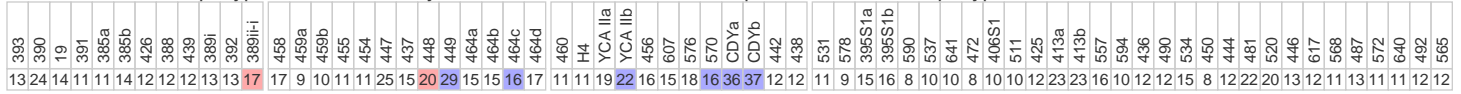
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	31	9.25%	48.51±5.59	1212.79±184.996



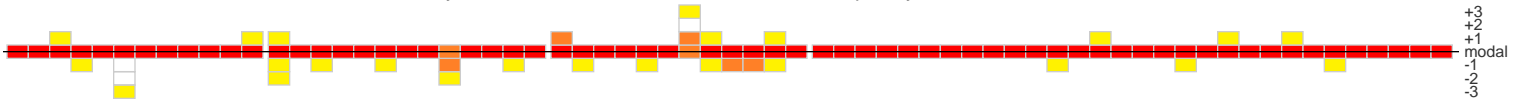
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1722

This is the modal haplotype for Mike's Variety 1722. The coloration is with respect to the modal haplotype of the full tree.

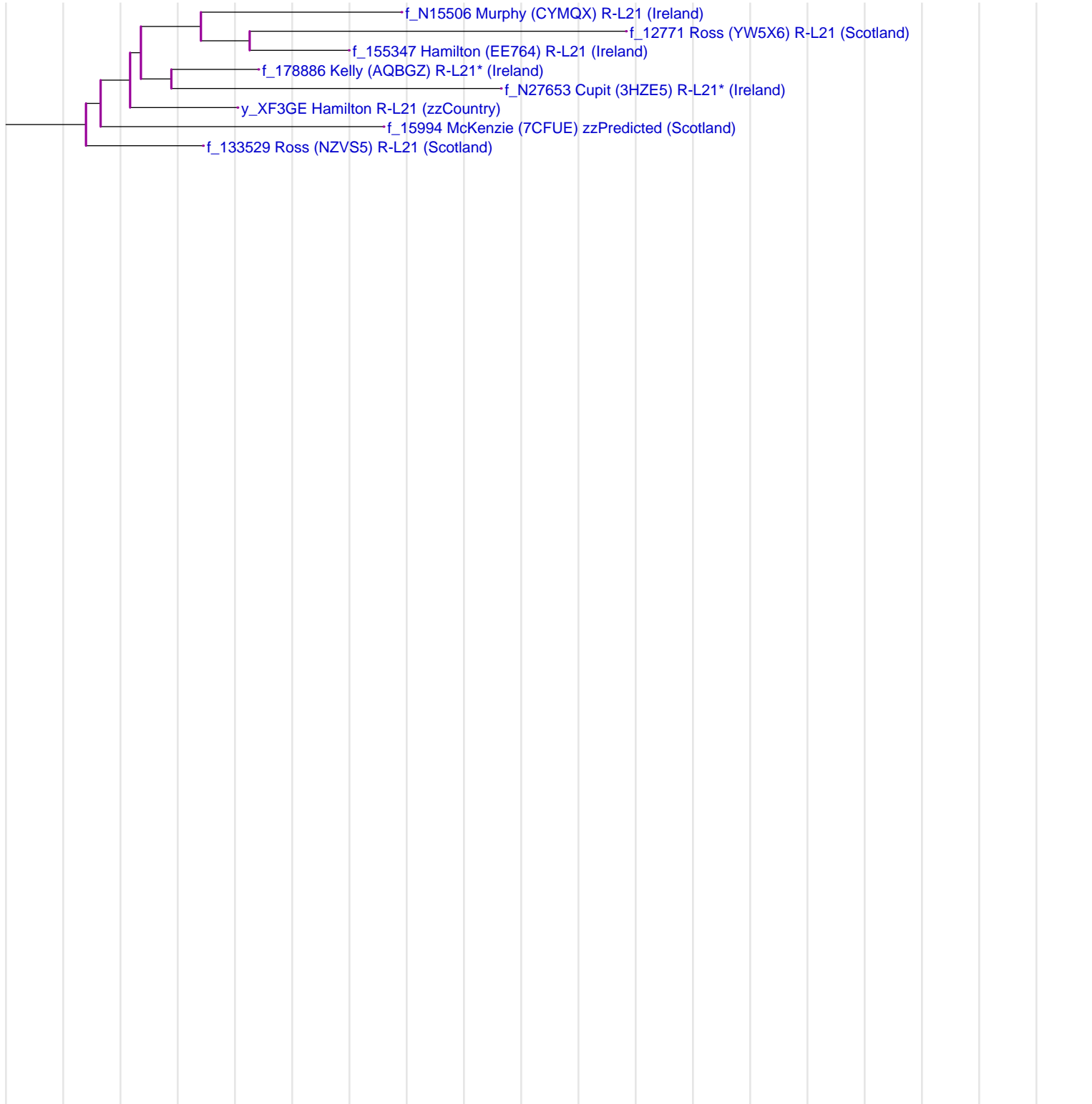


This is the marker distribution for Mike's Variety 1722. The color indicates the relative frequency of the alleles.



Age Analysis

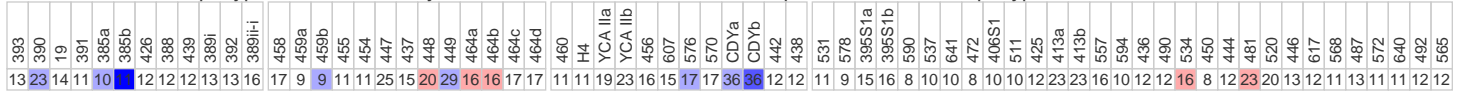
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
8	536	49	9.14%	47.90±5.26	1197.42±177.768



The vertical grey lines are separated 10 generations apart.

Mike's Variety 2399-Am

This is the modal haplotype for Mike's Variety 2399-Am. The coloration is with respect to the modal haplotype of the full tree.

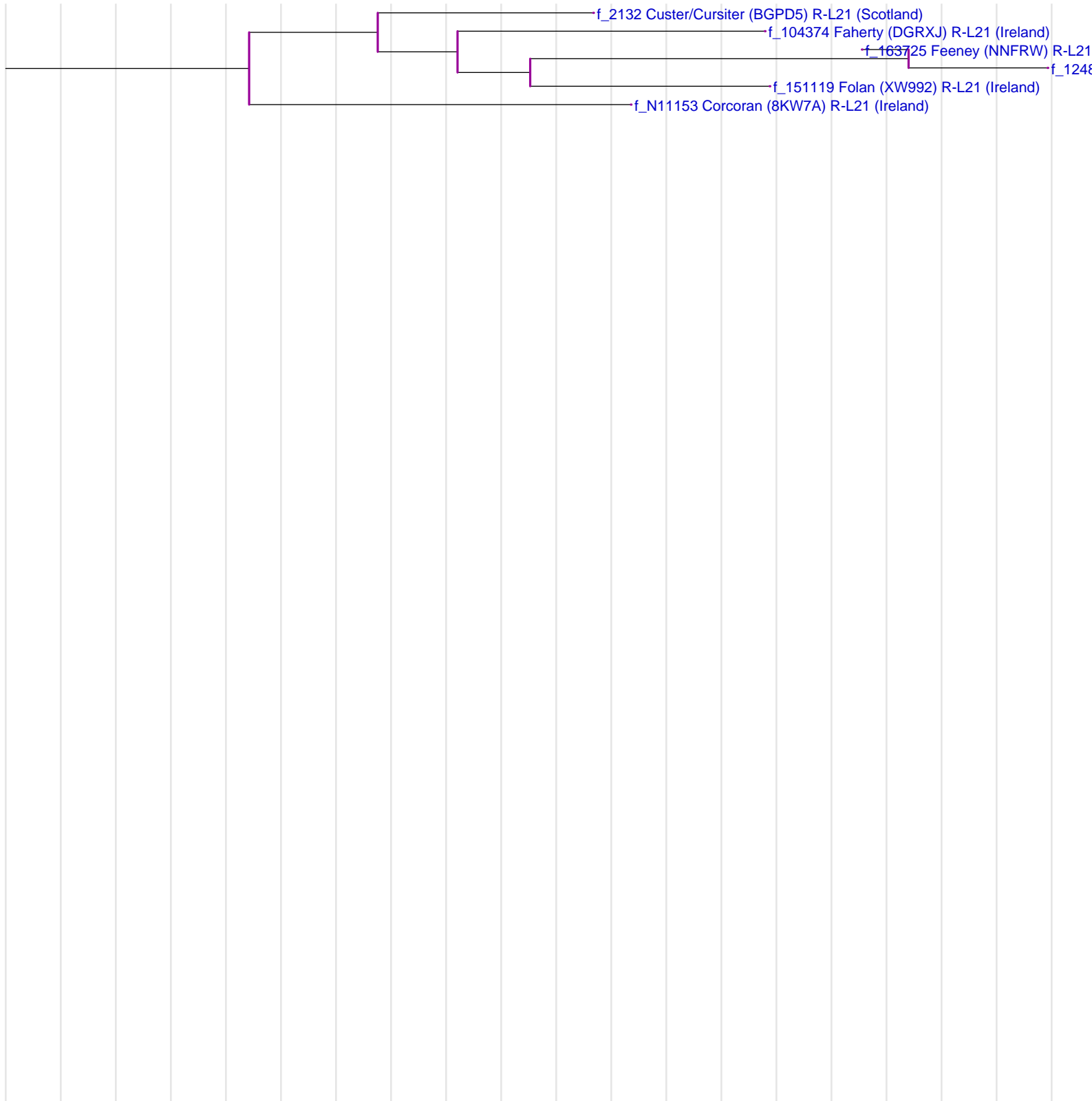


This is the marker distribution for Mike's Variety 2399-Am. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	49	12.19%	64.90±7.34	1622.39±244.975



The vertical grey lines are separated 10 generations apart.

Mike's Variety 590917

This is the modal haplotype for Mike's Variety 590917. The coloration is with respect to the modal haplotype of the full tree.

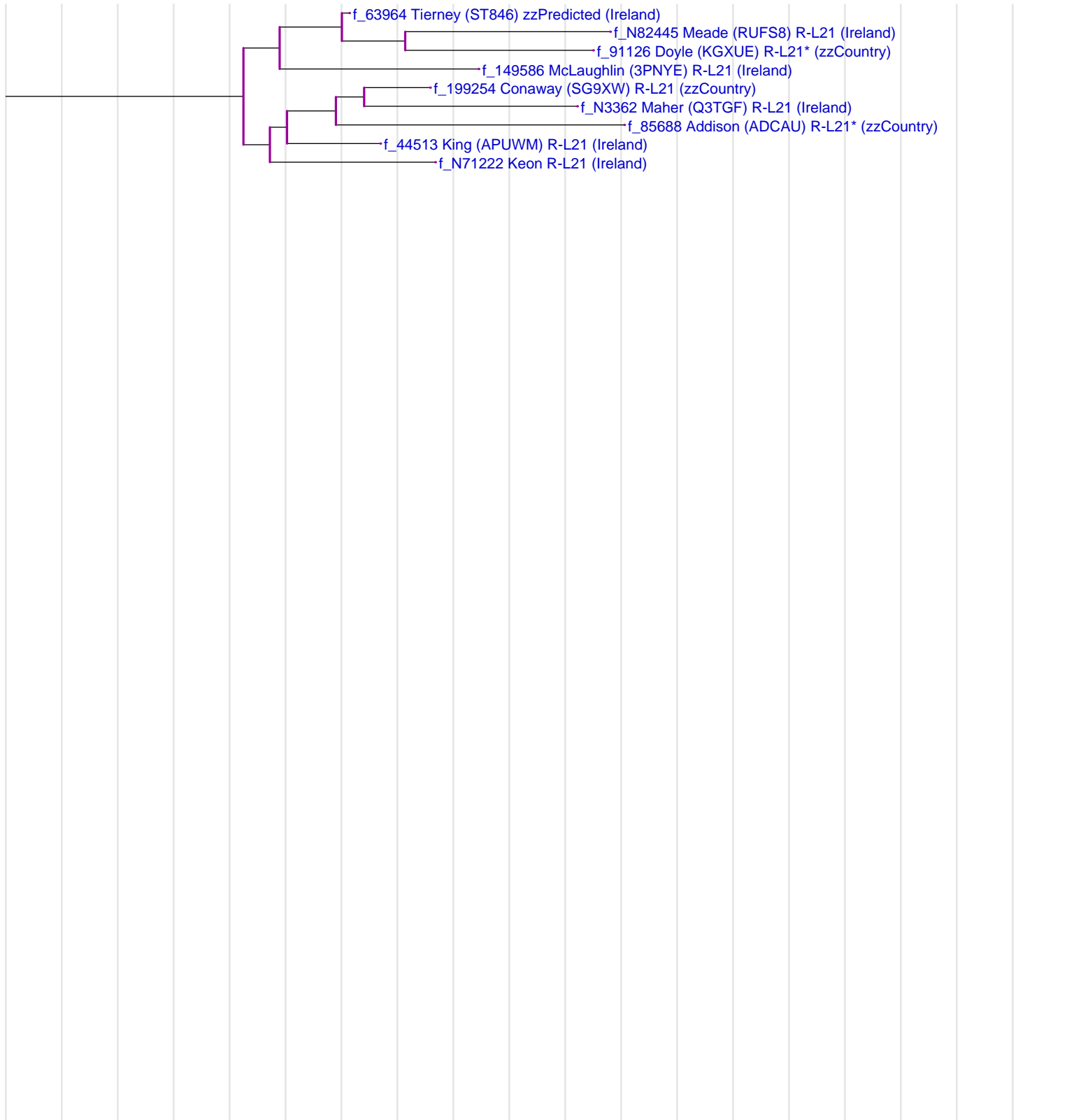
393	390	19	391	385a	385b	426	388	439	389i	392	389f-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	11	14	12	12	12	12	13	13	17	17	9	10	11	11	25	15	19	29	15	15	16	17	10	10	19	23	16	14	17	17	36	36	12	12	11	9	15	16	9	10	10	8	10	10	12	23	24	16	10	12	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 590917. The color indicates the relative frequency of the alleles.



Age Analysis

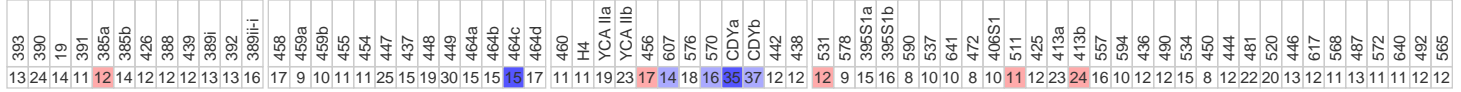
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
9	603	51	8.46%	44.15±4.80	1103.87±162.99



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1130-A

This is the modal haplotype for Mike's Variety 1130-A. The coloration is with respect to the modal haplotype of the full tree.

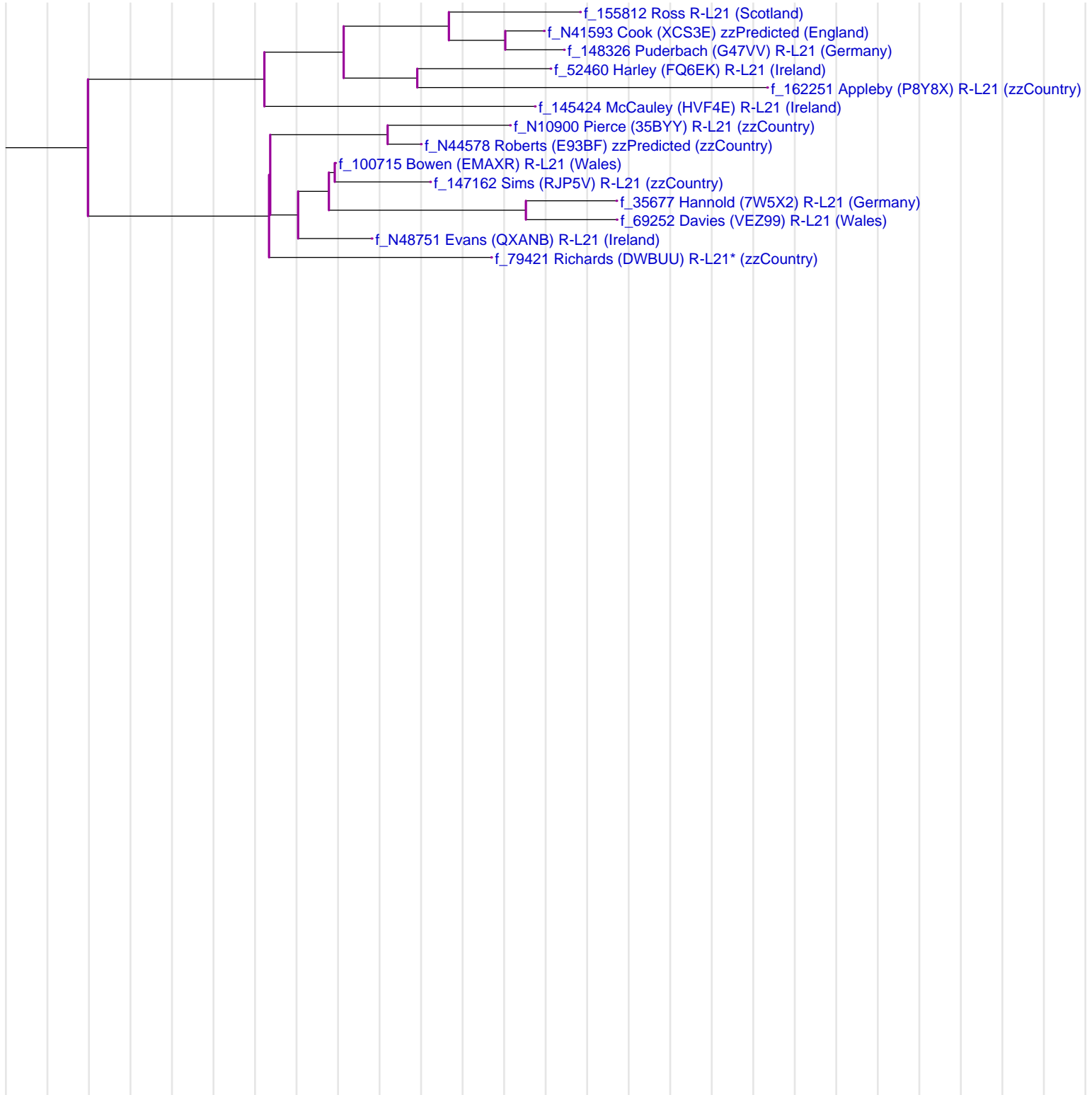


This is the marker distribution for Mike's Variety 1130-A. The color indicates the relative frequency of the alleles.



Age Analysis

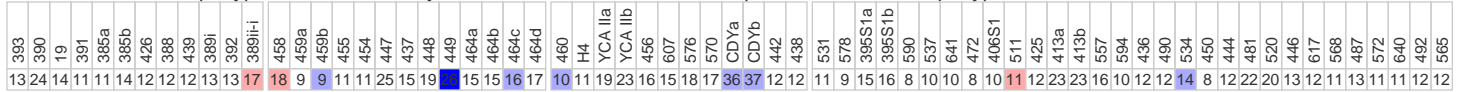
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
14	938	175	18.66%	102.85±10.92	2571.25±375.035



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1199

This is the modal haplotype for Mike's Variety 1199. The coloration is with respect to the modal haplotype of the full tree.

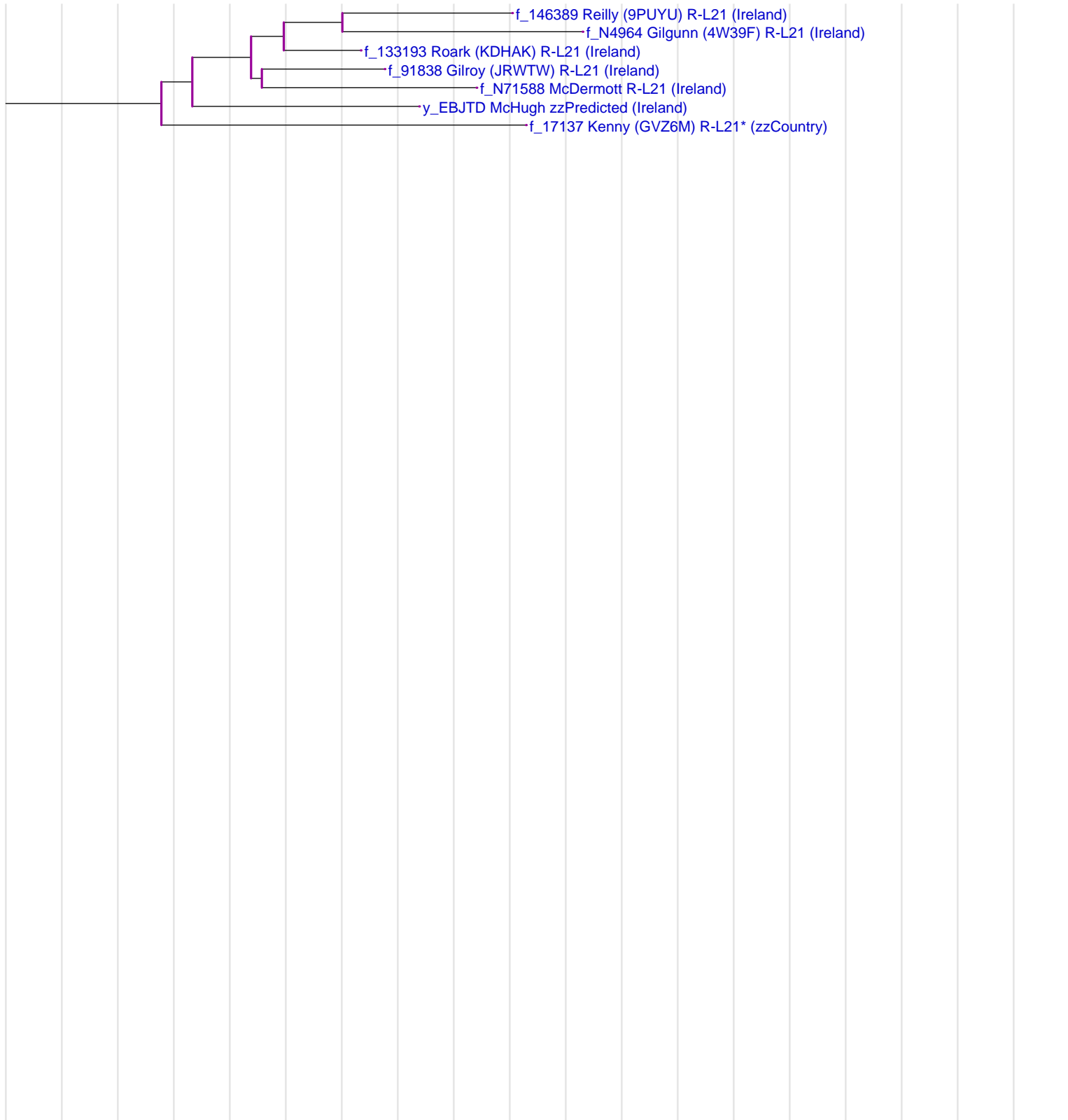


This is the marker distribution for Mike's Variety 1199. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
7	469	43	9.17%	48.04±5.34	1201.08±179.488



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1121

This is the modal haplotype for Mike's Variety 1121. The coloration is with respect to the modal haplotype of the full tree.

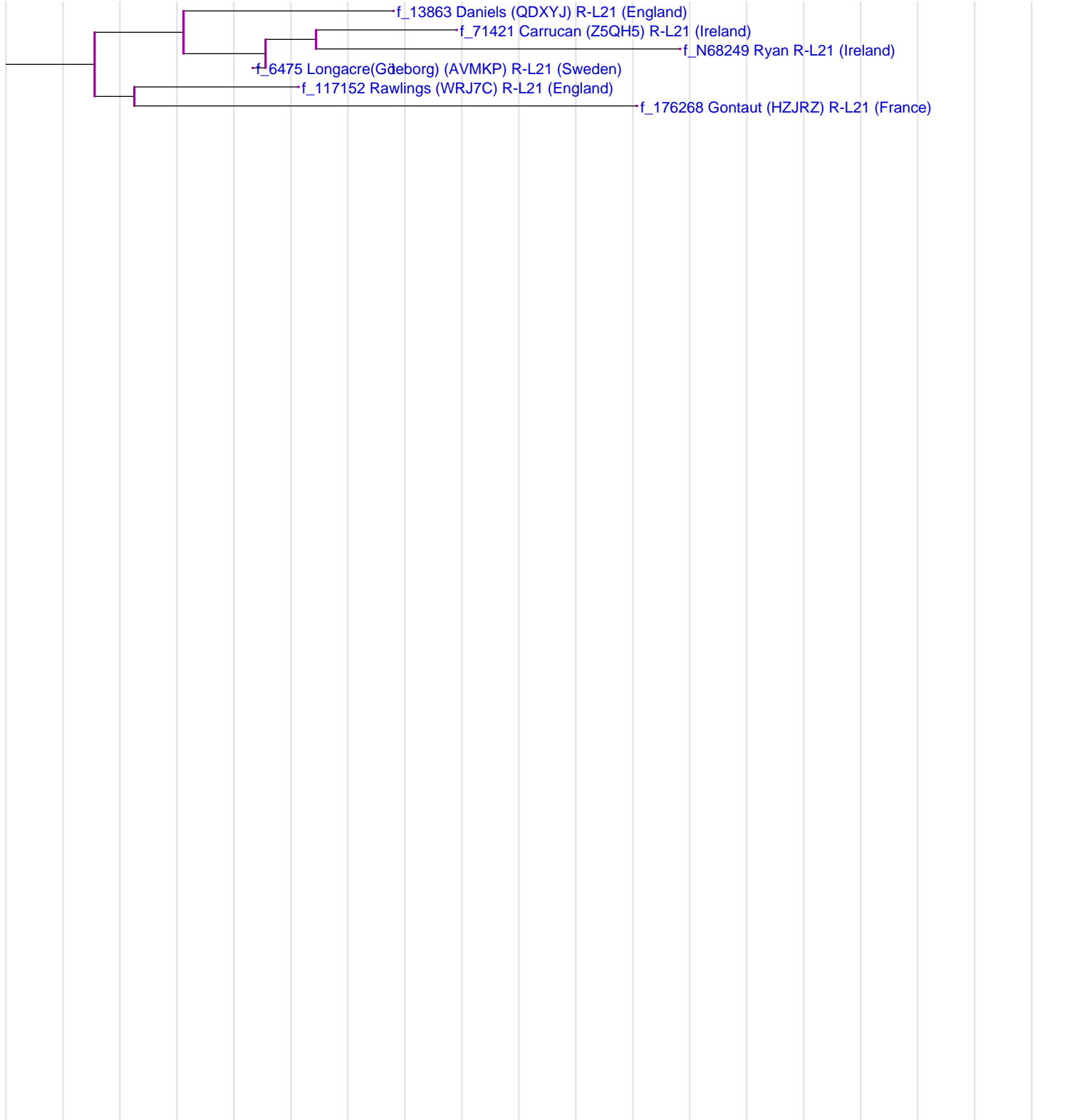
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	10	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	31	15	15	15	17	10	11	19	23	17	15	18	19	36	38	12	12	11	9	15	16	8	11	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	21	14	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 1121. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	43	10.70%	56.50±6.38	1412.54±213.105



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1416-A

This is the modal haplotype for Mike's Variety 1416-A. The coloration is with respect to the modal haplotype of the full tree.

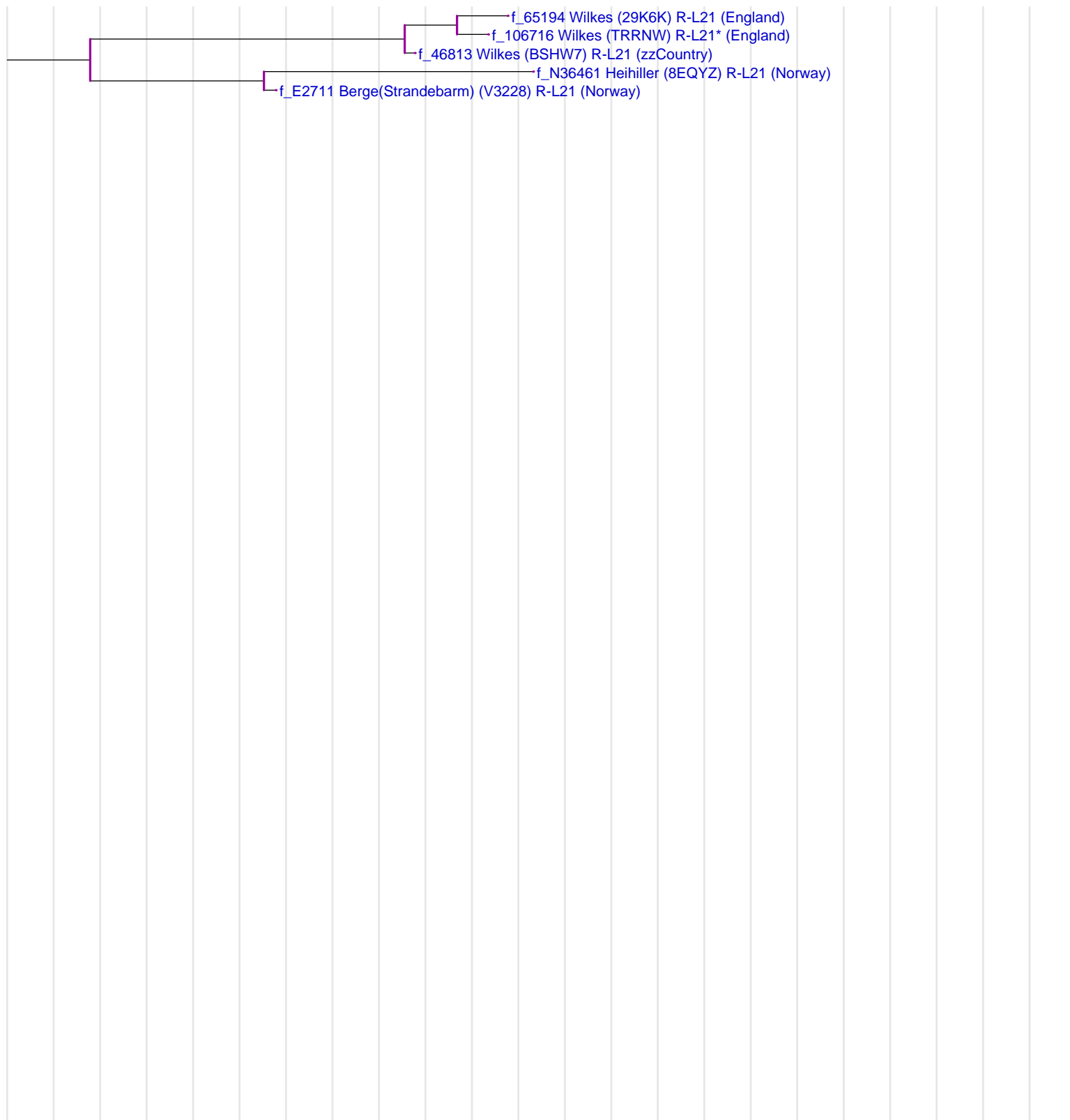
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	10	11	14	12	12	13	13	14	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	12	19	23	16	16	19	16	37	37	12	12	11	10	15	16	8	10	10	8	10	10	12	23	16	10	10	12	12	12	16	8	12	22	18	13	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 1416-A. The color indicates the relative frequency of the alleles.



Age Analysis

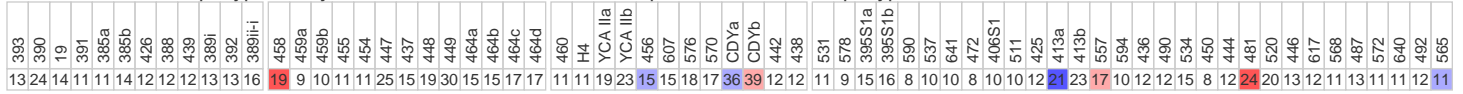
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	35	10.45%	55.12±6.36	1377.88±210.348



The vertical grey lines are separated 10 generations apart.

Hy-Maine

This is the modal haplotype for Hy-Maine. The coloration is with respect to the modal haplotype of the full tree.



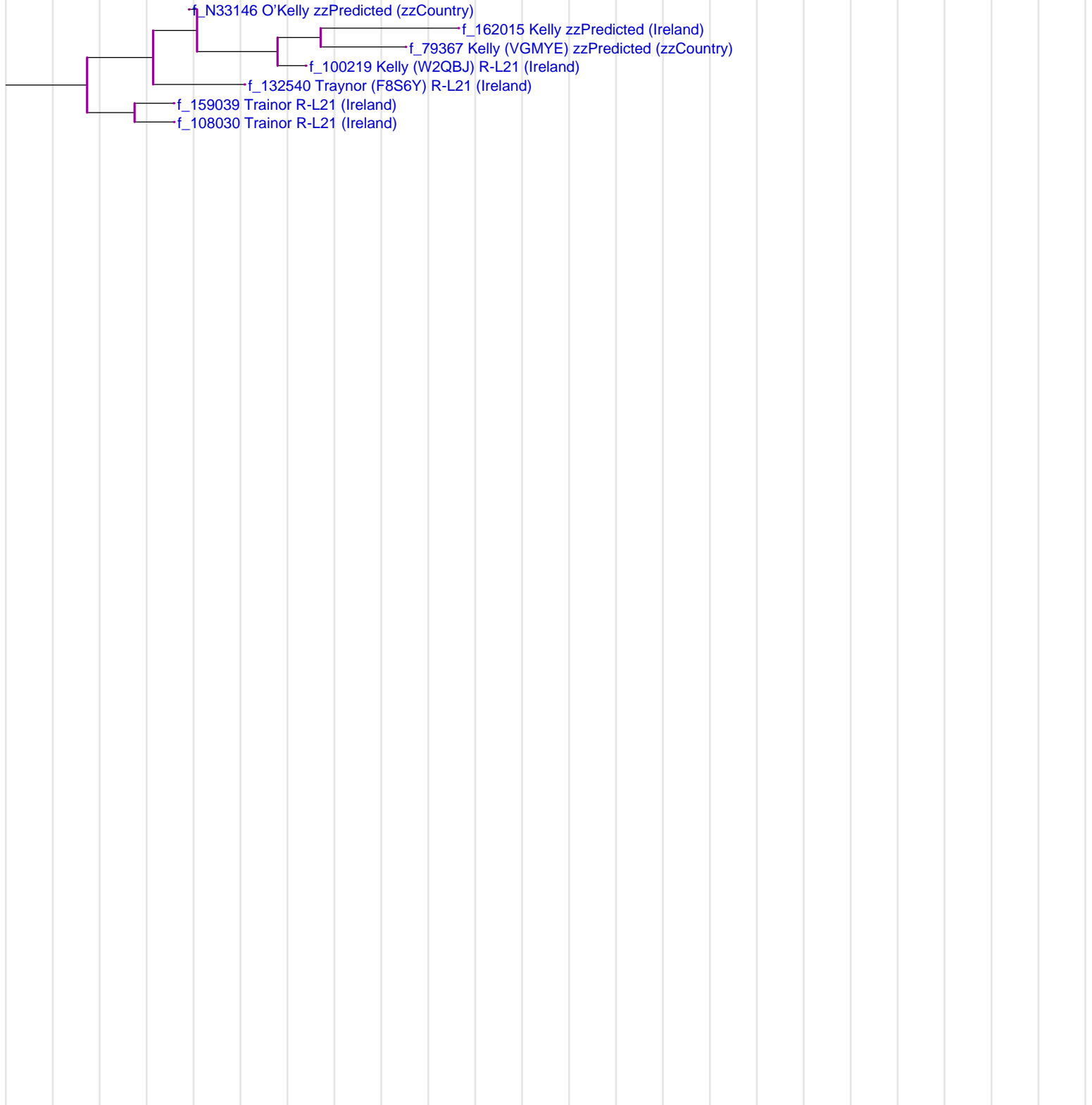
This is the marker distribution for Hy-Maine. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
7	469	29	6.18%	31.90±3.53	797.572±119.012

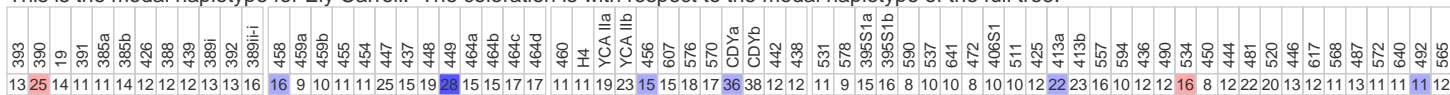
Note: This is Mike's Variety 2117



The vertical grey lines are separated 10 generations apart.

Ely Carroll

This is the modal haplotype for Ely Carroll. The coloration is with respect to the modal haplotype of the full tree.



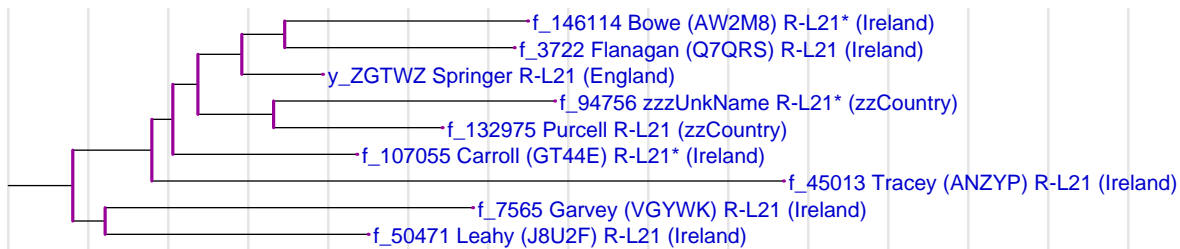
This is the marker distribution for Ely Carroll. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
9	603	54	8.96%	46.87±5.09	1171.84±173.06

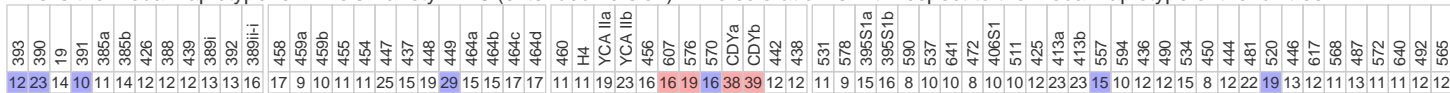
Note: This group of men constitute only the core group of Mike's 49211 men.



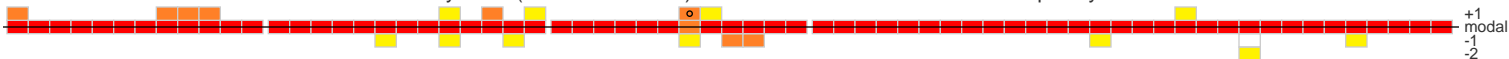
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1223 (extended version)

This is the modal haplotype for Mike's Variety 1223 (extended version). The coloration is with respect to the modal haplotype of the full tree.



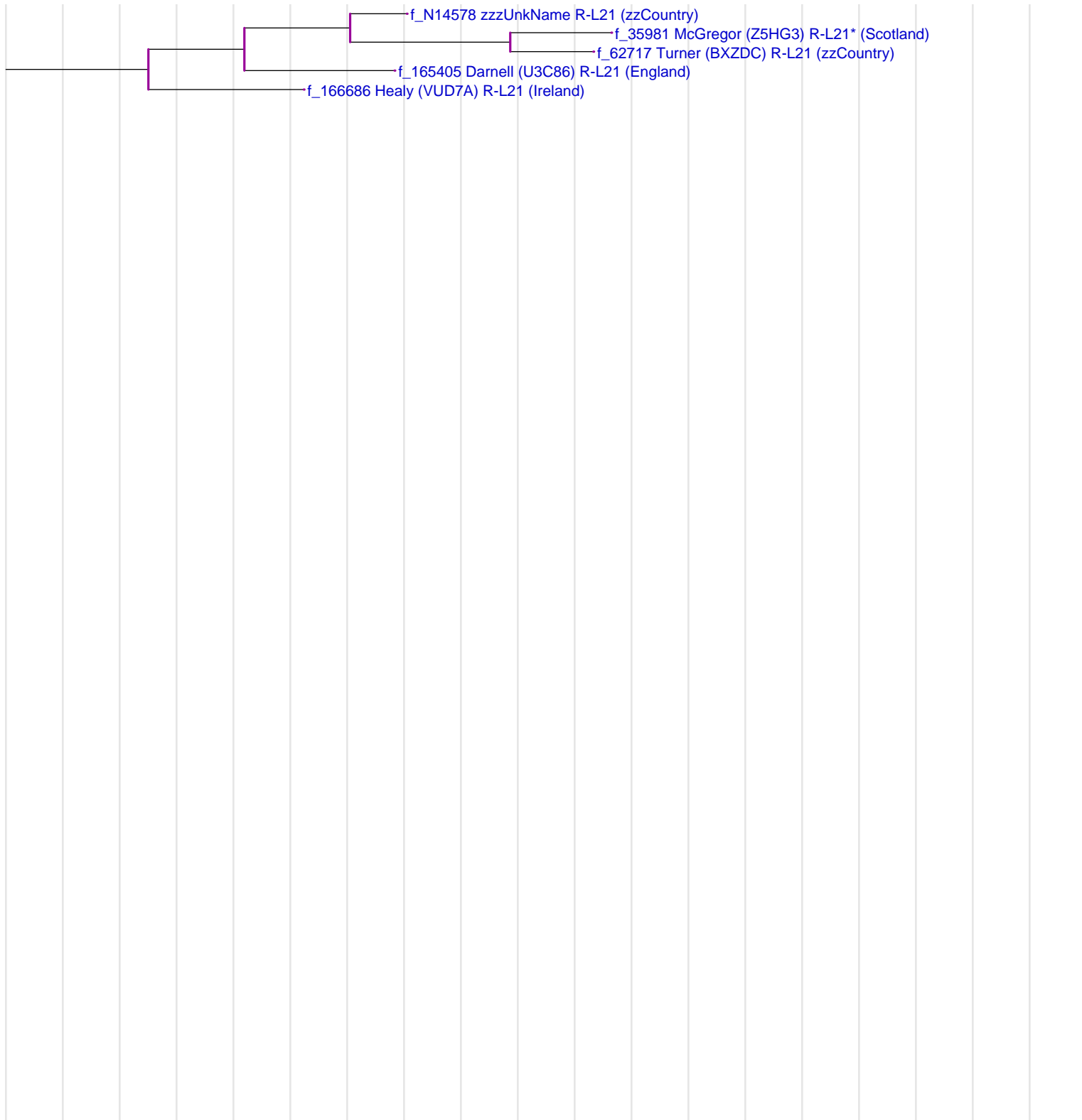
This is the marker distribution for Mike's Variety 1223 (extended version). The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	28	8.36%	43.61±5.02	1090.31±166.214

Note: Mike's variety does not include Healy or Darnell.



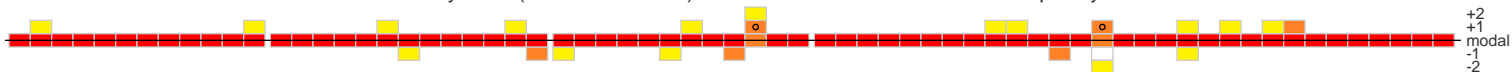
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1116 (extended version)

This is the modal haplotype for Mike's Variety 1116 (extended version). The coloration is with respect to the modal haplotype of the full tree.

393	390	19	301	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	572	640	492	565	
13	23	14	11	11	12	12	11	13	13	16	16	9	10	11	11	24	15	19	28	15	16	17	18	11	11	19	23	15	15	17	17	38	38	12	12	11	9	15	16	8	10	10	8	10	10	12	22	23	16	16	10	12	12	14	8	12	22	20	12	12	11	13	11	11	12	12

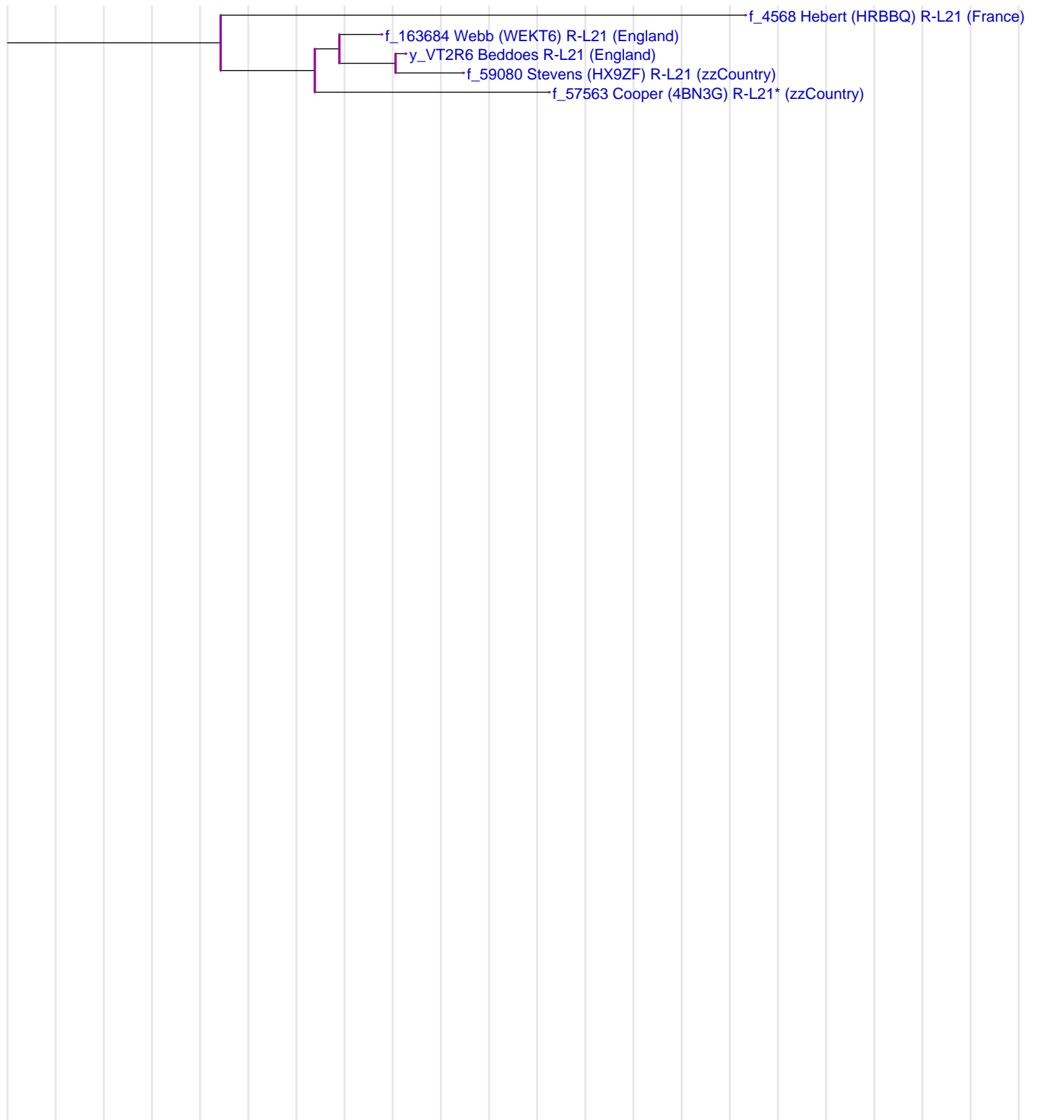
This is the marker distribution for Mike's Variety 1116 (extended version). The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	30	8.96%	46.87±5.40	1171.84±178.714

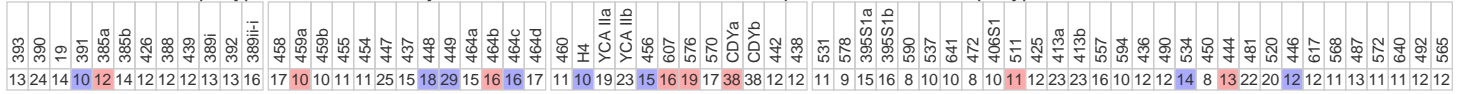
Note: Mike's variety does not include Hebert.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1810-W2

This is the modal haplotype for Mike's Variety 1810-W2. The coloration is with respect to the modal haplotype of the full tree.

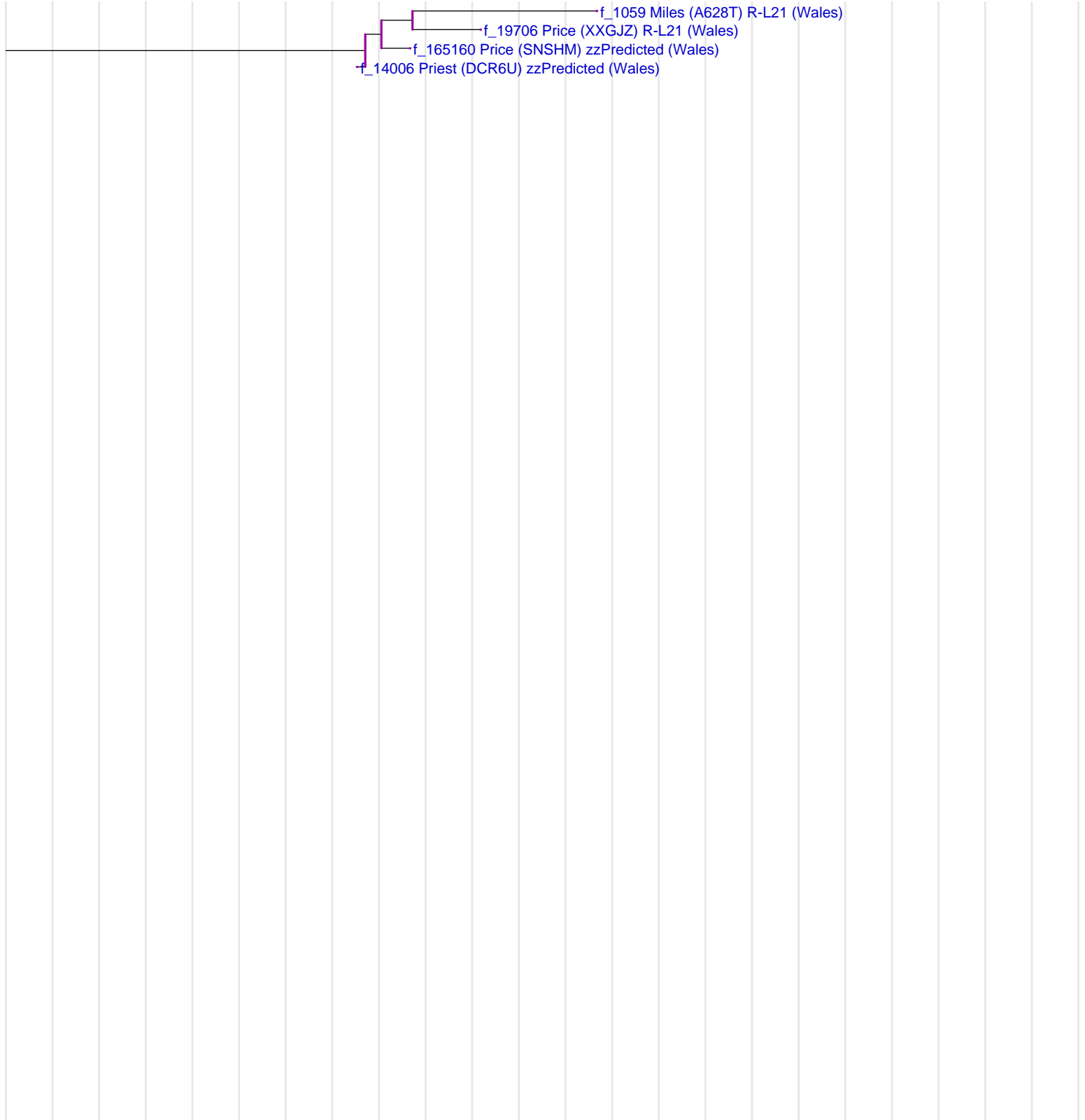


This is the marker distribution for Mike's Variety 1810-W2. The color indicates the relative frequency of the alleles.



Age Analysis

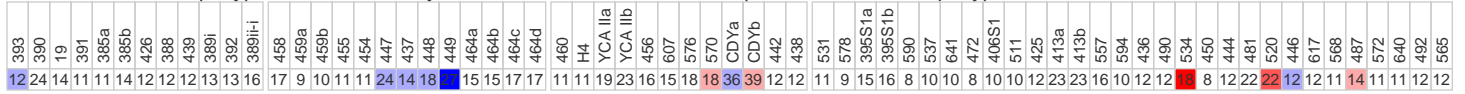
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	10	3.73%	19.01±2.24	475.284±73.4339



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1214

This is the modal haplotype for Mike's Variety 1214. The coloration is with respect to the modal haplotype of the full tree.

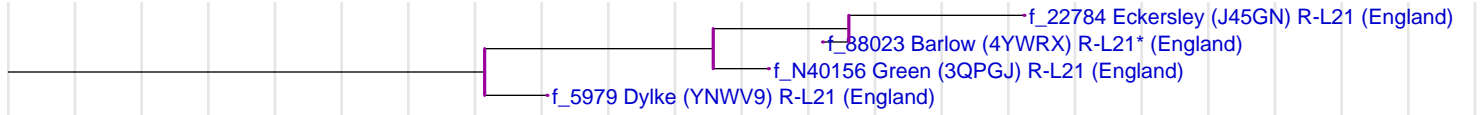


This is the marker distribution for Mike's Variety 1214. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	15	5.60%	28.79±3.40	719.764±111.373



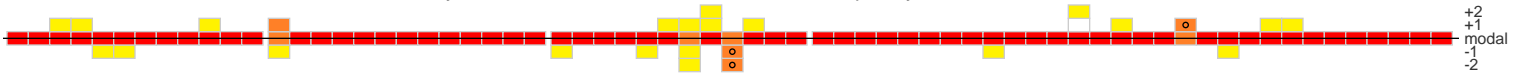
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1413

This is the modal haplotype for Mike's Variety 1413. The coloration is with respect to the modal haplotype of the full tree.

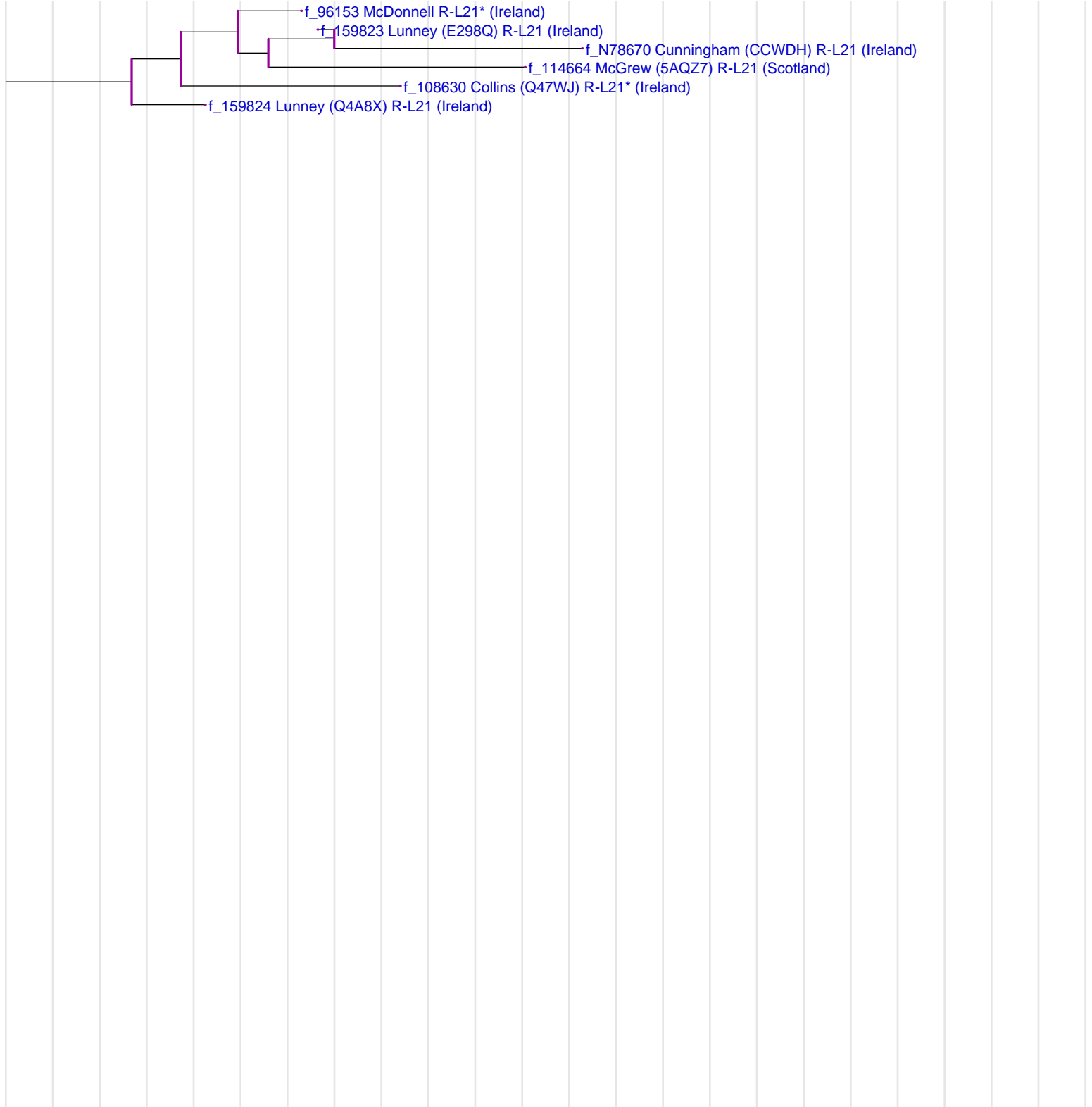
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	10	11	15	12	12	13	13	14	16	18	9	10	11	11	25	15	19	30	15	15	17	17	11	11	19	23	16	15	19	17	37	37	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	17	10	12	12	15	8	12	22	21	13	13	11	13	11	11	12	12	12

This is the marker distribution for Mike's Variety 1413. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	35	8.71%	45.51±5.13	1137.81±171.462



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1014

This is the modal haplotype for Mike's Variety 1014. The coloration is with respect to the modal haplotype of the full tree.

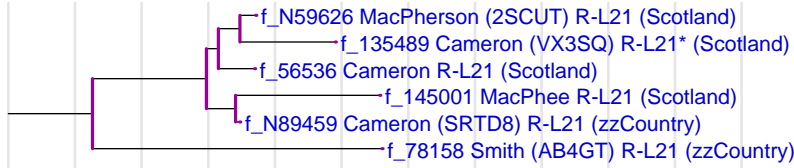
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565		
13	24	14	10	11	14	12	12	12	14	13	16	17	9	10	11	11	26	15	19	29	15	15	15	16	16	11	11	19	23	17	15	18	17	35	40	12	12	11	9	15	16	8	10	10	8	10	10	12	24	24	16	10	10	12	12	15	8	13	22	20	13	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 1014. The color indicates the relative frequency of the alleles.



Age Analysis

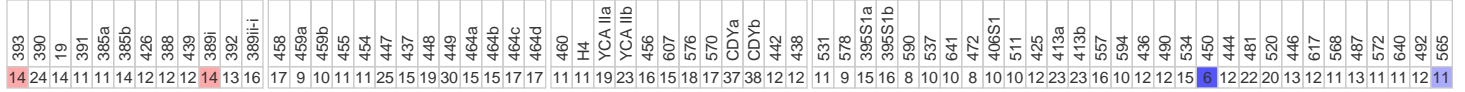
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	16	3.98%	20.30±2.28	507.613±76.2899



The vertical grey lines are separated 10 generations apart.

Mike's Variety 14611

This is the modal haplotype for Mike's Variety 14611. The coloration is with respect to the modal haplotype of the full tree.

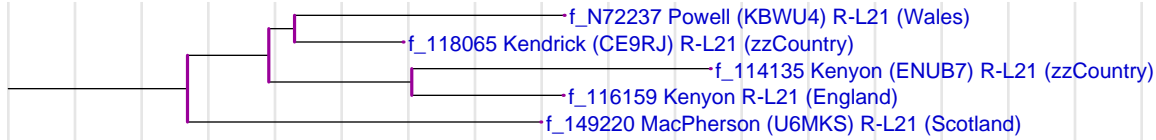


This is the marker distribution for Mike's Variety 14611. The color indicates the relative frequency of the alleles.



Age Analysis

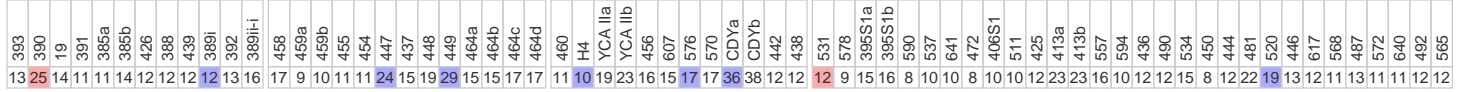
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	32	9.55%	50.15±5.78	1253.87±191.301



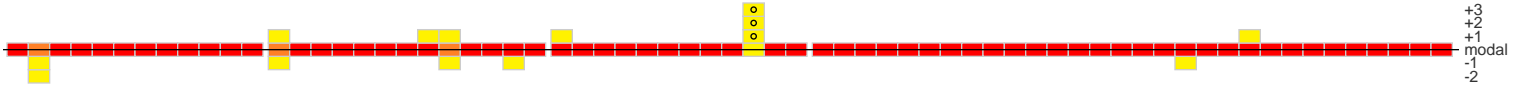
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1212

This is the modal haplotype for Mike's Variety 1212. The coloration is with respect to the modal haplotype of the full tree.

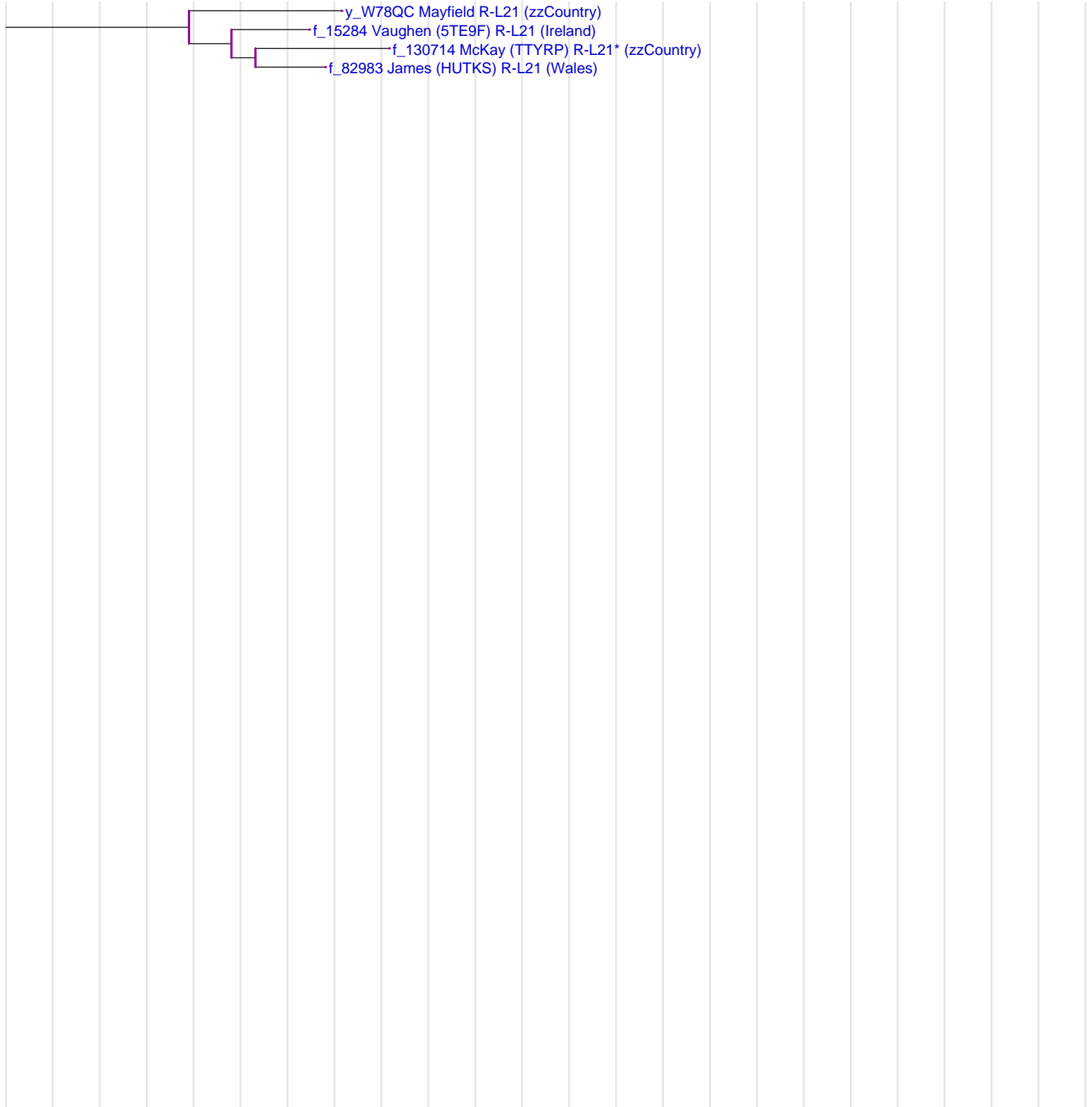


This is the marker distribution for Mike's Variety 1212. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	18	6.72%	34.75±4.11	868.714±134.542



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1430

This is the modal haplotype for Mike's Variety 1430. The coloration is with respect to the modal haplotype of the full tree.

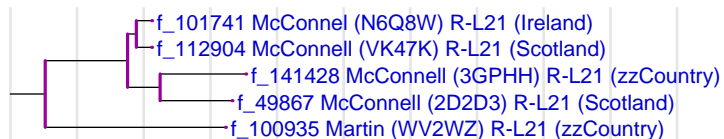
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	14	12	12	12	14	13	16	17	9	10	11	11	25	15	19	30	15	15	17	17	11	10	19	23	16	15	18	17	39	41	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	17	10	12	12	15	15	8	12	22	20	14	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 1430. The color indicates the relative frequency of the alleles.



Age Analysis

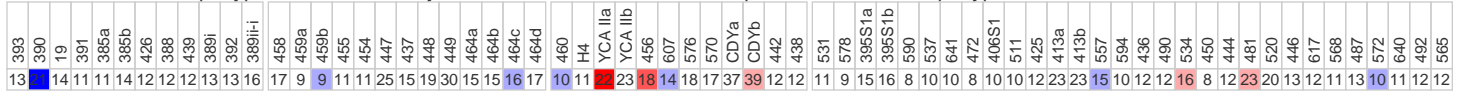
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	11	3.28%	16.69±1.91	417.298±63.4017



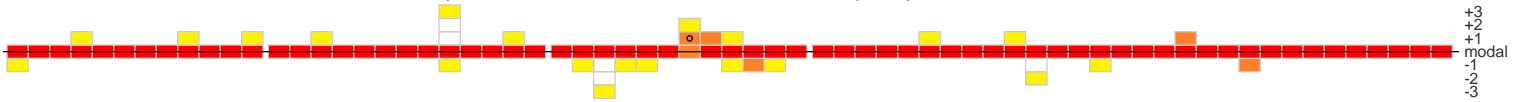
The vertical grey lines are separated 10 generations apart.

Mike's Variety 2110

This is the modal haplotype for Mike's Variety 2110. The coloration is with respect to the modal haplotype of the full tree.



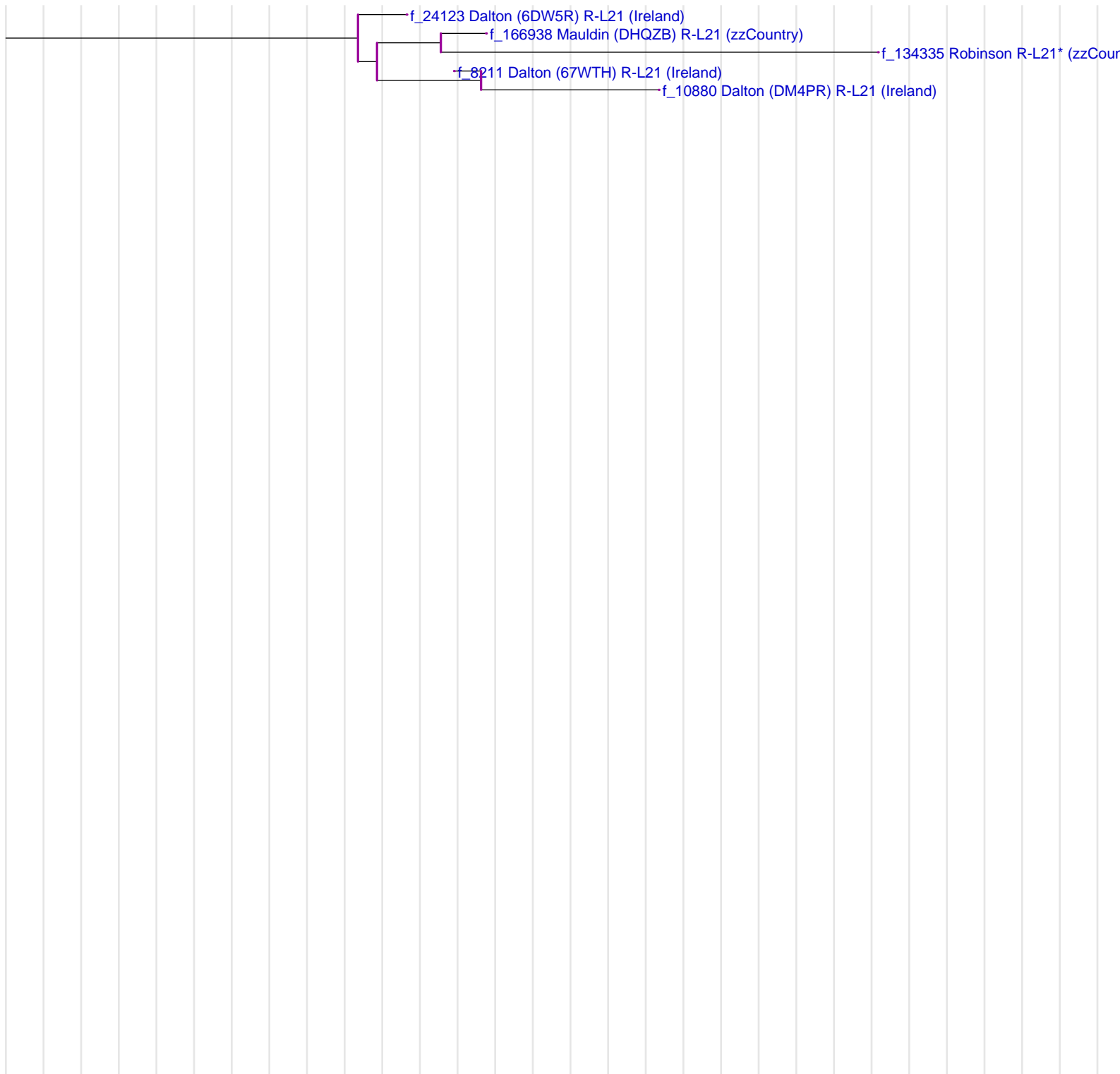
This is the marker distribution for Mike's Variety 2110. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	33	9.85%	51.80±5.97	1295.08±197.627

Note: Robinson (134335) is not a very good fit to this group.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1426

This is the modal haplotype for Mike's Variety 1426. The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	14	12	12	12	13	14	16	16	17	9	10	11	11	26	16	19	29	15	15	17	17	11	11	19	23	15	15	20	17	35	37	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	14	8	12	21	20	13	12	10	11	11	12	12	

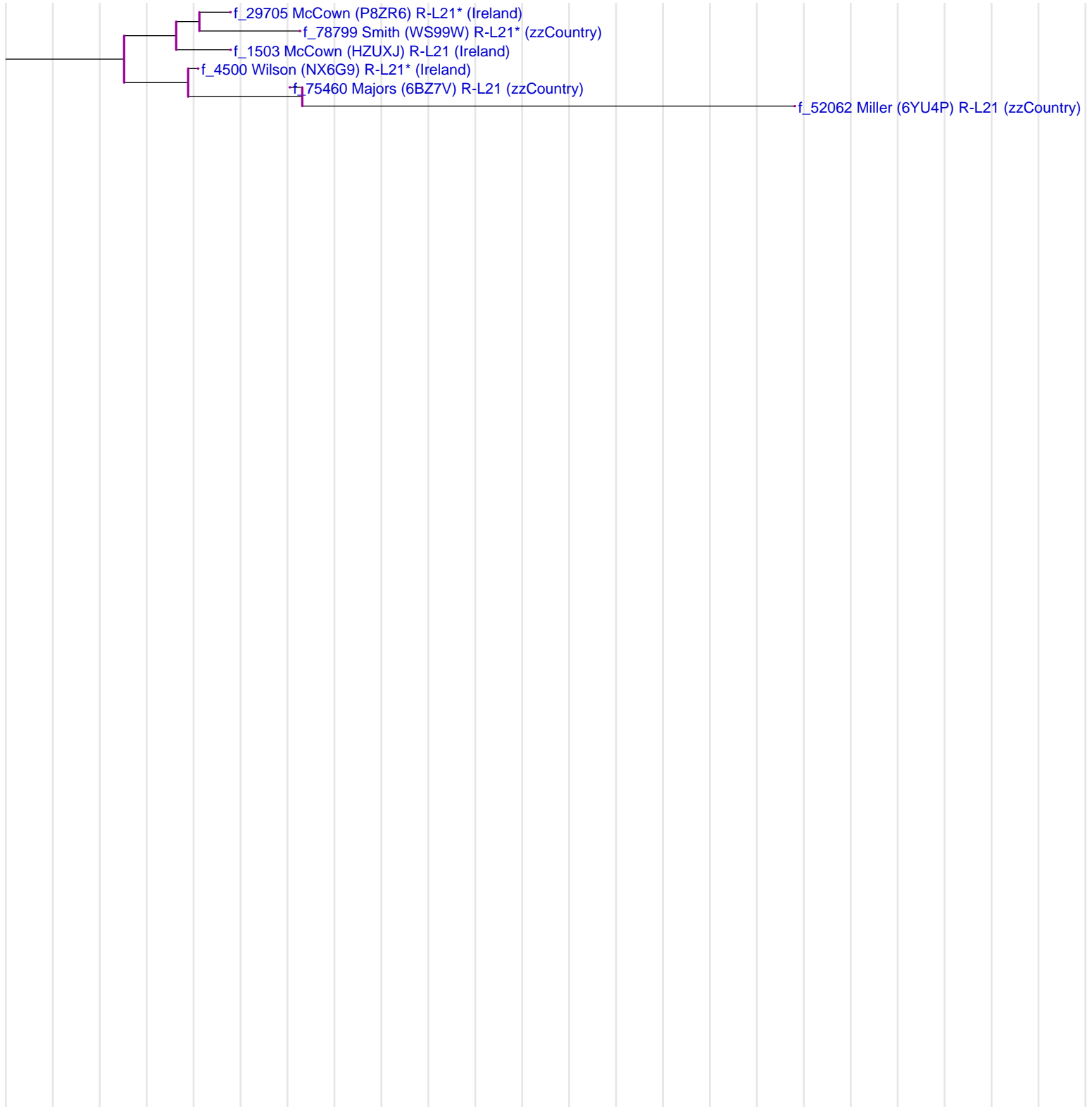
This is the marker distribution for Mike's Variety 1426. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	32	7.96%	41.45±4.67	1036.25±156.09

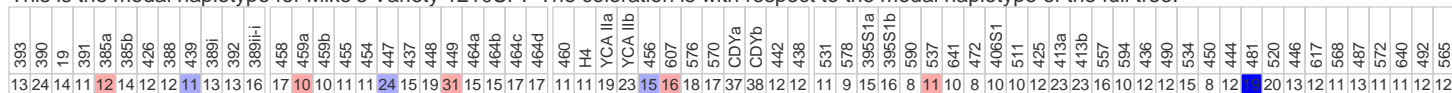
Note: Miller's haplotype is a little odd, but it does share the same slow moving off-modal markers as the others.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1210SP

This is the modal haplotype for Mike's Variety 1210SP. The coloration is with respect to the modal haplotype of the full tree.

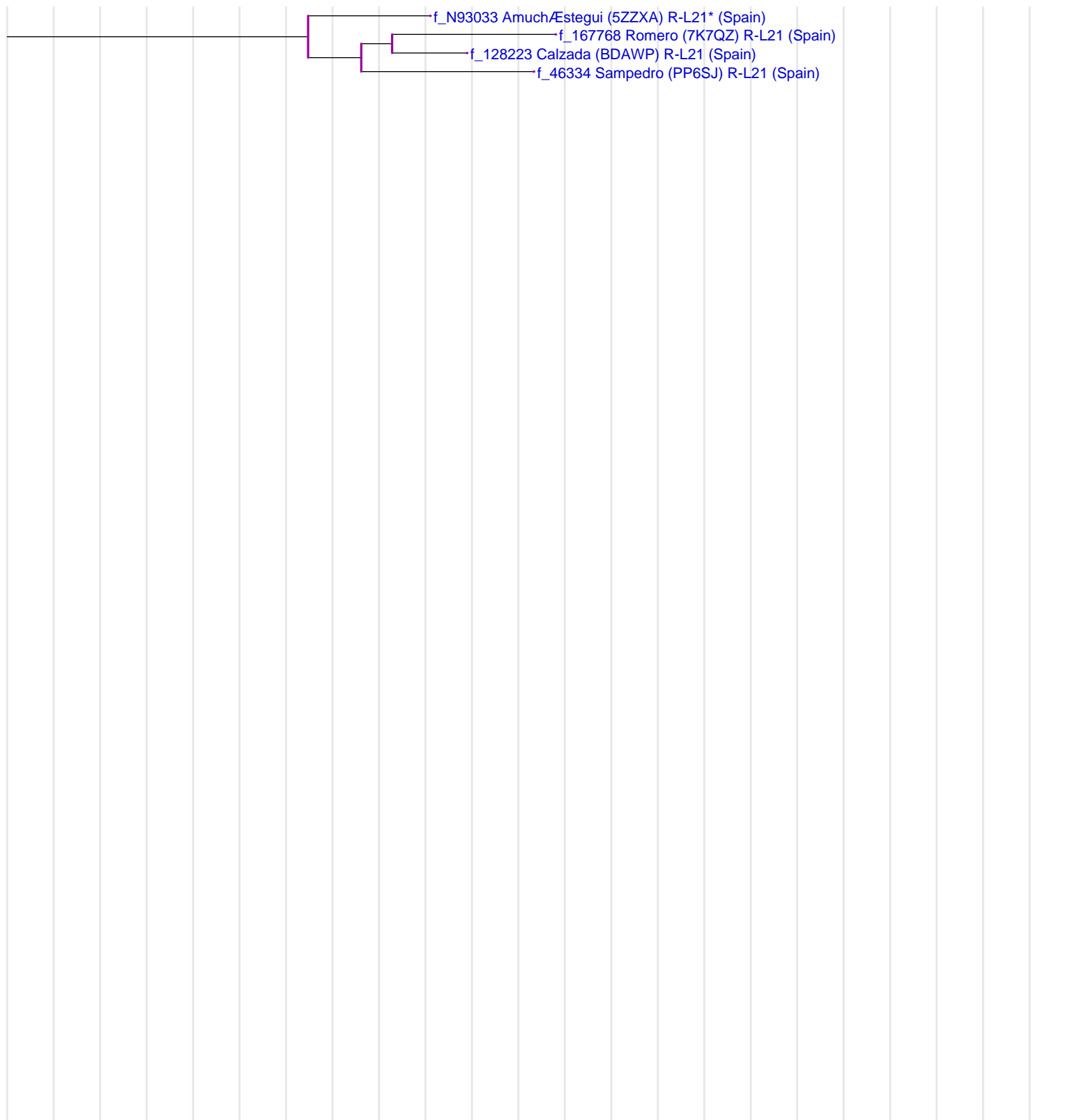


This is the marker distribution for Mike's Variety 1210SP. The color indicates the relative frequency of the alleles.



Age Analysis

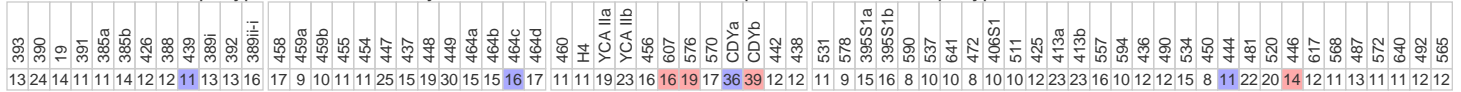
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	19	7.09%	36.75±4.35	918.748±142.334



The vertical grey lines are separated 10 generations apart.

Mike's Variety 3016

This is the modal haplotype for Mike's Variety 3016. The coloration is with respect to the modal haplotype of the full tree.



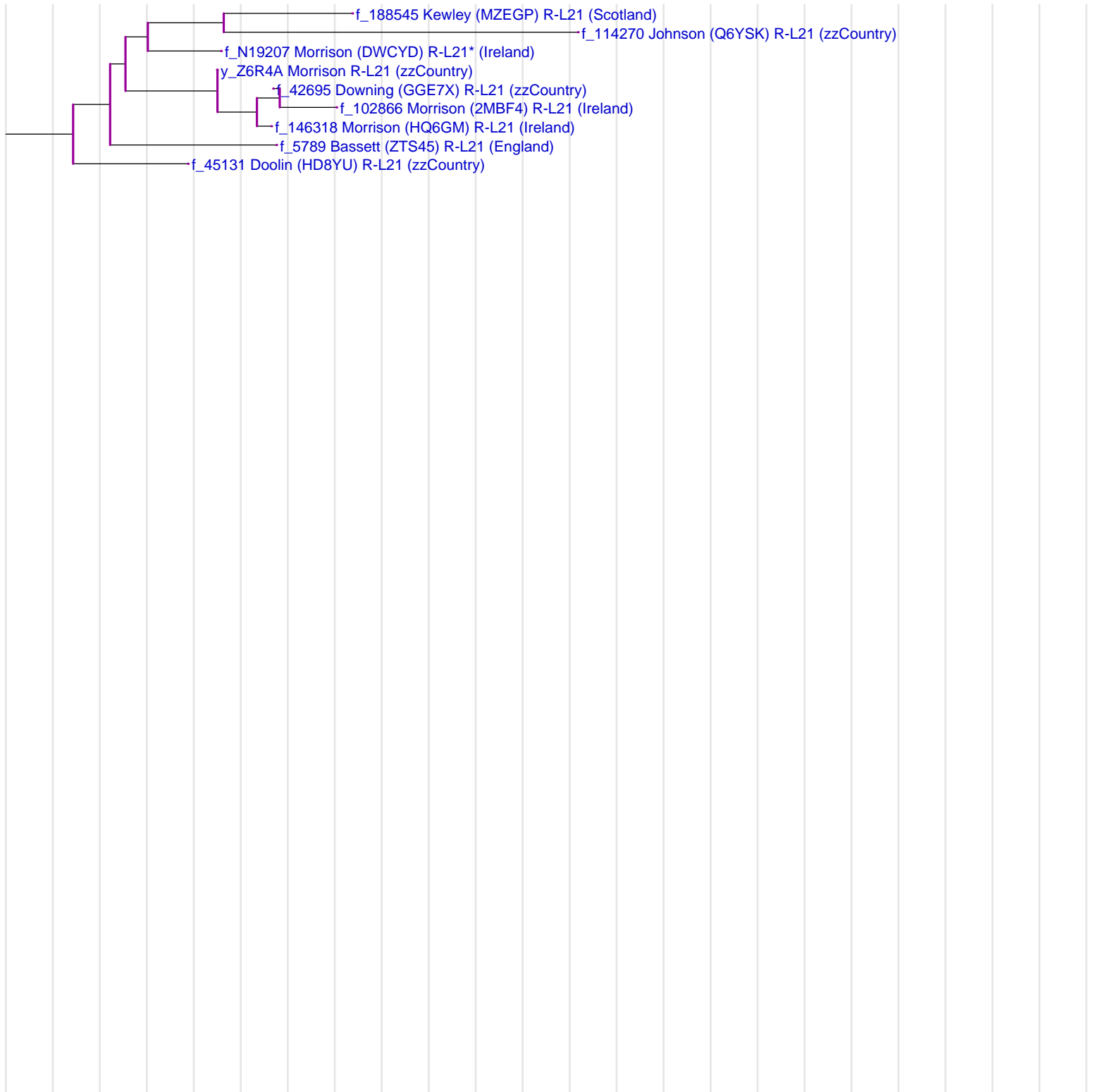
This is the marker distribution for Mike's Variety 3016. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
9	603	46	7.63%	39.65±4.31	991.36±146.33

Note: This is approximately Mike's variety 3016. Moore, just outside the group is also 3016.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 11169-B

This is the modal haplotype for Mike's Variety 11169-B. The coloration is with respect to the modal haplotype of the full tree.

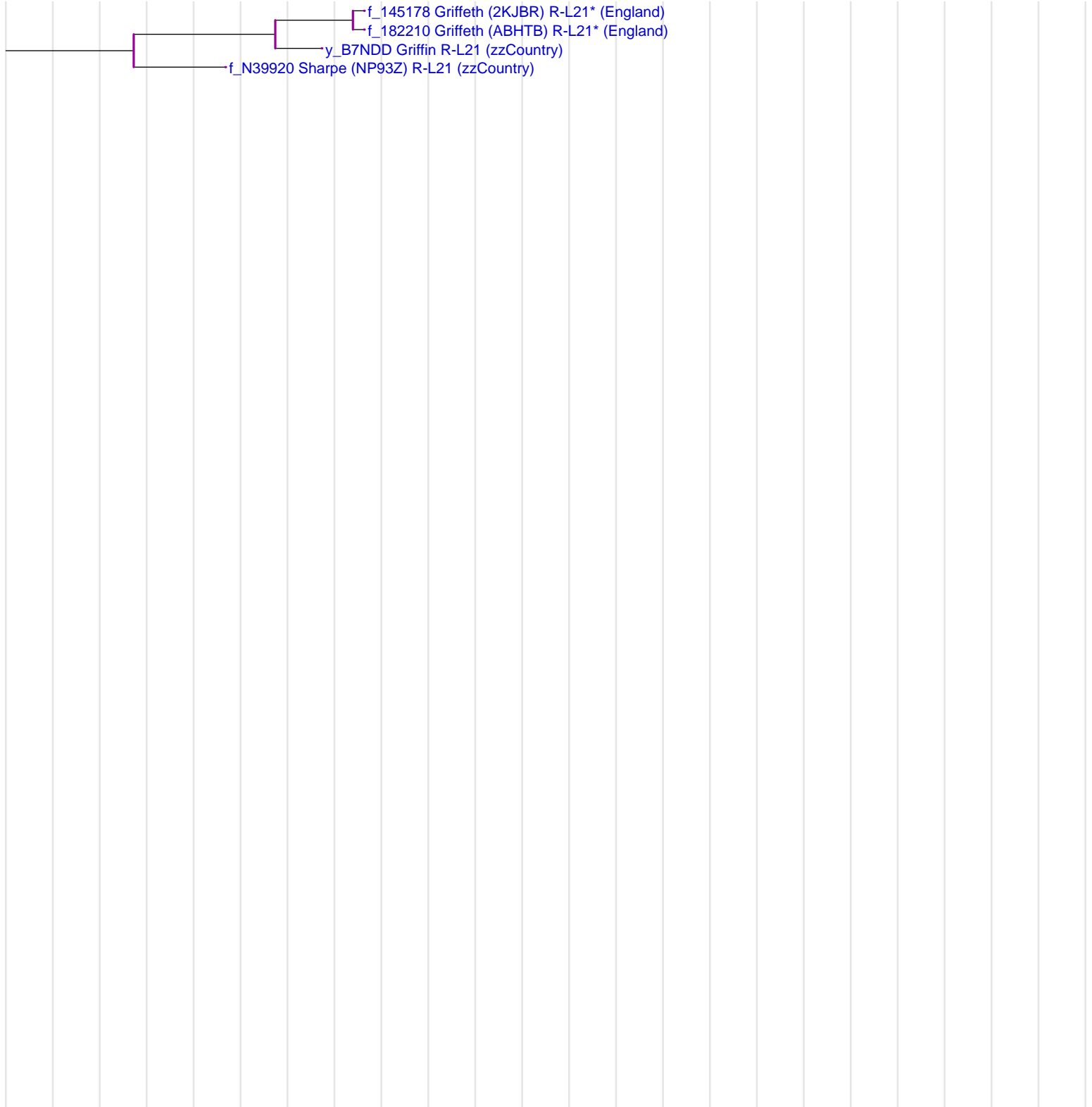
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	11	11	14	12	12	12	13	13	16	15	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	17	15	15	19	37	38	11	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	10	12	12	16	9	12	22	20	13	12	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 11169-B. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	13	4.85%	24.86±2.93	621.412±96.0972



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1422

This is the modal haplotype for Mike's Variety 1422. The coloration is with respect to the modal haplotype of the full tree.

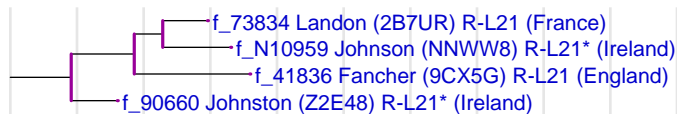
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	11	14	12	12	12	14	13	16	16	9	10	11	11	24	15	19	31	14	15	16	17	11	11	19	22	16	15	19	17	36	38	13	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	12	24	20	13	12	11	13	11	11	12	12		

This is the marker distribution for Mike's Variety 1422. The color indicates the relative frequency of the alleles.



Age Analysis

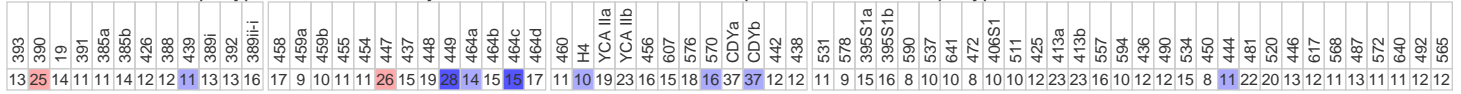
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	8	2.99%	15.15±1.78	378.787±58.4899



The vertical grey lines are separated 10 generations apart.

Mike's Variety 2510

This is the modal haplotype for Mike's Variety 2510. The coloration is with respect to the modal haplotype of the full tree.

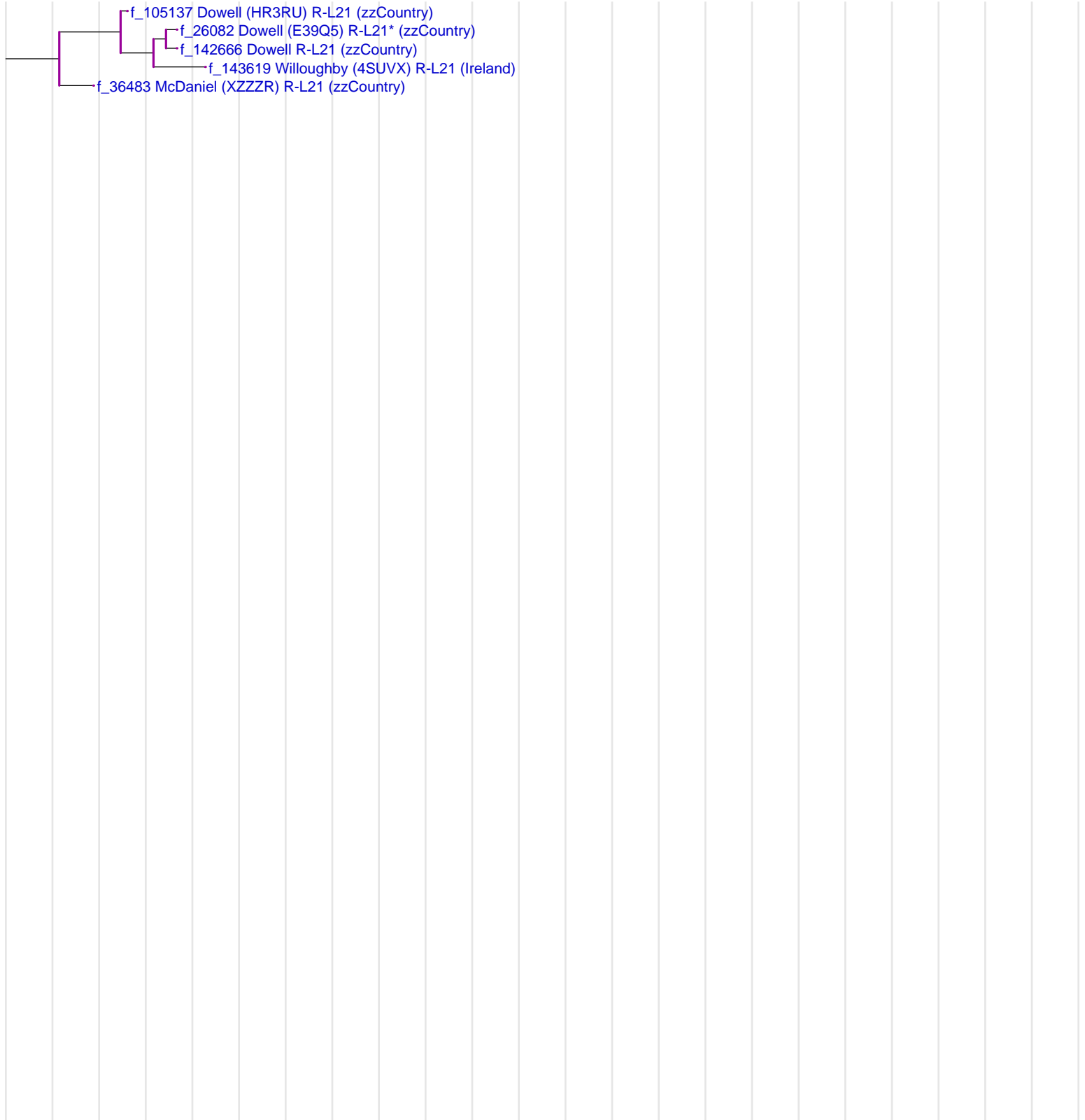


This is the marker distribution for Mike's Variety 2510. The color indicates the relative frequency of the alleles.



Age Analysis

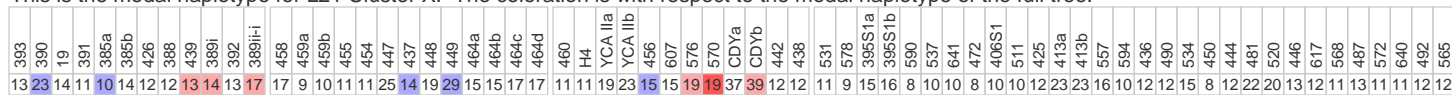
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	6	1.79%	9.04±1.03	225.904±34.2888



The vertical grey lines are separated 10 generations apart.

L21 Cluster X

This is the modal haplotype for L21 Cluster X. The coloration is with respect to the modal haplotype of the full tree.



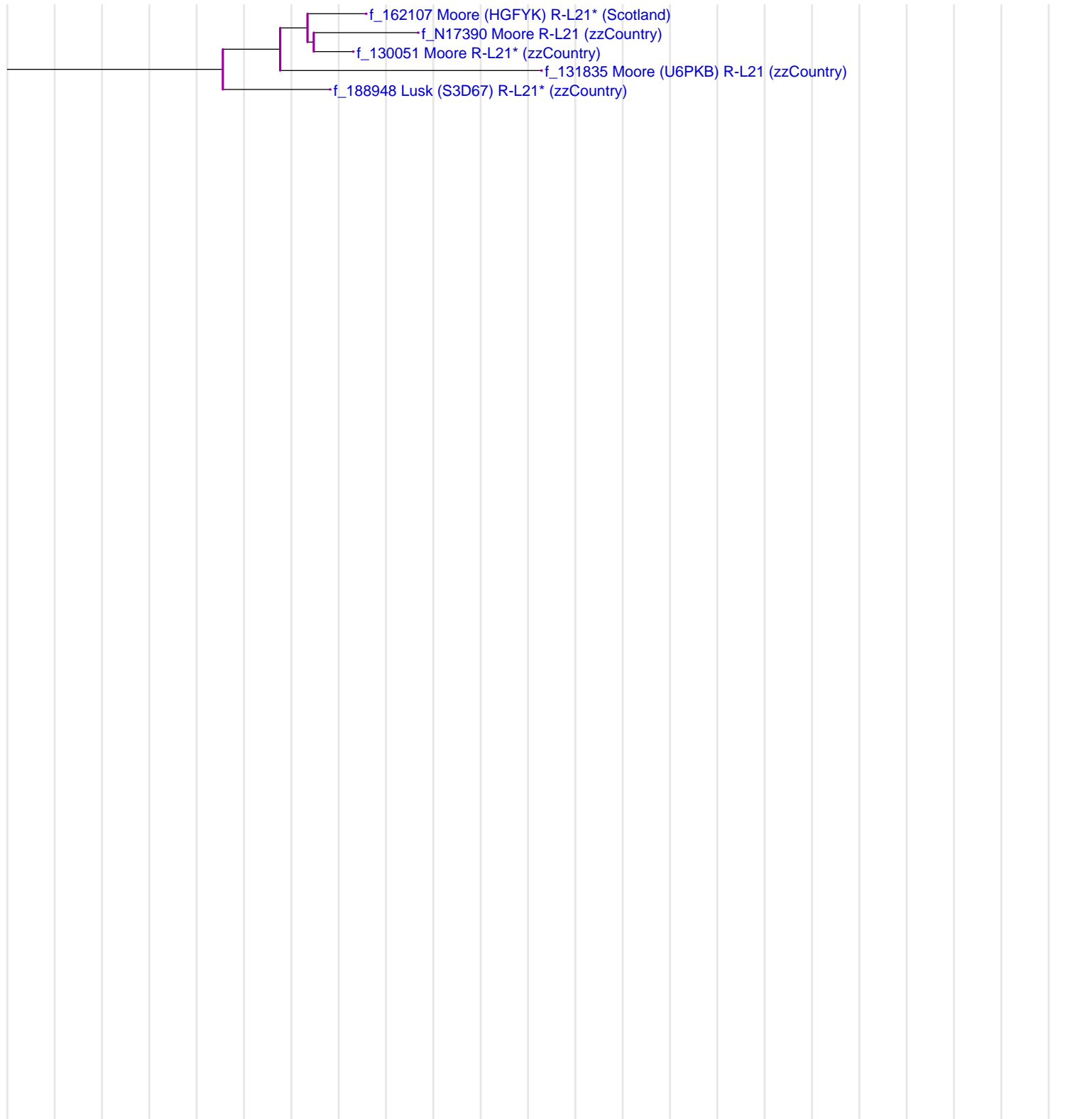
This is the marker distribution for L21 Cluster X. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	18	5.37%	27.61±3.17	690.179±105.006

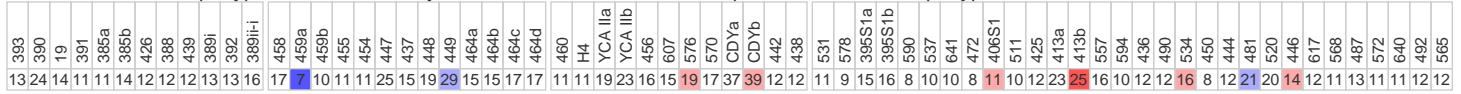
Note: This is John Walden's L21 Cluster X.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 711

This is the modal haplotype for Mike's Variety 711. The coloration is with respect to the modal haplotype of the full tree.



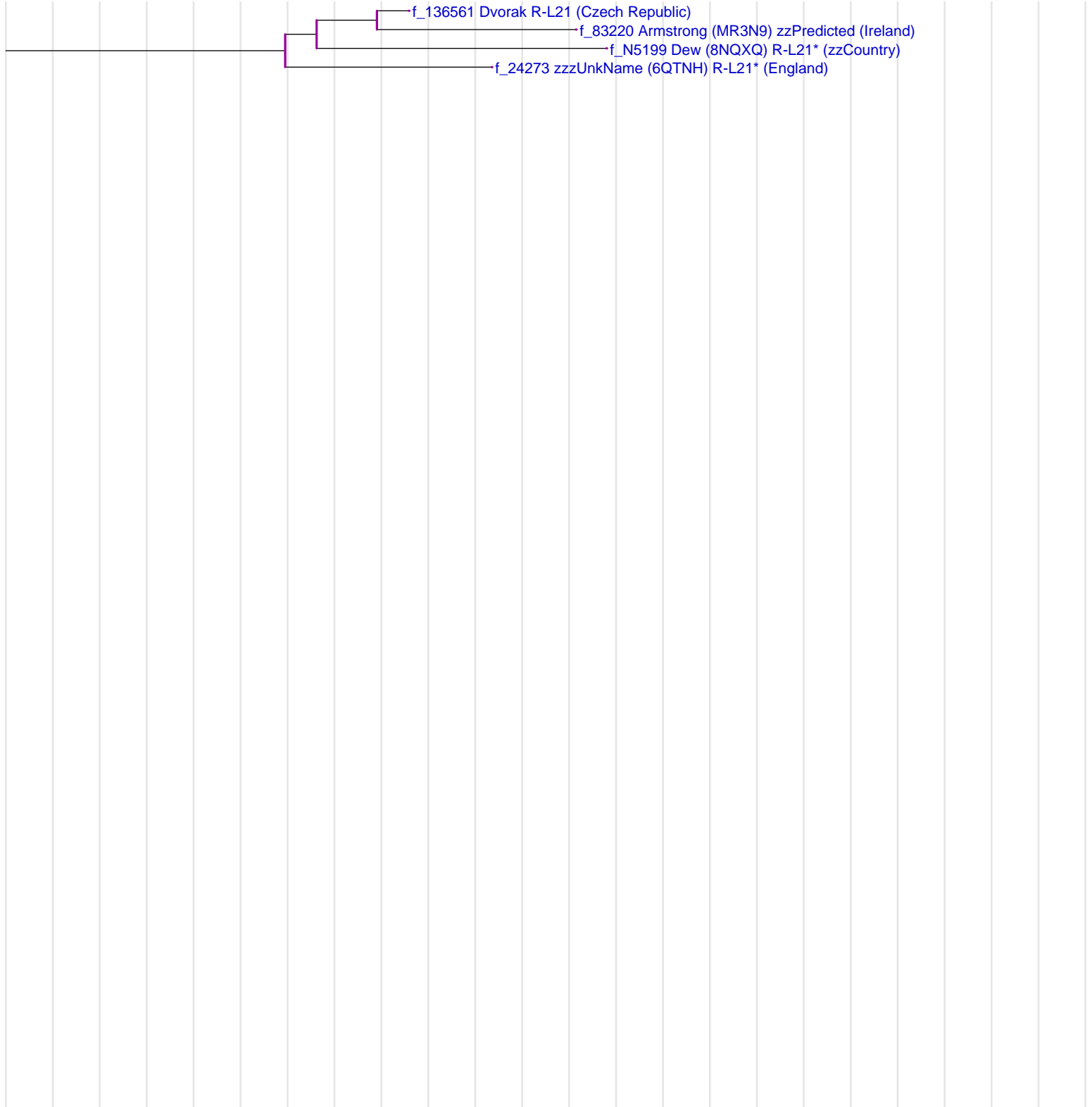
This is the marker distribution for Mike's Variety 711. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	21	7.84%	40.78±4.83	1019.4±158.021

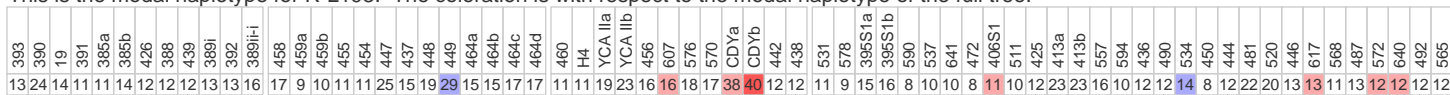
Note: This is Mike Walsh's variety 711, although Armstrong is in Mike's variety 1113-A.



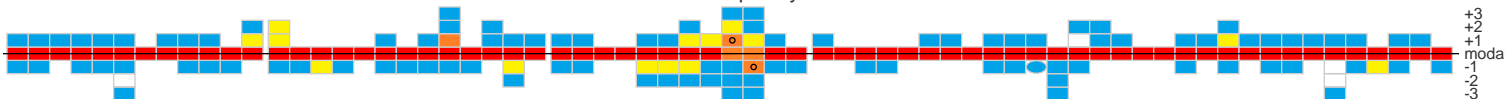
The vertical grey lines are separated 10 generations apart.

R-L193

This is the modal haplotype for R-L193. The coloration is with respect to the modal haplotype of the full tree.



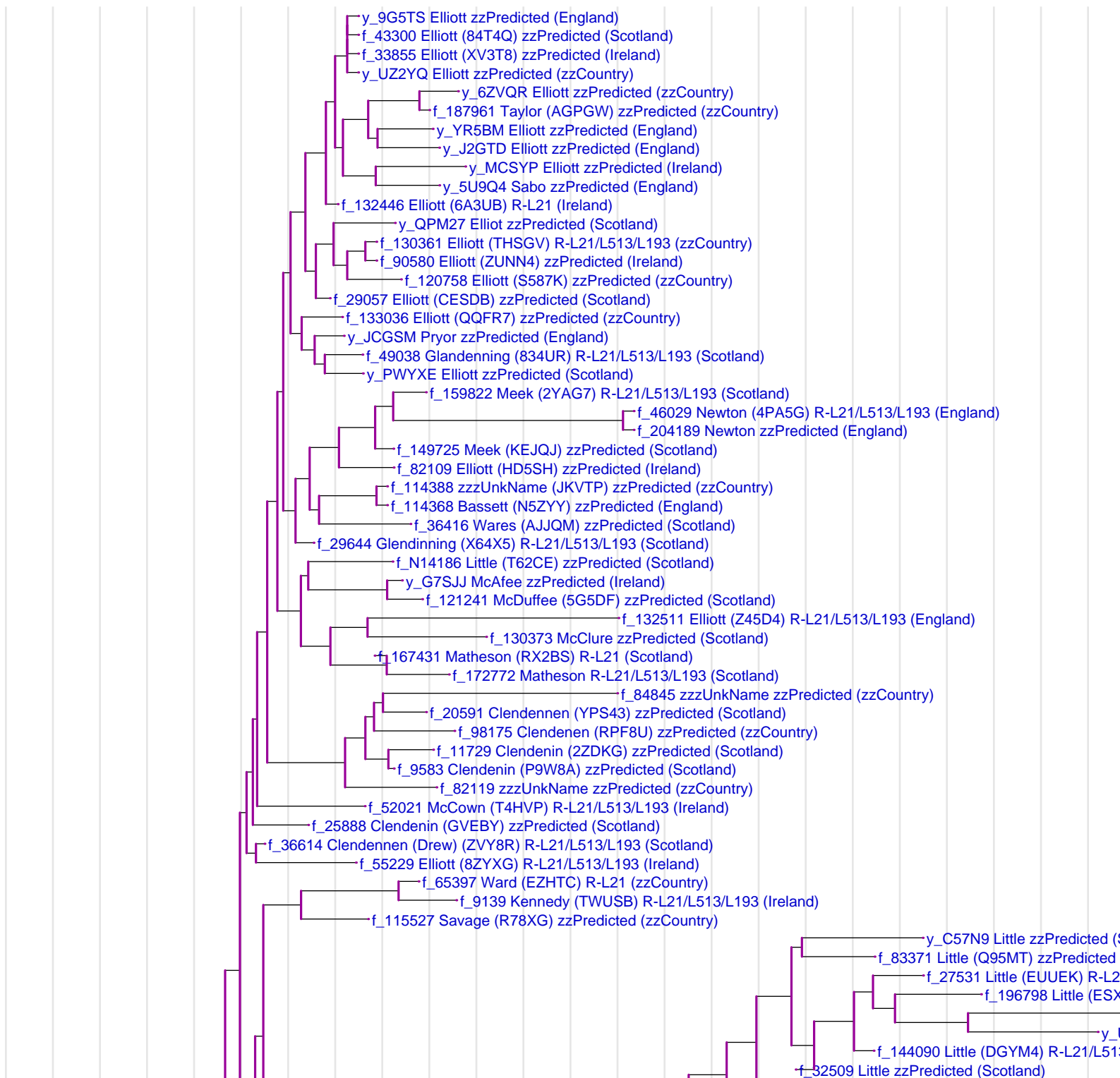
This is the marker distribution for R-L193. The color indicates the relative frequency of the alleles.



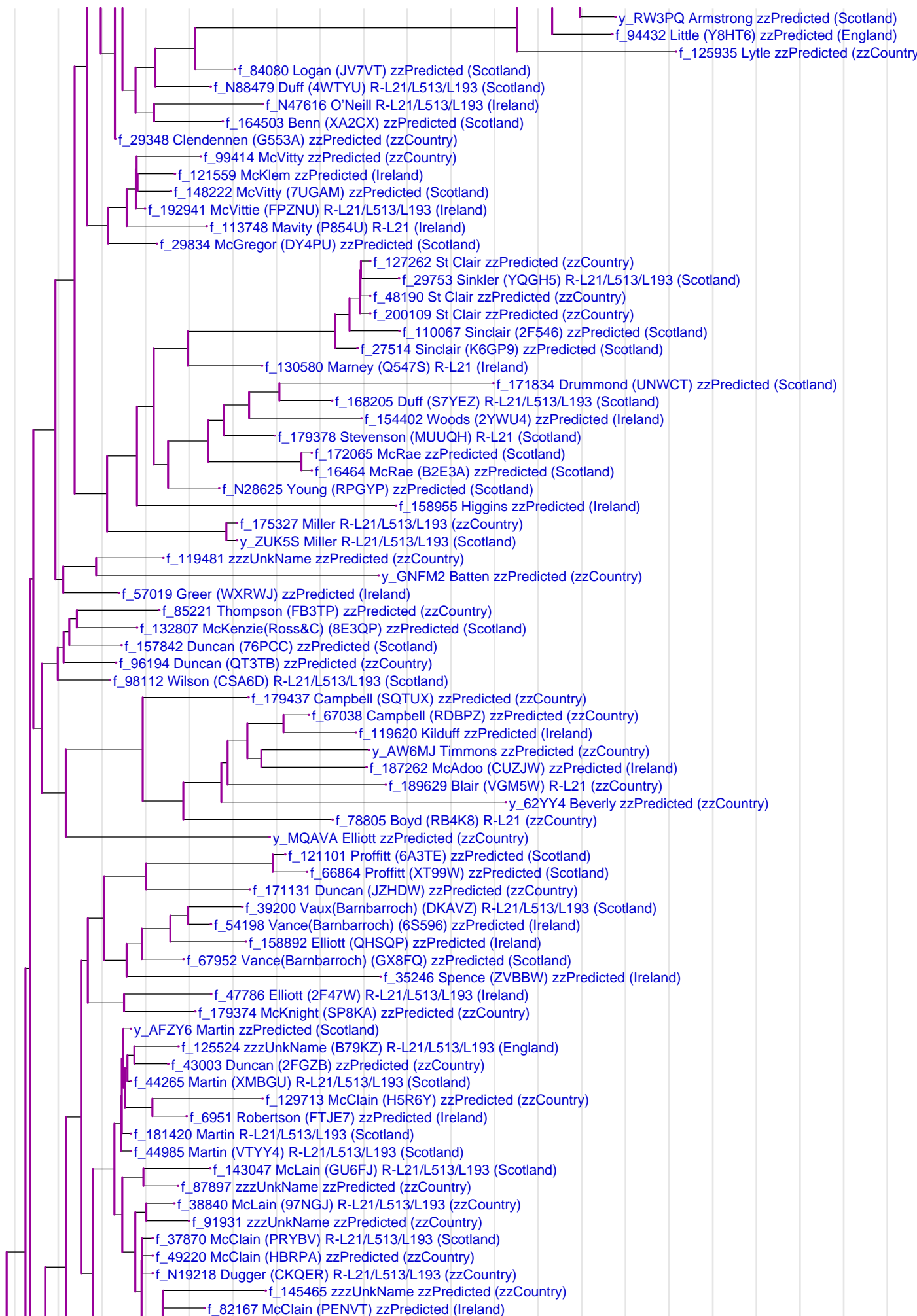
Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
183	12261	1194	9.74%	51.18±5.14	1279.53±181.358

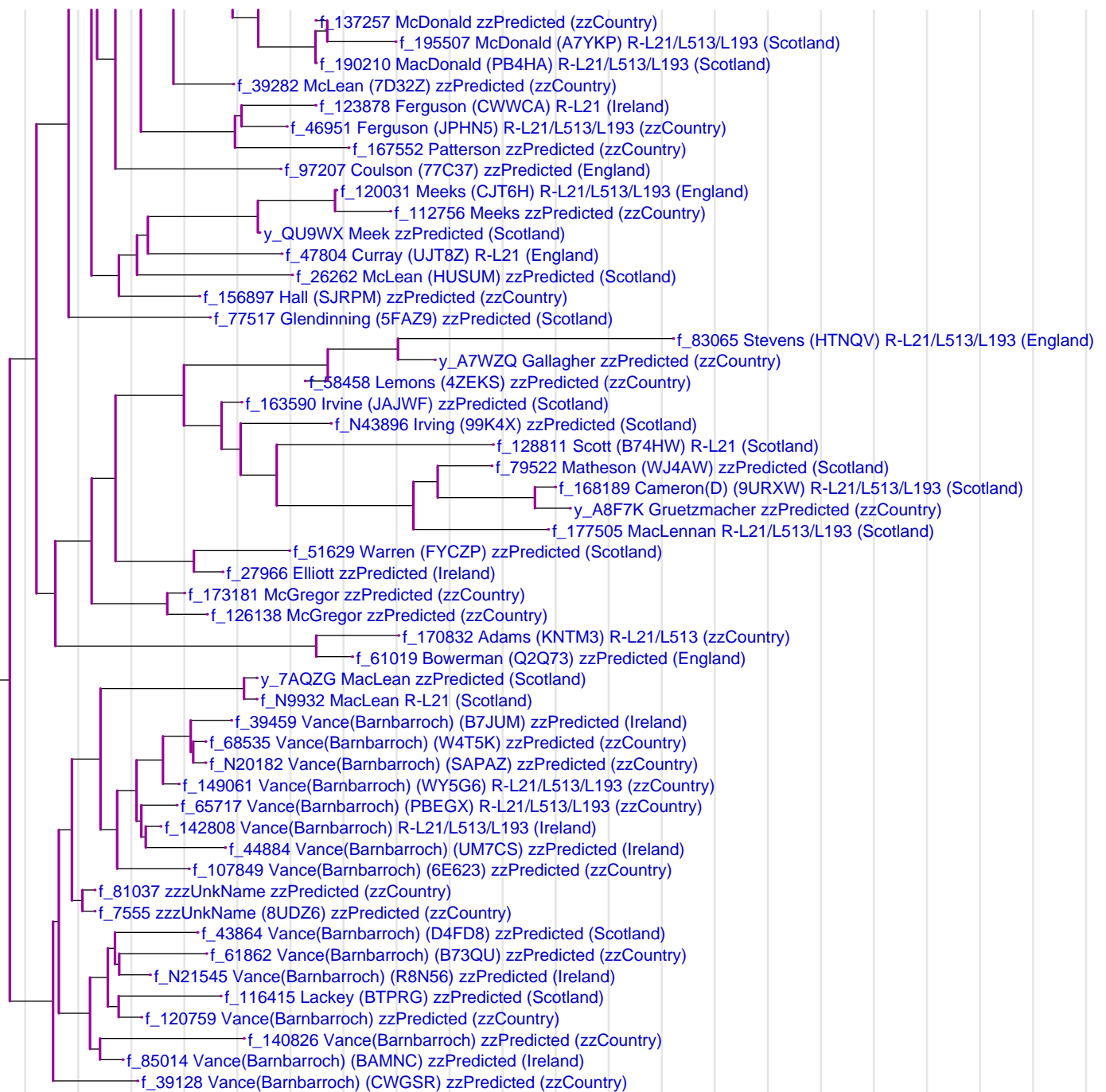
Note: Unlike everyone else in the cluster, MacLean (N9932) has DYS 572 = 11 and not 12.



The vertical grey lines are separated 10 generations apart.



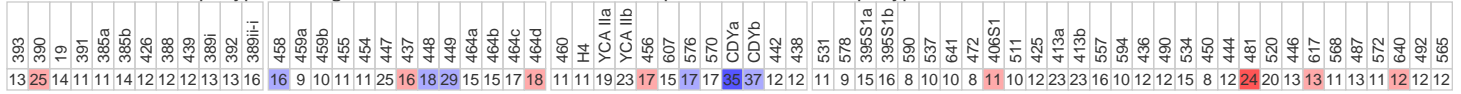
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

Airghialla 2

This is the modal haplotype for Airghialla 2. The coloration is with respect to the modal haplotype of the full tree.



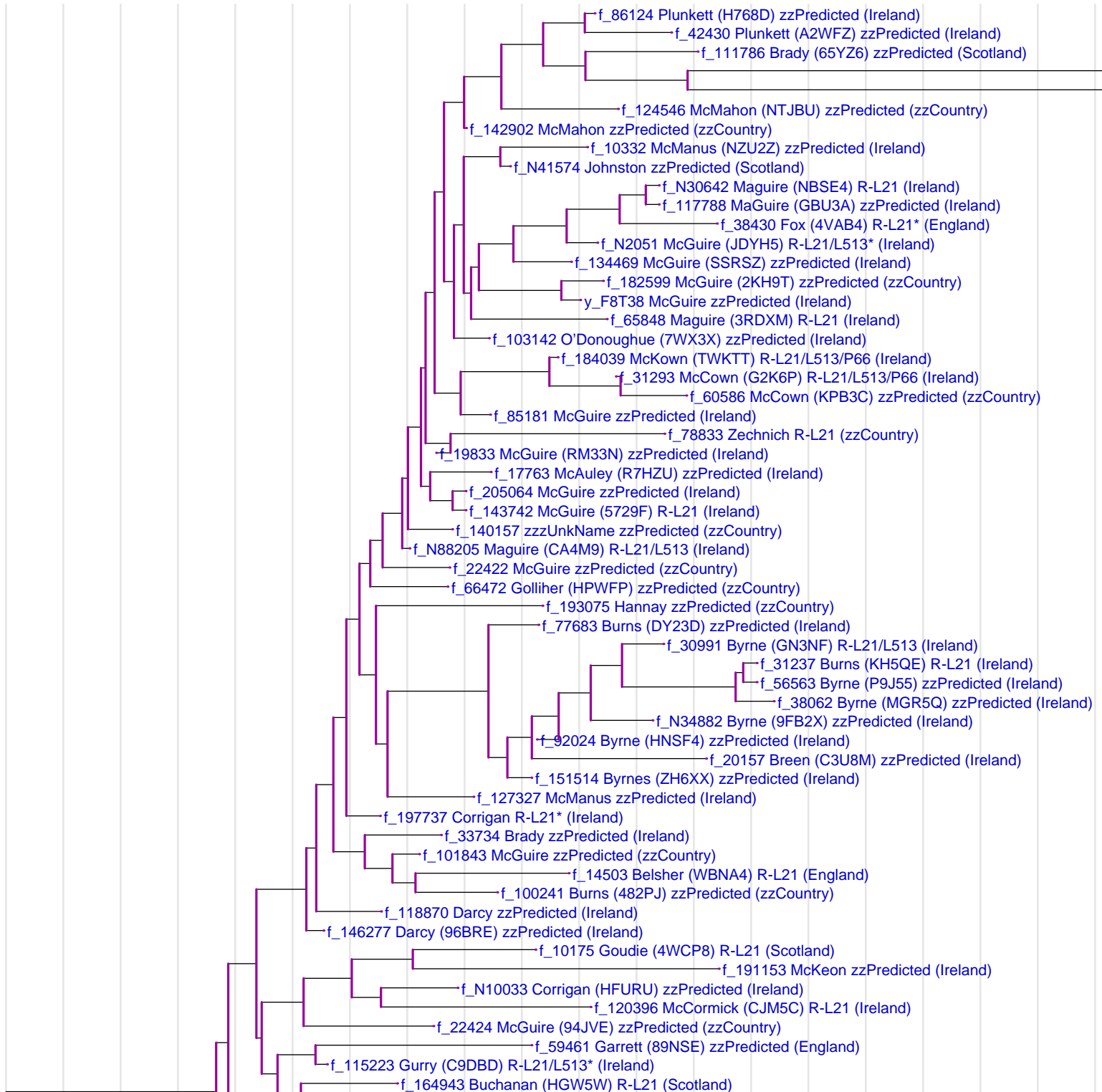
This is the marker distribution for Airghialla 2. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
60	4020	246	6.12%	31.56±3.20	789.061±112.325

Note: Mike has referred to the majority of these men as 1113-A-2-M, but several are also 1113-A-2-B, and 1113-A-2.

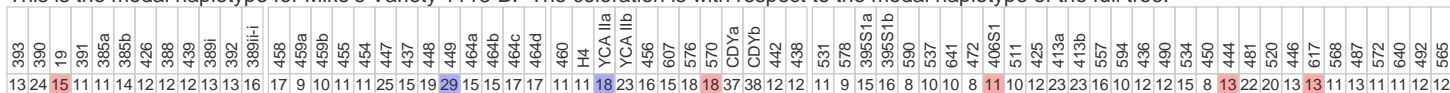


The vertical grey lines are separated 10 generations apart.

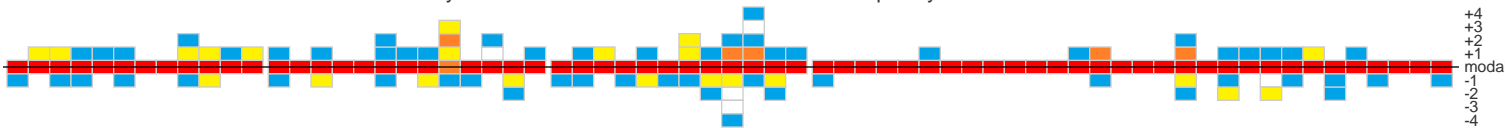
f_108324 zzzUnkName zzPredicted (zzCountry)
f_109682 Corrigan (PSUVS) zzPredicted (Ireland)
y_P5NZV McGuire zzPredicted (zzCountry)

Mike's Variety 1113-B

This is the modal haplotype for Mike's Variety 1113-B. The coloration is with respect to the modal haplotype of the full tree.



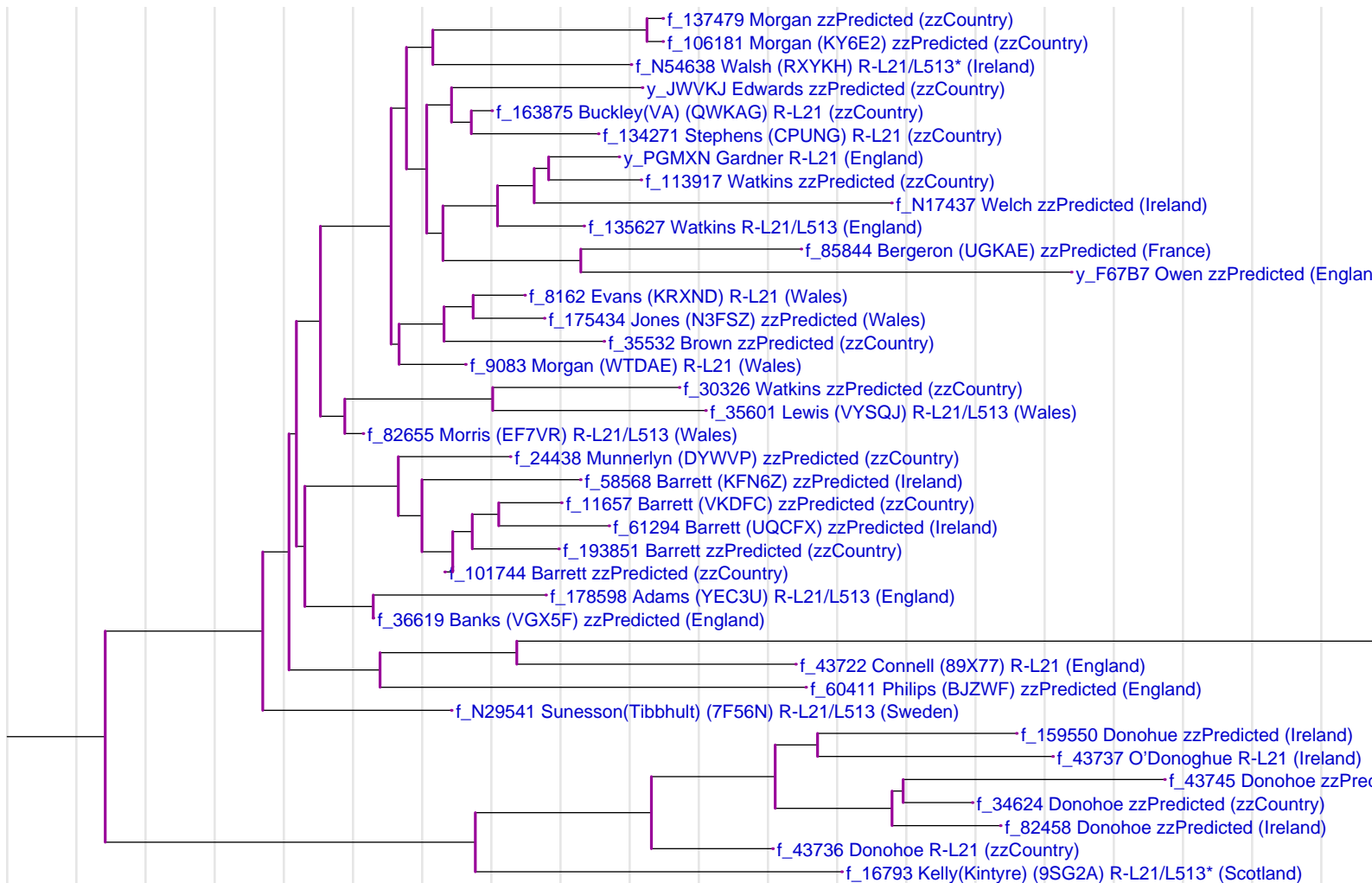
This is the marker distribution for Mike's Variety 1113-B. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
38	2546	319	12.53%	66.83±6.83	1670.71±238.88

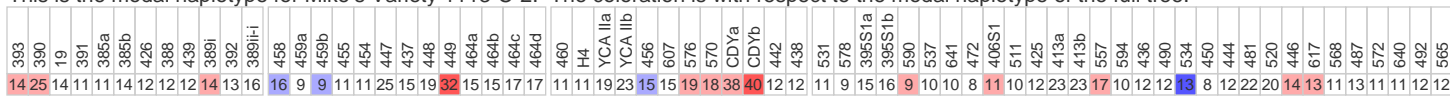
Note: Includes Mike's Varieties 1113-B-2 and 1113-B-2-W.



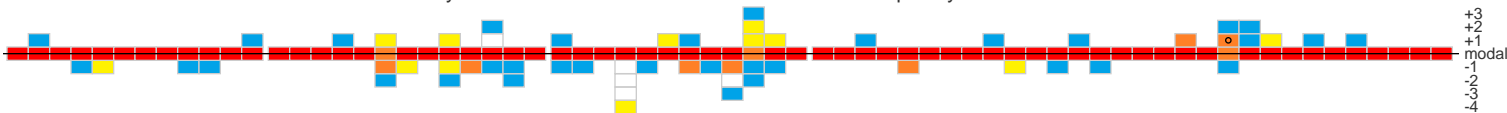
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-C-2

This is the modal haplotype for Mike's Variety 1113-C-2. The coloration is with respect to the modal haplotype of the full tree.



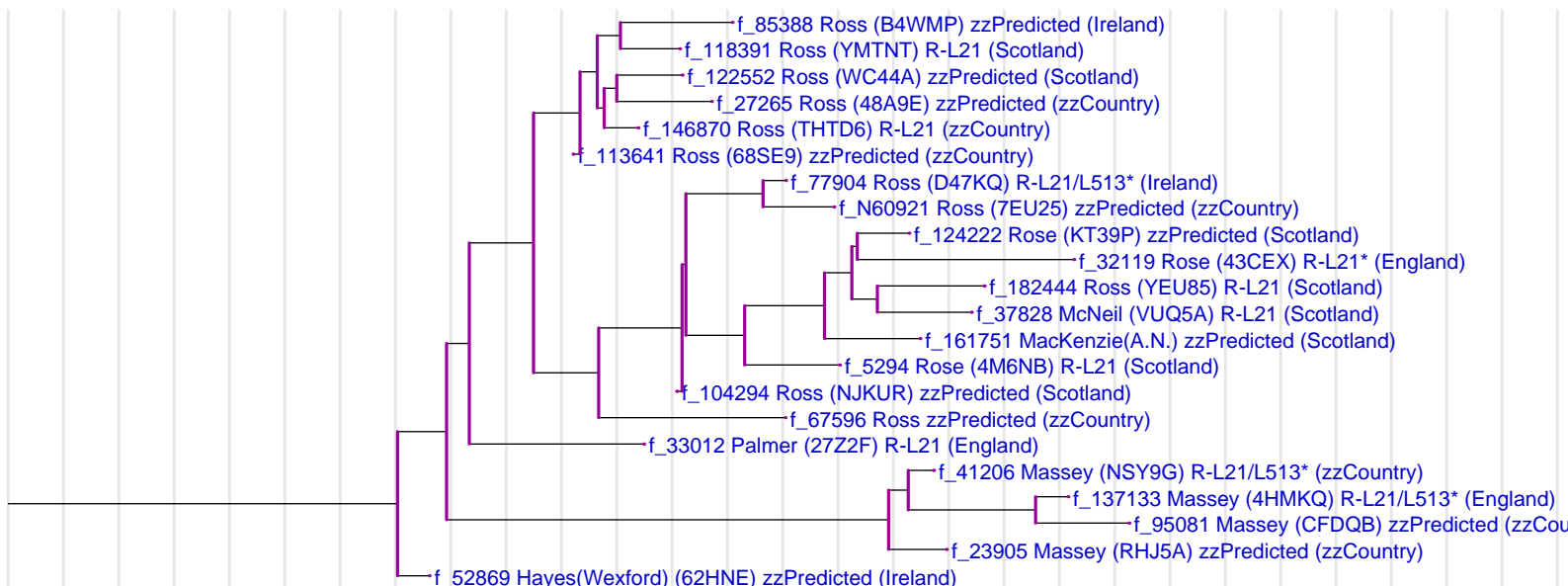
This is the marker distribution for Mike's Variety 1113-C-2. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
22	1474	158	10.72%	56.63±5.87	1415.69±203.944

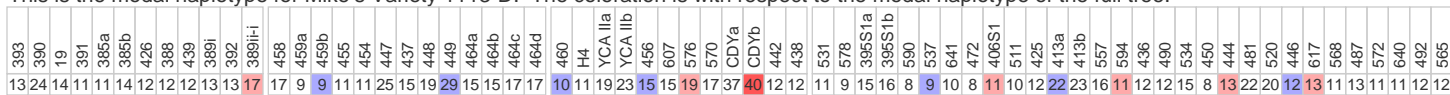
Note: The Masseys are 1113-C-2-M, the Roses (or Rosses) are 1113-C-2-R.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-D

This is the modal haplotype for Mike's Variety 1113-D. The coloration is with respect to the modal haplotype of the full tree.



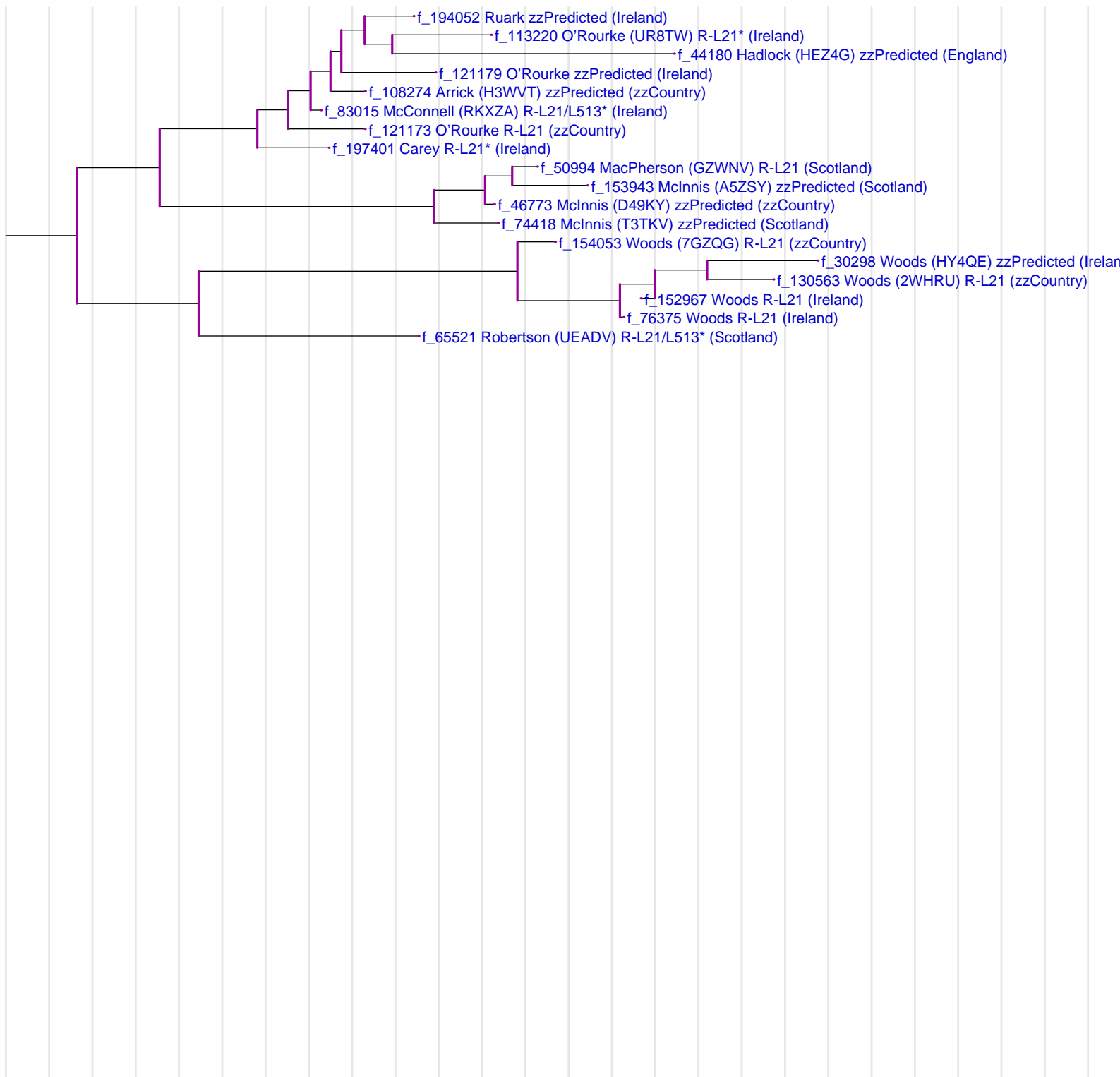
This is the marker distribution for Mike's Variety 1113-D. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
18	1206	184	15.26%	82.57±8.64	2064.3±298.864

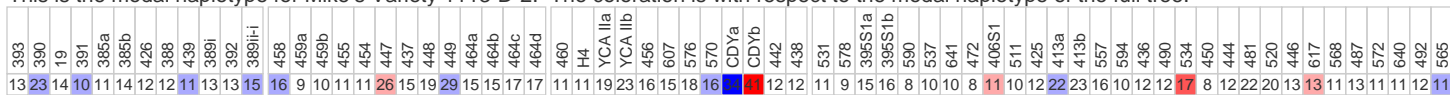
Note: Includes variety 1113-D-1, but looks as though other divisions are possible.



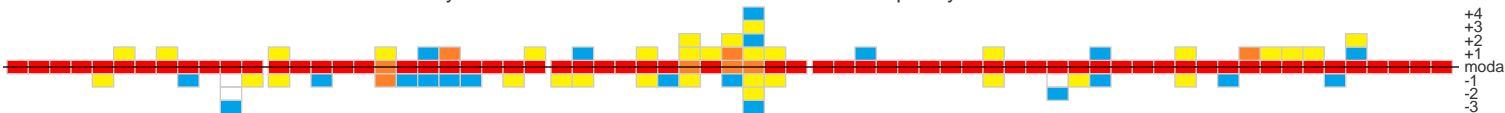
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-D-2

This is the modal haplotype for Mike's Variety 1113-D-2. The coloration is with respect to the modal haplotype of the full tree.



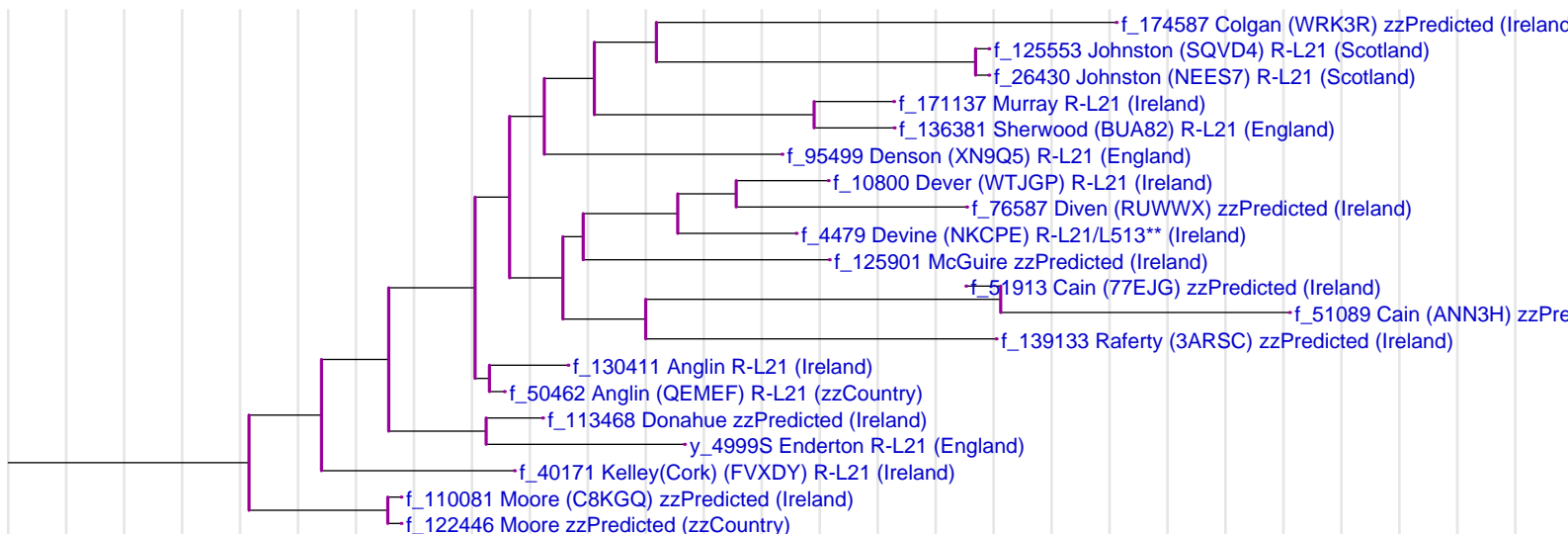
This is the marker distribution for Mike's Variety 1113-D-2. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
20	1340	175	13.06%	69.85±7.28	1746.33±252.144

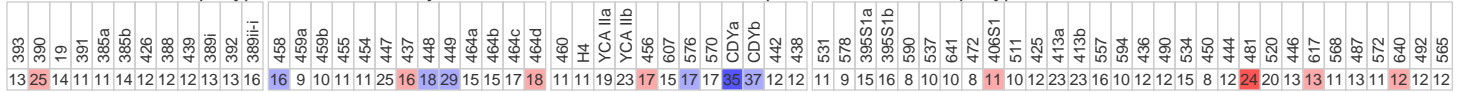
Note: Donahue (f113468), Enderton (y4999S) and Kelley (f40171) have DYS617=13, but not DYS406S1=11.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-E

This is the modal haplotype for Mike's Variety 1113-E. The coloration is with respect to the modal haplotype of the full tree.



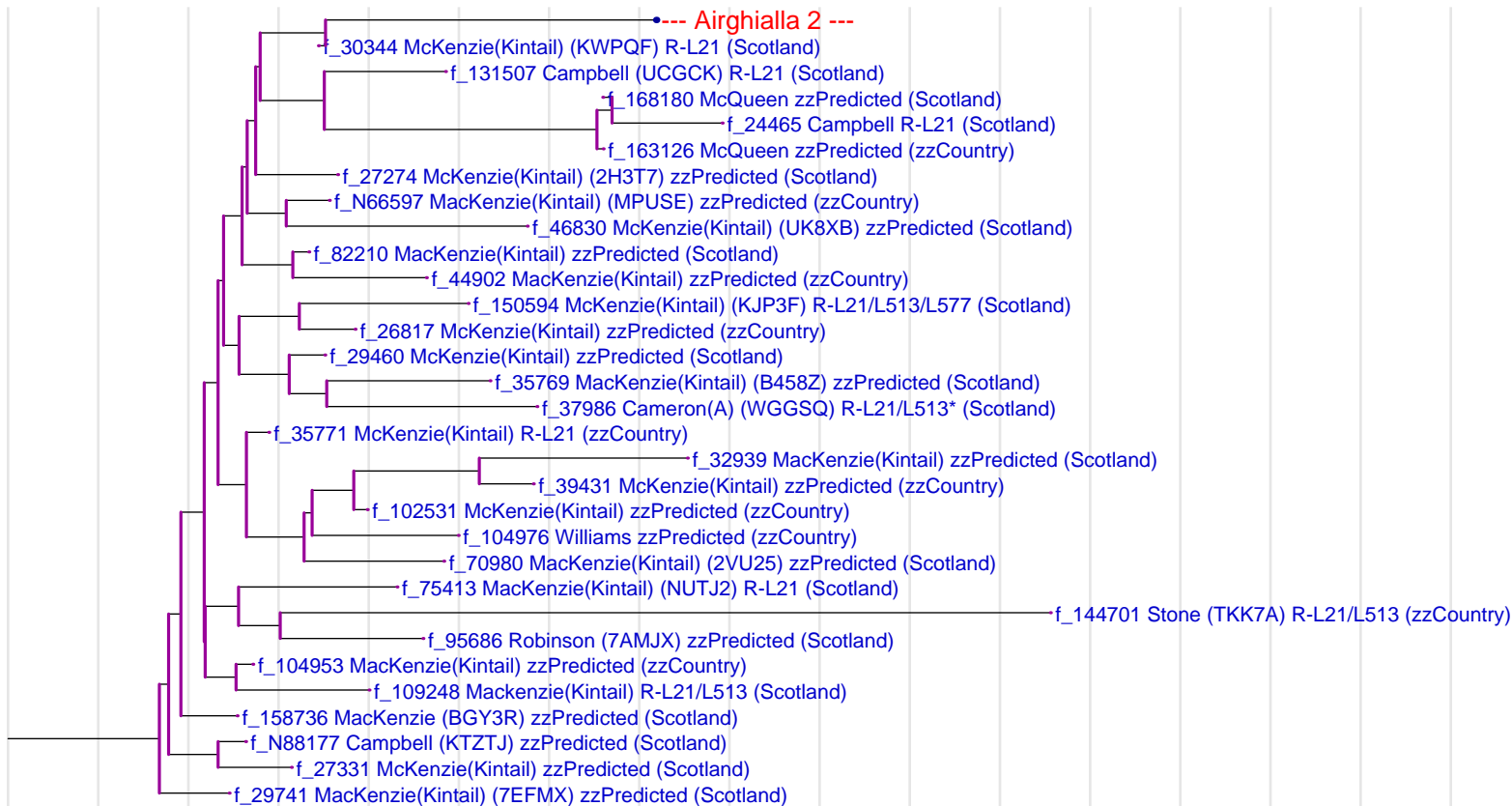
This is the marker distribution for Mike's Variety 1113-E. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
90	6030	579	9.60%	50.43±5.09	1260.73±179.104

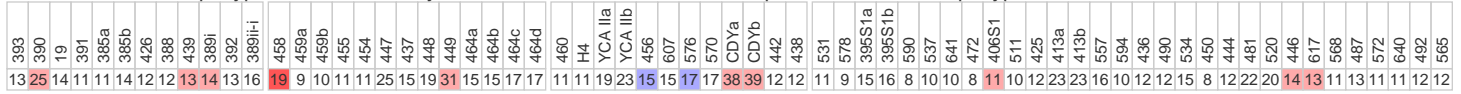
Note: Stone is not 1113-E although he is 1113.



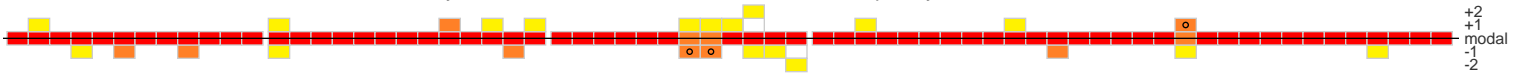
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-F

This is the modal haplotype for Mike's Variety 1113-F. The coloration is with respect to the modal haplotype of the full tree.



This is the marker distribution for Mike's Variety 1113-F. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	35	10.45%	55.12±6.36	1377.88±210.348



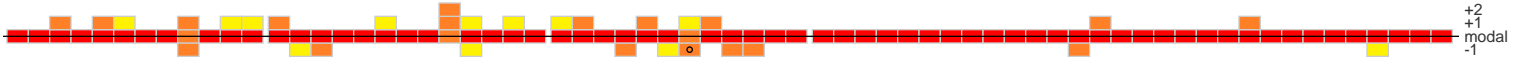
The vertical grey lines are separated 10 generations apart.

Mike's Vareity 1113-FA

This is the modal haplotype for Mike's Vareity 1113-FA. The coloration is with respect to the modal haplotype of the full tree.

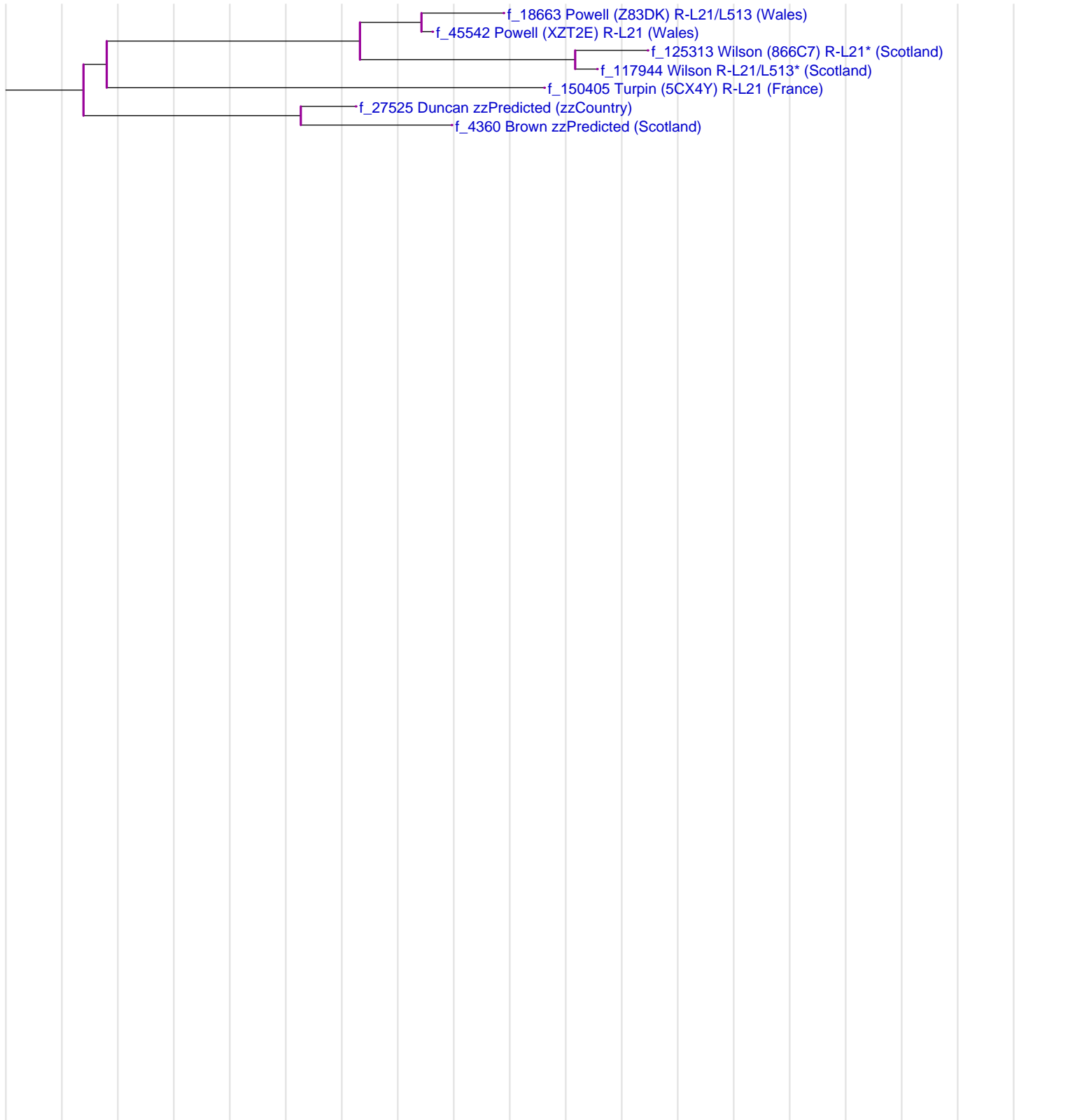
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	12	14	12	12	12	13	13	16	16	9	10	11	11	25	15	19	28	15	16	16	17	11	11	19	23	15	15	18	16	37	39	12	12	11	9	15	16	8	10	10	8	11	10	12	23	24	16	10	12	12	15	8	12	21	20	13	13	11	13	11	11	12	12

This is the marker distribution for Mike's Vareity 1113-FA. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
7	469	58	12.37%	65.90±7.34	1647.59±246.611



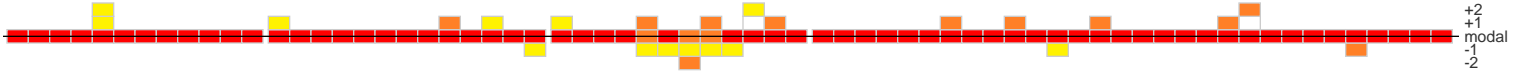
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-FB/G (617=14)

This is the modal haplotype for Mike's Variety 1113-FB/G (617=14). The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	10	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	16	17	11	11	19	23	16	14	19	17	37	40	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	15	8	12	20	14	14	11	14	11	11	11	12	12

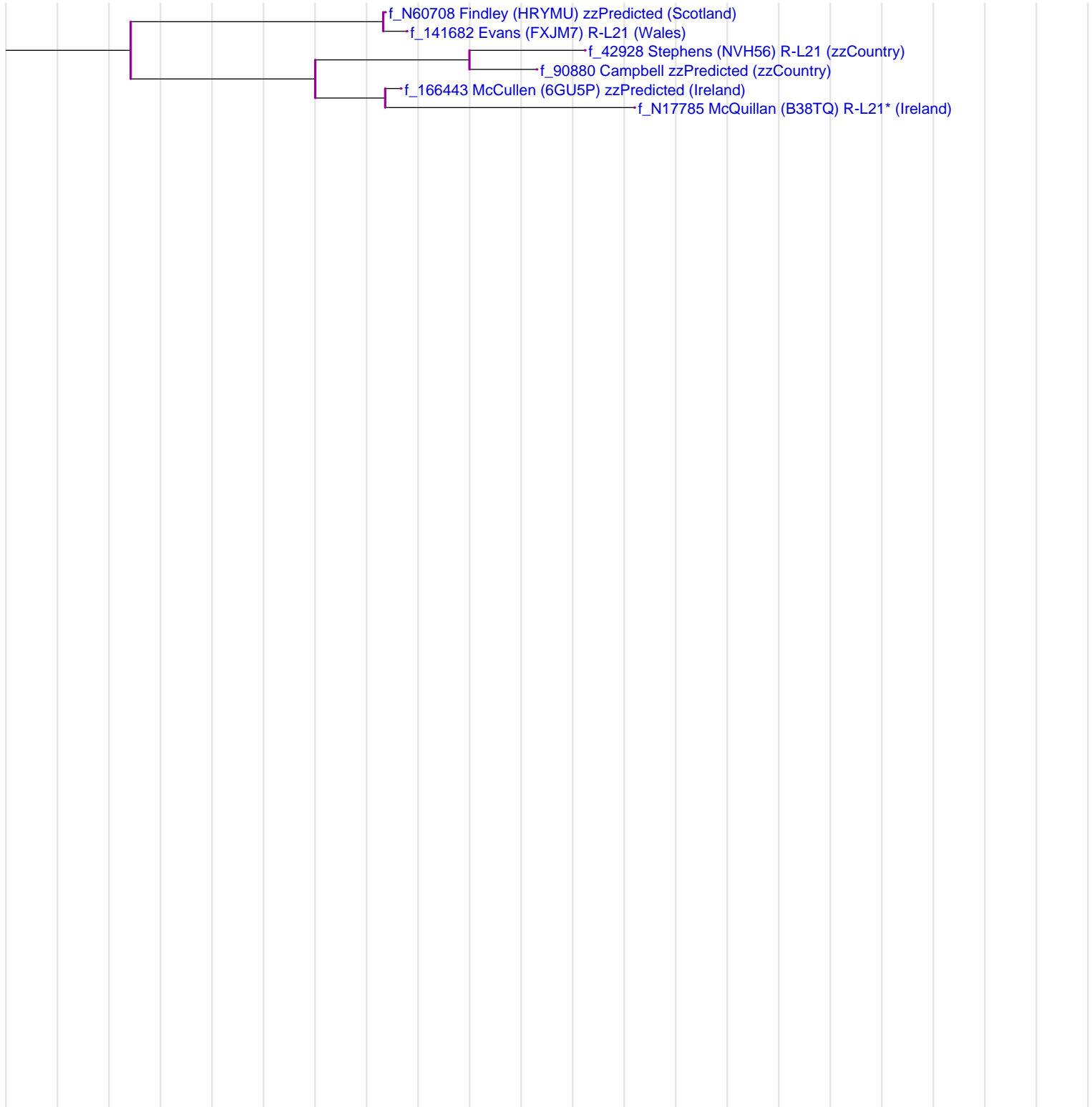
This is the marker distribution for Mike's Variety 1113-FB/G (617=14). The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	41	10.20%	53.73±6.07	1343.32±202.604

Note: Mikes 1113-G (with *DYS617=14*) top, and 1113-FB bottom.



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-G (617=13)

This is the modal haplotype for Mike's Variety 1113-G (617=13). The coloration is with respect to the modal haplotype of the full tree.

393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	444	481	520	446	617	568	487	572	640	492	565	
13	24	14	10	11	14	12	12	12	13	13	16	18	9	10	11	11	25	15	19	29	15	15	16	17	11	11	19	23	16	15	18	17	35	38	13	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	12	16	8	12	22	20	13	13	11	13	11	11	12	12	12

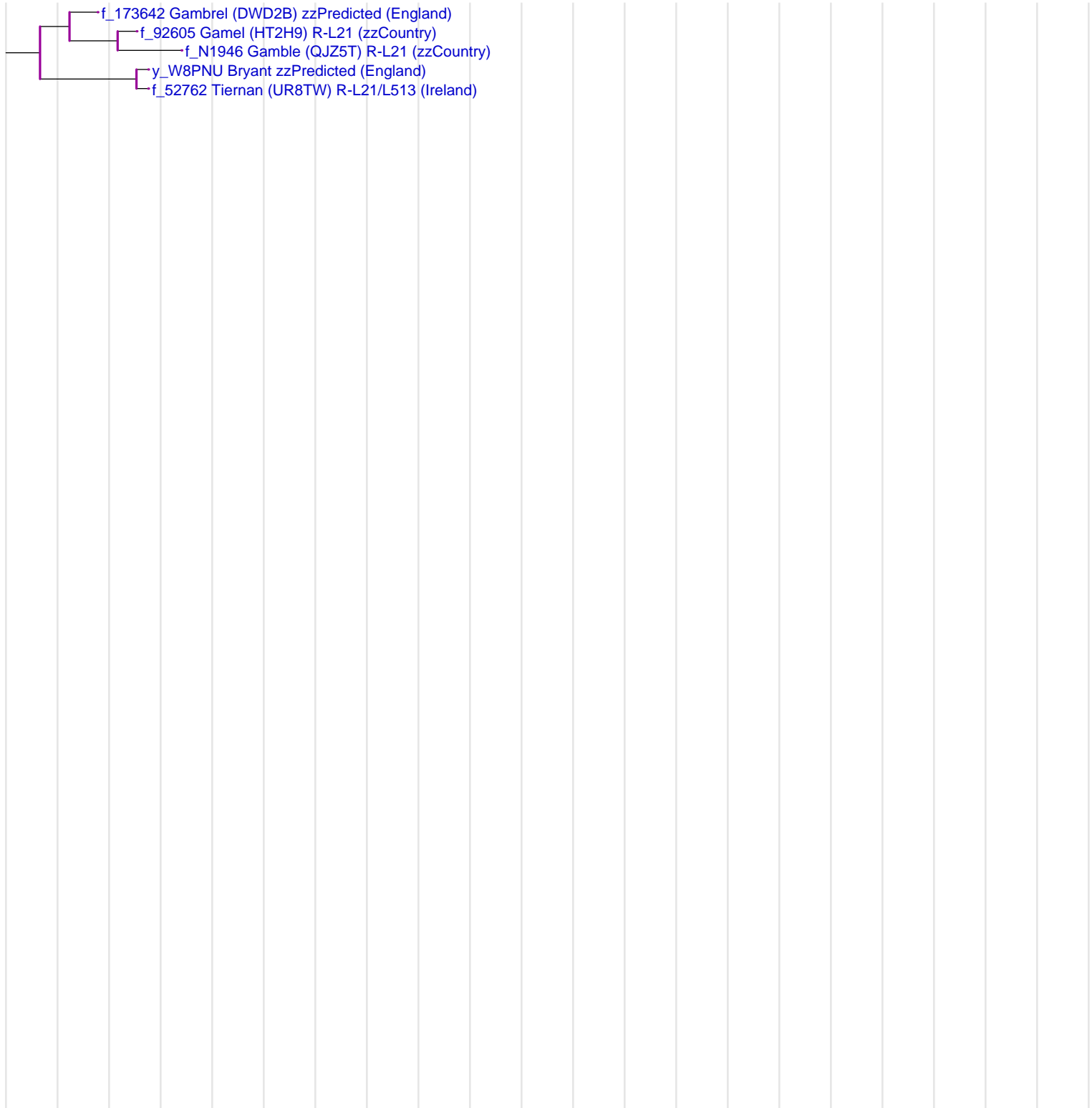
This is the marker distribution for Mike's Variety 1113-G (617=13). The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	12	3.58%	18.24±2.09	455.926±69.2842

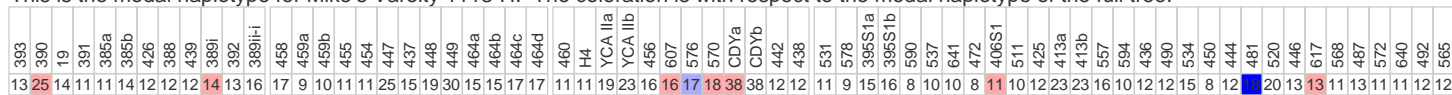
Note: This includes only those 1113-G men with DYS617=13, as opposed to 14.



The vertical grey lines are separated 10 generations apart.

Mike's Vareity 1113-H

This is the modal haplotype for Mike's Vareity 1113-H. The coloration is with respect to the modal haplotype of the full tree.

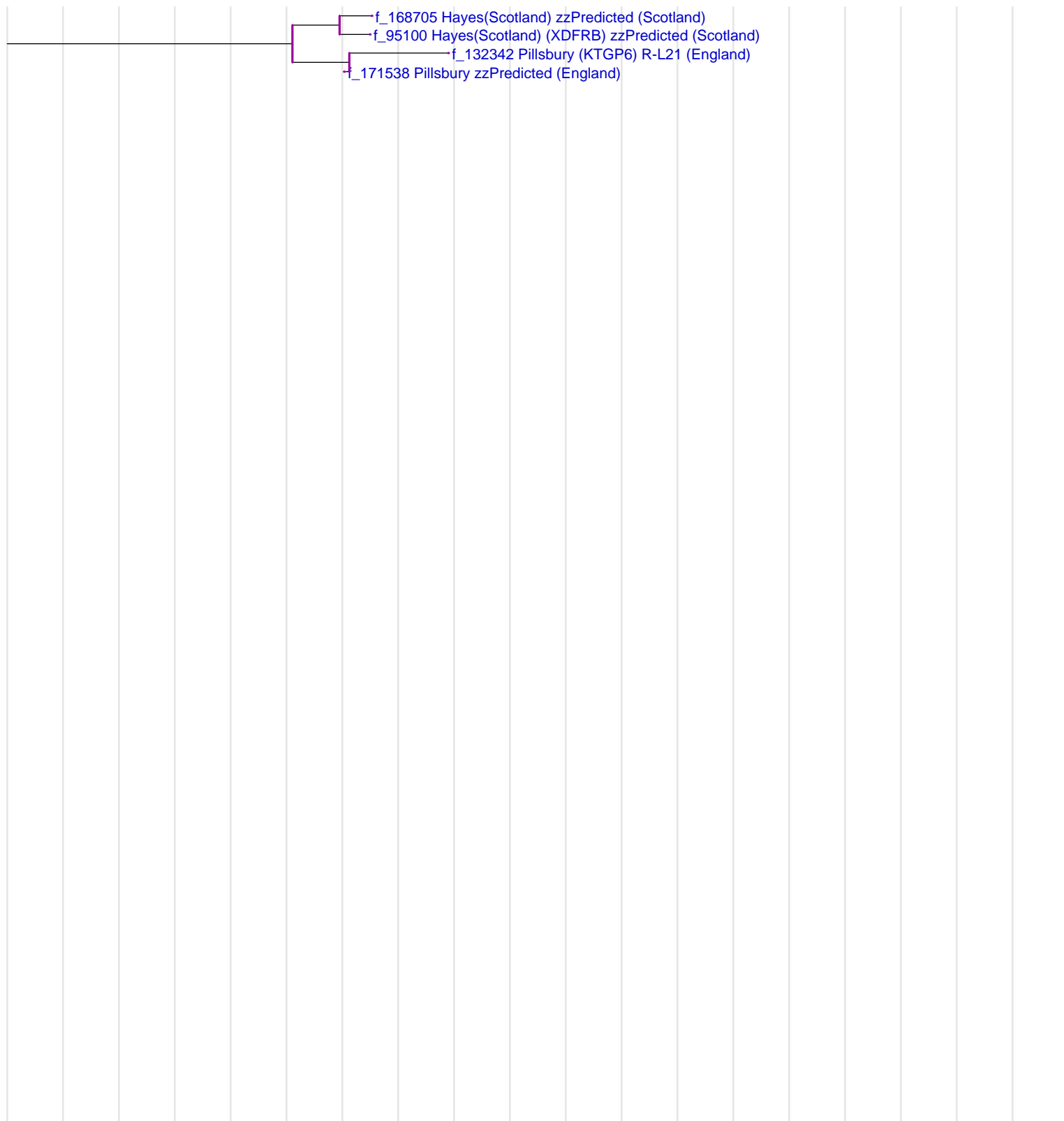


This is the marker distribution for Mike's Vareity 1113-H. The color indicates the relative frequency of the alleles.



Age Analysis

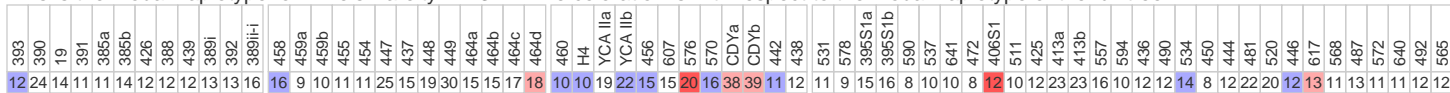
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	9	3.36%	17.08±2.01	426.944±65.9455



The vertical grey lines are separated 10 generations apart.

Mike's Vareity 1113-K

This is the modal haplotype for Mike's Vareity 1113-K. The coloration is with respect to the modal haplotype of the full tree.

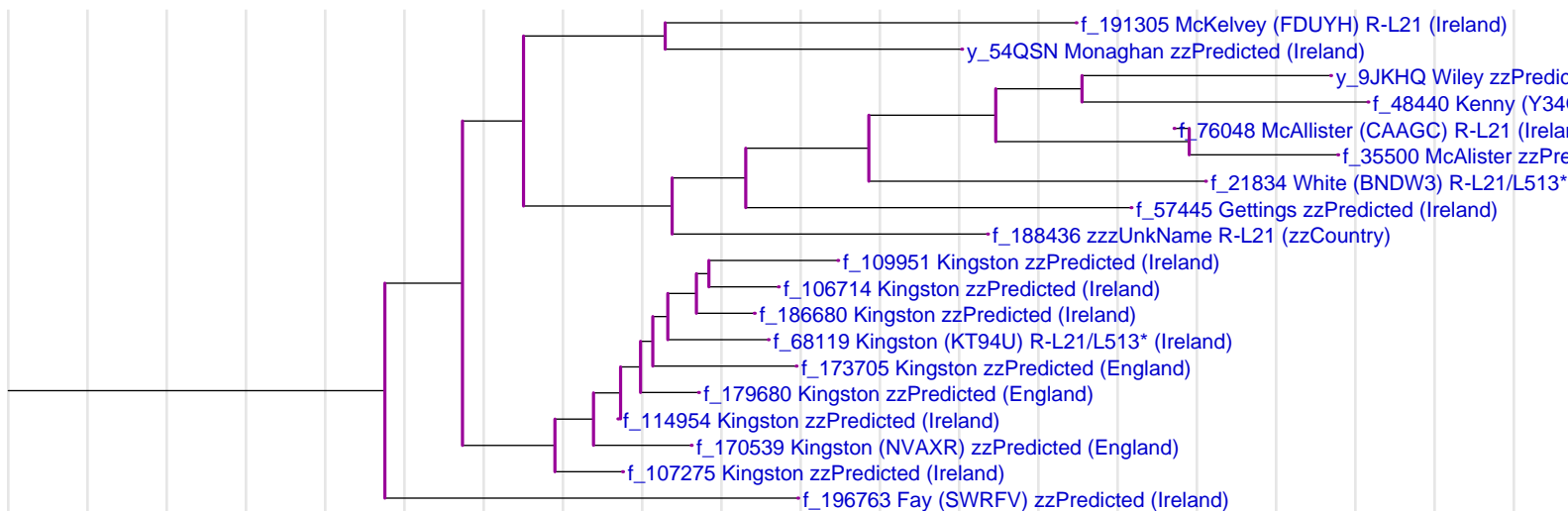


This is the marker distribution for Mike's Vareity 1113-K. The color indicates the relative frequency of the alleles.



Age Analysis

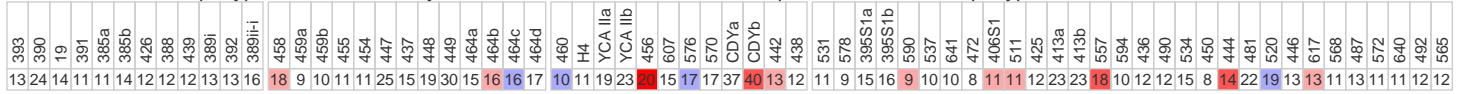
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
19	1273	134	10.53%	55.55±5.79	1388.82±200.637



The vertical grey lines are separated 10 generations apart.

Mike's Vareity 1113-nV

This is the modal haplotype for Mike's Vareity 1113-nV. The coloration is with respect to the modal haplotype of the full tree.

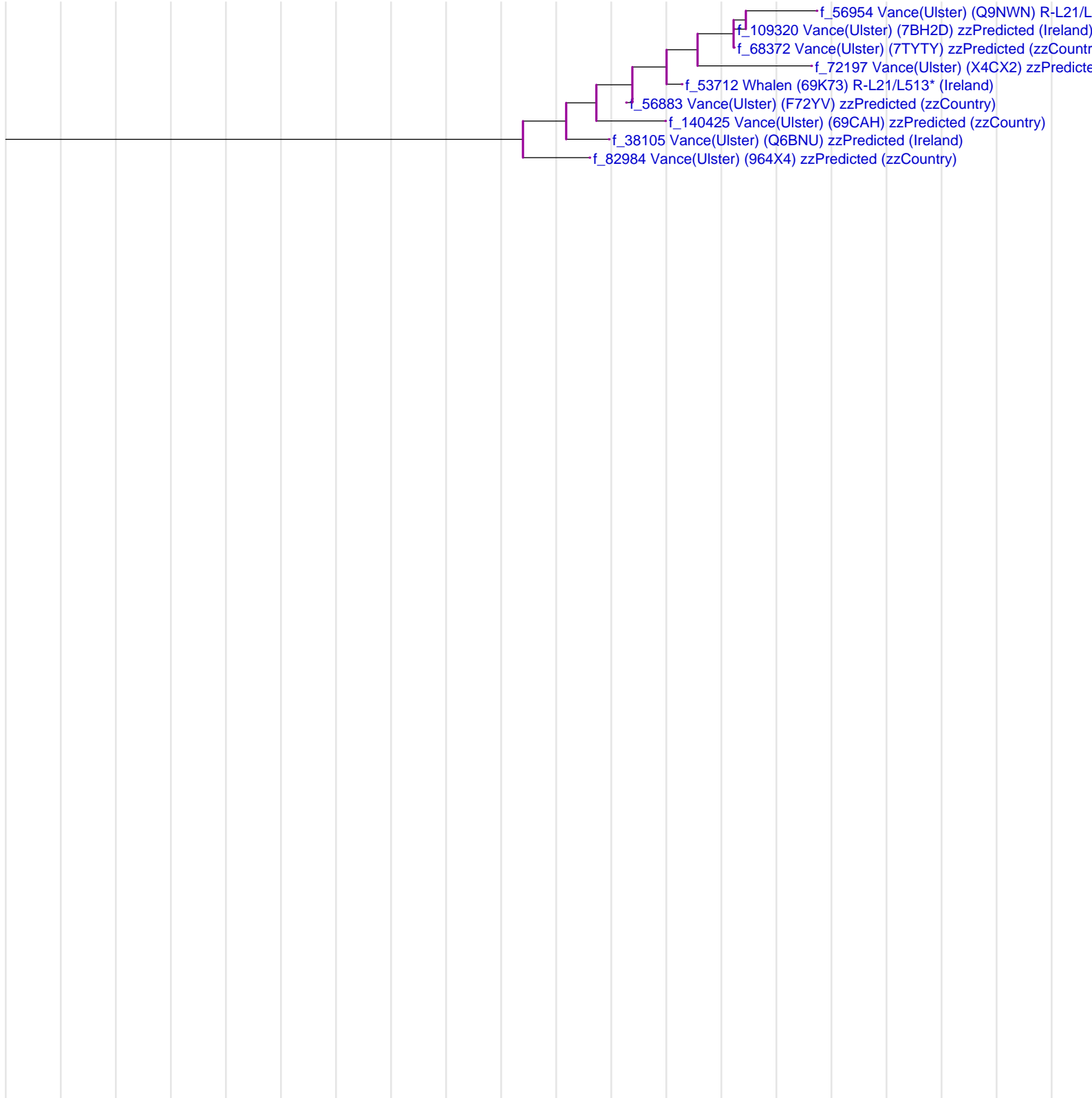


This is the marker distribution for Mike's Vareity 1113-nV. The color indicates the relative frequency of the alleles.



Age Analysis

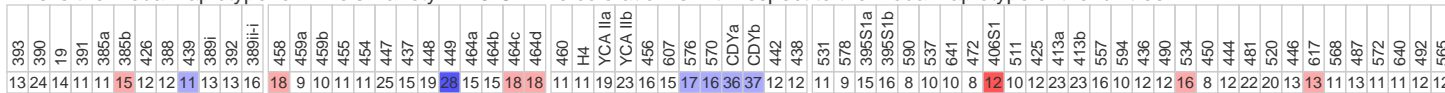
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
9	603	16	2.65%	13.45±1.45	336.134±49.5187



The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-O

This is the modal haplotype for Mike's Variety 1113-O. The coloration is with respect to the modal haplotype of the full tree.



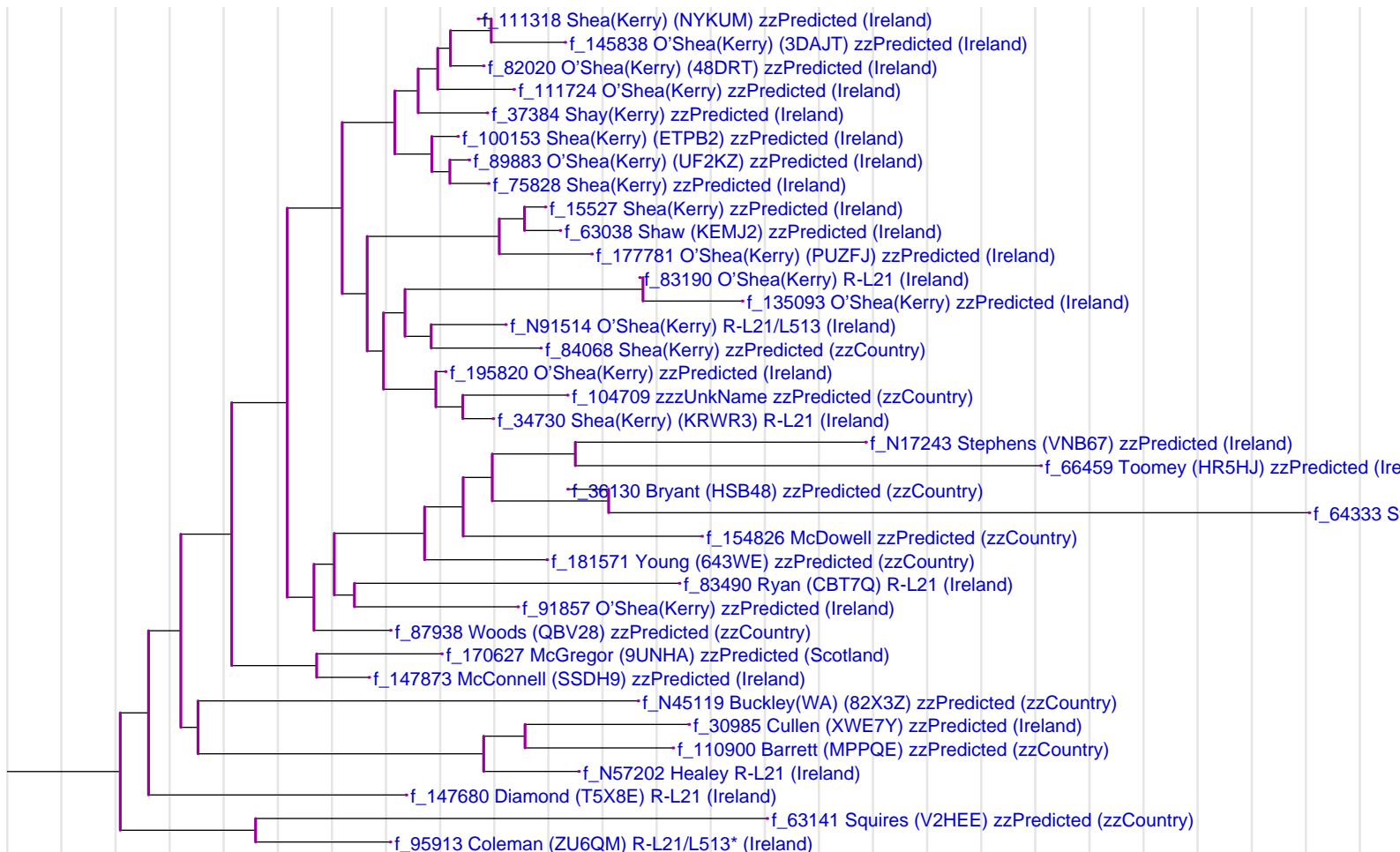
This is the marker distribution for Mike's Variety 1113-O. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
36	2412	267	11.07%	58.59±5.99	1464.69±209.516

Note: Includes varieties 1113-O-A, 1113-N as well as 2 men from 1113-C and one 1113-E man.



The vertical grey lines are separated 10 generations apart.

Notes

The Tree

The tree was generated using the neighbor-joining algorithm provided by the PHYLIP phylogeny package. This algorithm requires a distance matrix, for which the data came from the 2011-06-19 version of Mike Walsh's Excel spreadsheet. Only members with at least the 67 FTDNA markers, and who tested, or were predicted positive for RL21 were used. For now, only the markers in FTDNA's standard set of 67 were used to calculate the matrix, but I will use markers beyond these in the future.

Modal Values and Age Estimates

For each cluster on the tree, I provide both its modal haplotype determined from its descendant members on the tree, as well as an age analysis. The age analysis was completed in the style of what Anatole Klyosov describes in his Journal of Genetic Genealogy article, 5(2):186-216, 2009. I have not taken into consideration the up/down mutation asymmetry, but may do so in the future. I used a 67-marker average mutation rate of 0.002 and assumed 25 years per generation. I included a 10% uncertainty for the average mutation rate, and a 10% uncertainty for the average number of years in a generation.

For the calculation of the modal haplotypes, in the event of a tie for a particular marker, with two or more different allele values having the same count of haplotypes, the allele closest to the R-L21 modal haplotype was chosen. This was done so that the modal haplotype would more closely resemble what might be the ancestral haplotype for the cluster.

Allele Distribution Diagram

The allele distribution plot attempts to display relative frequency information of the various allele values for each marker. For each possible allele value of each marker, a different coloured box is used to represent the fraction of haplotypes, with that particular allele value. A red box indicates that more than 50% of the haplotypes have that particular value, an orange box indicates more than 33% have that particular value, yellow for more than 25%, and blue indicates that the fraction is simply greater than 0.

If the fraction for an allele is within 5% of what it is for the modal value, I have indicated that allele with a small circle. The idea here, is that if the other allele value is so close, then if you were to use different sample data, you could potentially end up with a different modal value.

- - greater than 0% of haplotypes
- - greater than 25% of haplotypes
- - greater than 33% of haplotypes
- - greater than 50% of haplotypes

Consider the following example of DYS 464c for the whole of R-L21. We look at what fraction of the 1483 people in this cluster have a particular allele value. The modal value is clearly 17, but 16 is not far behind. As 16 is within 5% of the modal value, I have indicated that close relationship with a small circle.

Allele	Count	Fraction	Colour
19	0	0.00%	
18	14	0.94%	■
17	694	46.80%	■
16	626	42.21%	■
15	145	9.78%	■
14	2	0.13%	■
13	2	0.13%	■
12	0	0.00%	

