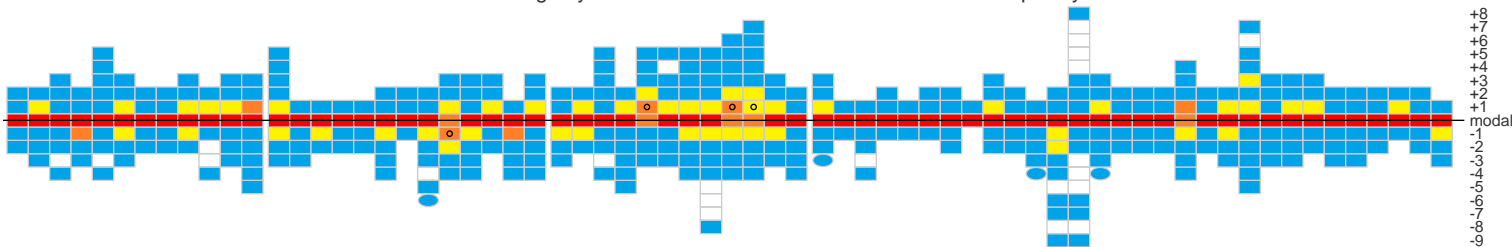


# R-L21

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

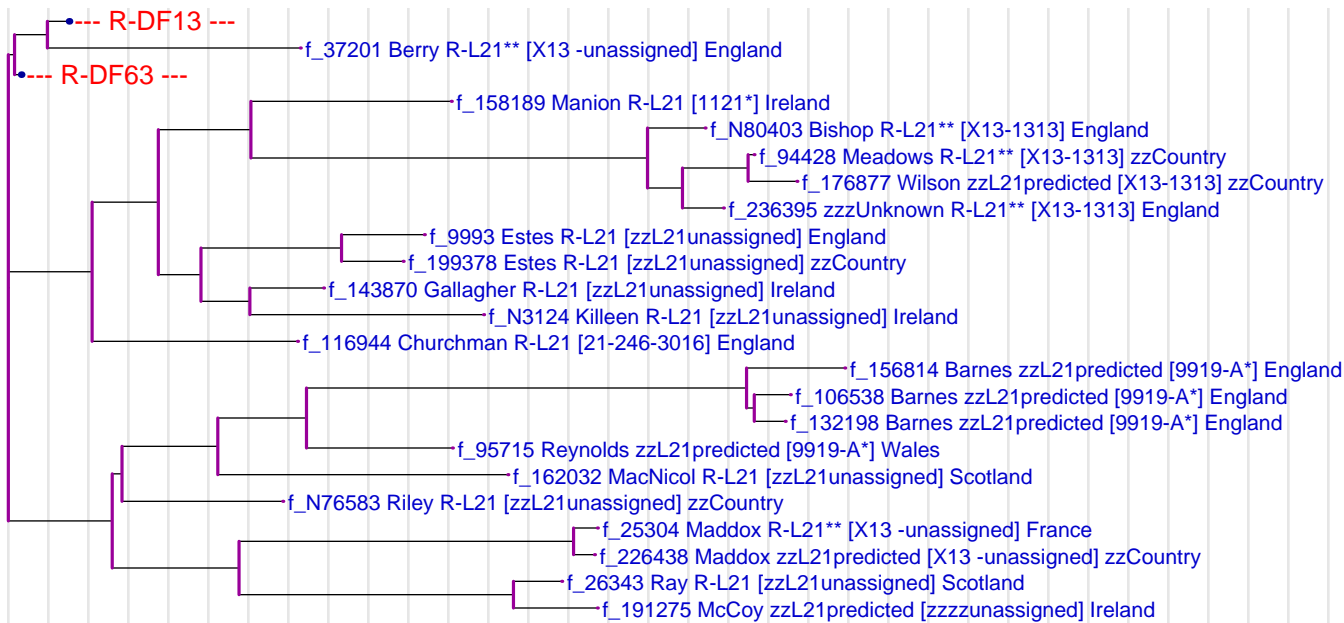
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	572	640	492	565	
13	24	14	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	30	15	15	17	17	11	11	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	8	10	10	12	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

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



## Age Analysis

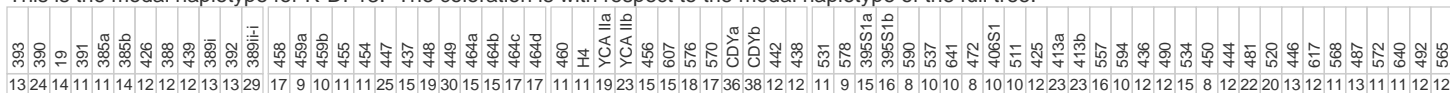
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5514	369438	90747	24.56%	139.92±13.99	3497.9±494.72



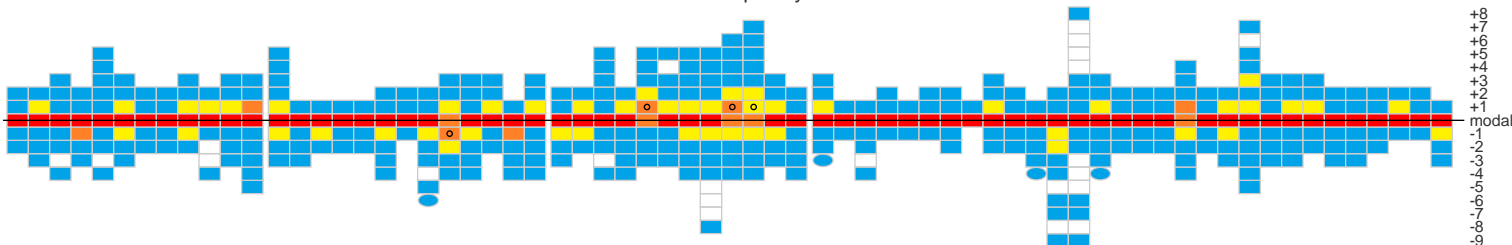
The vertical grey lines are separated 10 generations apart.

# R-DF13

This is the modal haplotype for R-DF13. The coloration is with respect to the modal haplotype of the full tree.

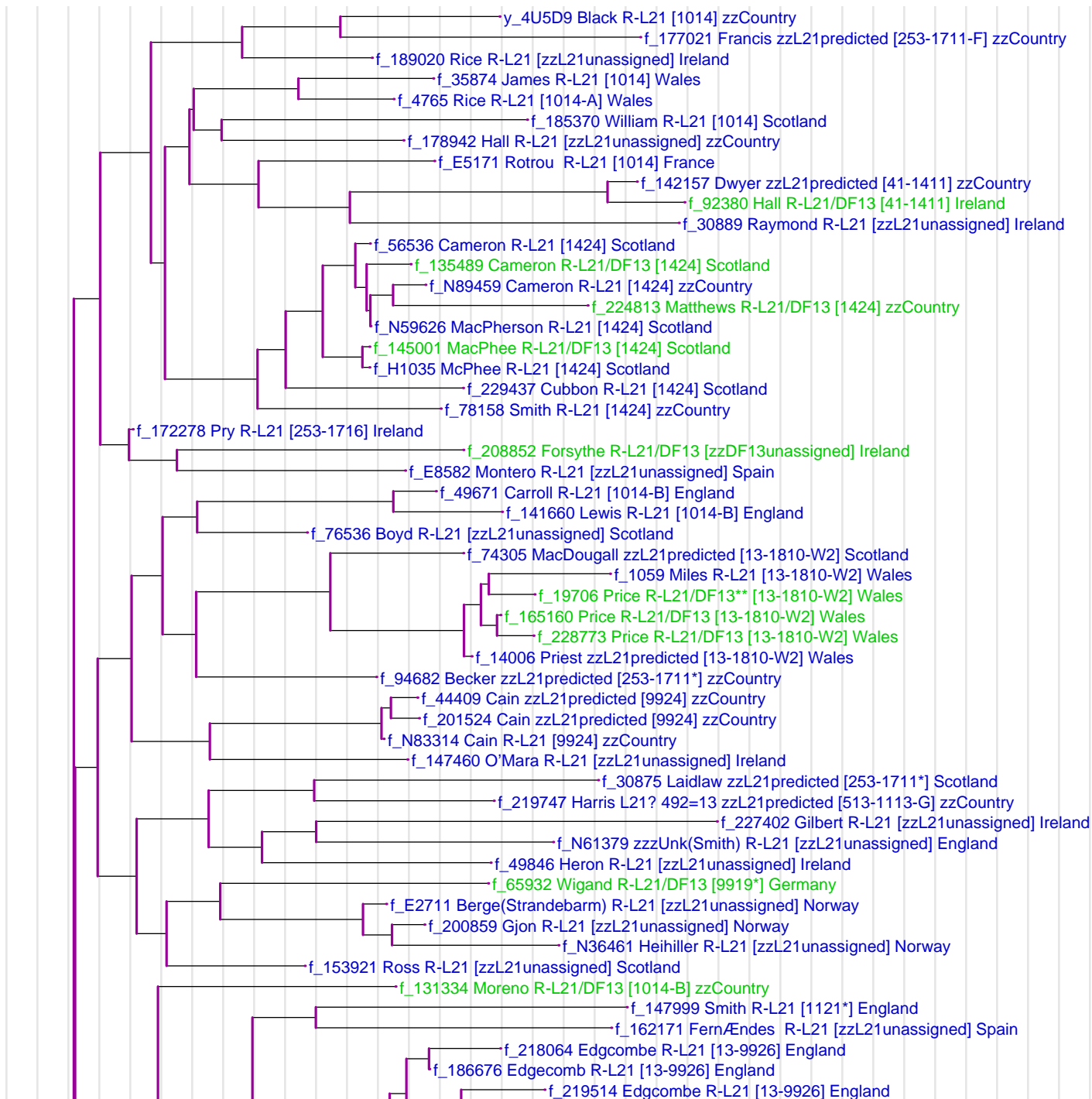


This is the marker distribution for R-DF13. The color indicates the relative frequency of the alleles.

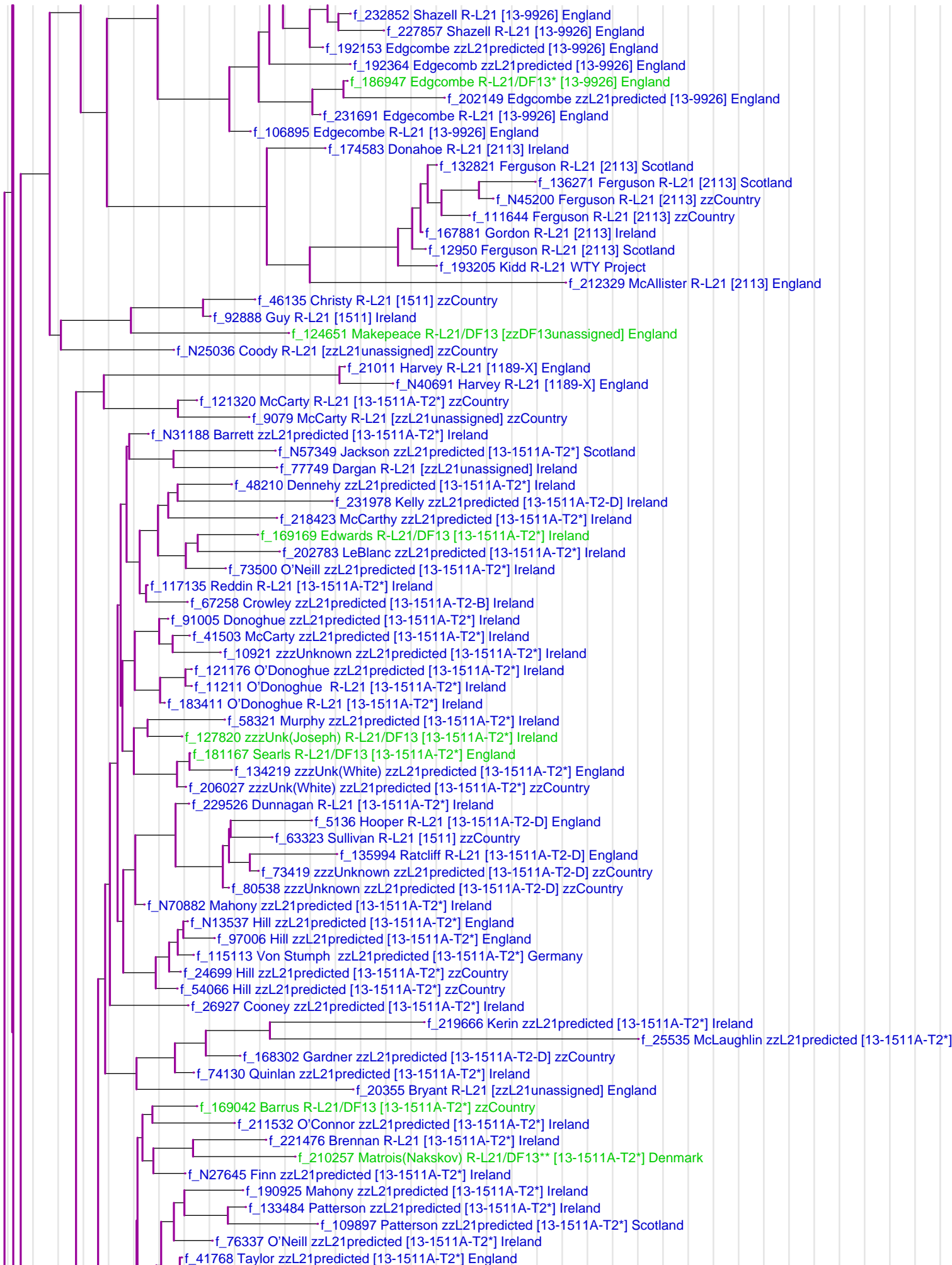


## Age Analysis

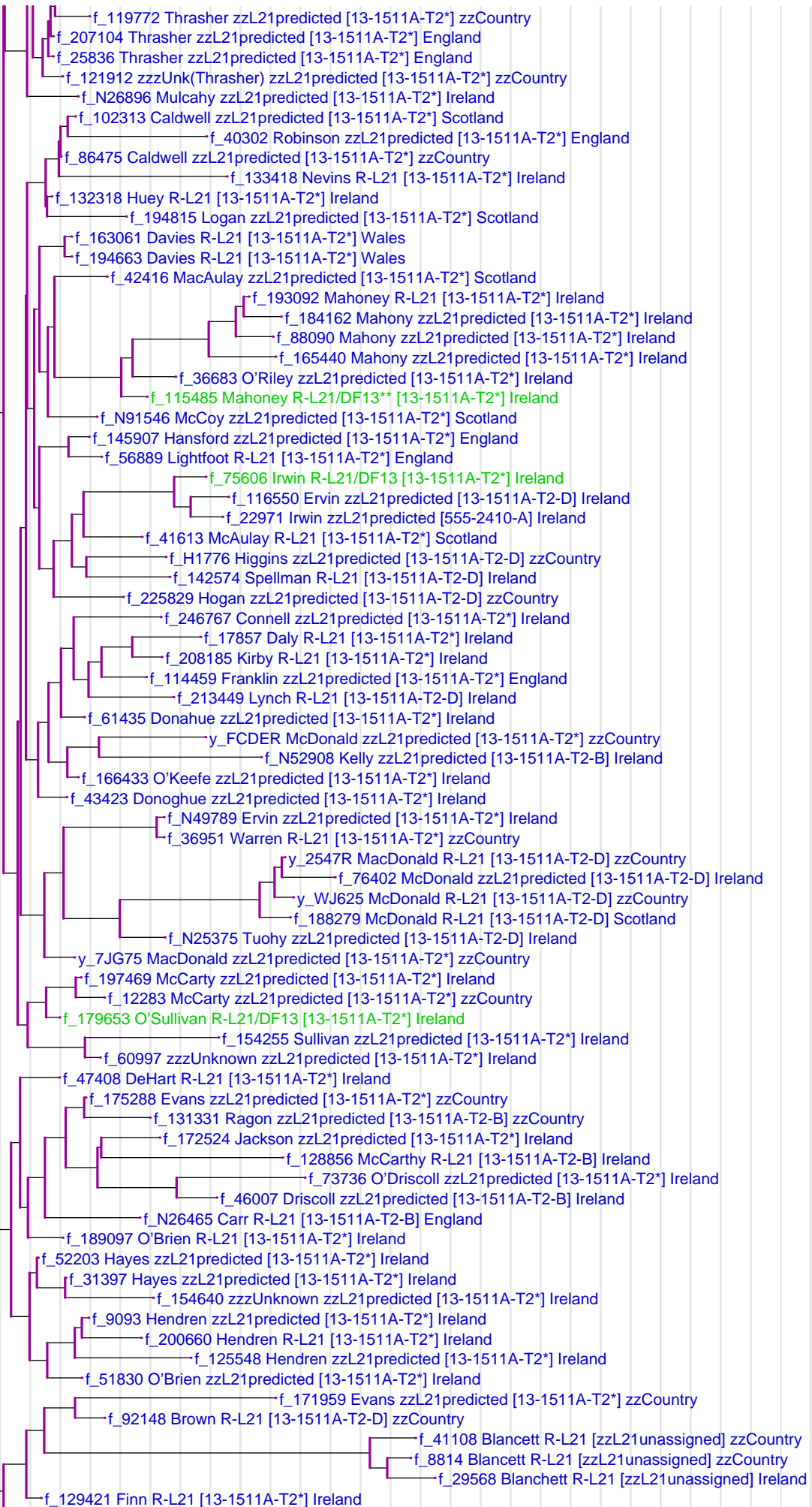
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5450	365150	89834	24.60%	140.16±14.02	3504.12±495.601



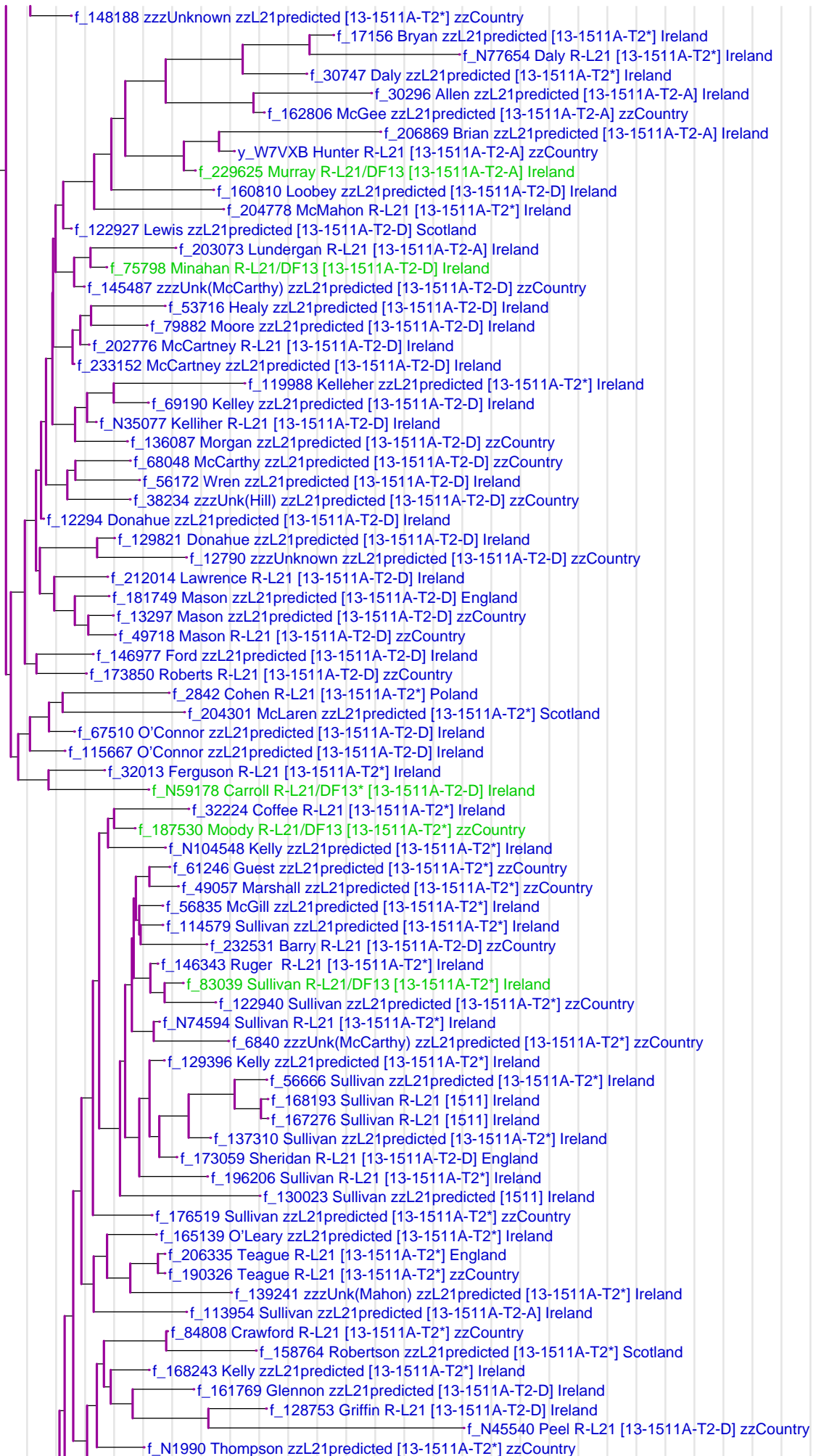
The vertical grey lines are separated 10 generations apart.



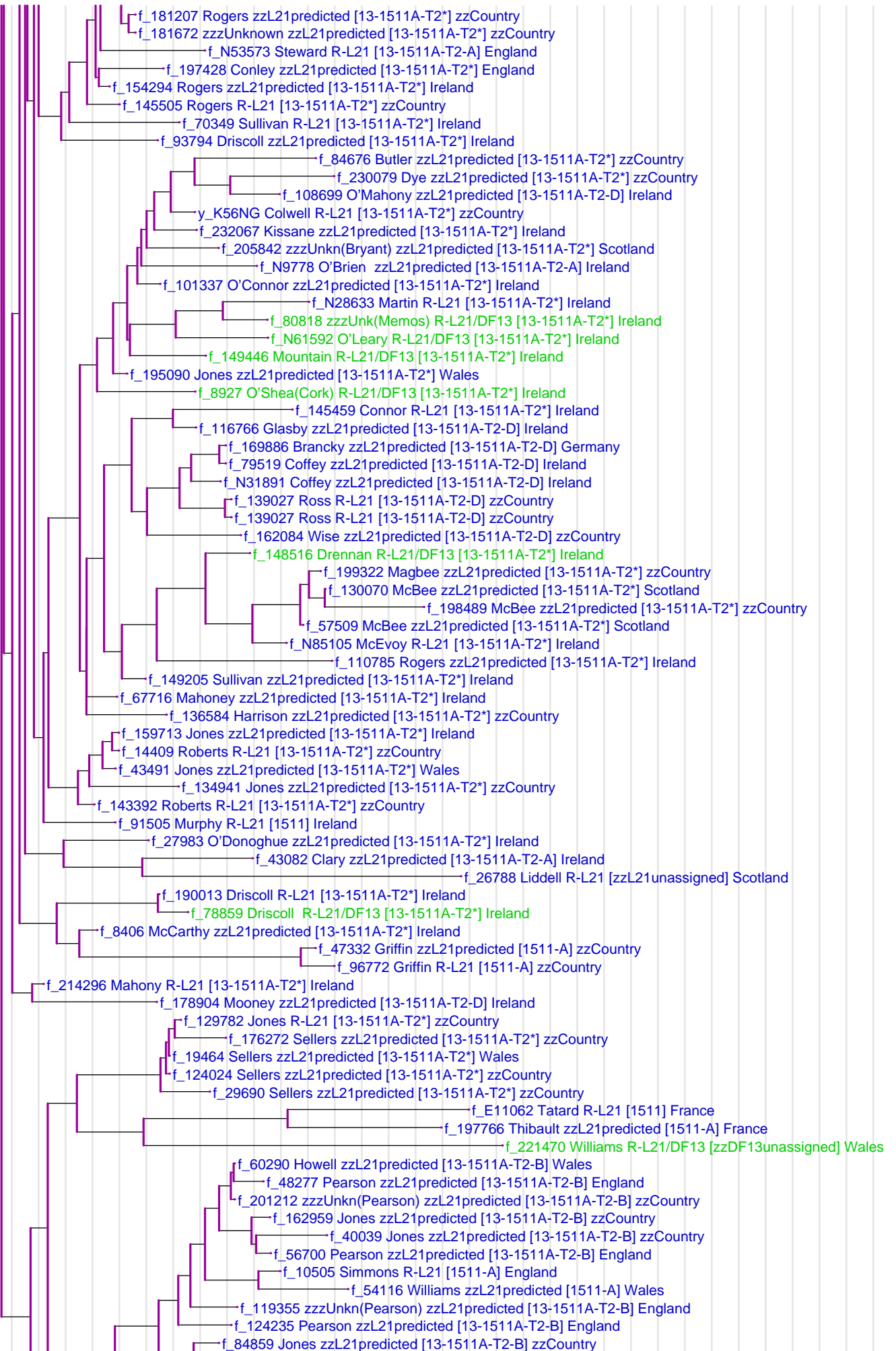
The vertical grey lines are separated 10 generations apart.



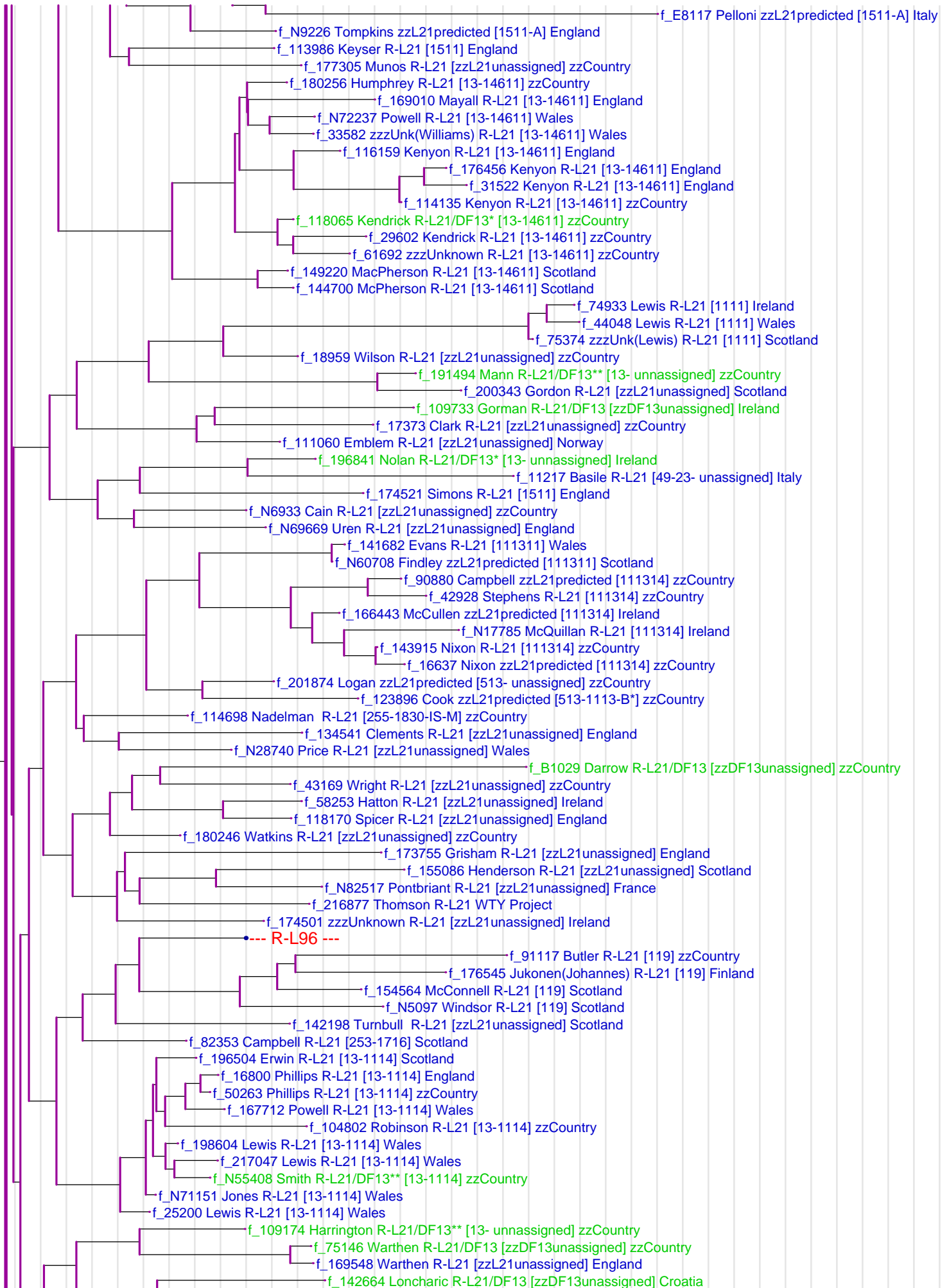
The vertical grey lines are separated 10 generations apart.



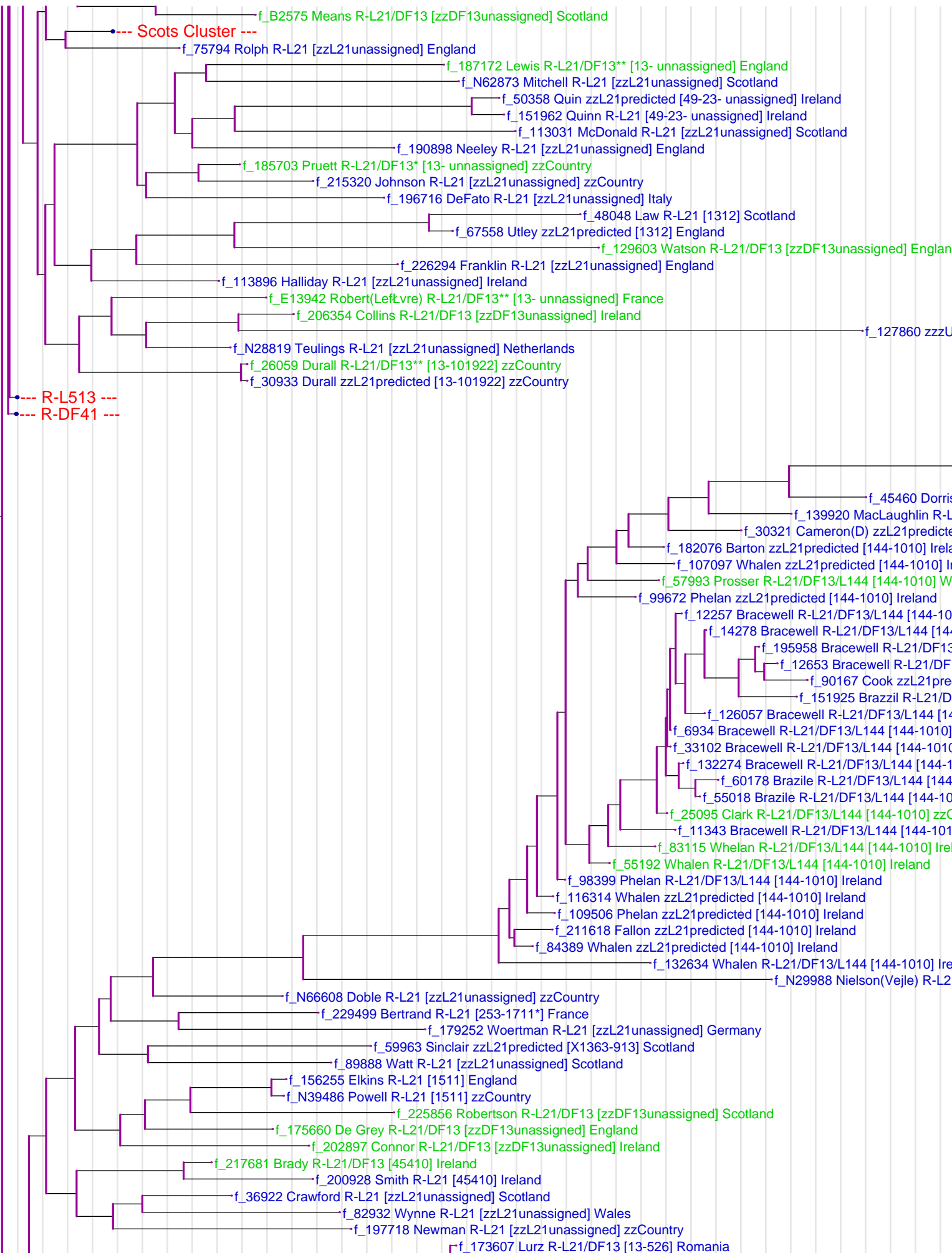
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

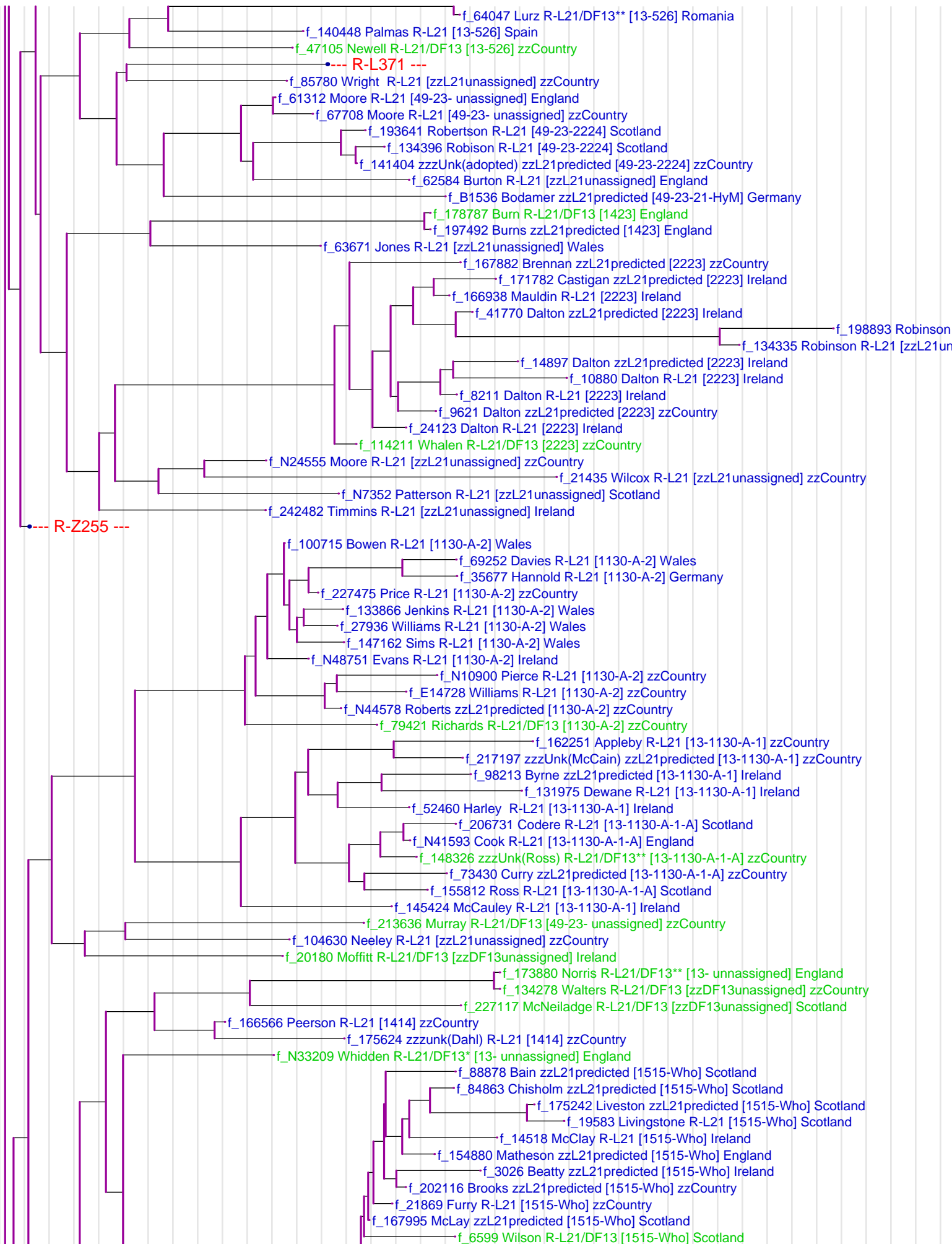


The vertical grey lines are separated 10 generations apart.

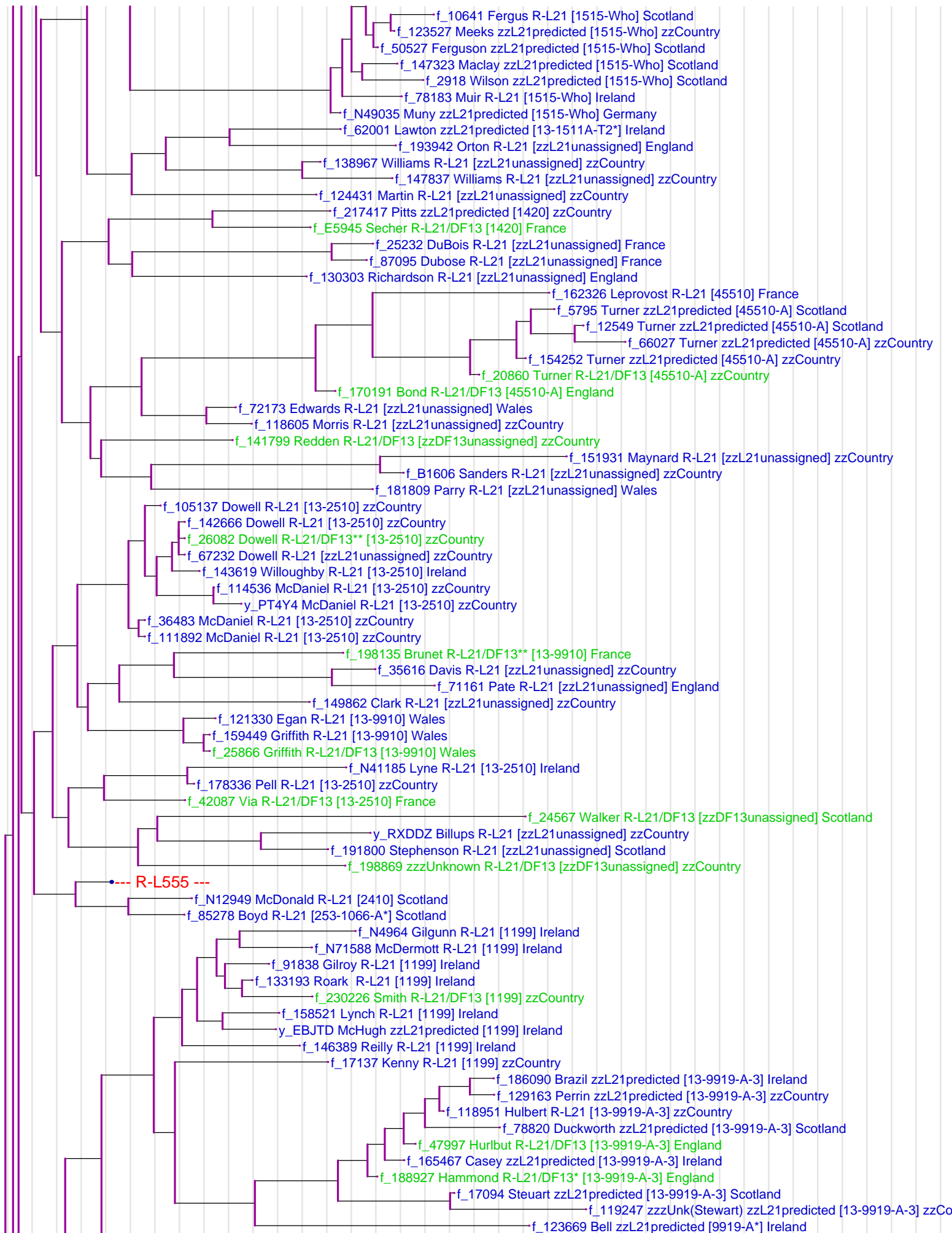


The vertical grey lines are separated 10 generations apart.

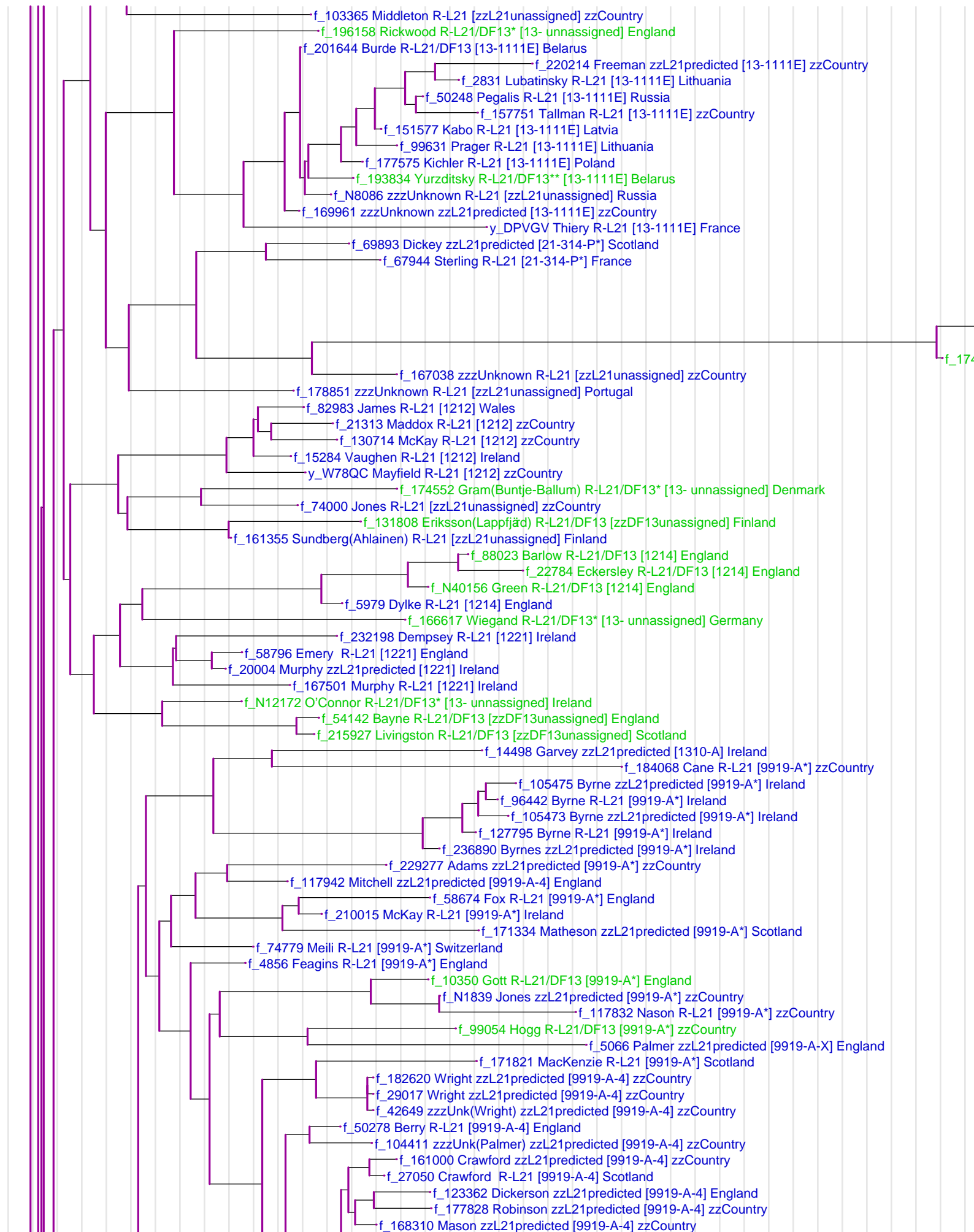




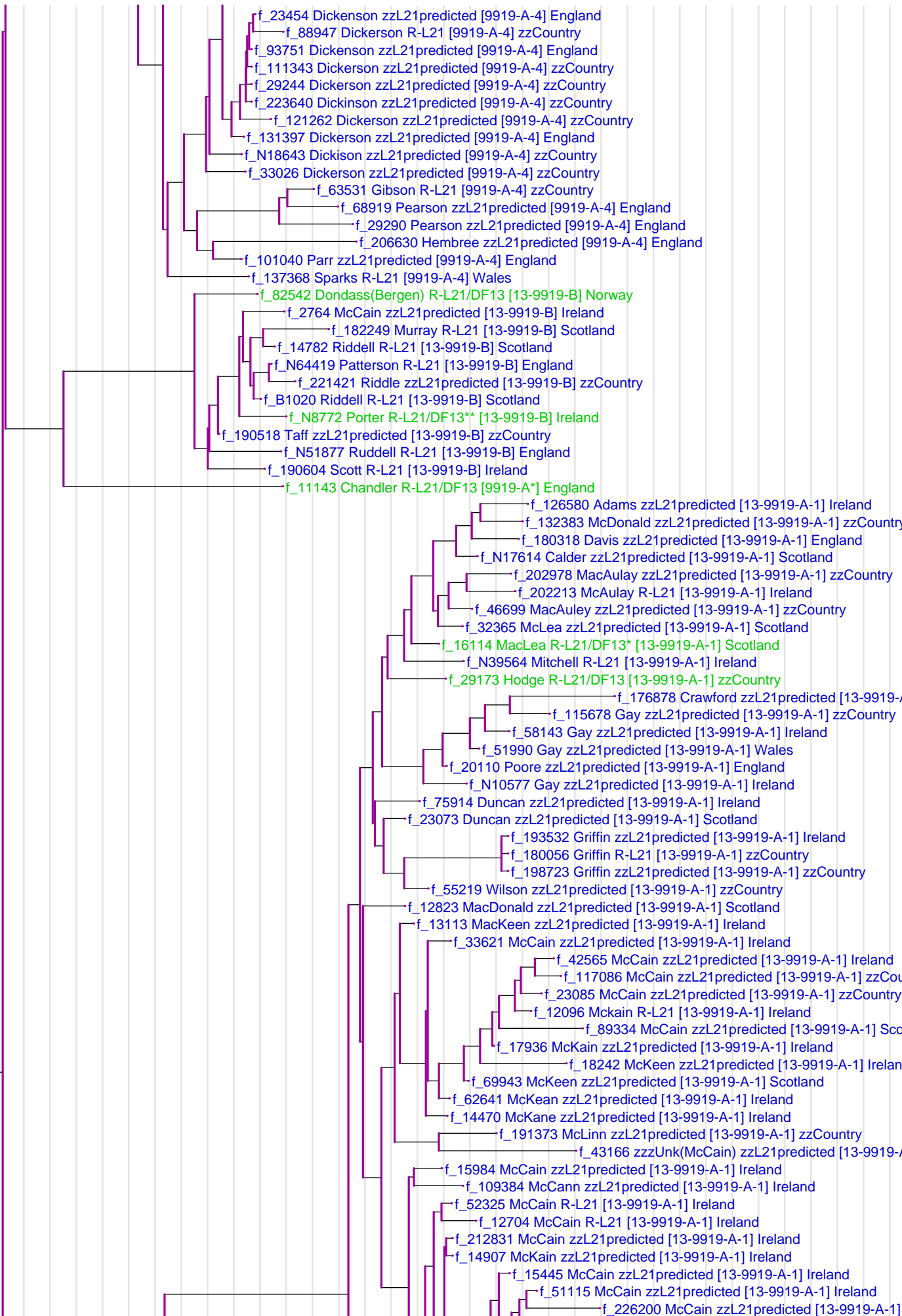
The vertical grey lines are separated 10 generations apart.



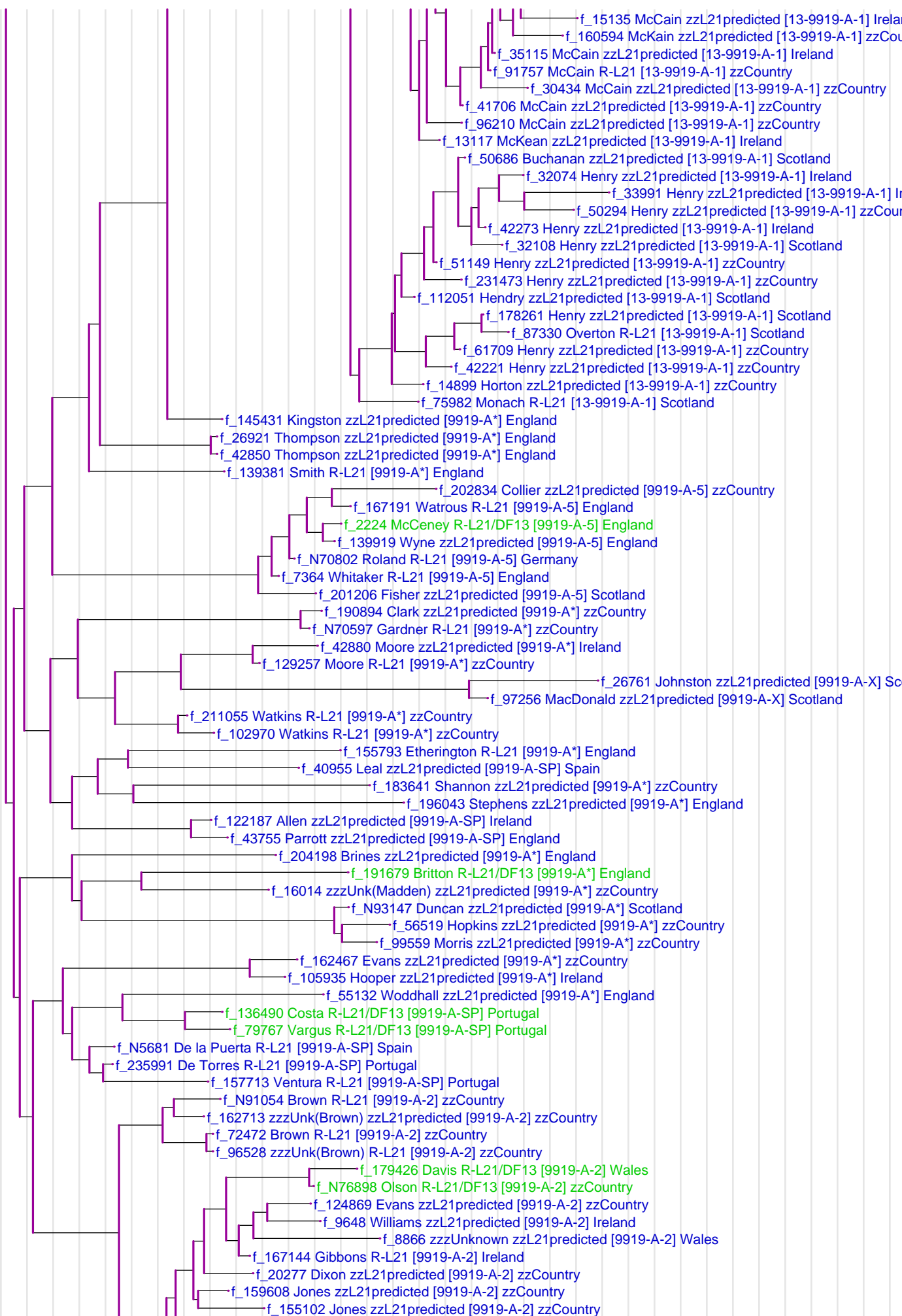
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



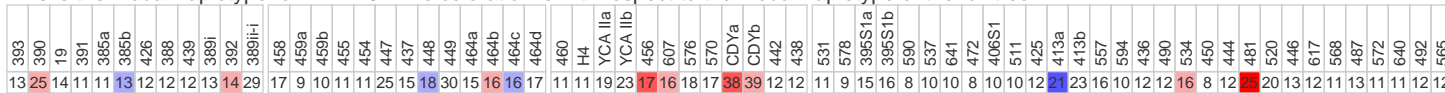
The vertical grey lines are separated 10 generations apart.



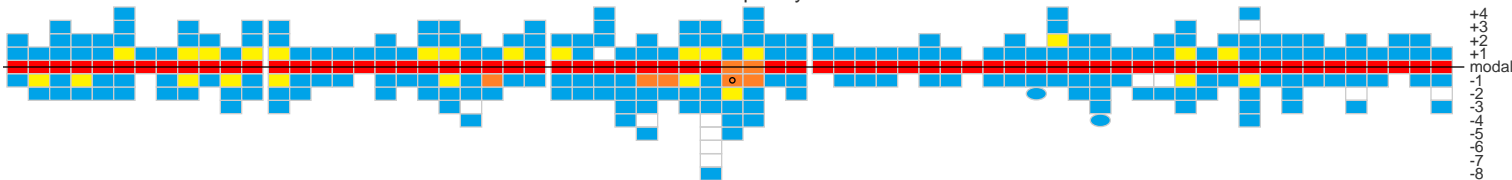
The vertical grey lines are separated 10 generations apart.

# R-DF49

This is the modal haplotype for R-DF49. The coloration is with respect to the modal haplotype of the full tree.

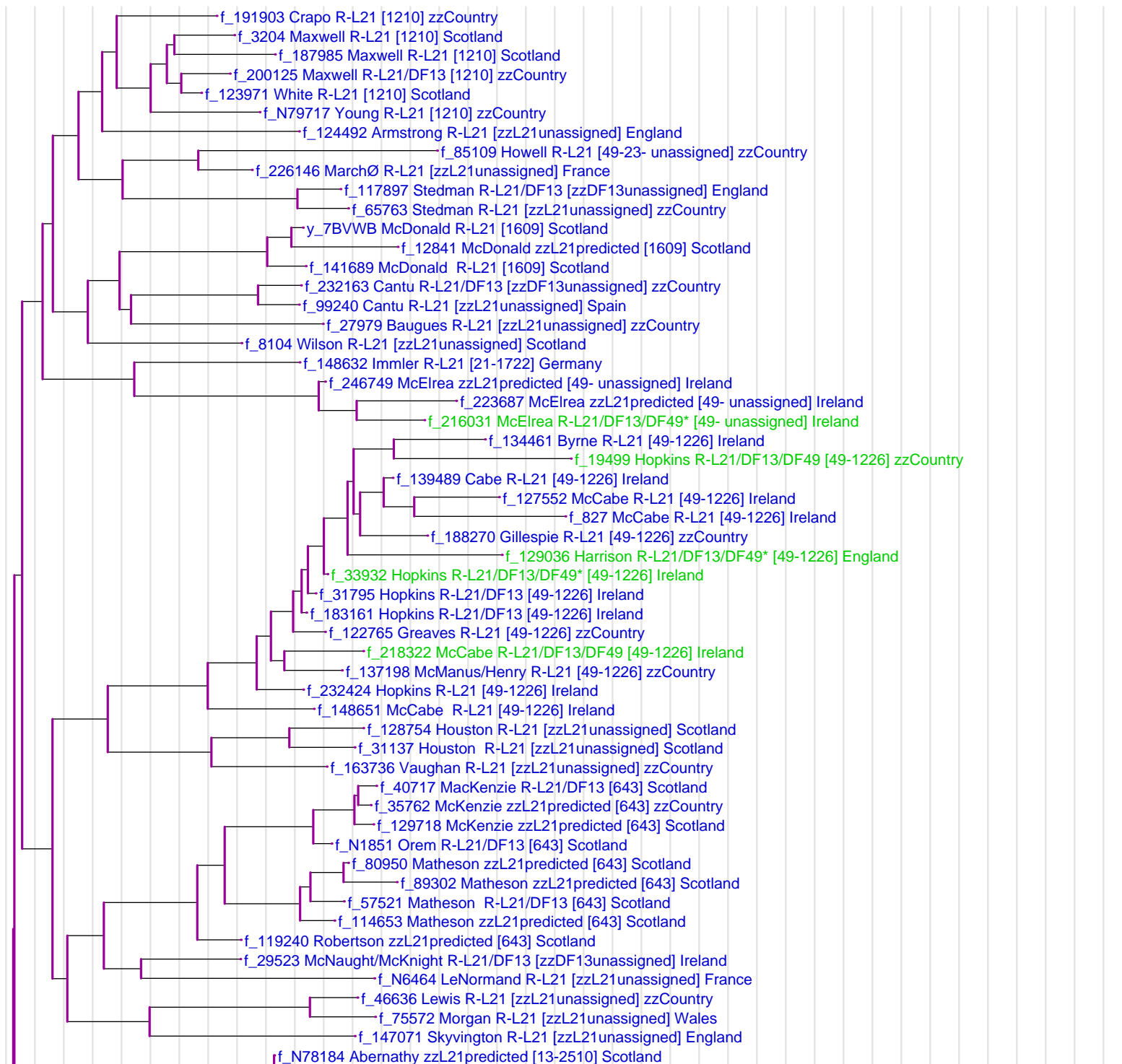


This is the marker distribution for R-DF49. The color indicates the relative frequency of the alleles.

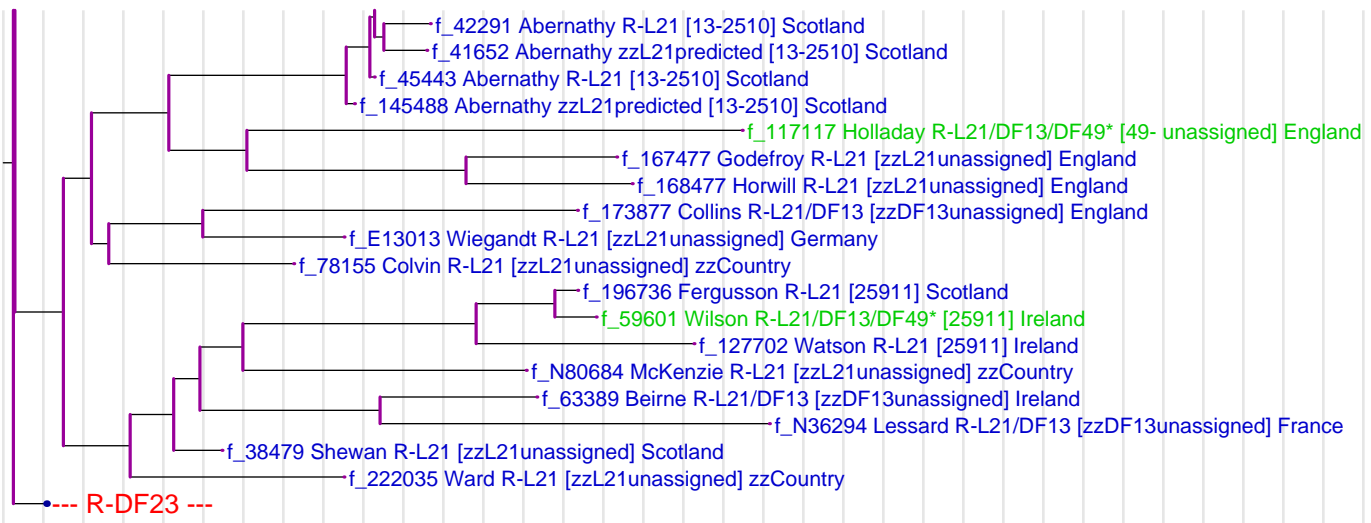


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
933	62511	10674	17.08%	93.33±9.34	2333.14±330.111



The vertical grey lines are separated 10 generations apart.

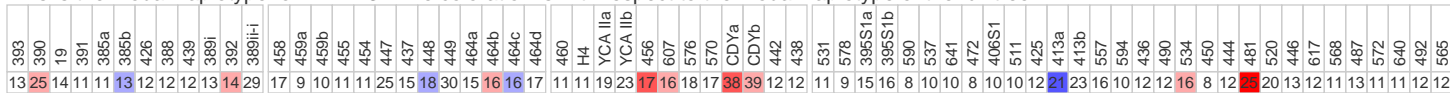


The vertical grey lines are separated 10 generations apart.

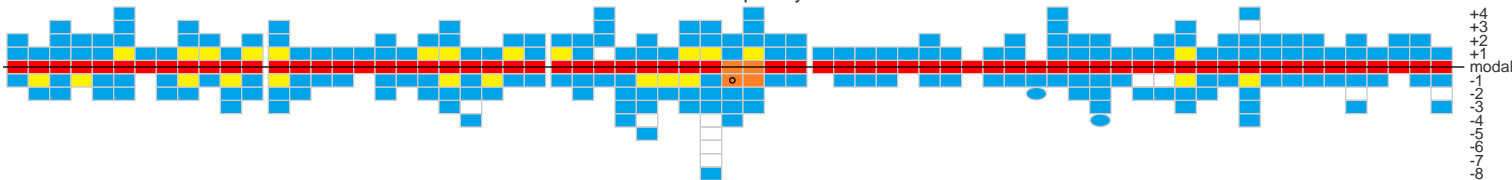


# R-DF23

This is the modal haplotype for R-DF23. The coloration is with respect to the modal haplotype of the full tree.

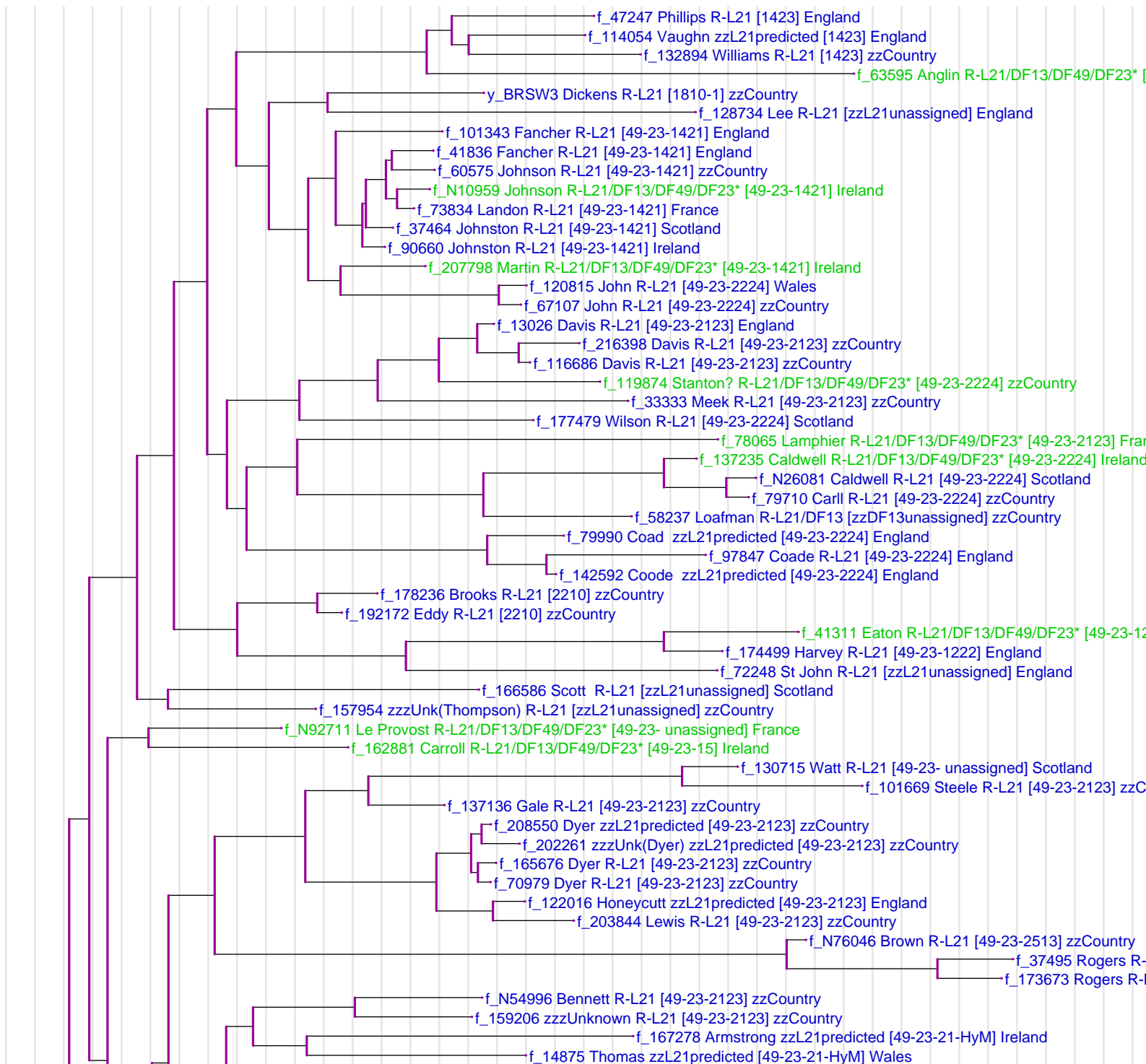


This is the marker distribution for R-DF23. The color indicates the relative frequency of the alleles.

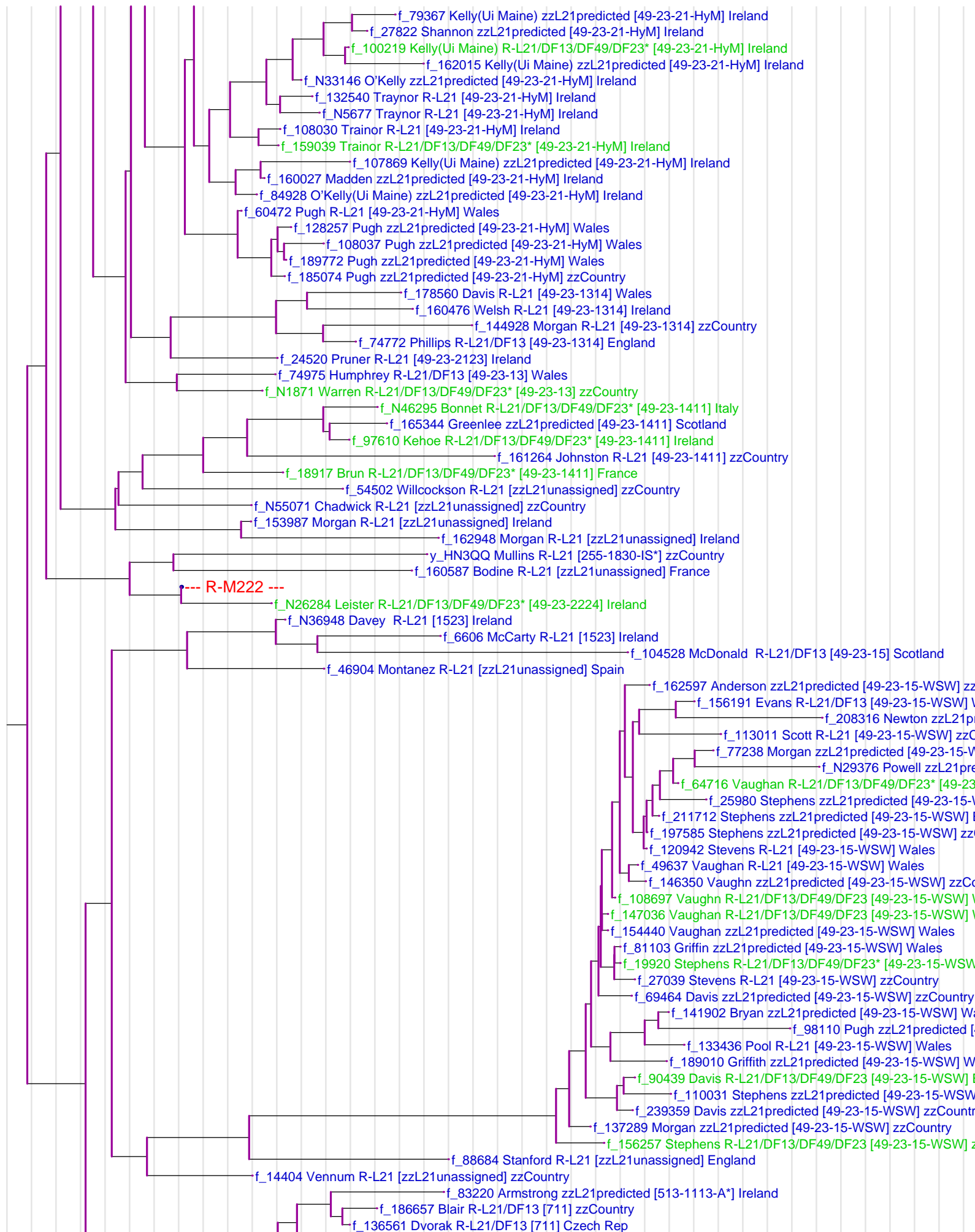


## Age Analysis

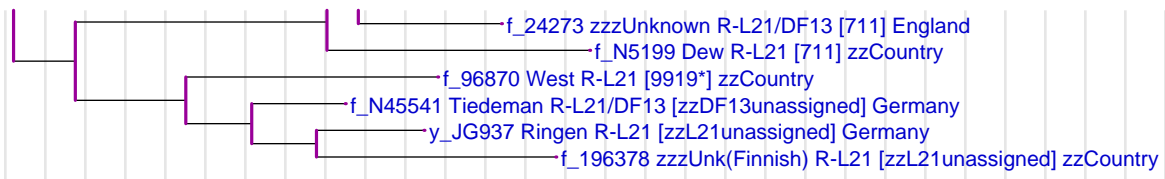
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
860	57620	8764	15.21%	82.30±8.24	2057.42±291.109



The vertical grey lines are separated 10 generations apart.



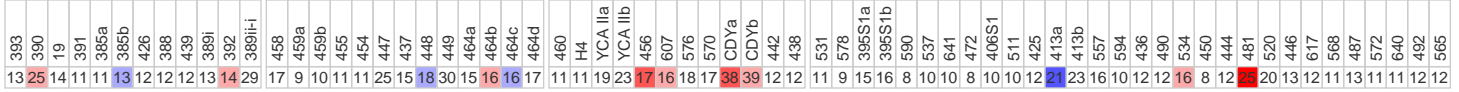
The vertical grey lines are separated 10 generations apart.



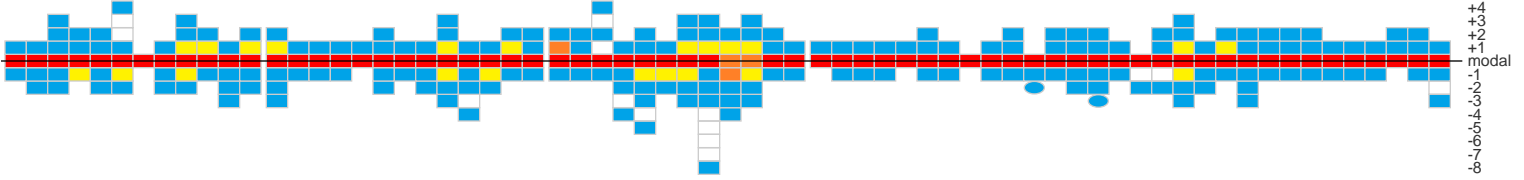
The vertical grey lines are separated 10 generations apart.

# R-M222

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

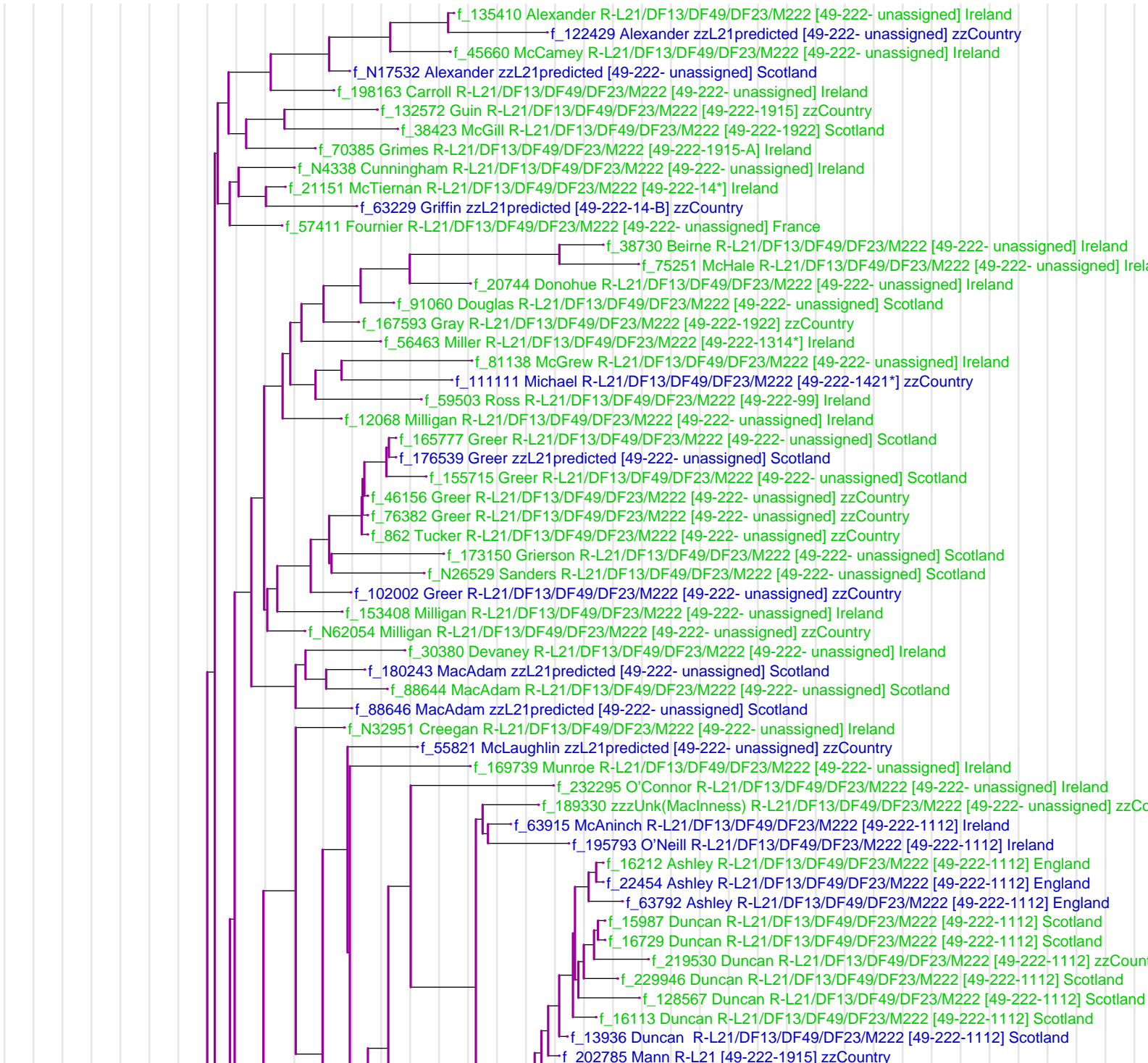


This is the marker distribution for R-M222. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
725	48575	5649	11.63%	61.73±6.18	1543.32±218.384



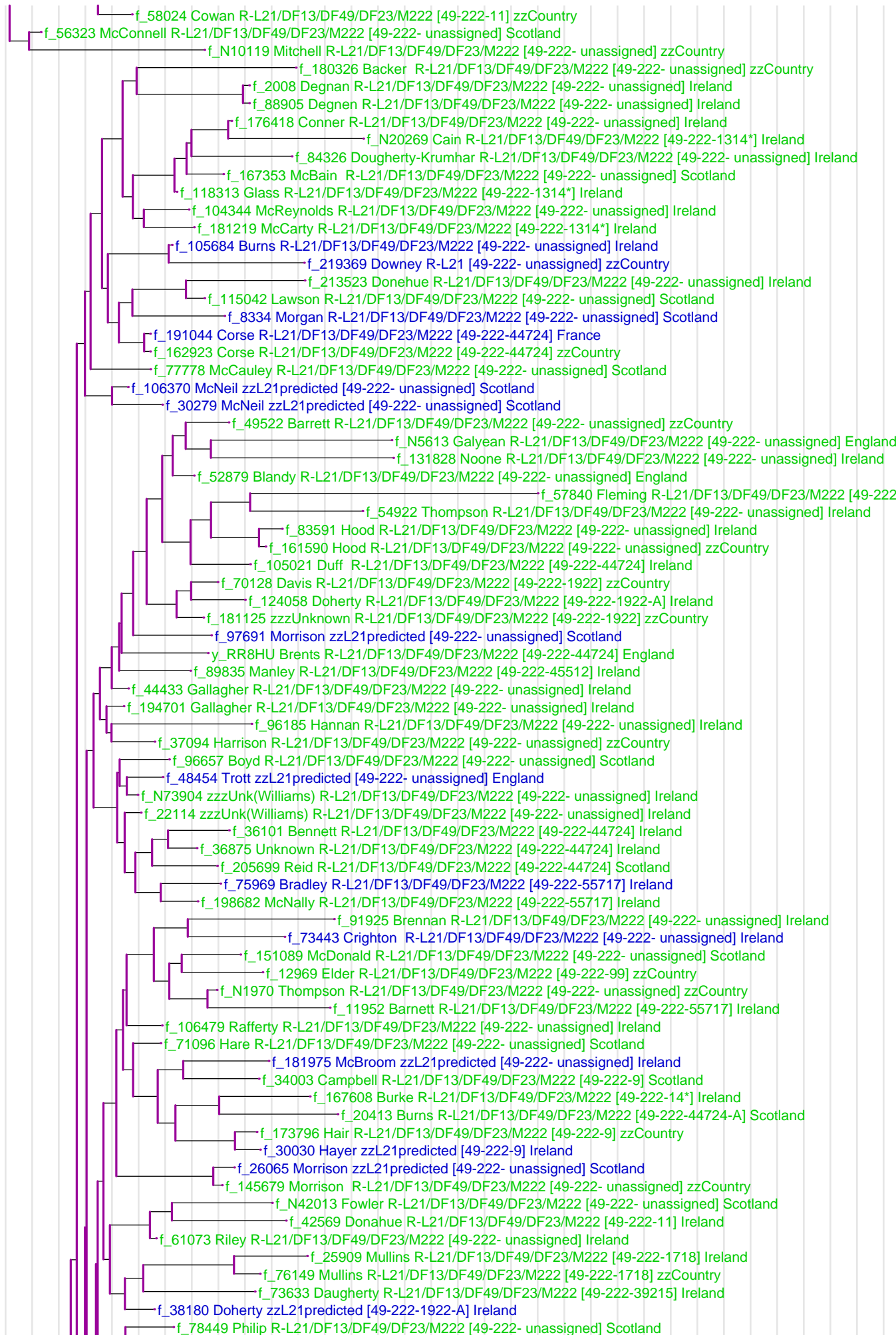
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

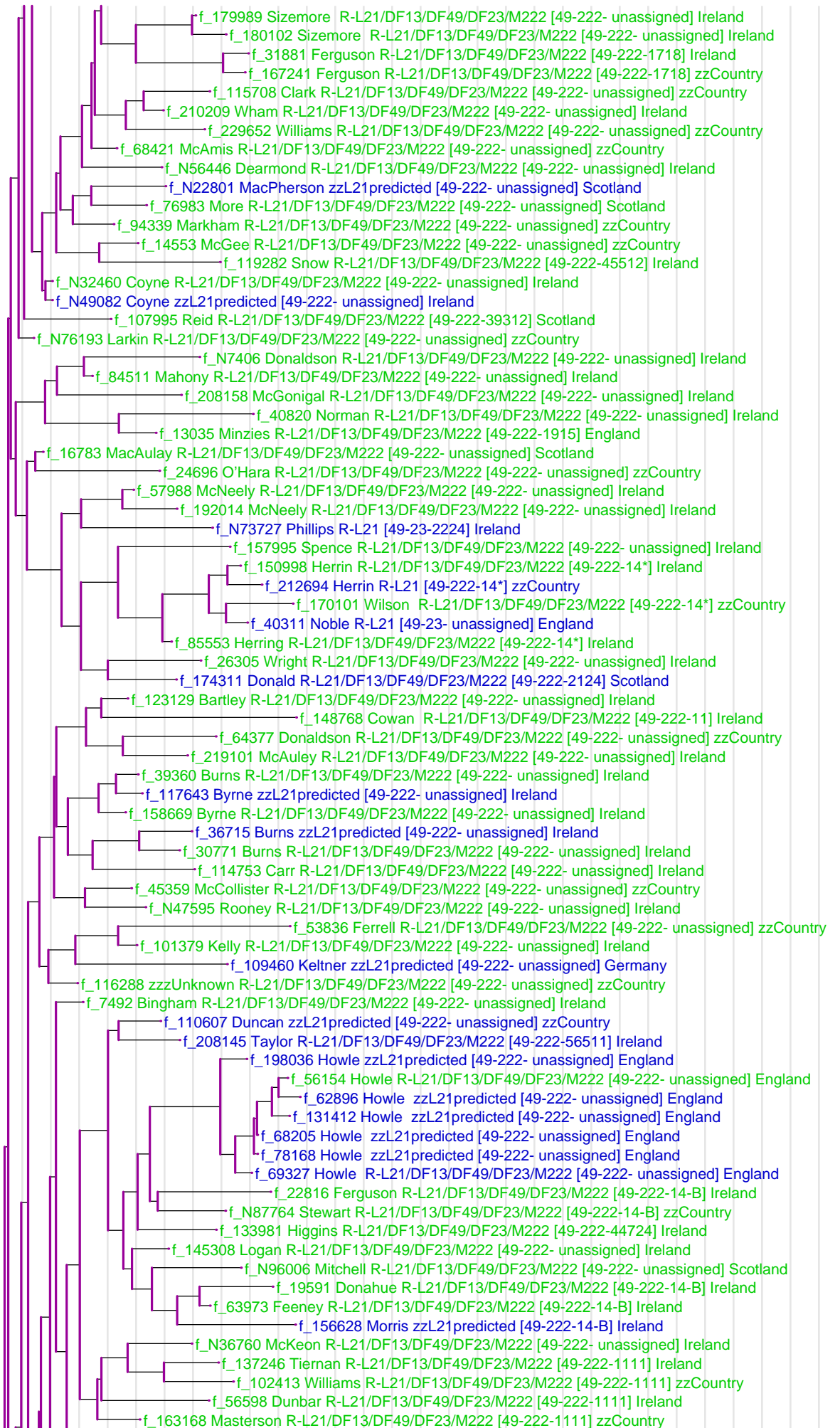


The vertical grey lines are separated 10 generations apart.

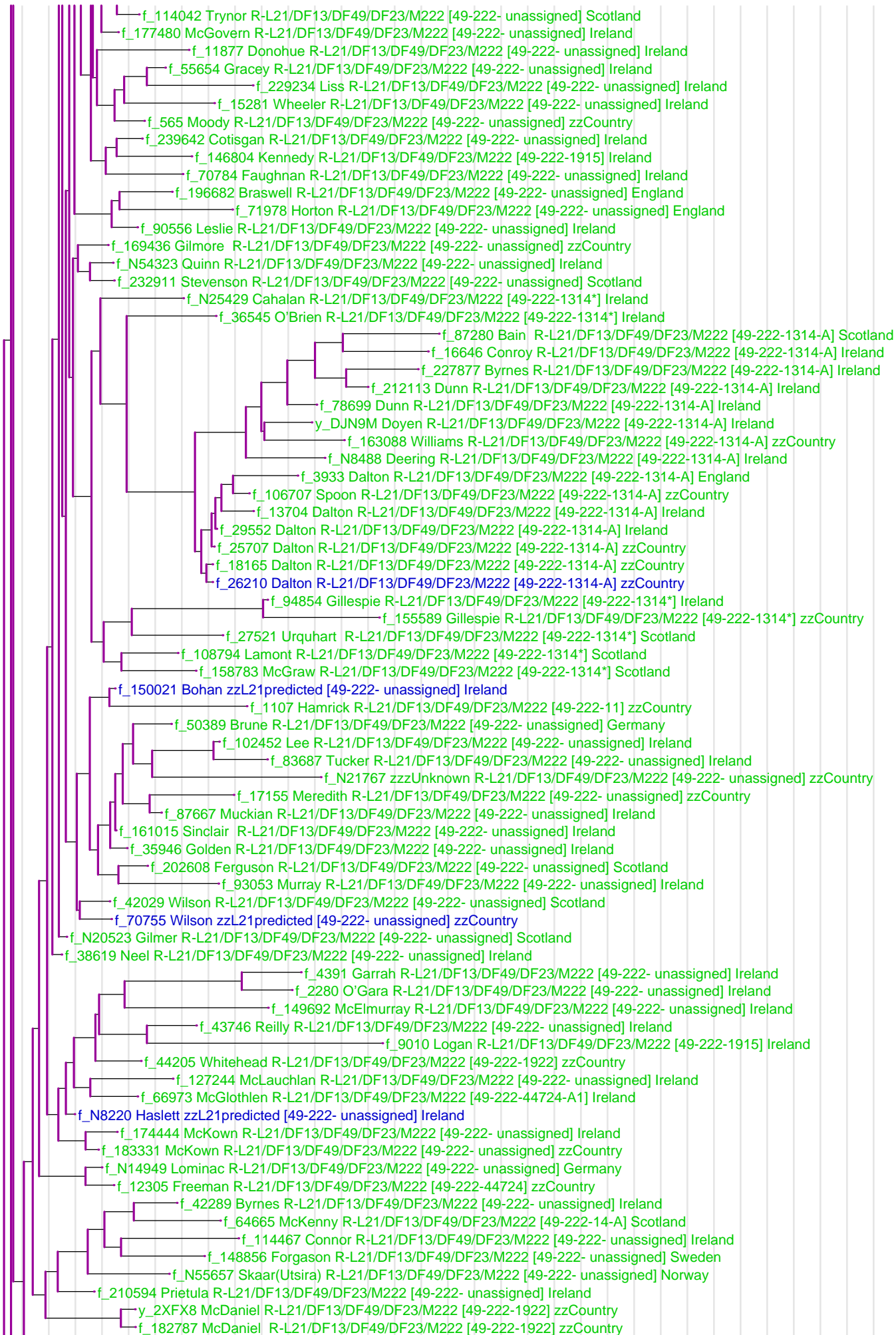


The vertical grey lines are separated 10 generations apart.





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.



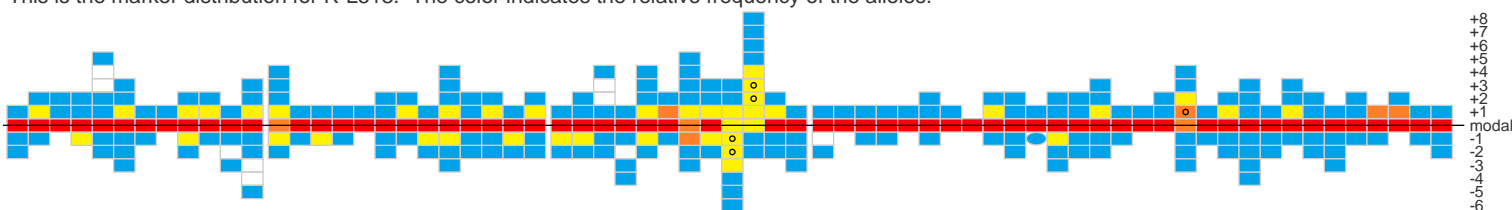
The vertical grey lines are separated 10 generations apart.

# R-L513

This is the modal haplotype for R-L513. The coloration is with respect to the modal haplotype of the full tree.

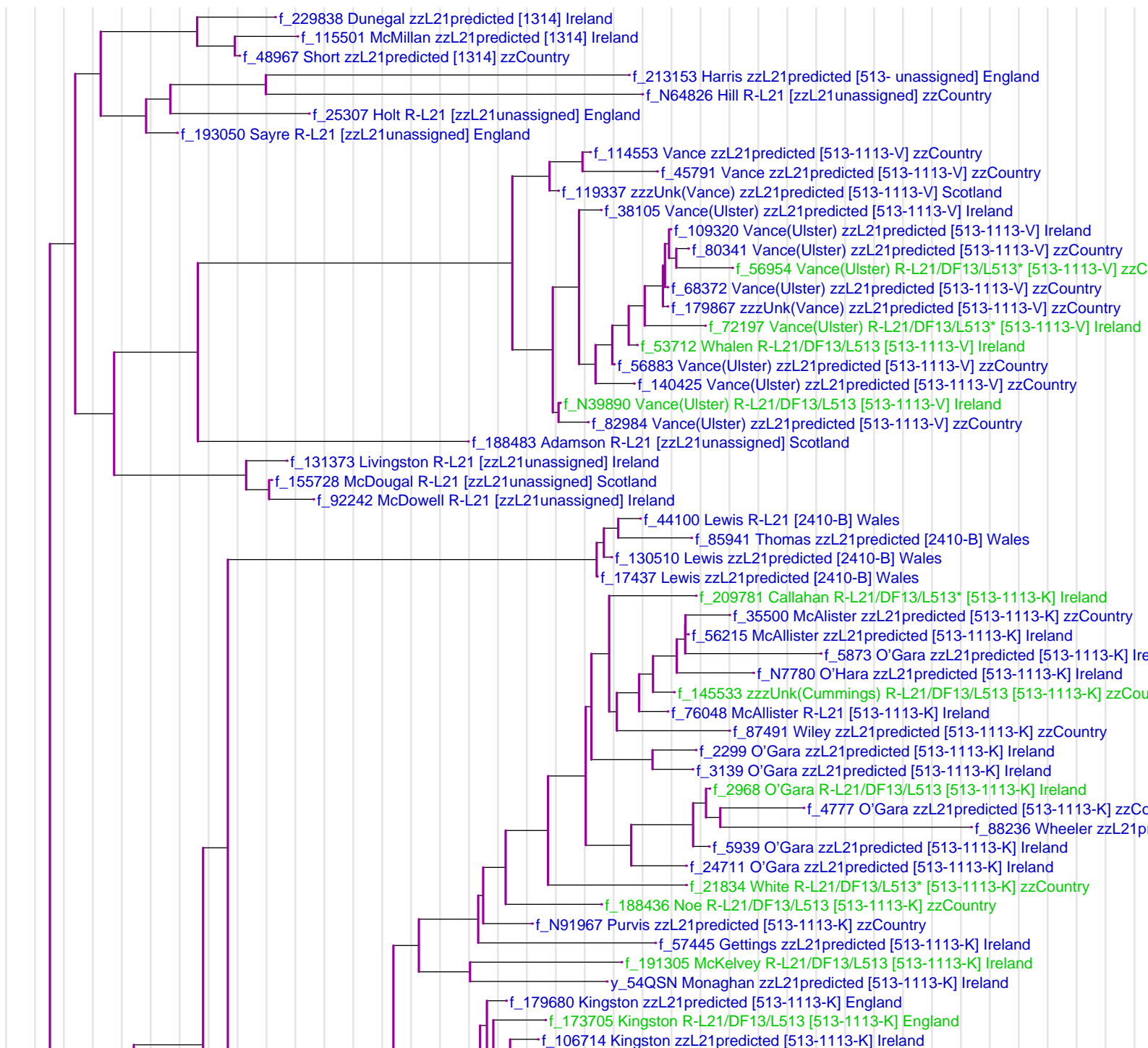
393	390	19	391	385a	385b	426	388	439	389i	392	389f-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	572	640	492	565
13	24	14	11	14	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	11	19	23	16	15	18	17	38	37	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	11	12	12	

This is the marker distribution for R-L513. The color indicates the relative frequency of the alleles.

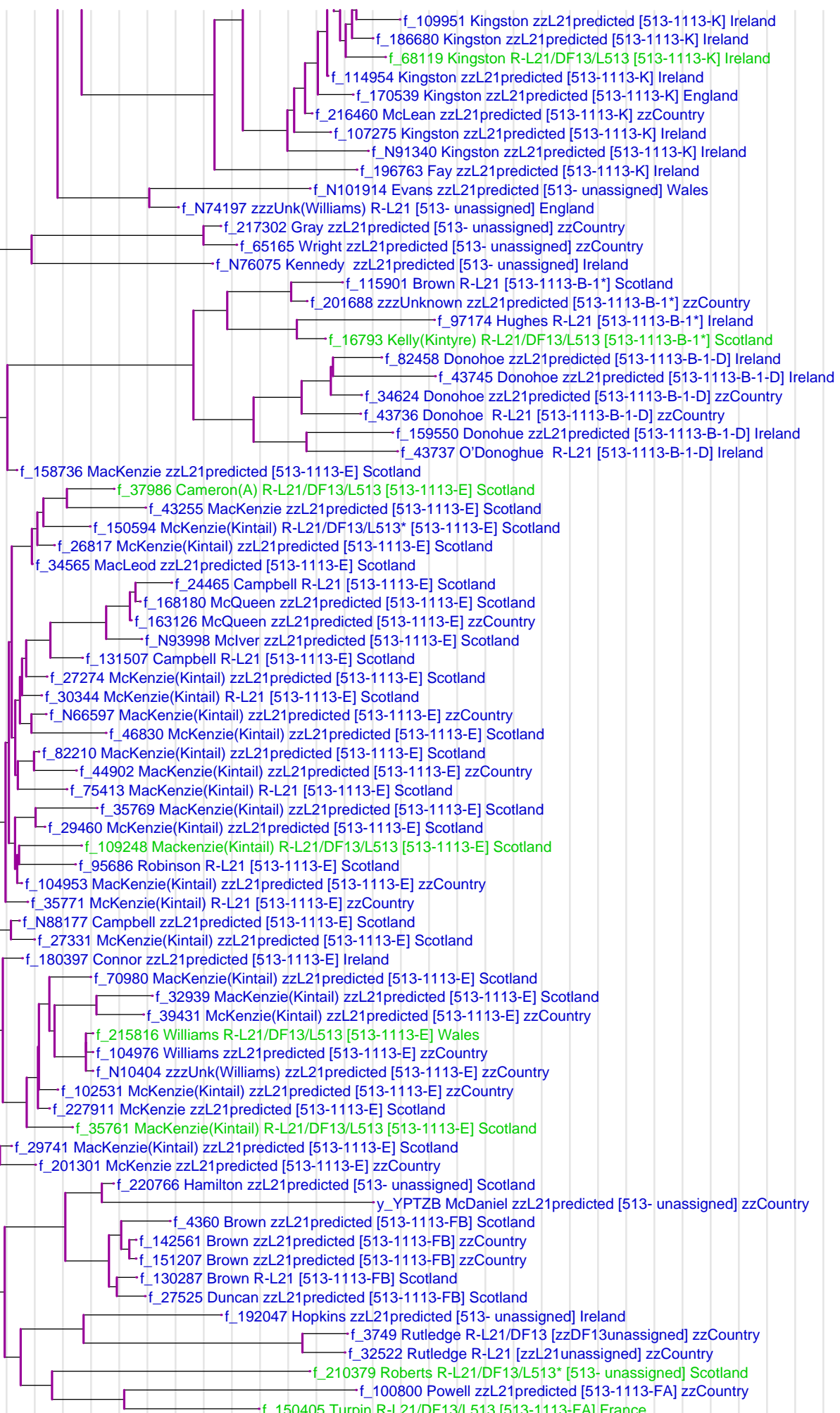


## Age Analysis

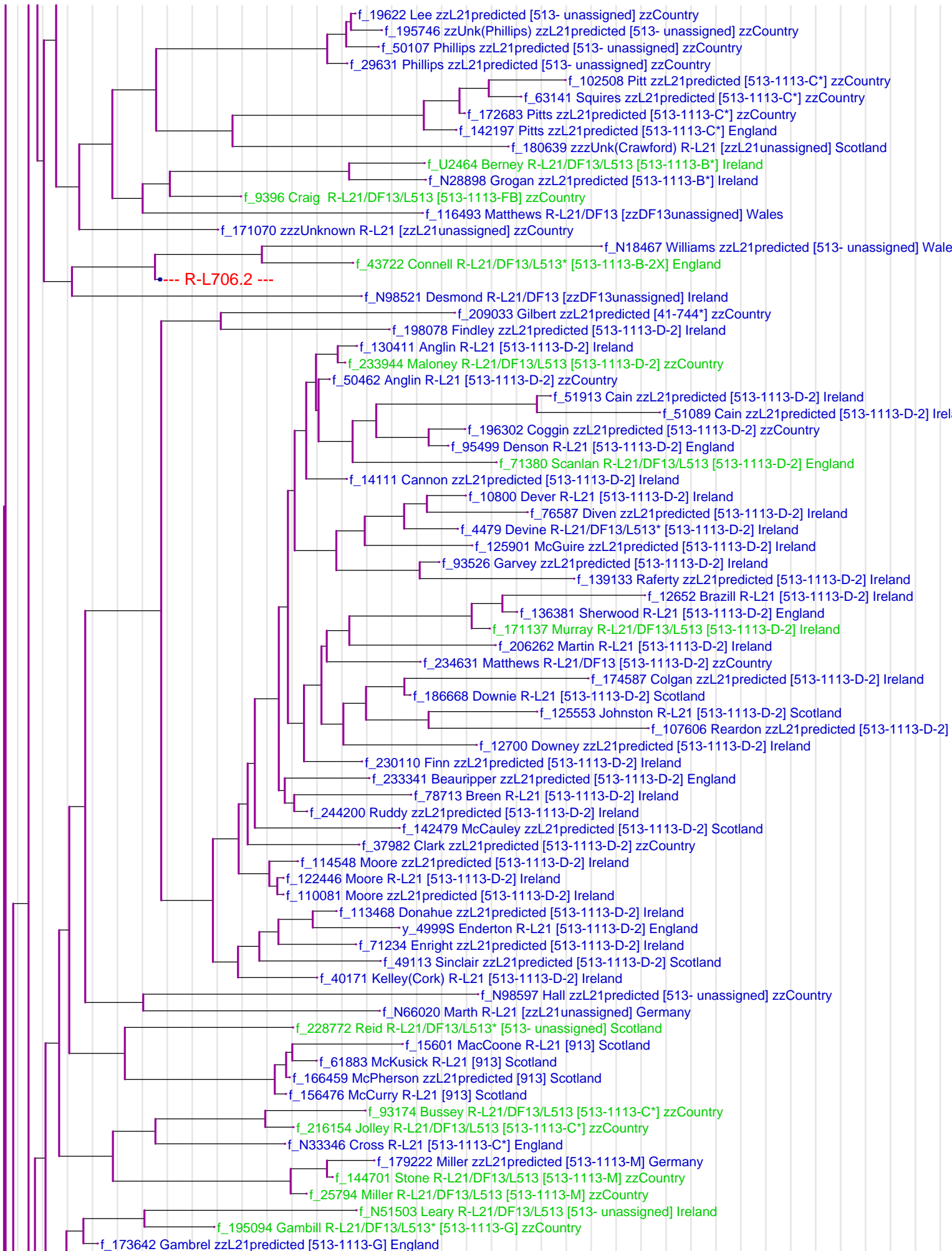
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
849	56883	12321	21.66%	121.40±12.15	3034.94±429.437



The vertical grey lines are separated 10 generations apart.

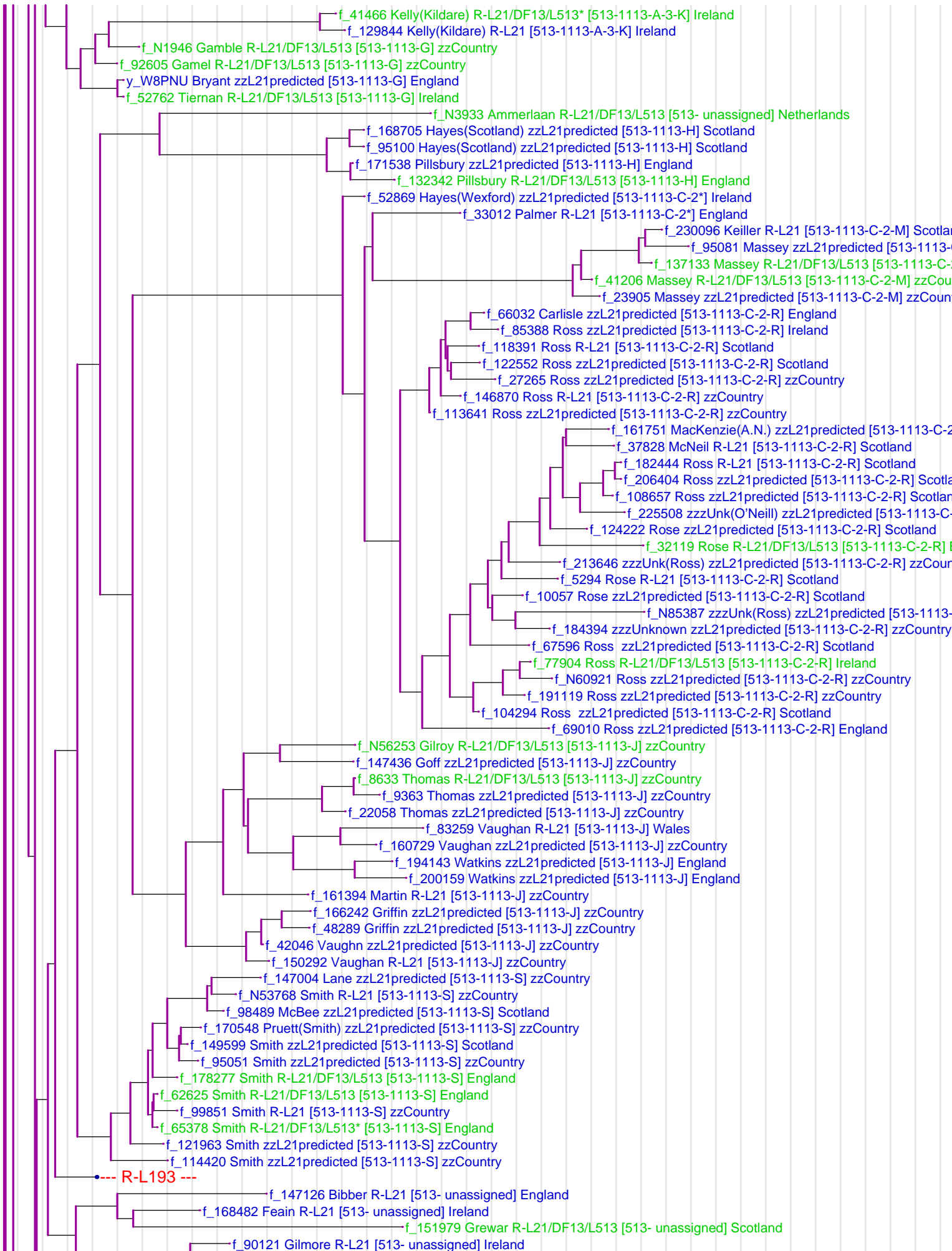


The vertical grey lines are separated 10 generations apart.

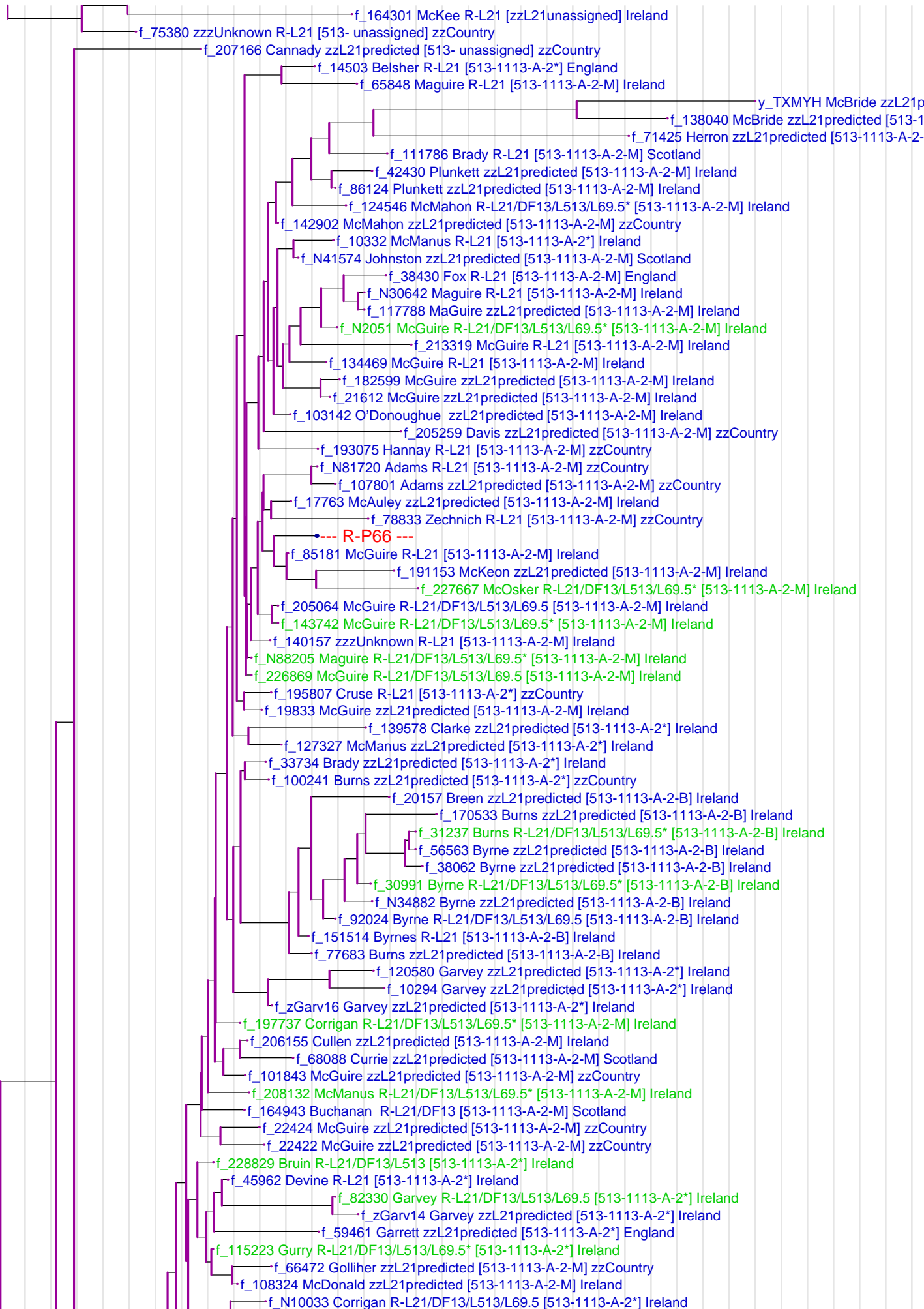


The vertical grey lines are separated 10 generations apart.

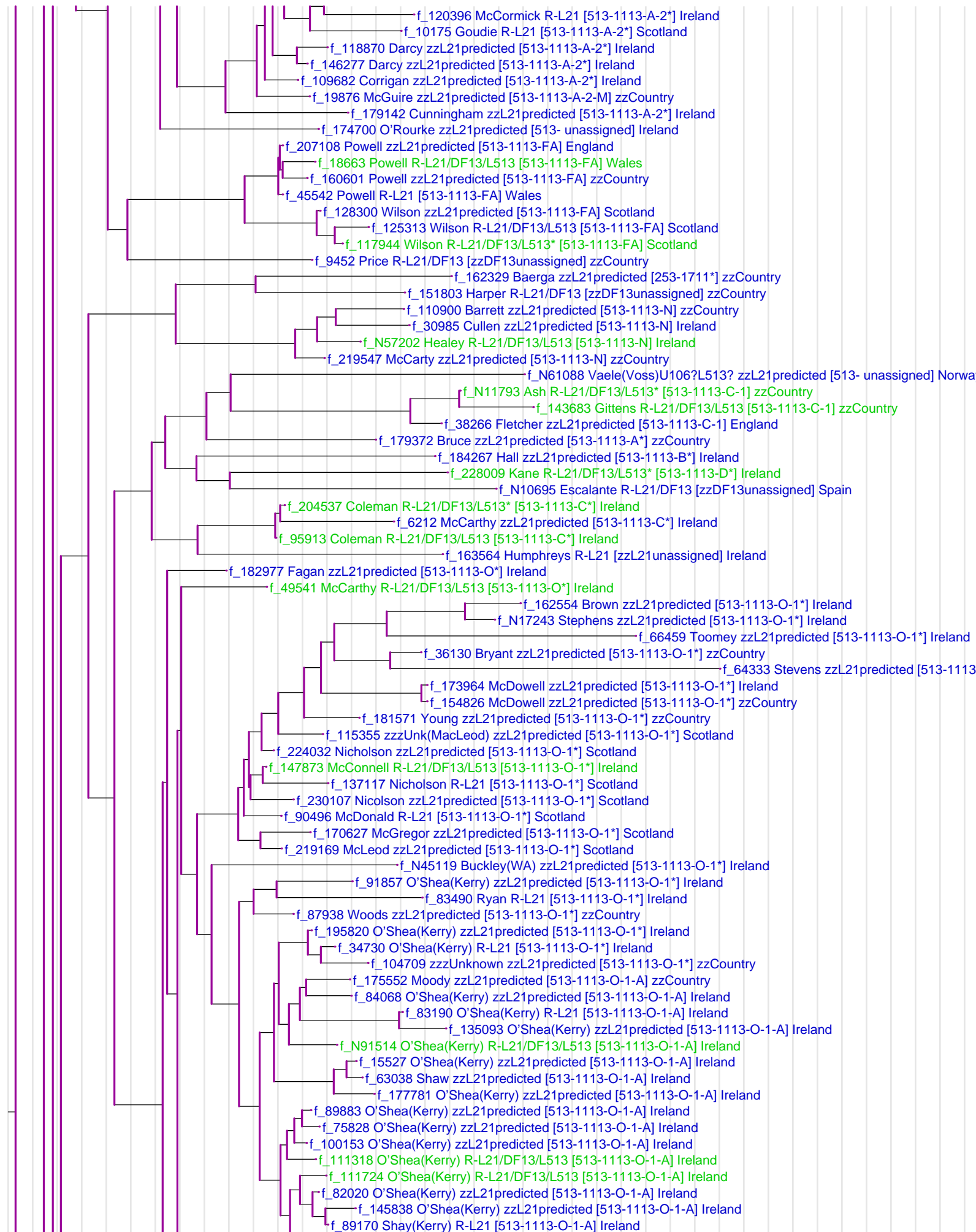




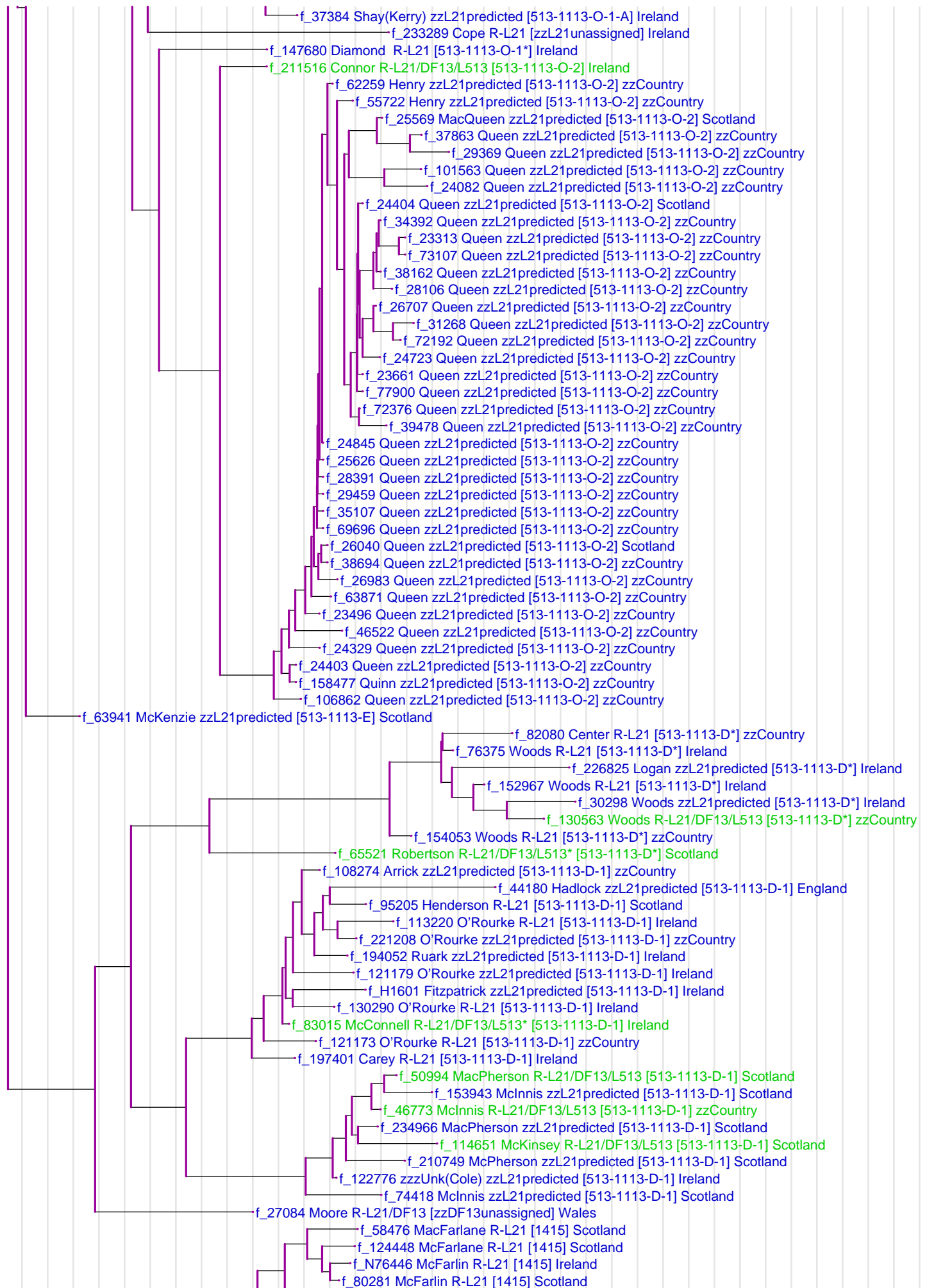
The vertical grey lines are separated 10 generations apart.



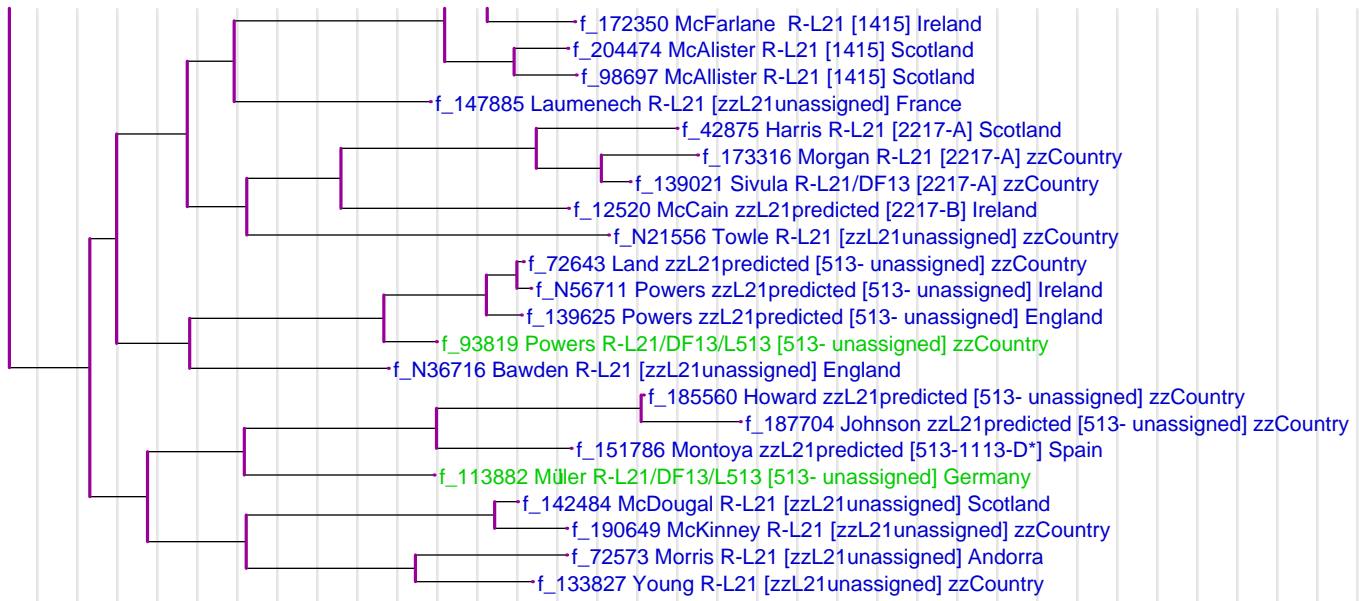
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



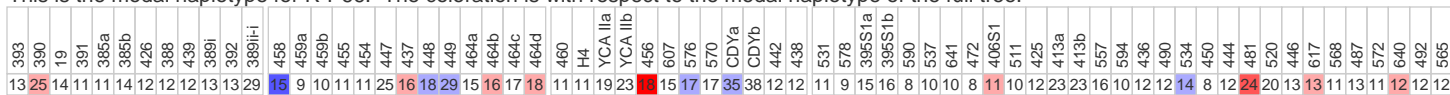
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

# R-P66

This is the modal haplotype for R-P66. The coloration is with respect to the modal haplotype of the full tree.

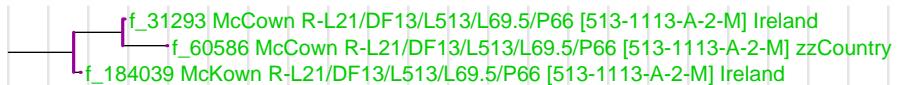


This is the marker distribution for R-P66. The color indicates the relative frequency of the alleles.



## Age Analysis

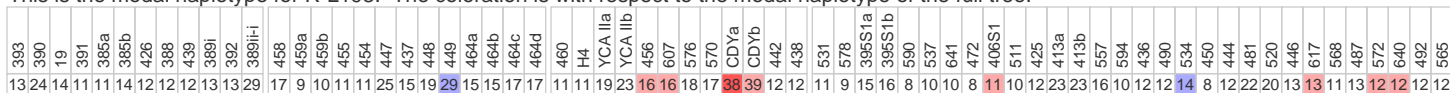
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	3	1.49%	7.52±0.92	187.97±29.7502



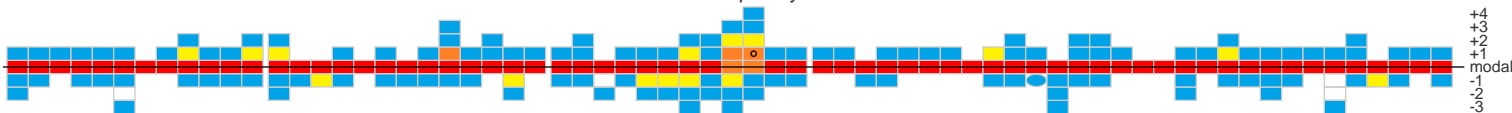
The vertical grey lines are separated 10 generations apart.

# R-L193

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

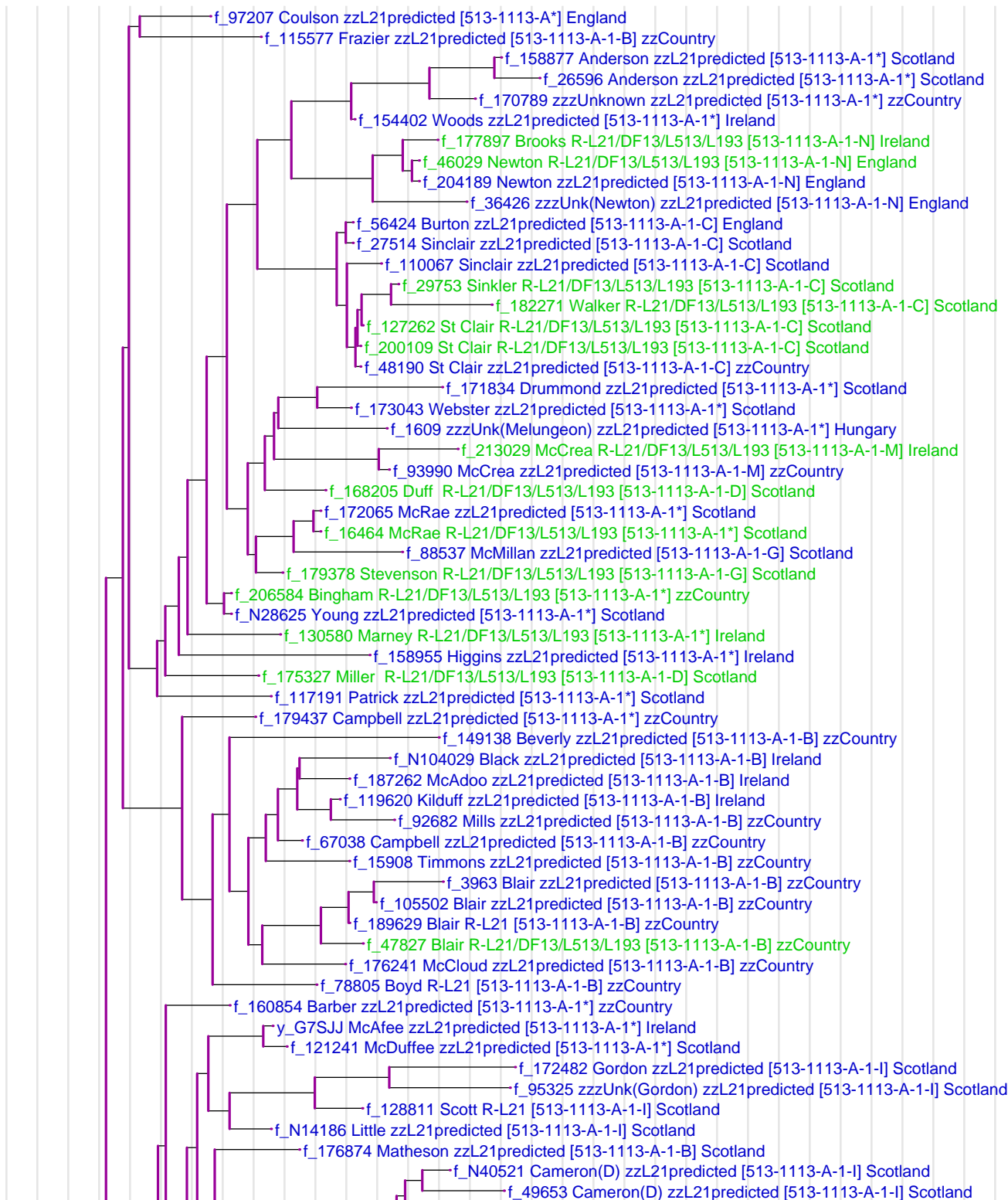


This is the marker distribution for R-L193. The color indicates the relative frequency of the alleles.

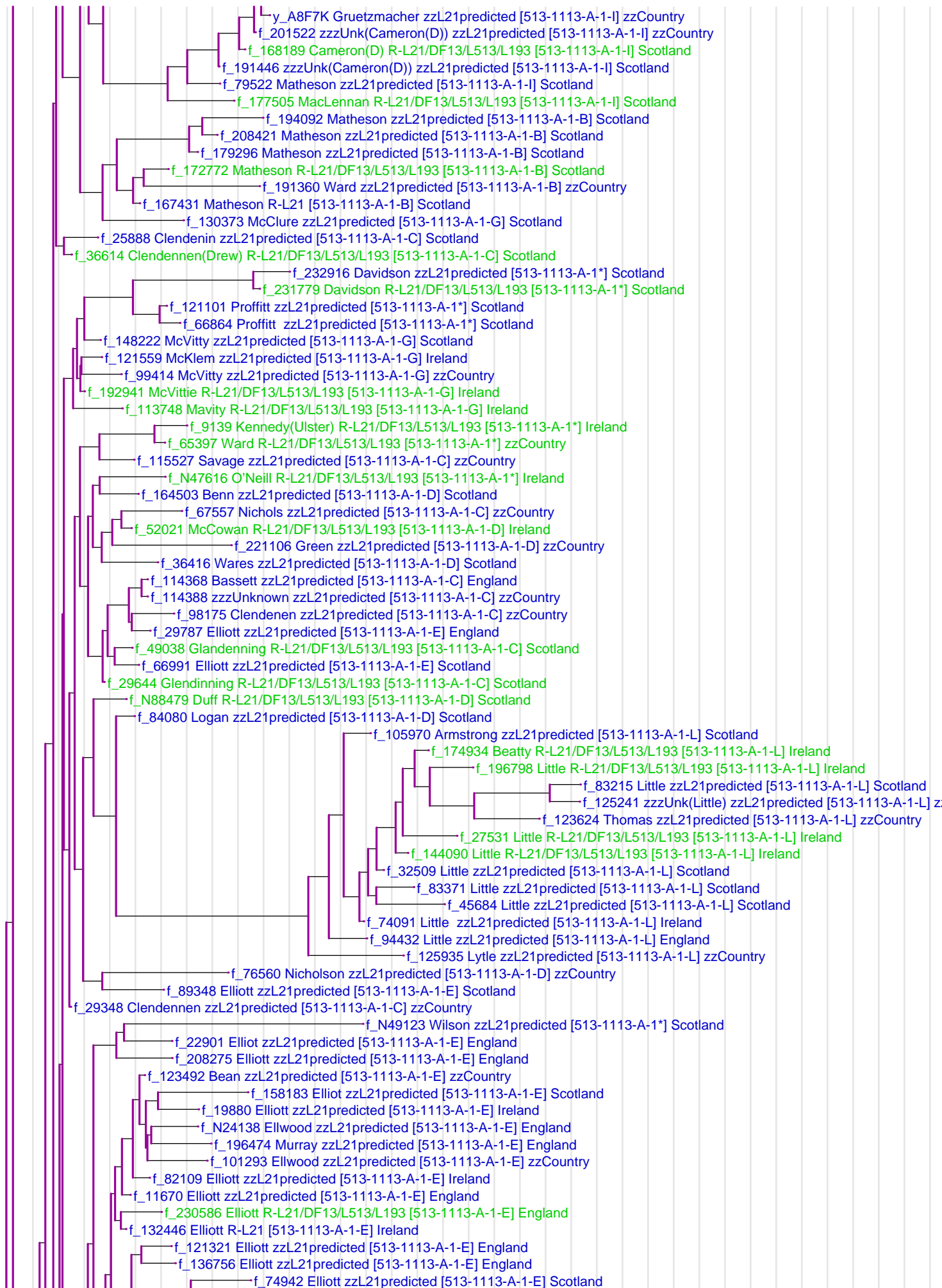


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
275	18425	1986	10.78%	56.96±5.71	1424.03±201.691

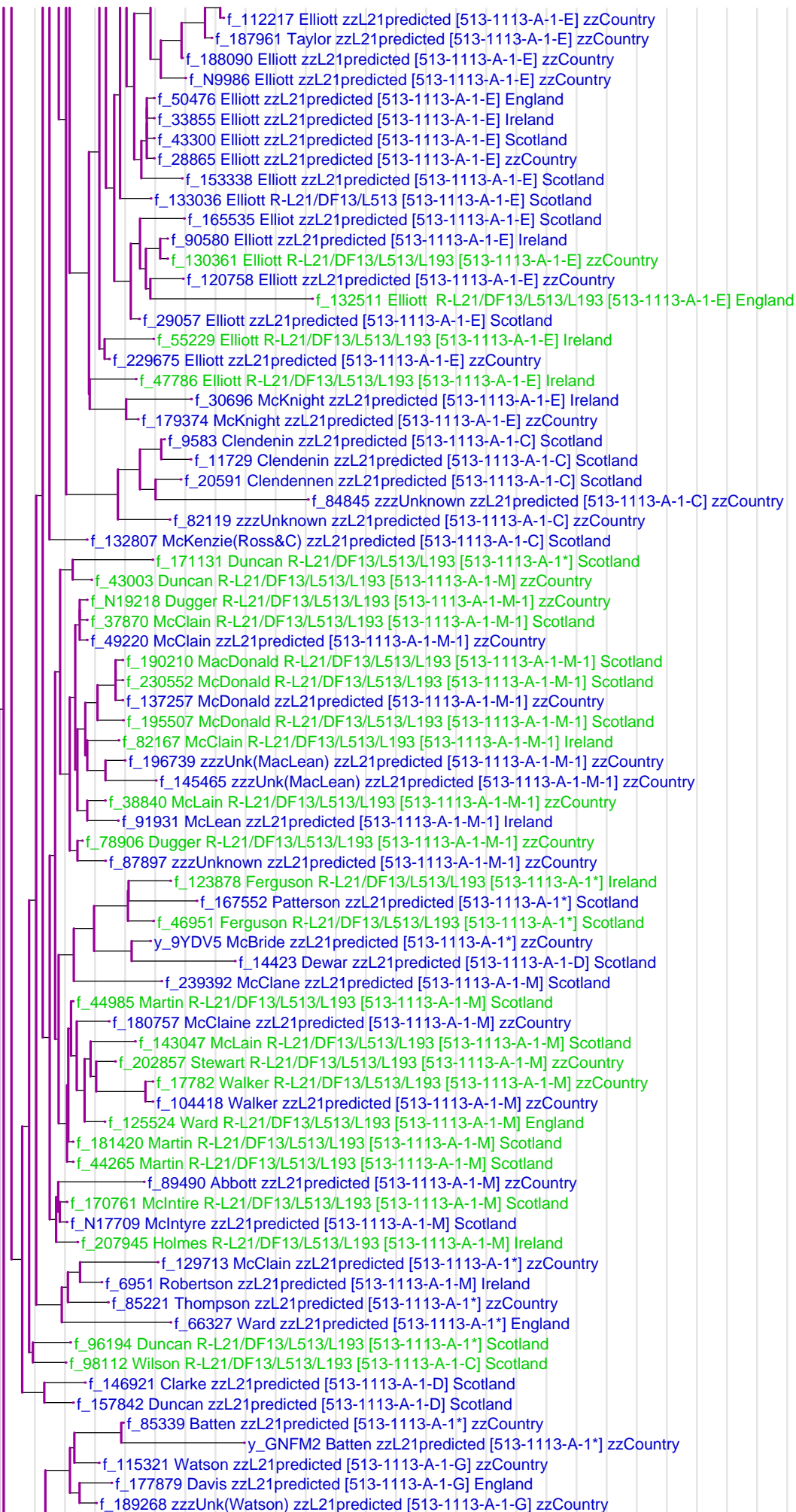


The vertical grey lines are separated 10 generations apart.

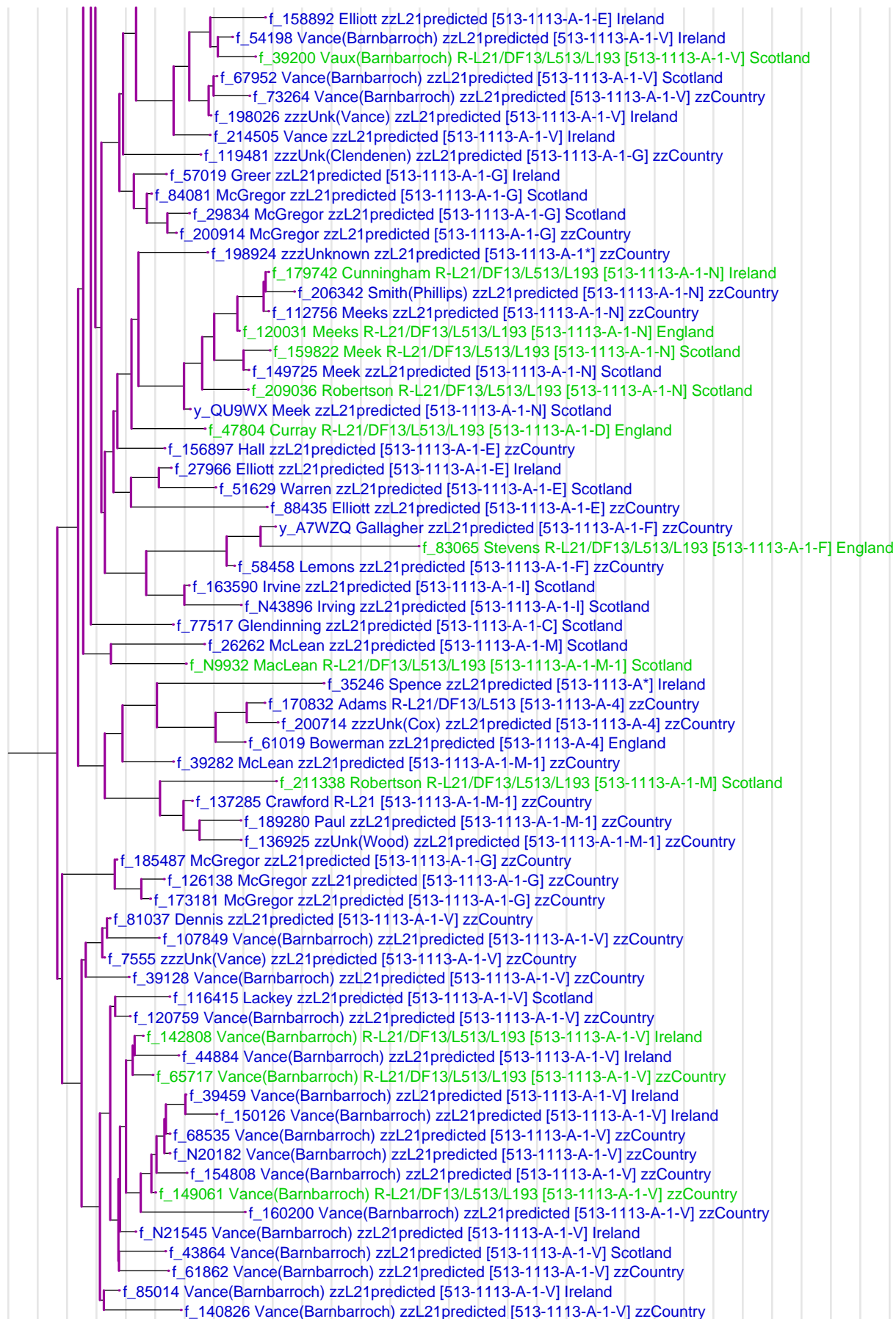


The vertical grey lines are separated 10 generations apart.





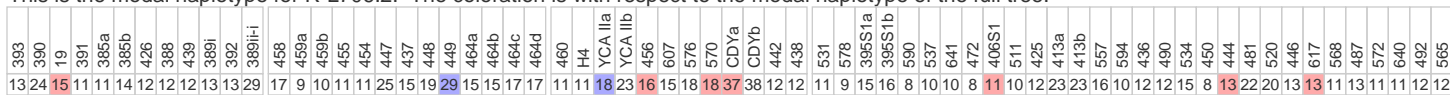
The vertical grey lines are separated 10 generations apart.



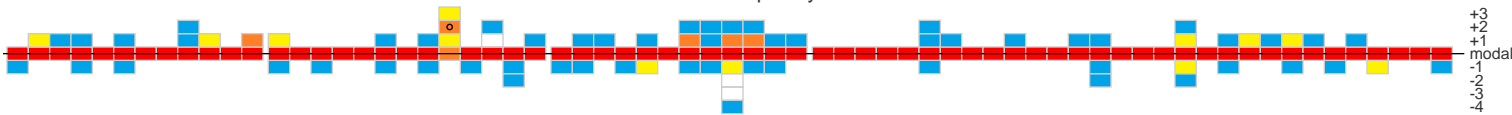
The vertical grey lines are separated 10 generations apart.

# R-L706.2

This is the modal haplotype for R-L706.2. The coloration is with respect to the modal haplotype of the full tree.



This is the marker distribution for R-L706.2. The color indicates the relative frequency of the alleles.



## Age Analysis

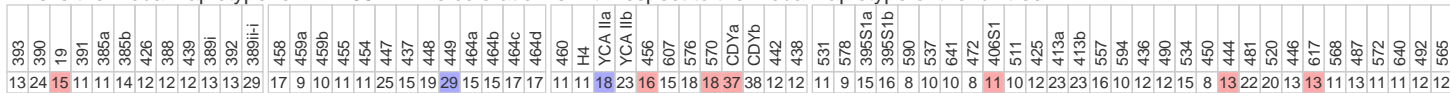
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
48	3216	303	9.42%	49.44±5.03	1235.88±176.264



The vertical grey lines are separated 10 generations apart.

# R-L705.2

This is the modal haplotype for R-L705.2. The coloration is with respect to the modal haplotype of the full tree.

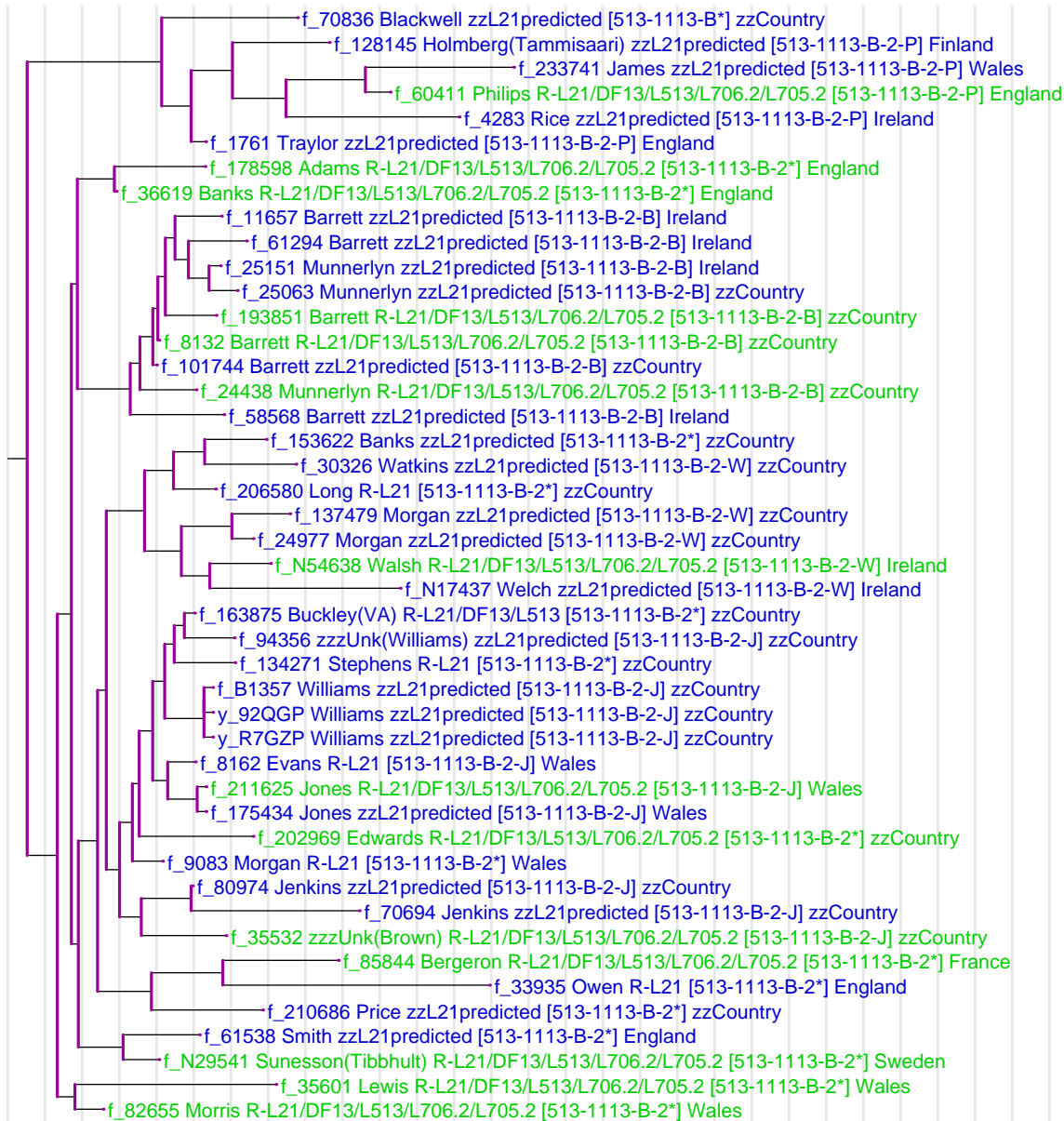


This is the marker distribution for R-L705.2. The color indicates the relative frequency of the alleles.



## Age Analysis

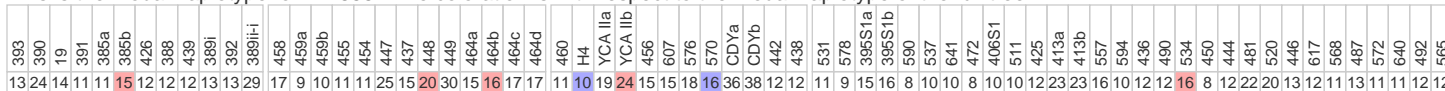
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
45	3015	285	9.45%	49.61±5.05	1240.16±176.973



The vertical grey lines are separated 10 generations apart.

# R-L555

This is the modal haplotype for R-L555. The coloration is with respect to the modal haplotype of the full tree.

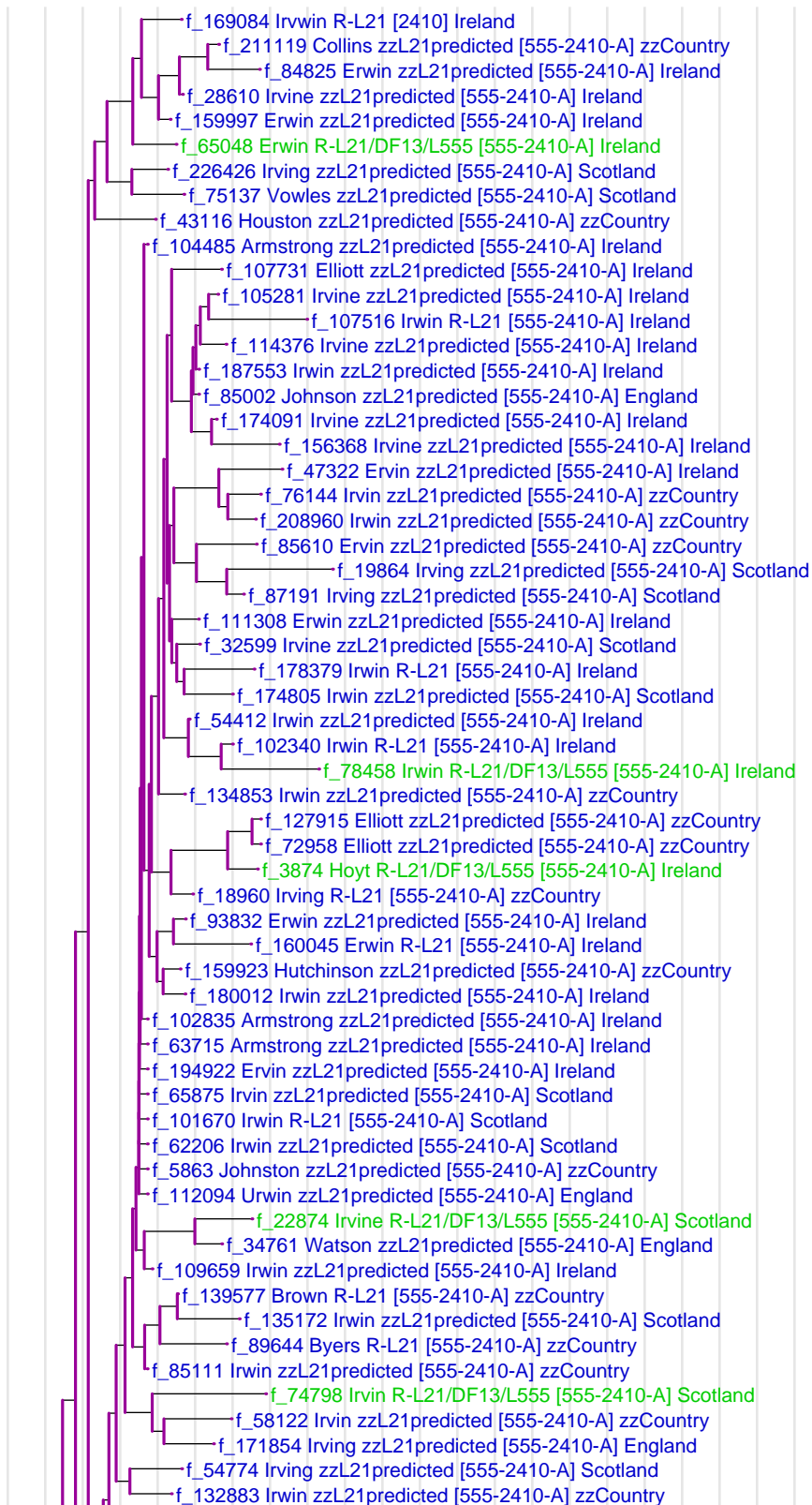


This is the marker distribution for R-L555. The color indicates the relative frequency of the alleles.

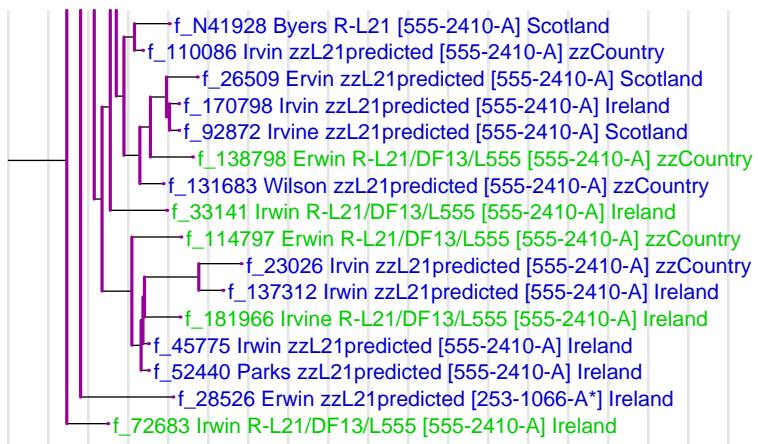


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
76	5092	181	3.55%	18.09±1.83	452.363±64.2984



The vertical grey lines are separated 10 generations apart.



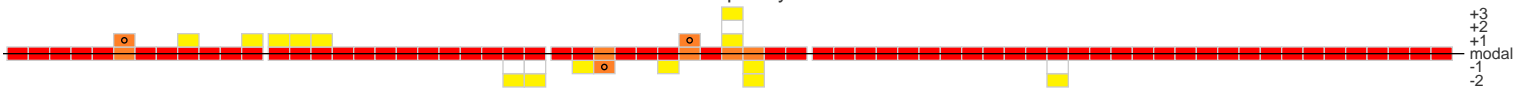
The vertical grey lines are separated 10 generations apart.

# R-L96

This is the modal haplotype for R-L96. The coloration is with respect to the modal haplotype of the full tree.

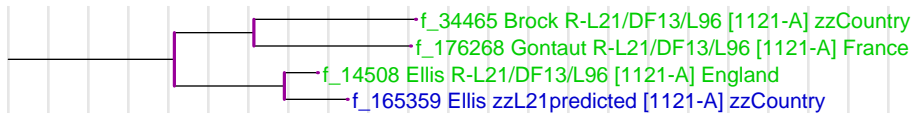
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565
13	24	14	10	11	14	12	12	12	13	13	28	17	9	10	11	11	24	15	19	29	15	15	17	17	11	11	19	23	16	15	19	19	35	39	12	12	11	9	15	16	8	11	10	8	10	10	12	23	23	17	10	12	12	15	8	12	23	21	13	12	11	13	11	11	12	12

This is the marker distribution for R-L96. The color indicates the relative frequency of the alleles.



## Age Analysis

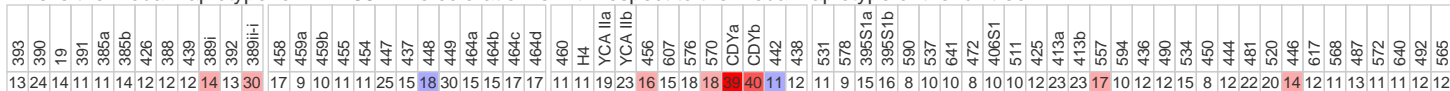
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	26	9.70%	50.98±6.05	1274.46±197.858



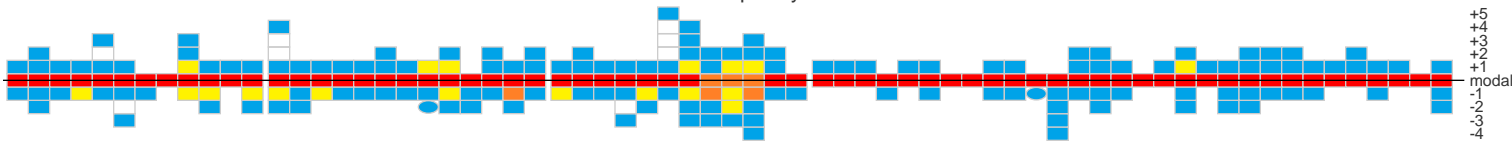
The vertical grey lines are separated 10 generations apart.

# R-Z255

This is the modal haplotype for R-Z255. The coloration is with respect to the modal haplotype of the full tree.

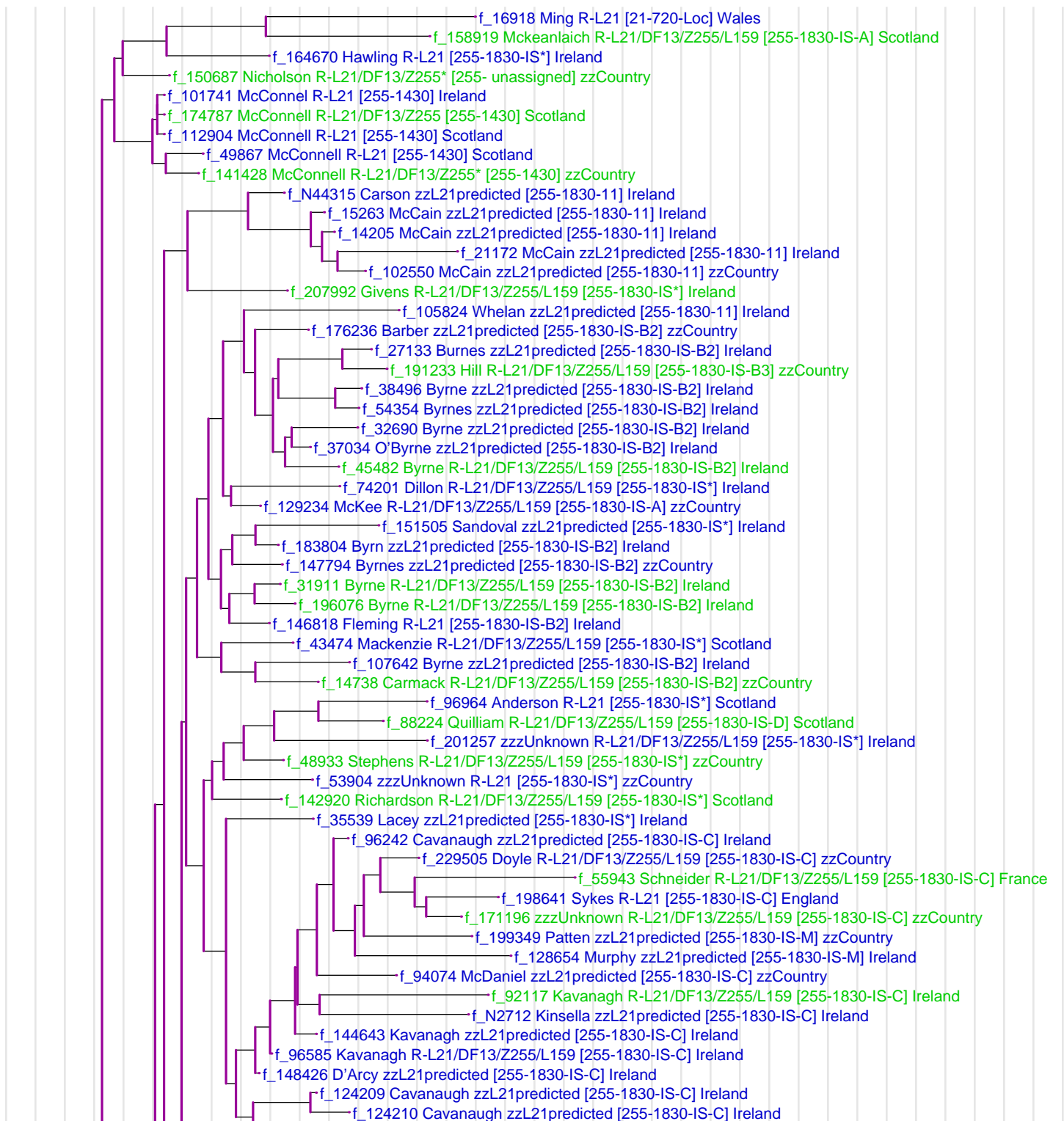


This is the marker distribution for R-Z255. The color indicates the relative frequency of the alleles.



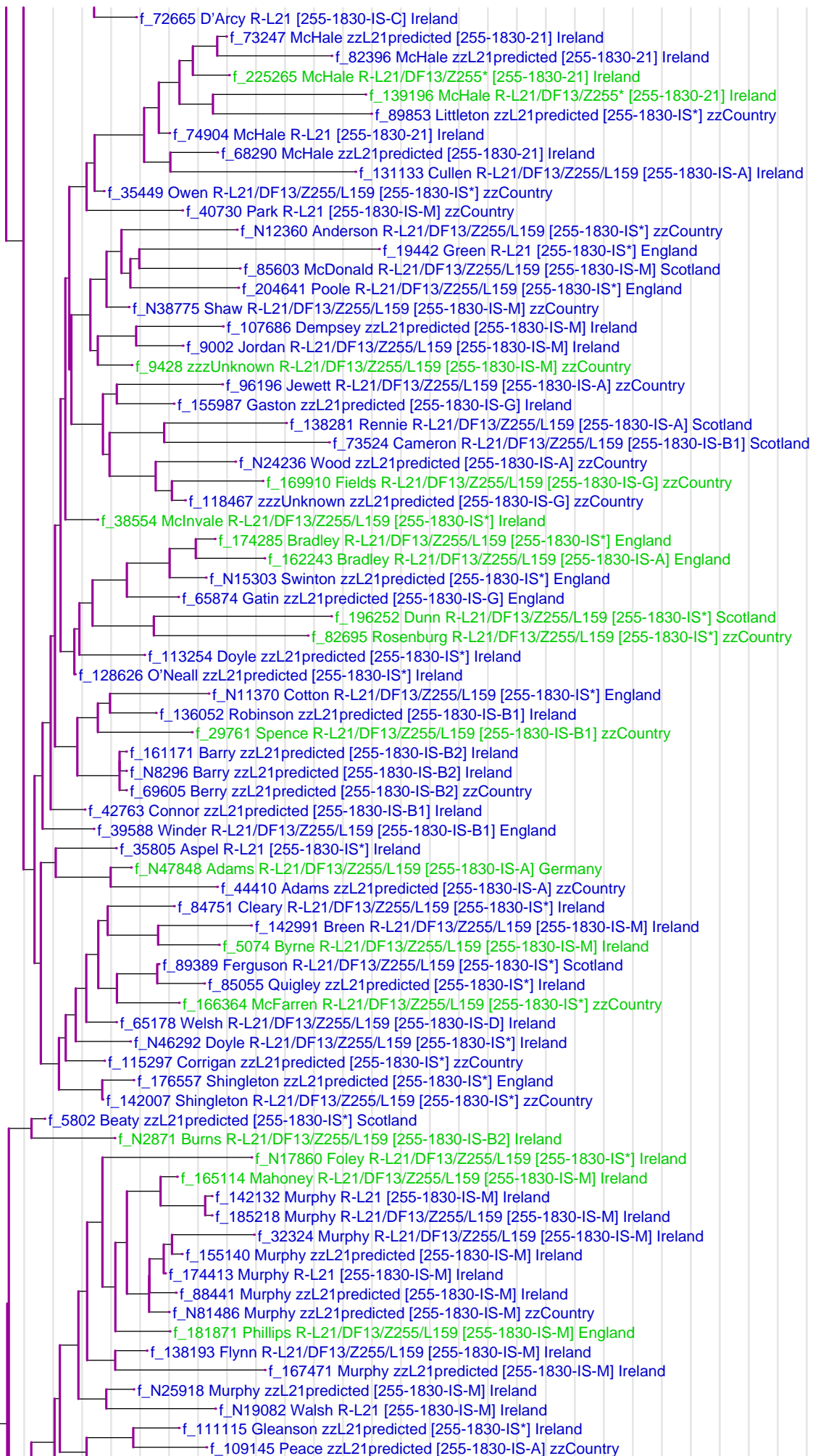
## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
263	17621	2207	12.52%	66.80±6.70	1670.05±236.559

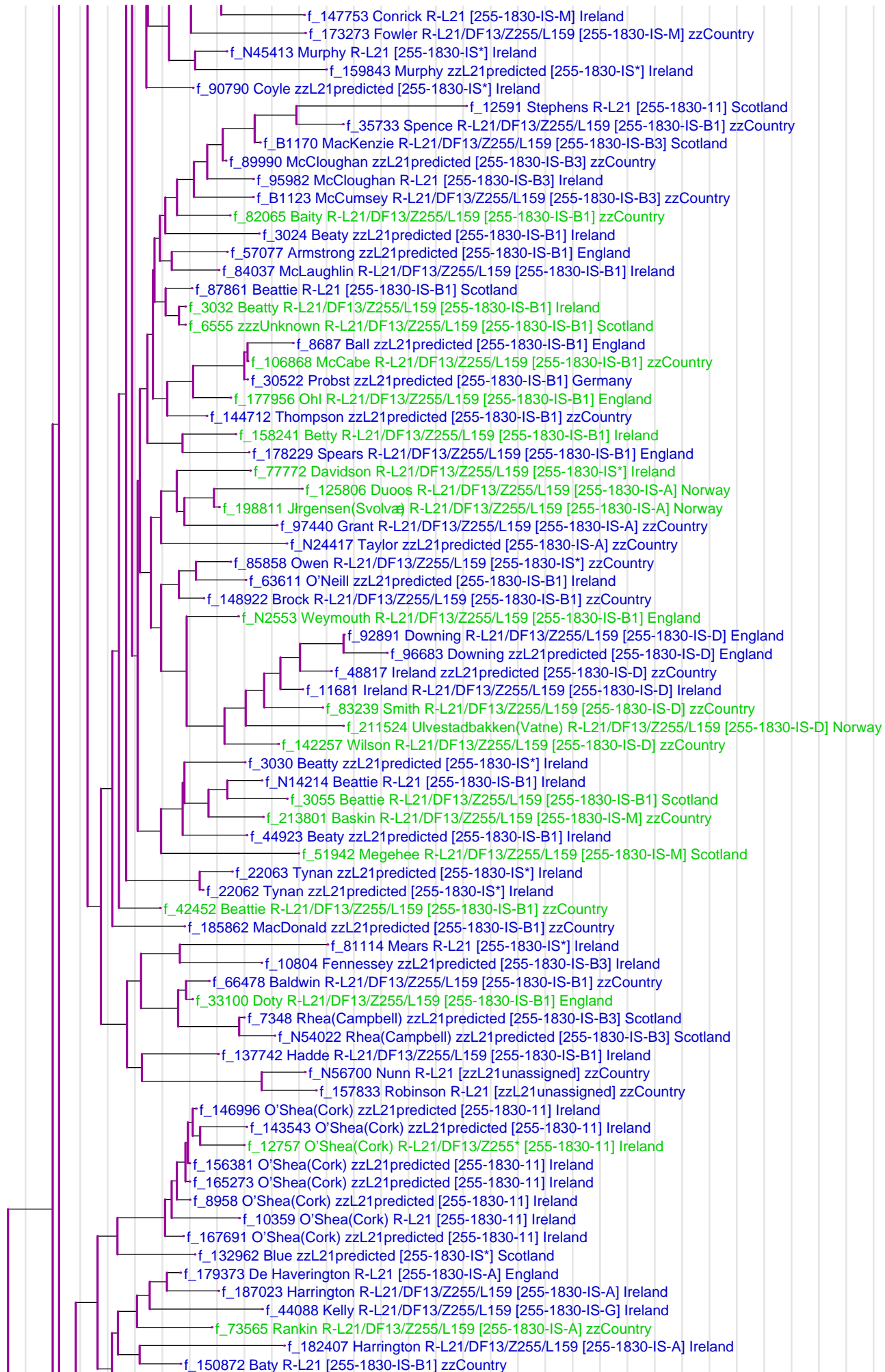


The vertical grey lines are separated 10 generations apart.

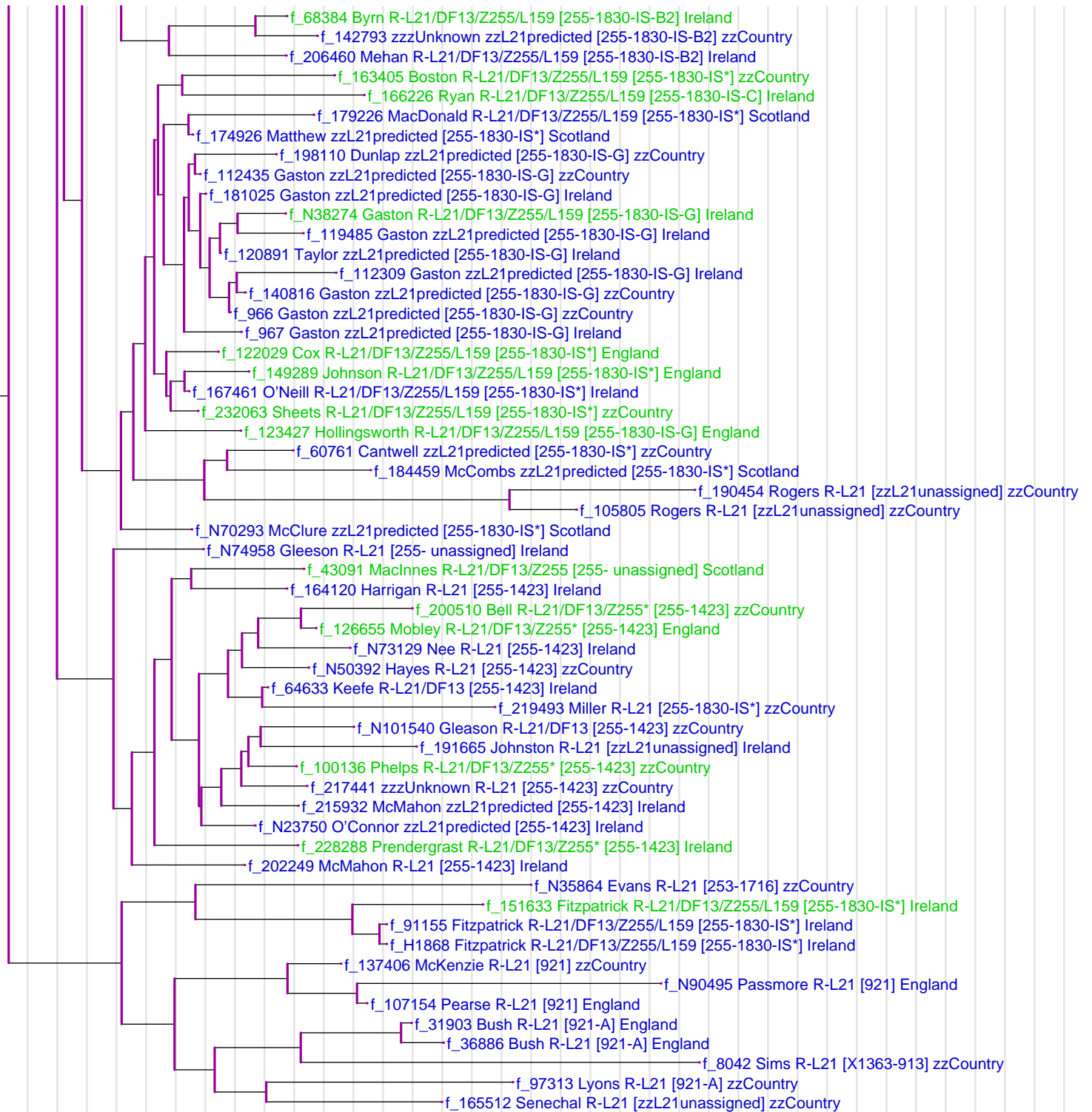




The vertical grey lines are separated 10 generations apart.



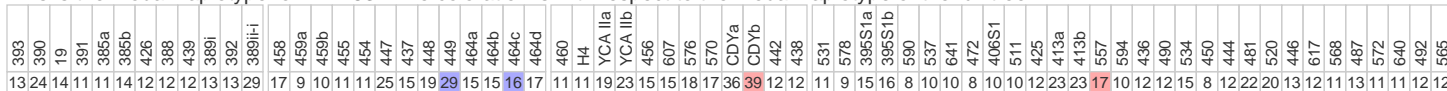
The vertical grey lines are separated 10 generations apart.



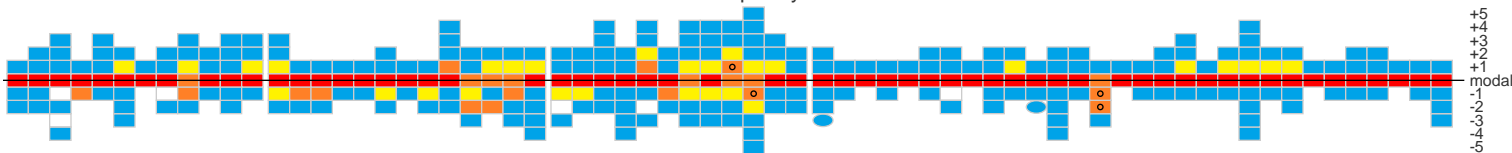
The vertical grey lines are separated 10 generations apart.

# R-Z253

This is the modal haplotype for R-Z253. The coloration is with respect to the modal haplotype of the full tree.

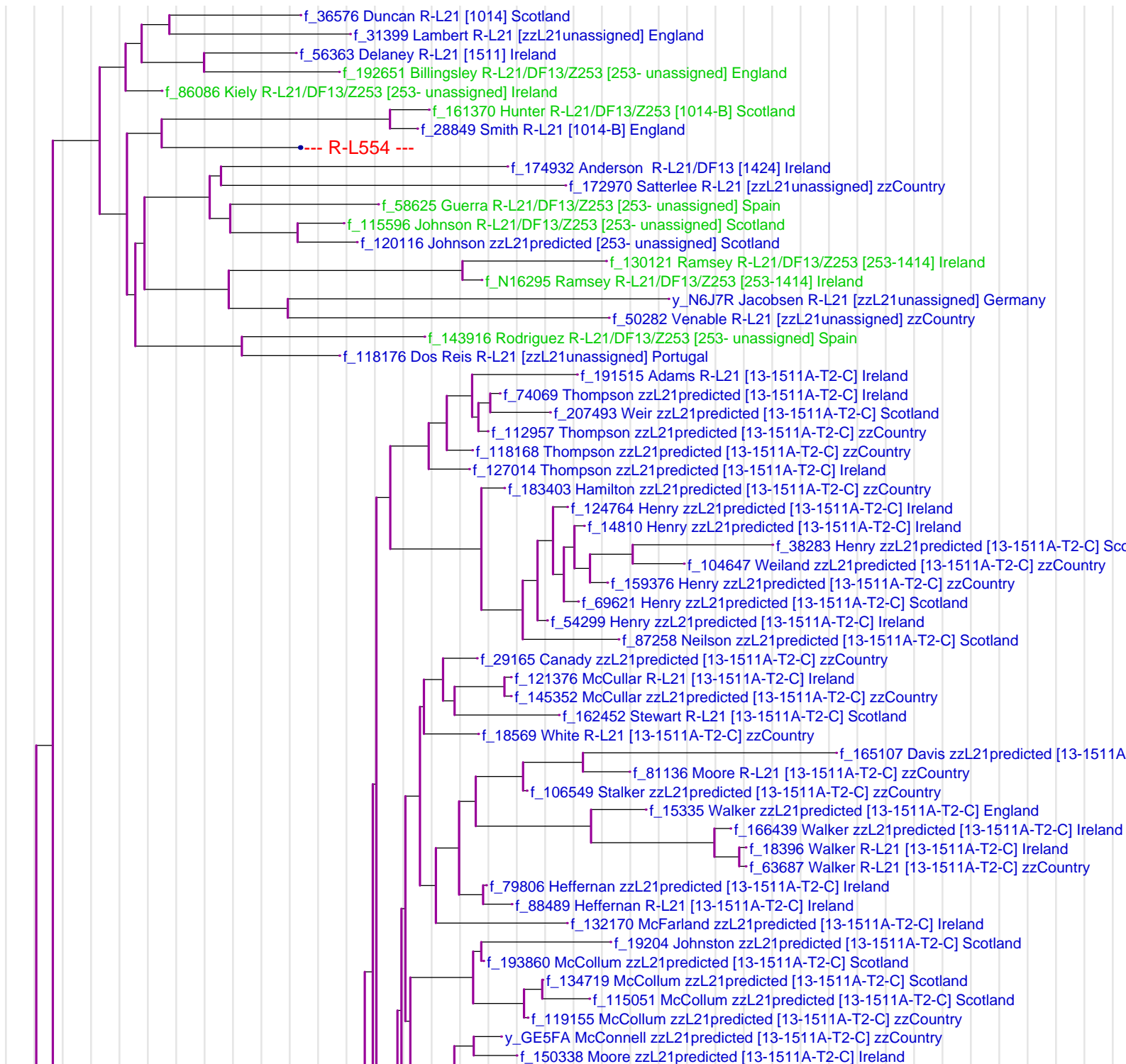


This is the marker distribution for R-Z253. The color indicates the relative frequency of the alleles.

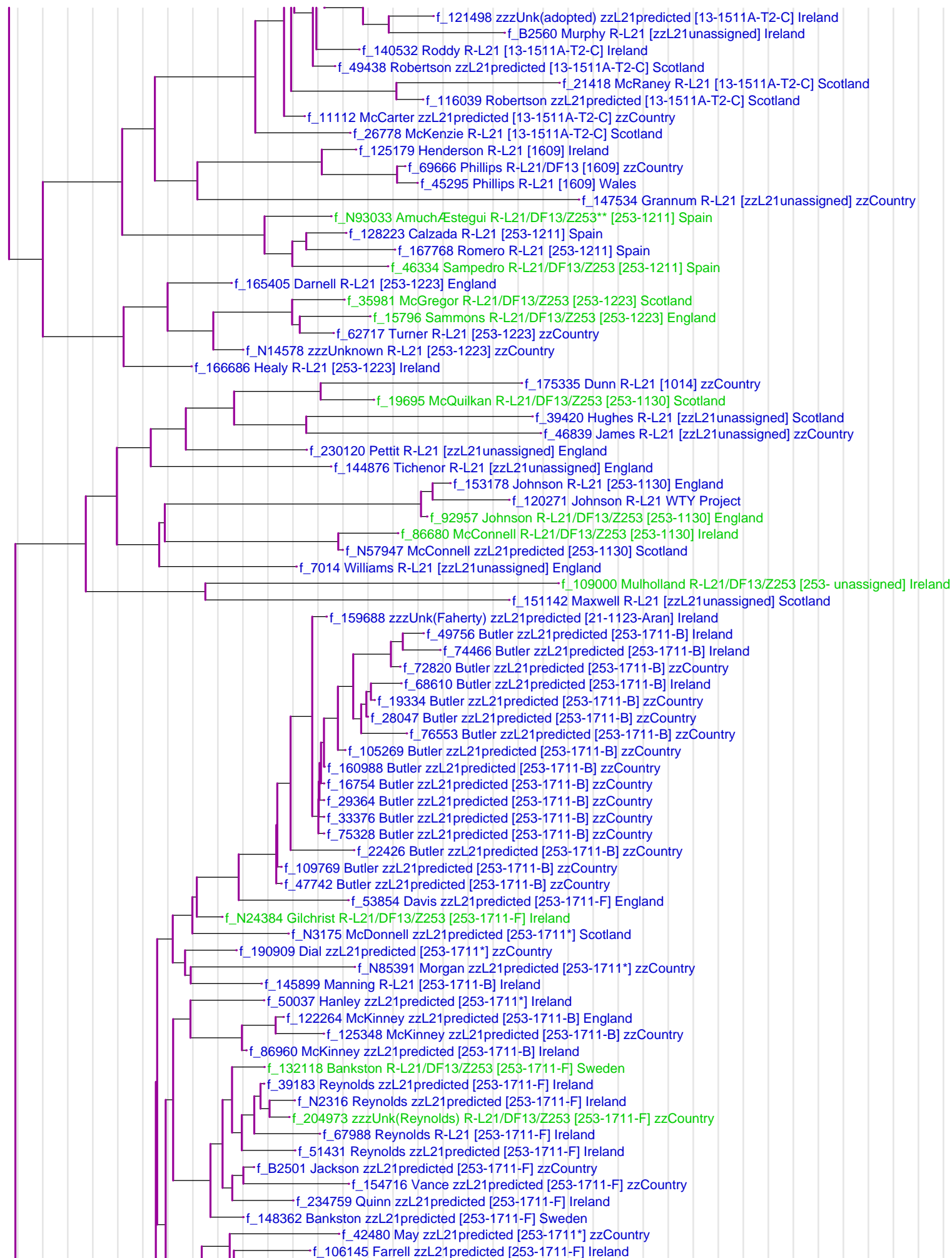


## Age Analysis

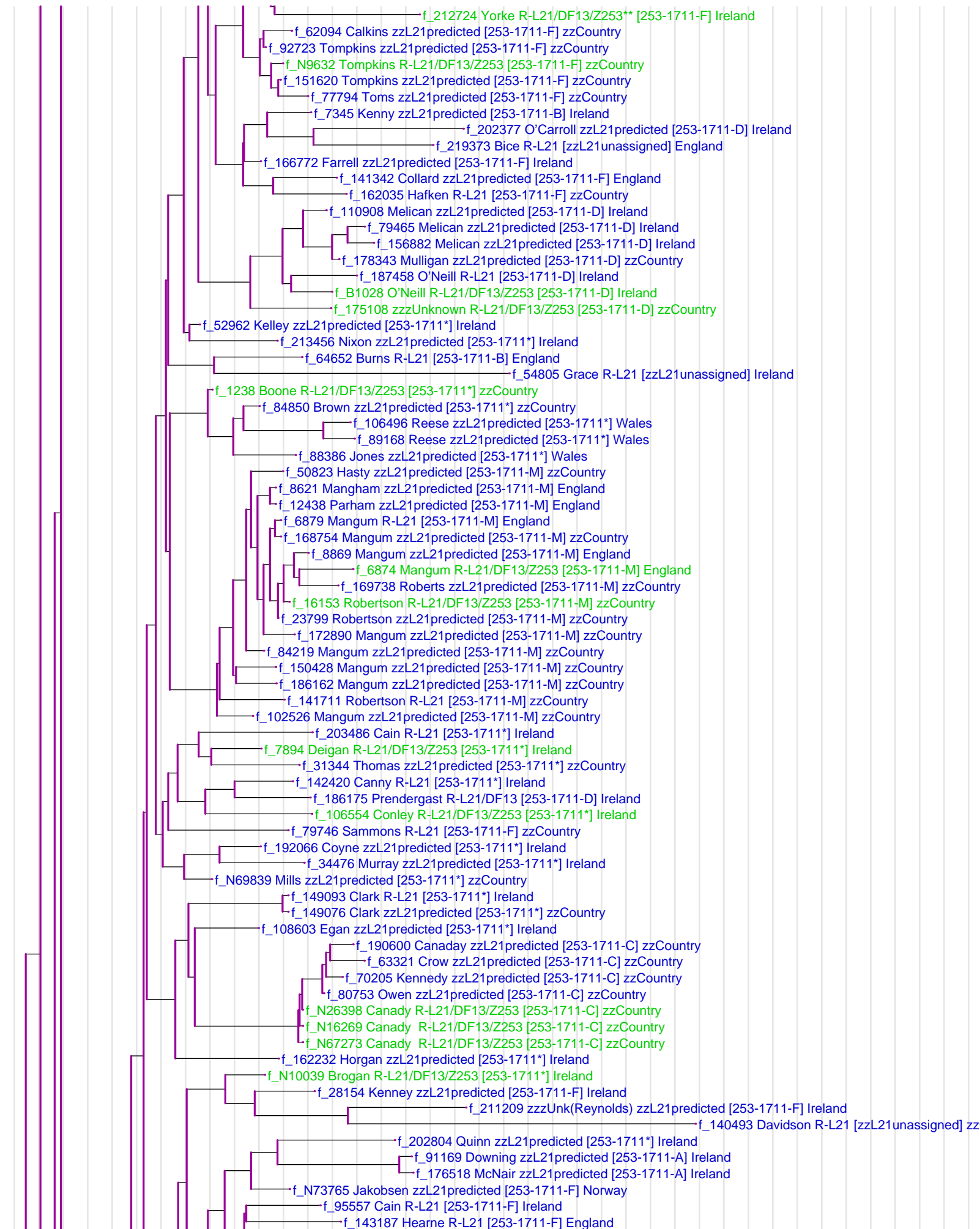
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
785	52595	11717	22.28%	125.29±12.54	3132.18±443.217



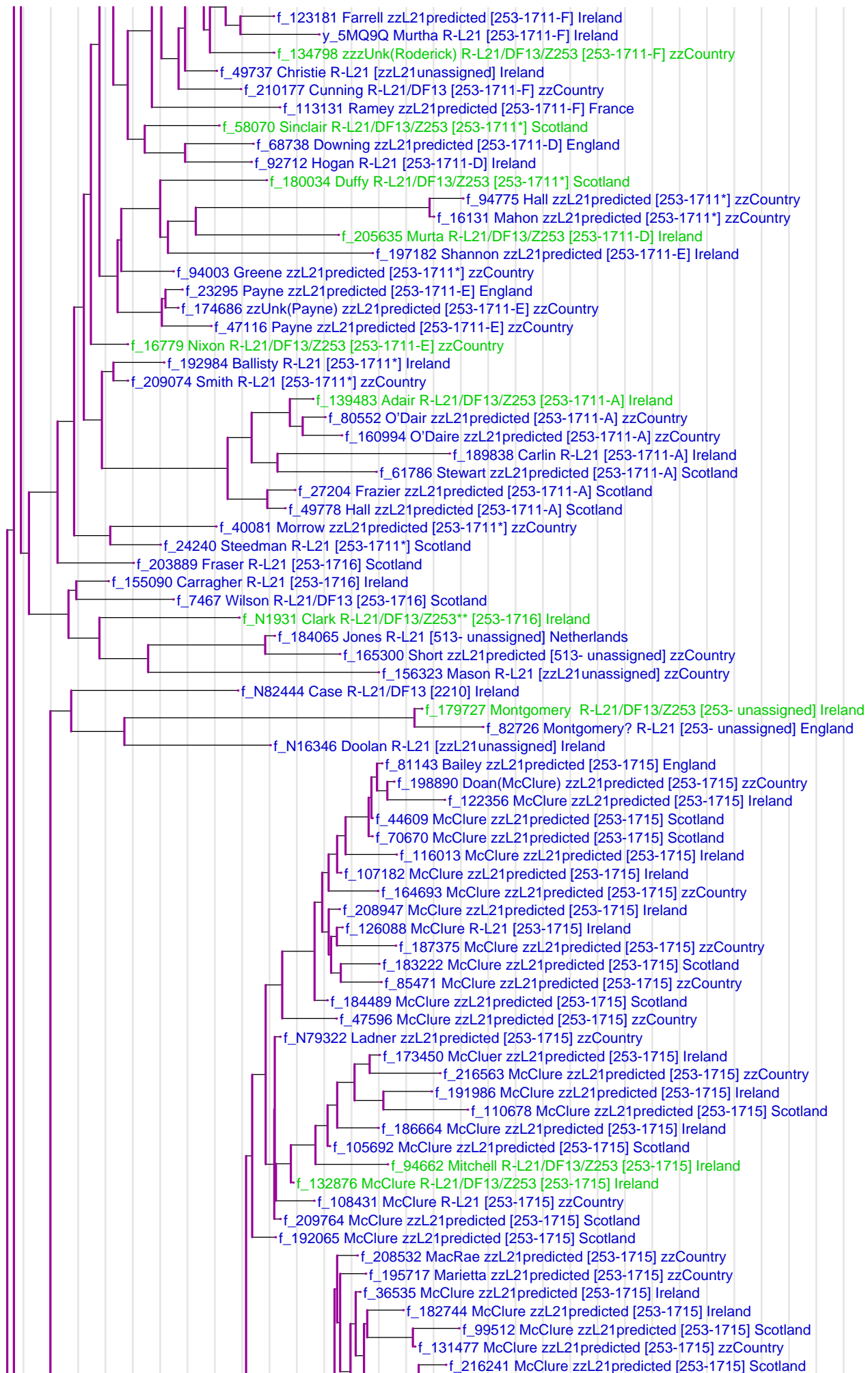
The vertical grey lines are separated 10 generations apart.



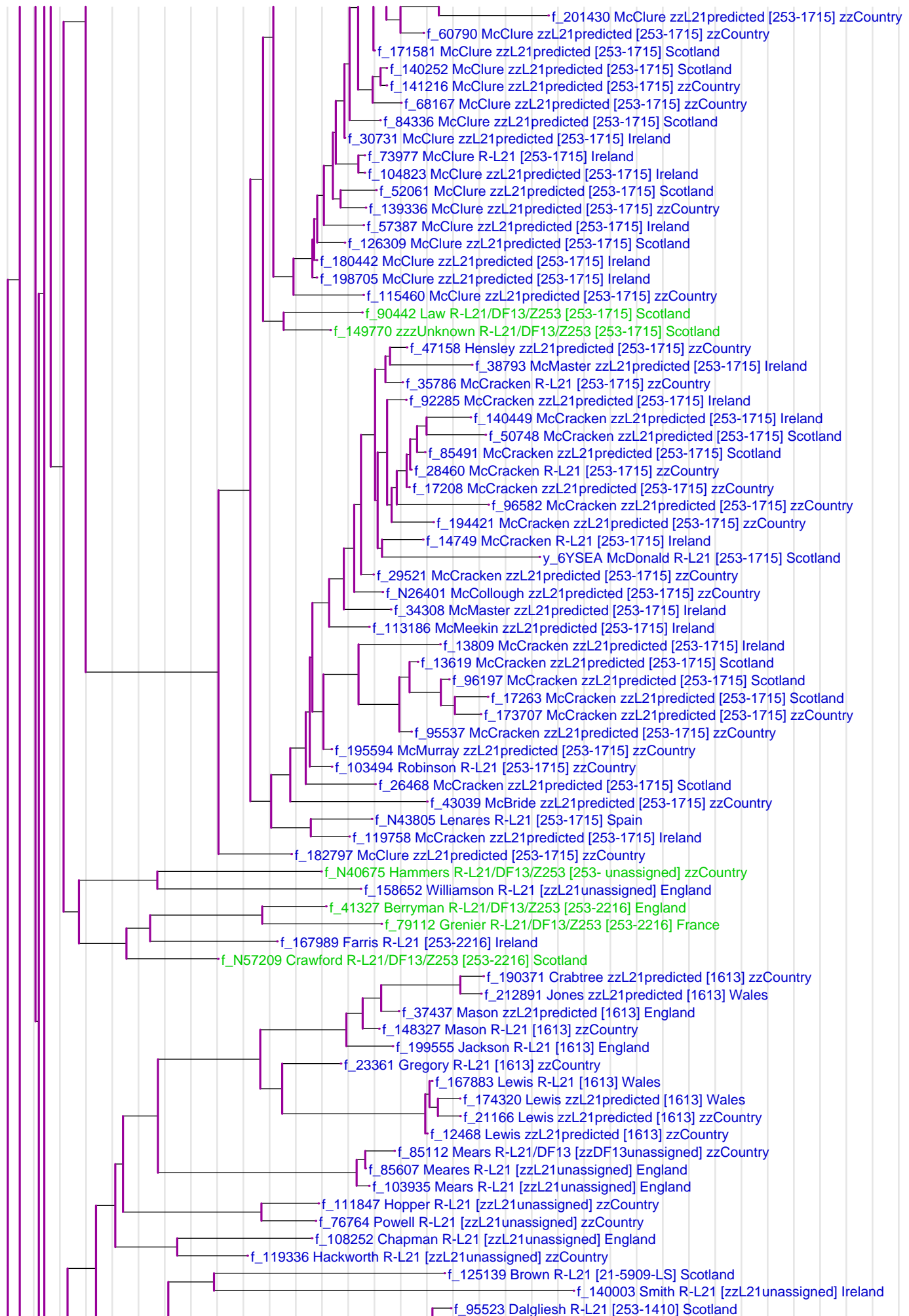
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

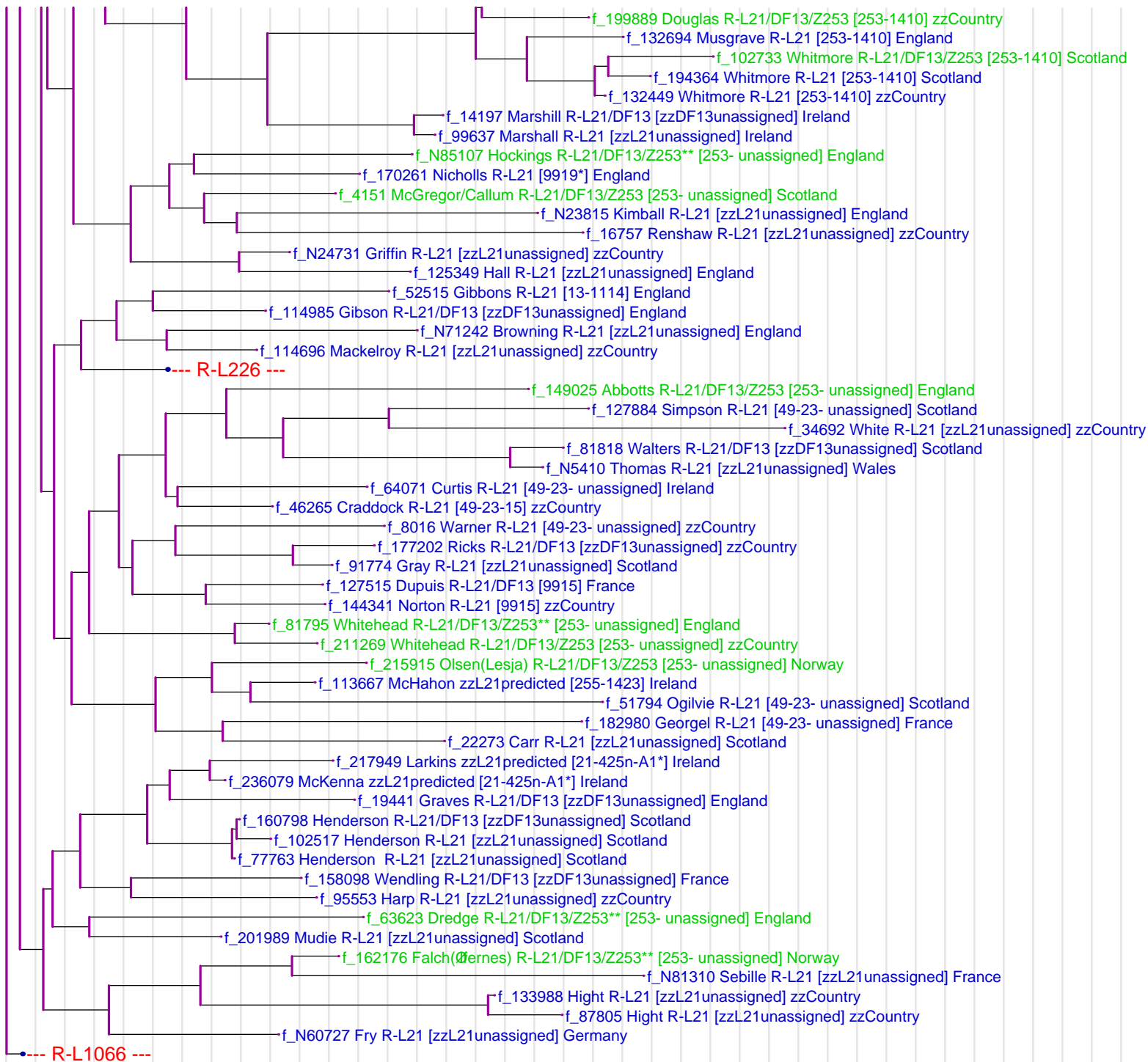


The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

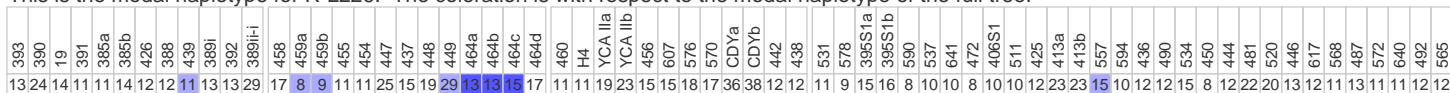




The vertical grey lines are separated 10 generations apart.

# R-L226

This is the modal haplotype for R-L226. The coloration is with respect to the modal haplotype of the full tree.

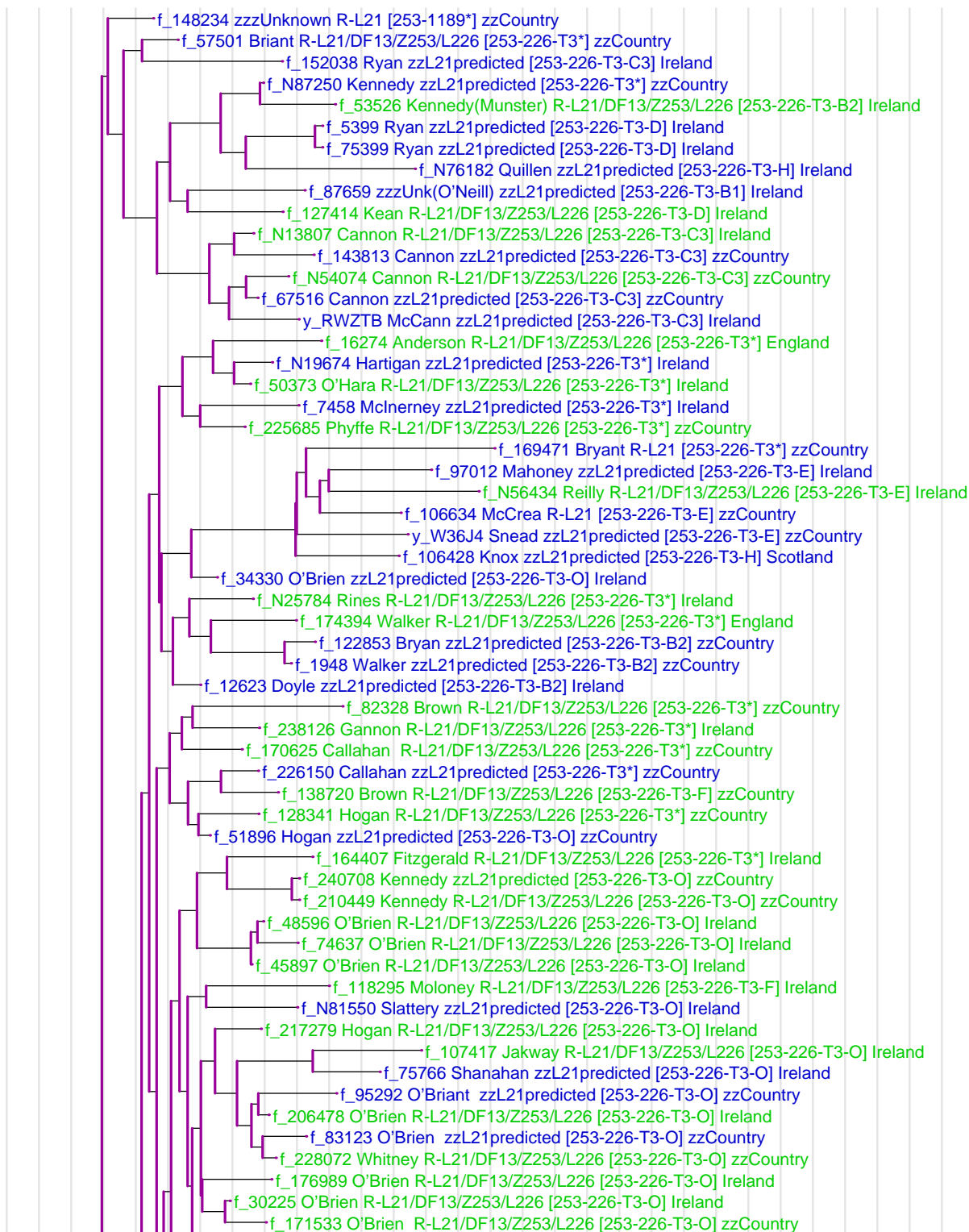


This is the marker distribution for R-L226. The color indicates the relative frequency of the alleles.

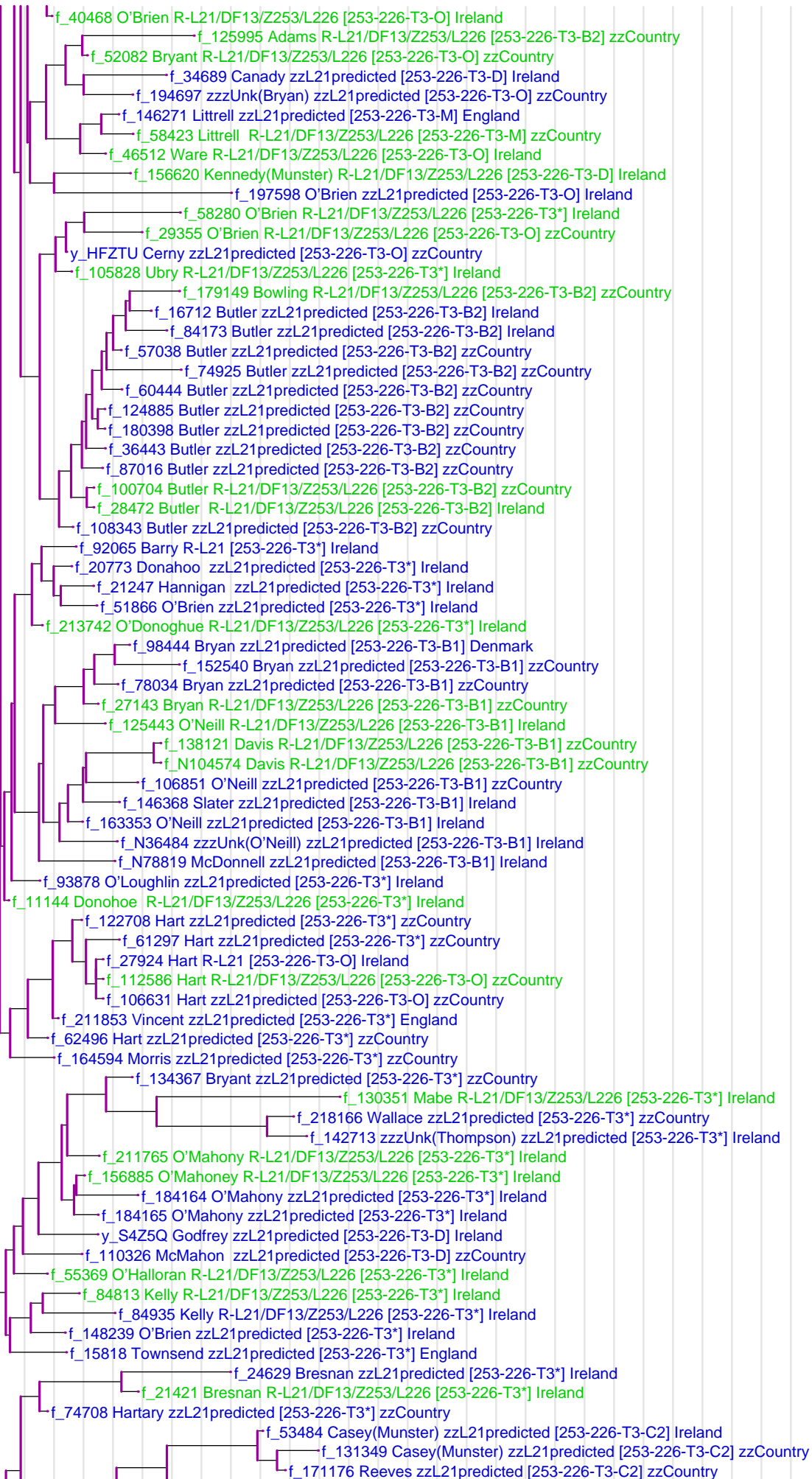


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
236	15812	1508	9.54%	50.07±5.02	1251.78±177.335



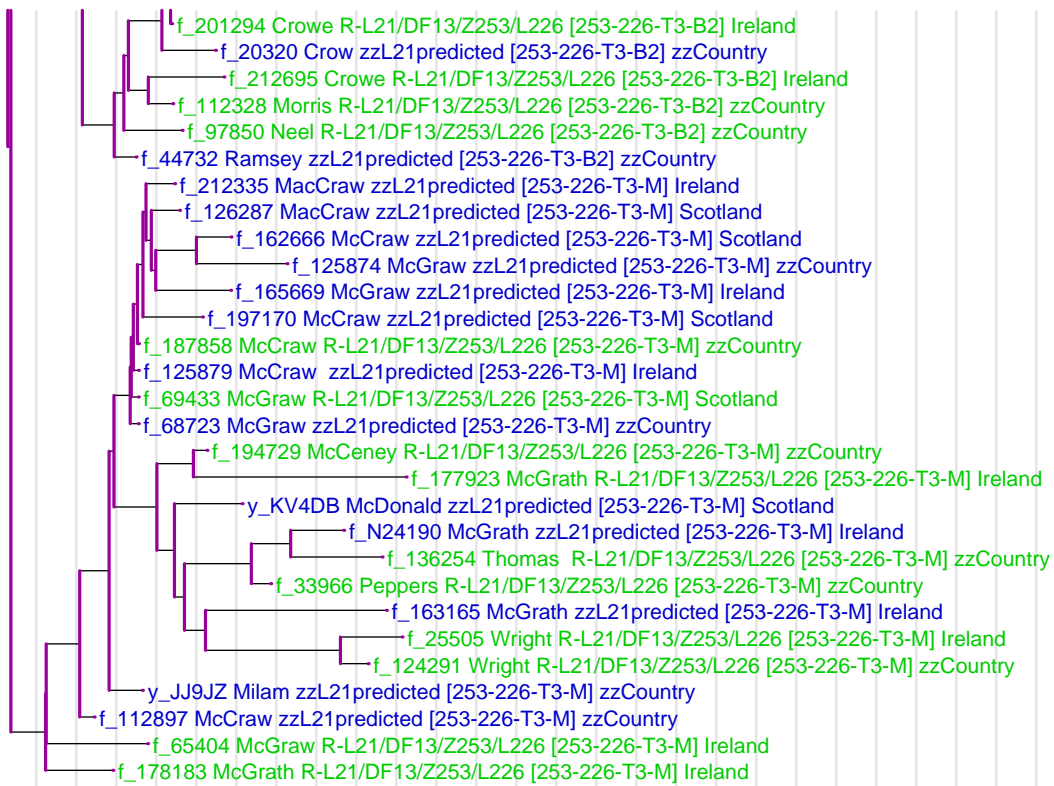
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



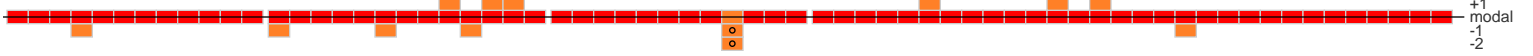
The vertical grey lines are separated 10 generations apart.

# R-L554

This is the modal haplotype for R-L554. The coloration is with respect to the modal haplotype of the full tree.

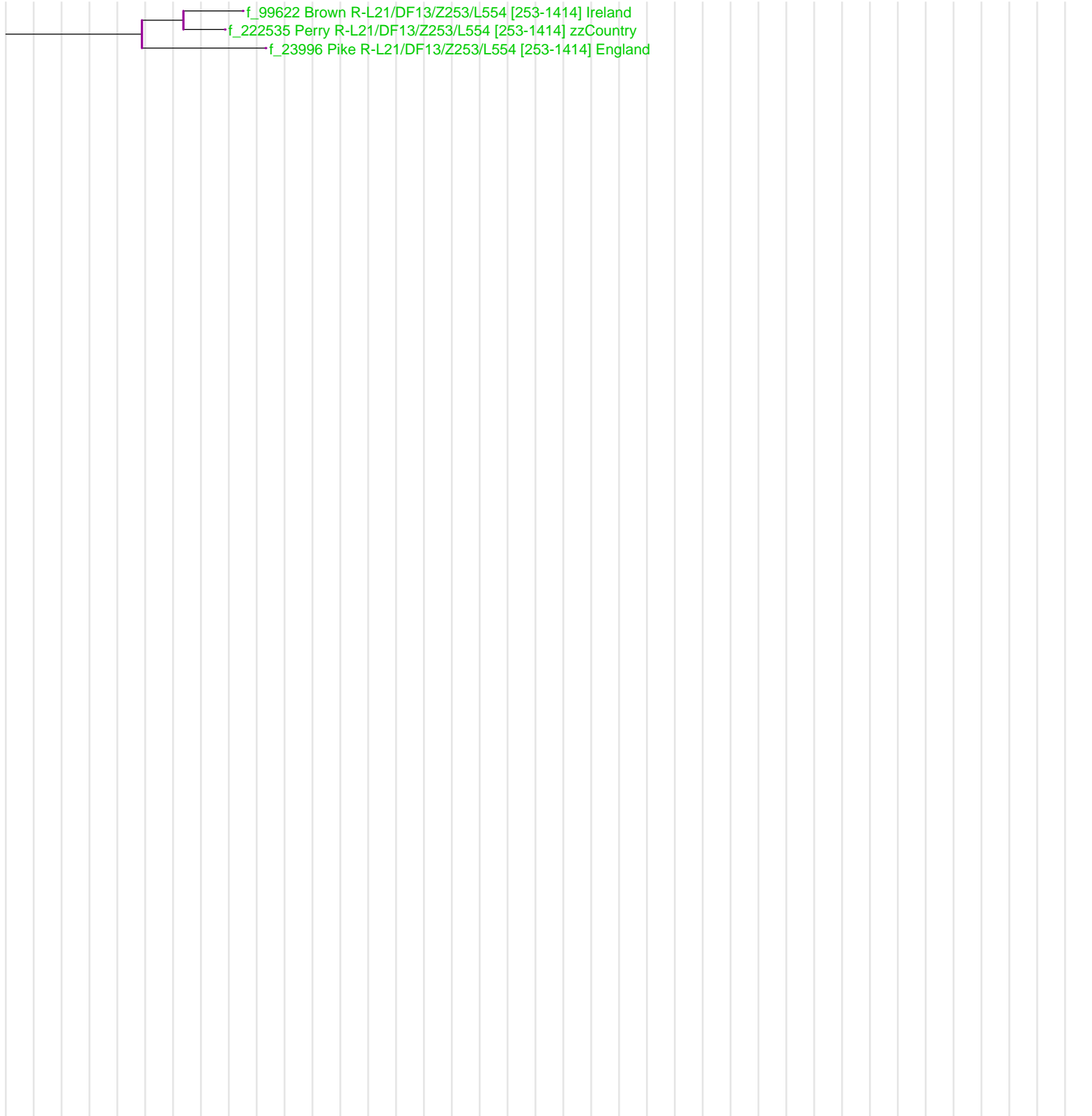
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565		
13	25	14	11	11	14	12	12	11	14	13	30	17	9	10	11	11	25	14	19	29	15	15	15	17	10	11	19	23	15	15	18	17	36	40	13	12	11	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	12	12	17	8	12	22	20	13	12	11	11	11	11	12	12

This is the marker distribution for R-L554. The color indicates the relative frequency of the alleles.



## Age Analysis

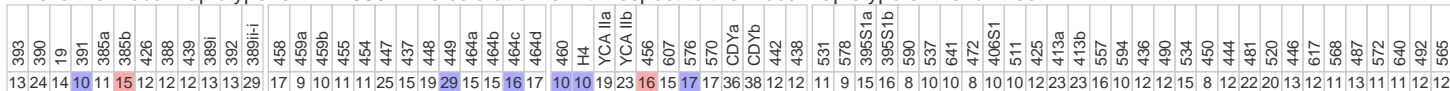
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	14	6.97%	36.08±4.47	902.049±143.558



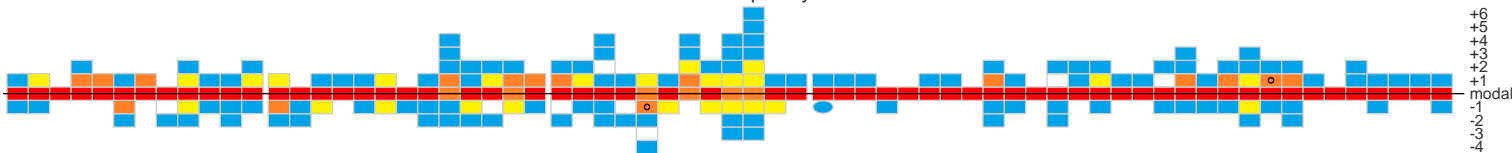
The vertical grey lines are separated 10 generations apart.

# R-L1066

This is the modal haplotype for R-L1066. The coloration is with respect to the modal haplotype of the full tree.

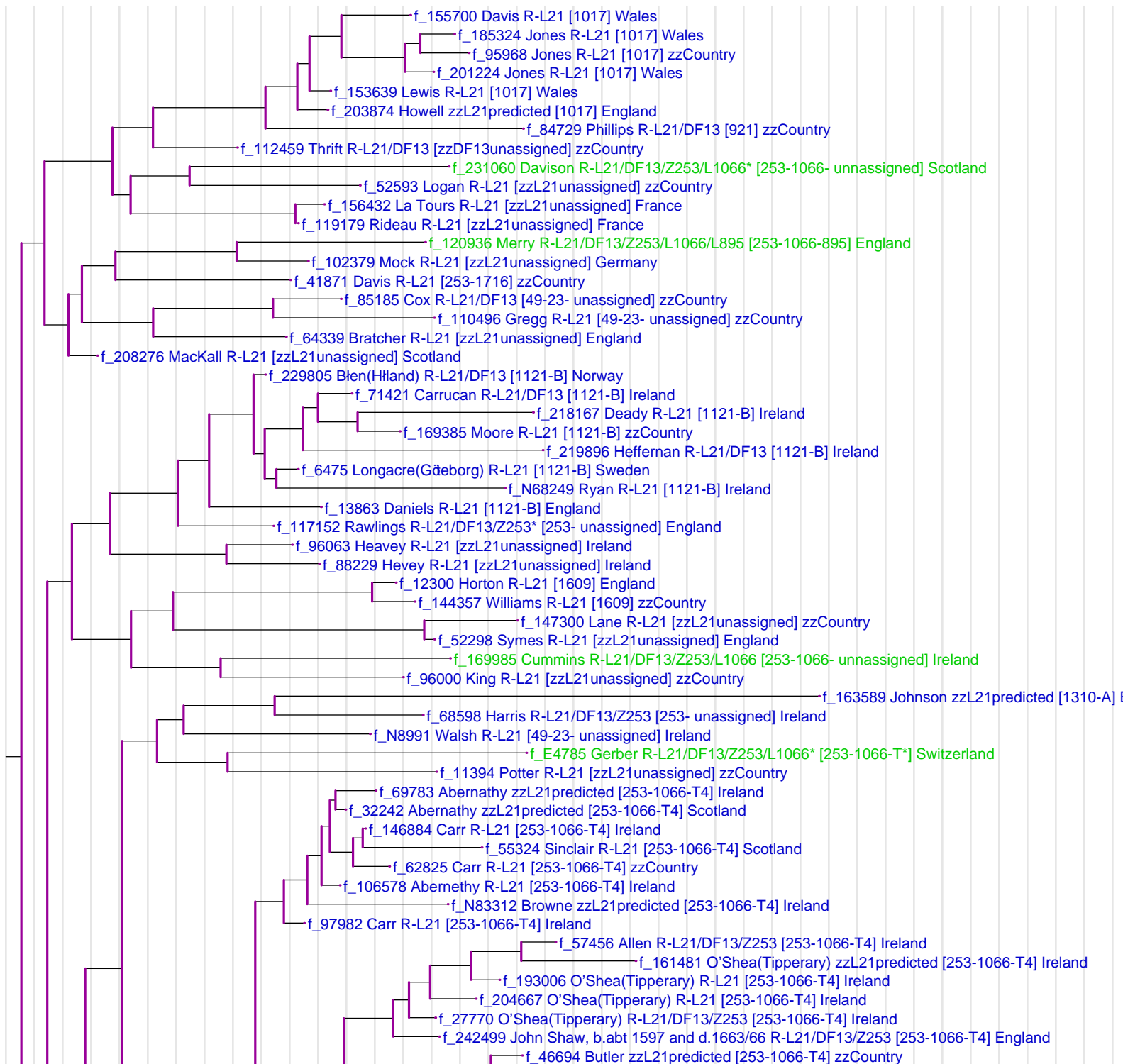


This is the marker distribution for R-L1066. The color indicates the relative frequency of the alleles.

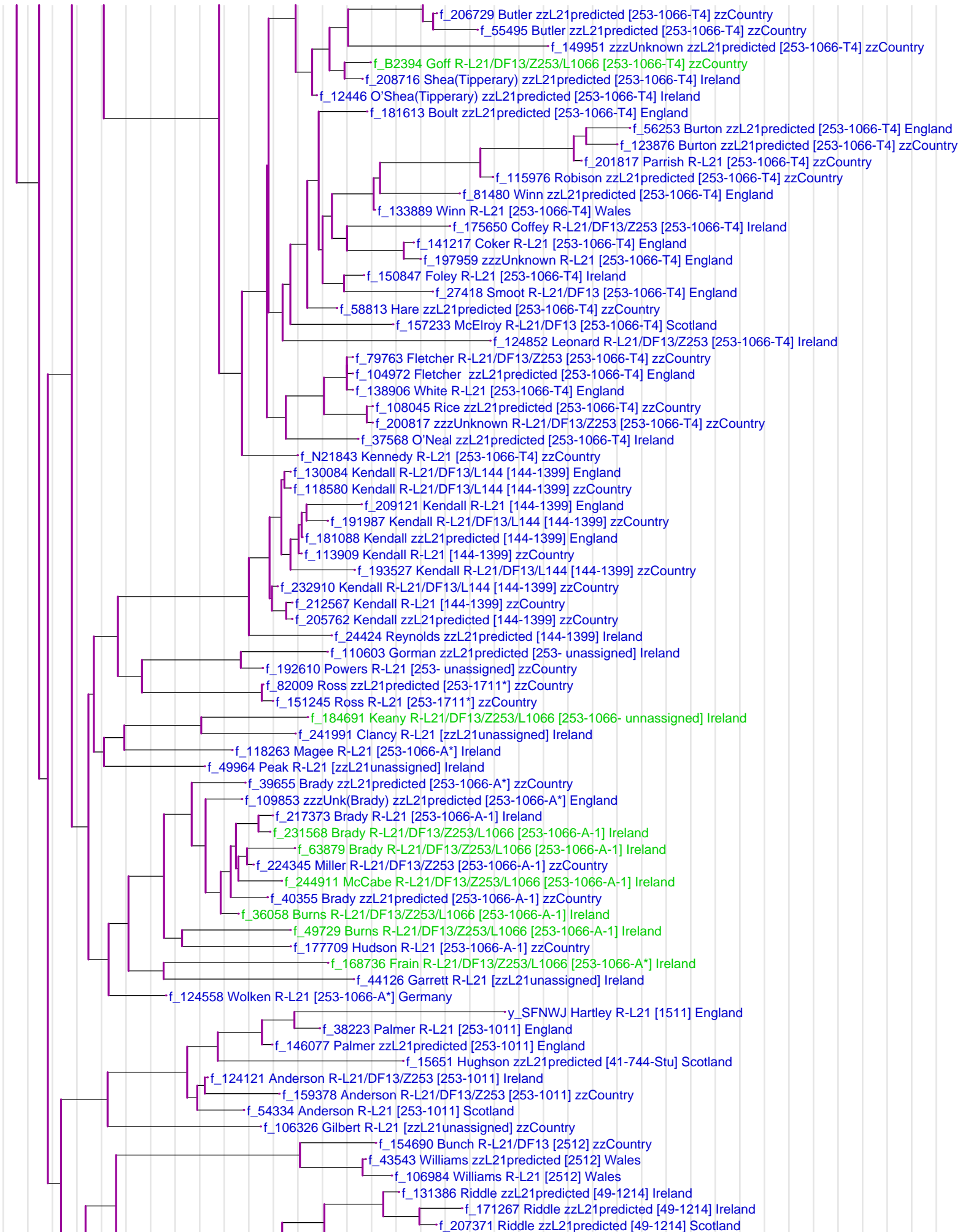


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
139	9313	2074	22.27%	125.24±12.61	3130.94±444.247

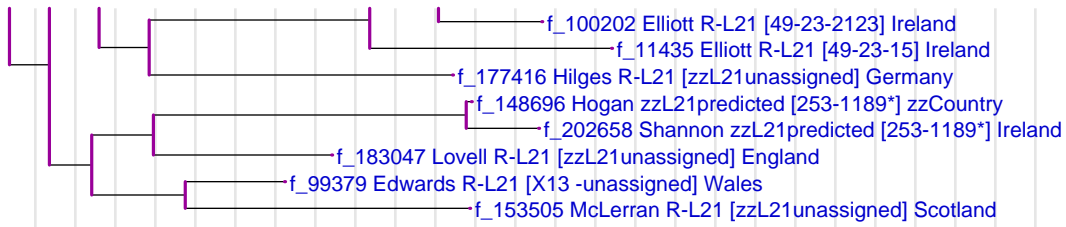


The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

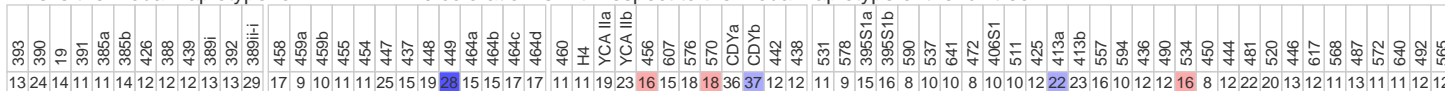




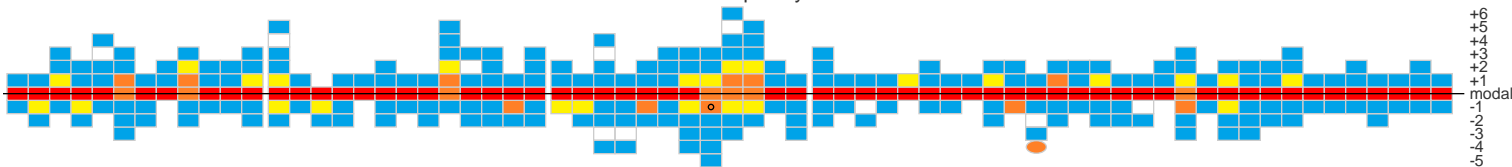
The vertical grey lines are separated 10 generations apart.

# R-DF21

This is the modal haplotype for R-DF21. The coloration is with respect to the modal haplotype of the full tree.

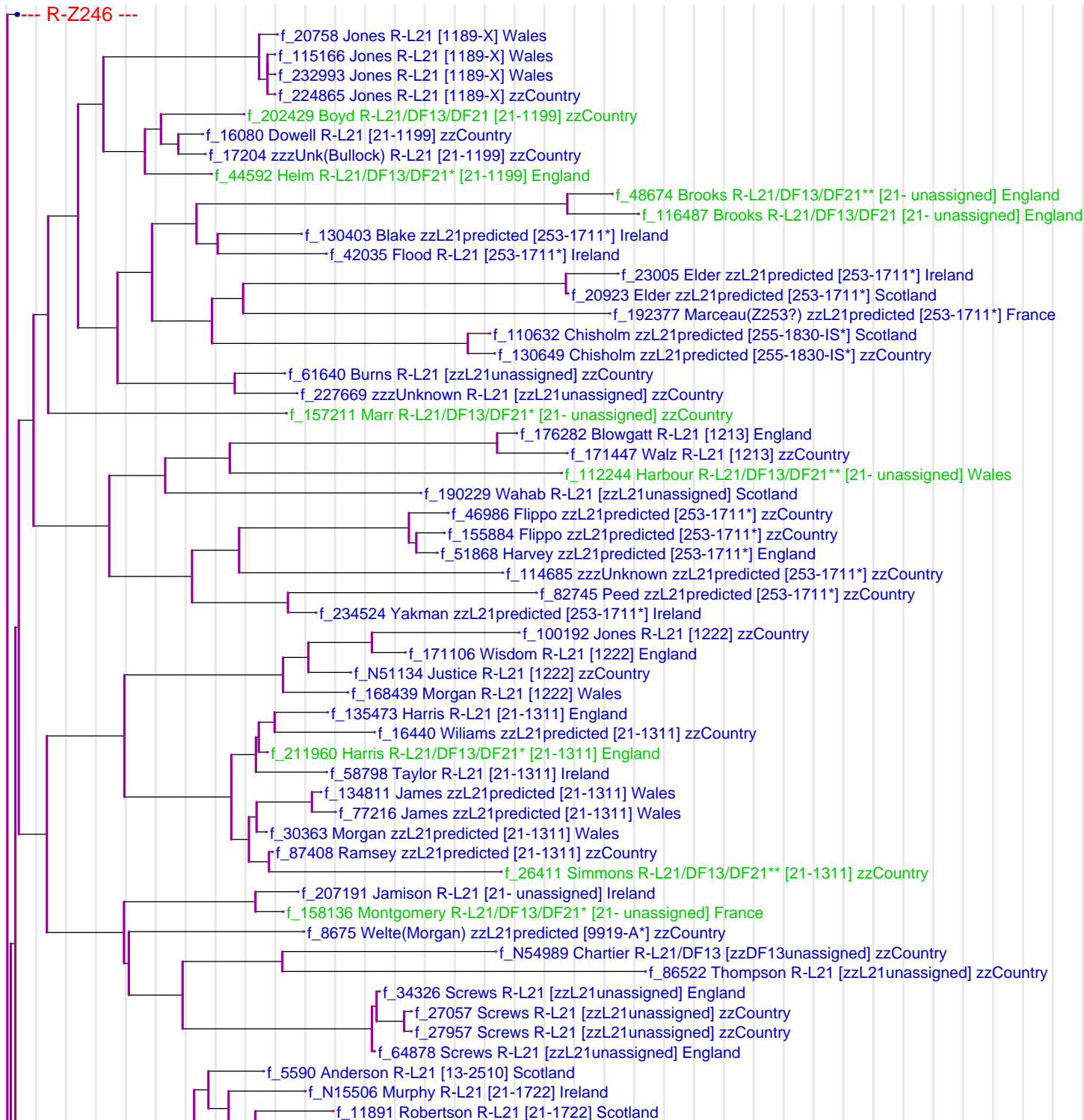


This is the marker distribution for R-DF21. The color indicates the relative frequency of the alleles.

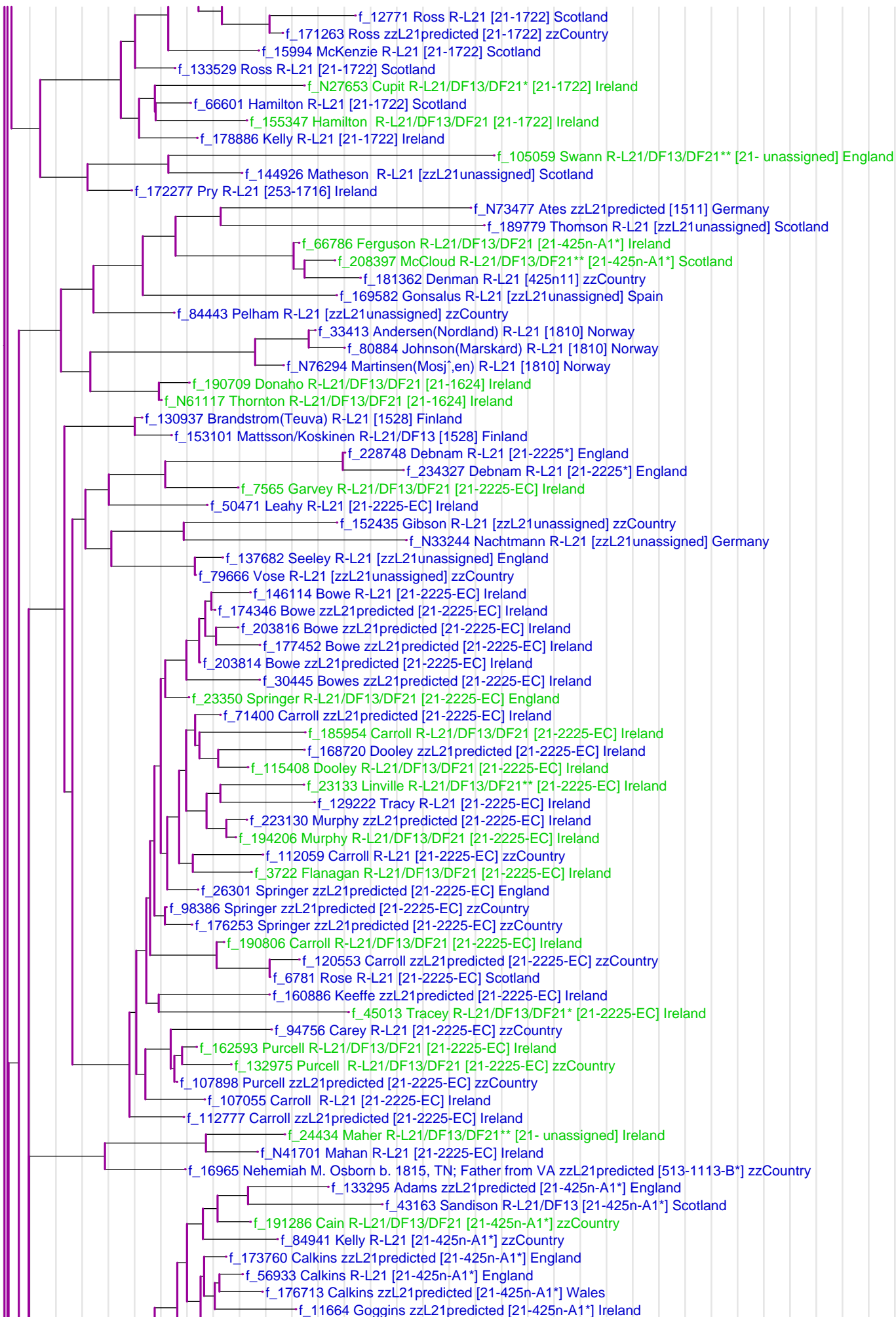


## Age Analysis

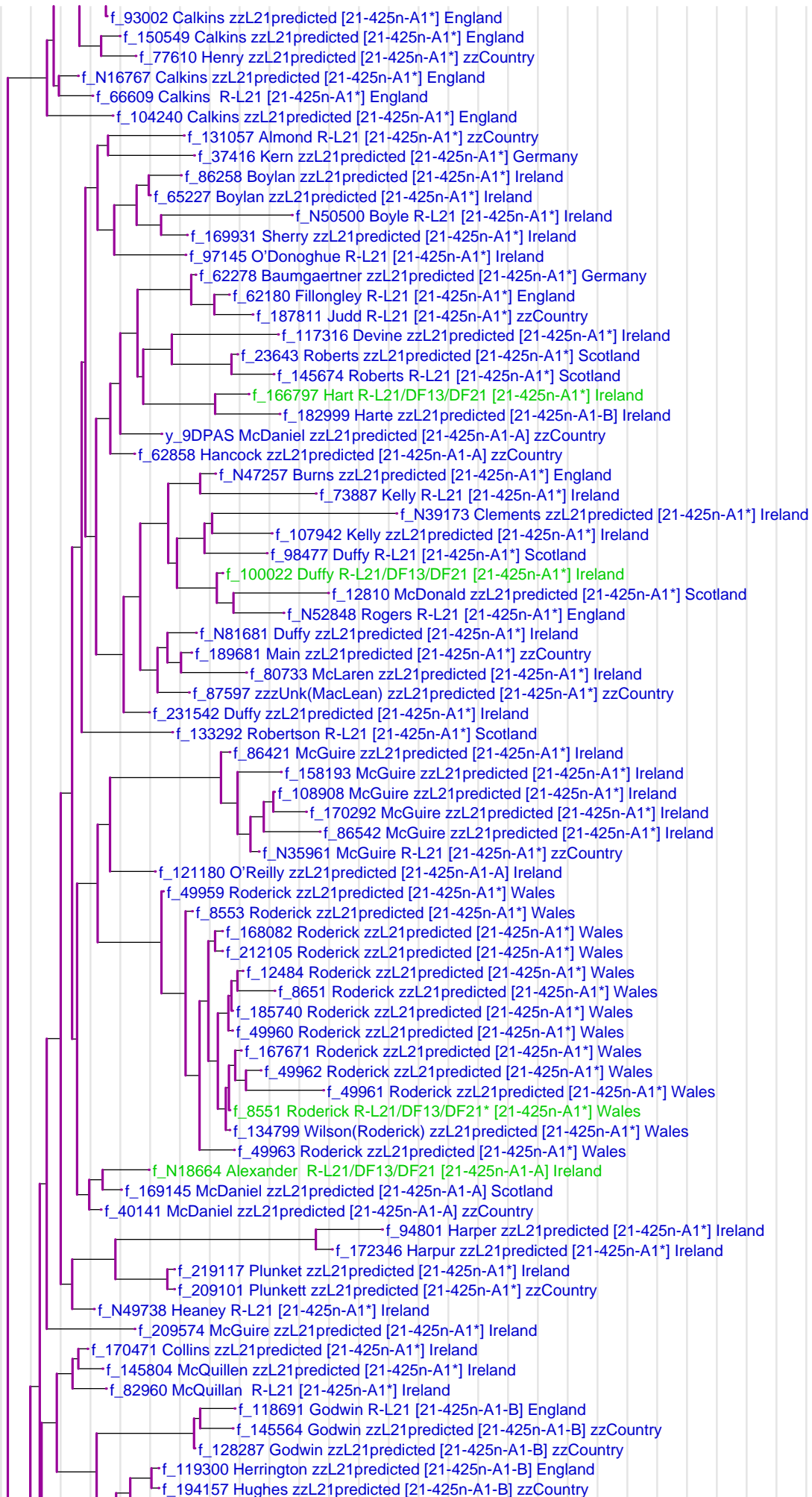
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
653	43751	9184	20.99%	117.22±11.74	2930.38±414.707



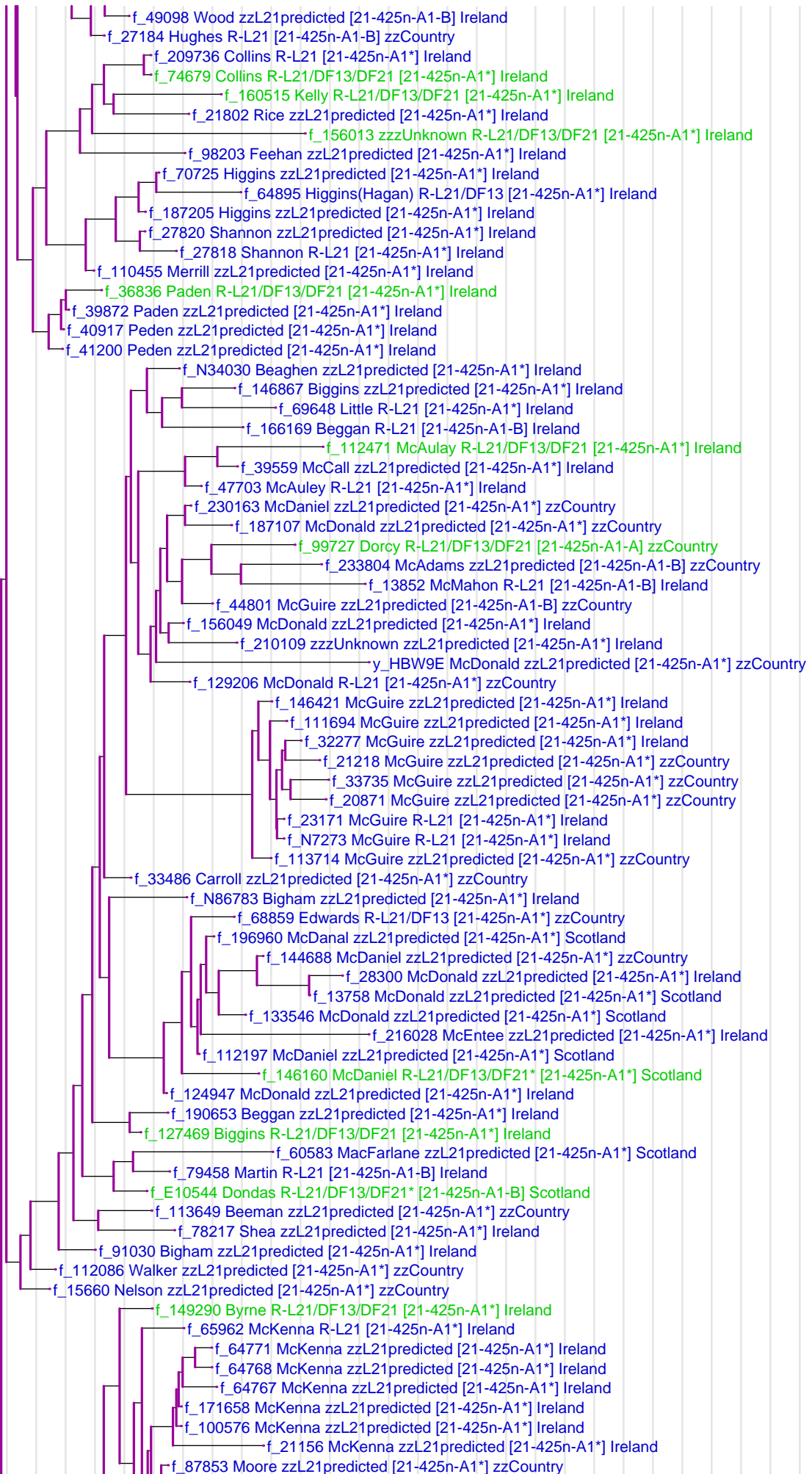
The vertical grey lines are separated 10 generations apart.



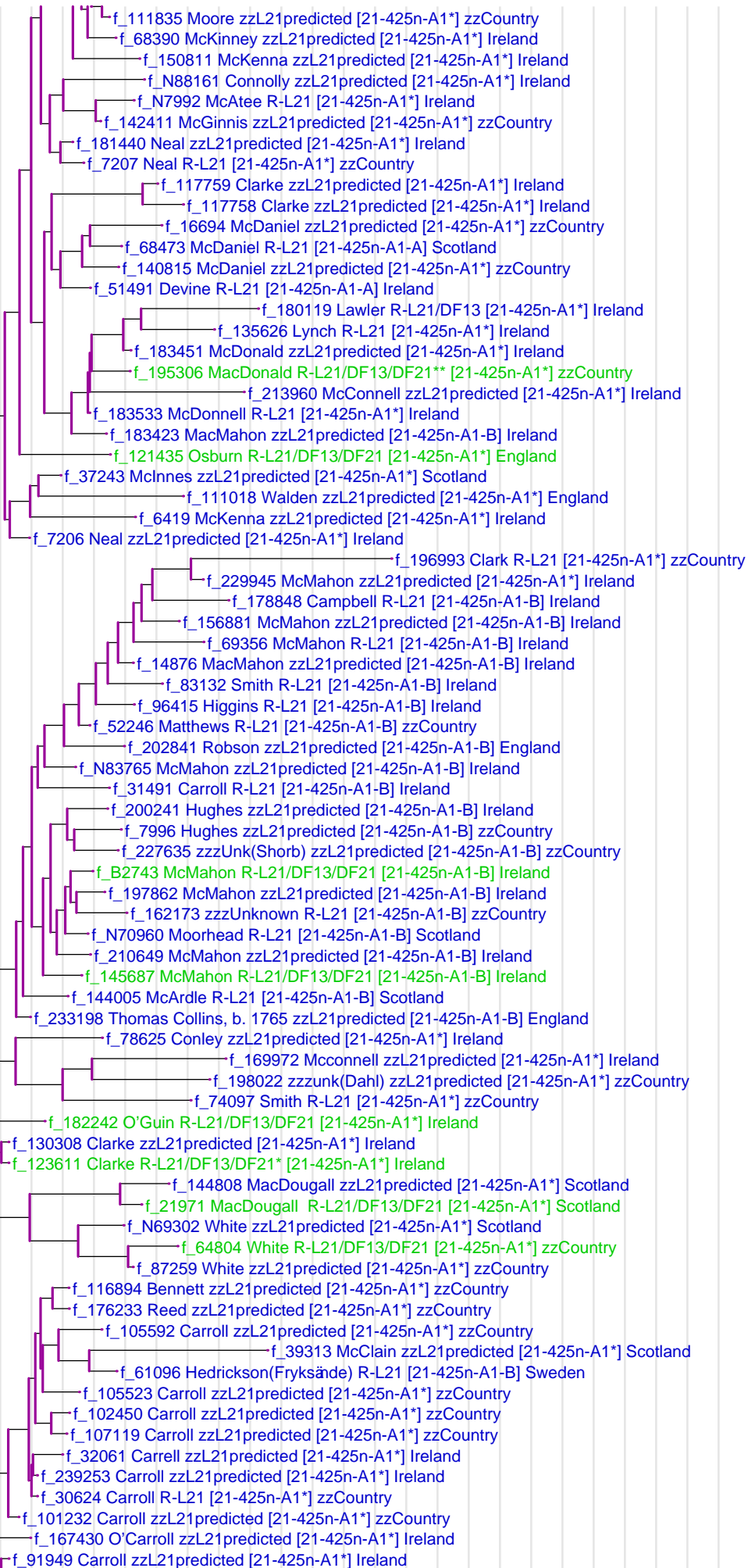
The vertical grey lines are separated 10 generations apart.



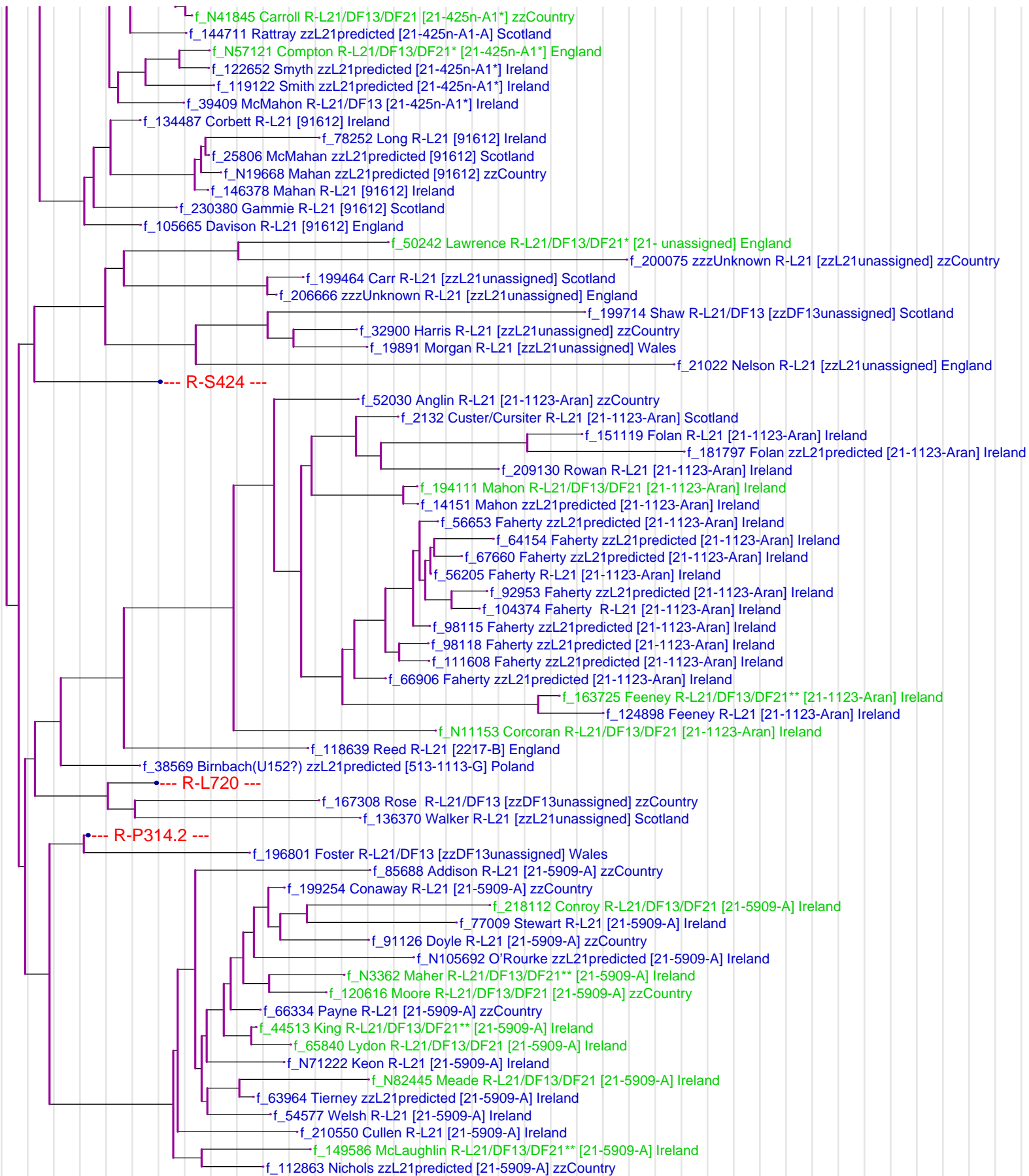
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



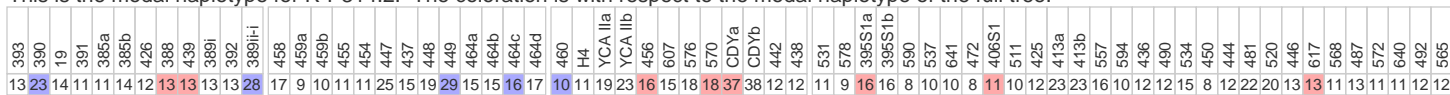
The vertical grey lines are separated 10 generations apart.



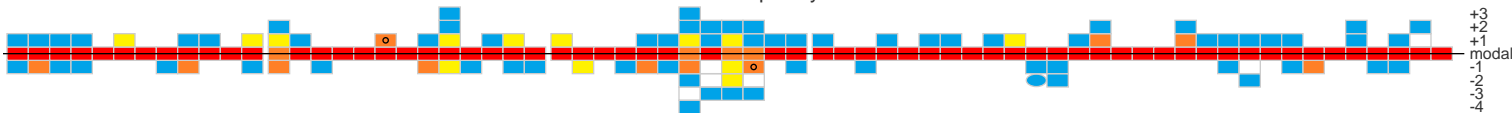
The vertical grey lines are separated 10 generations apart.

# R-P314.2

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

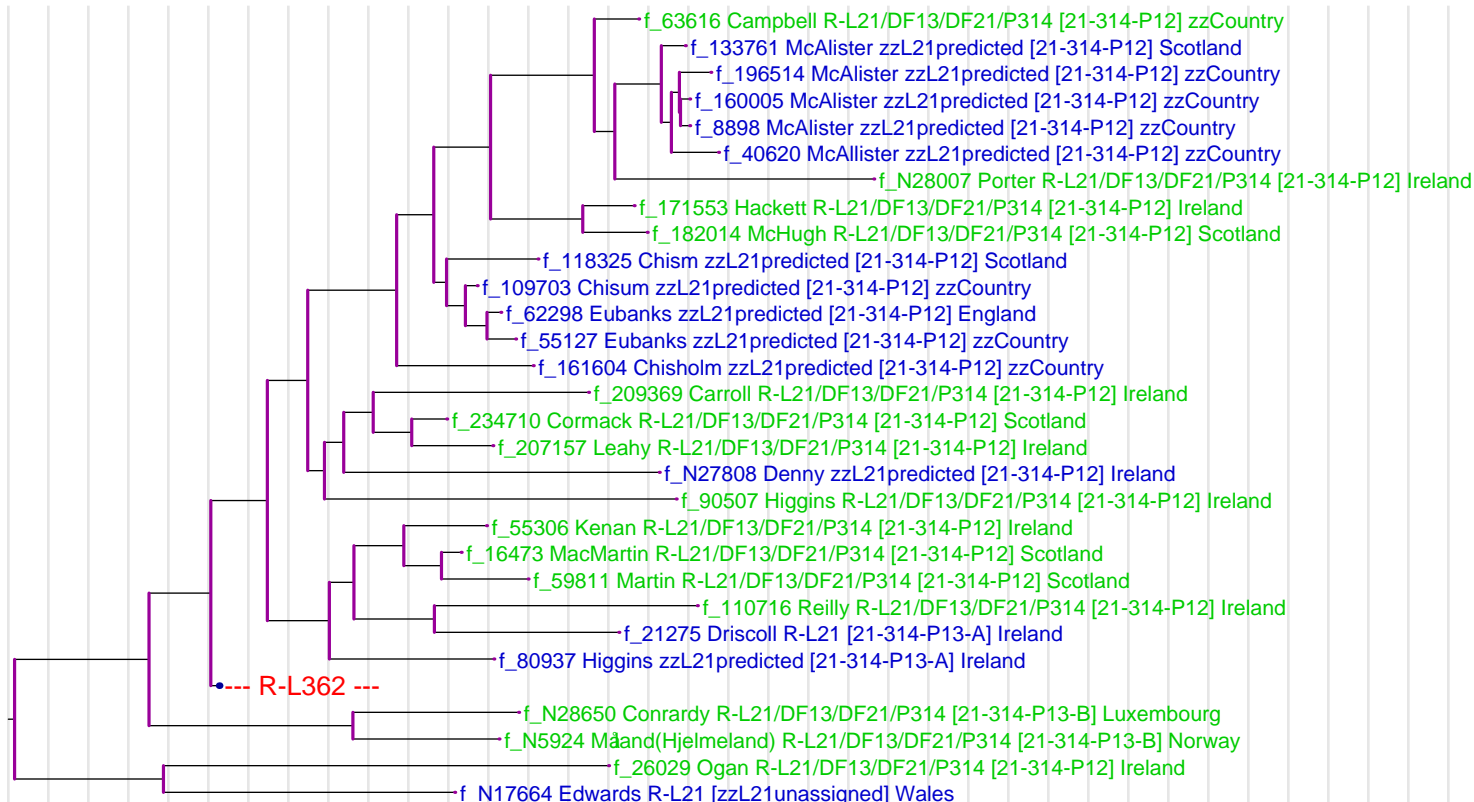


This is the marker distribution for R-P314.2. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
54	3618	517	14.29%	76.94±7.81	1923.4±274.159

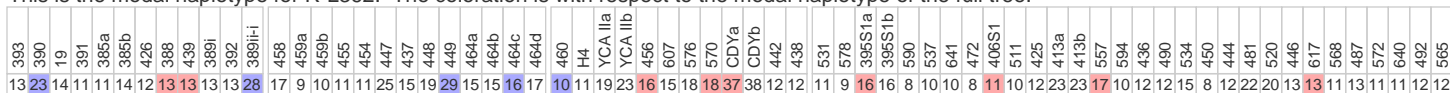


The vertical grey lines are separated 10 generations apart.



# R-L362

This is the modal haplotype for R-L362. The coloration is with respect to the modal haplotype of the full tree.

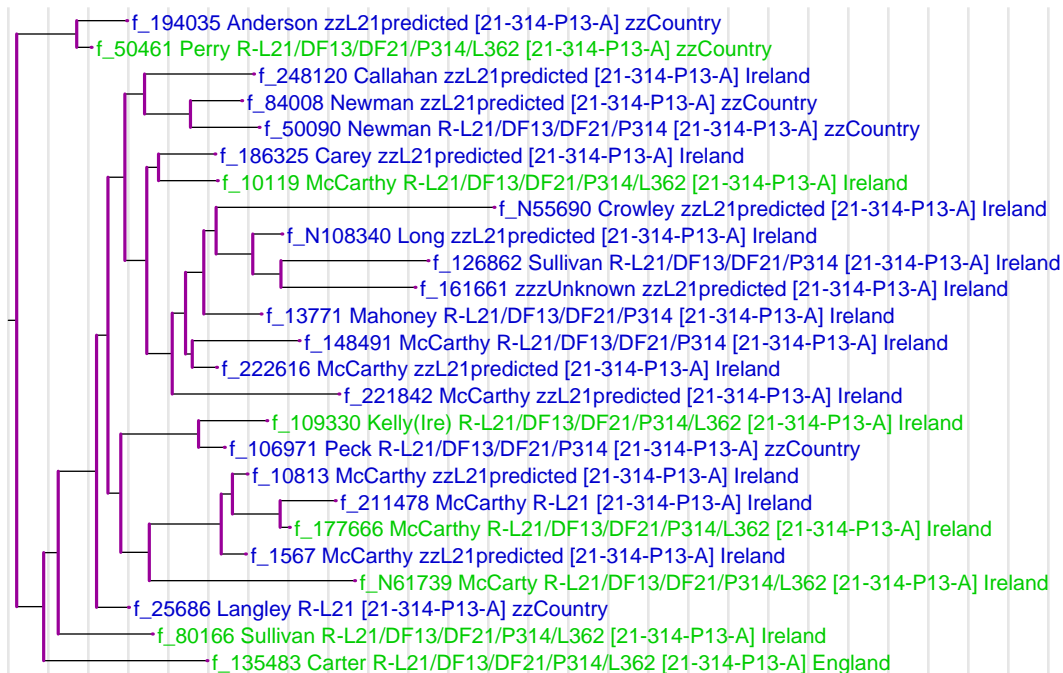


This is the marker distribution for R-L362. The color indicates the relative frequency of the alleles.



## Age Analysis

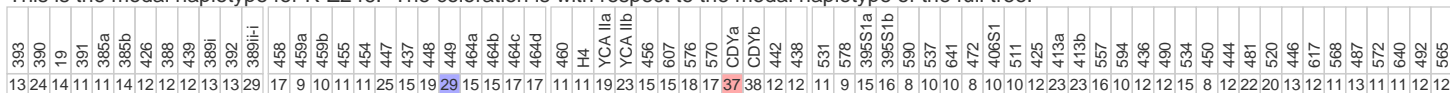
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
25	1675	137	8.18%	42.64±4.40	1065.96±153.167



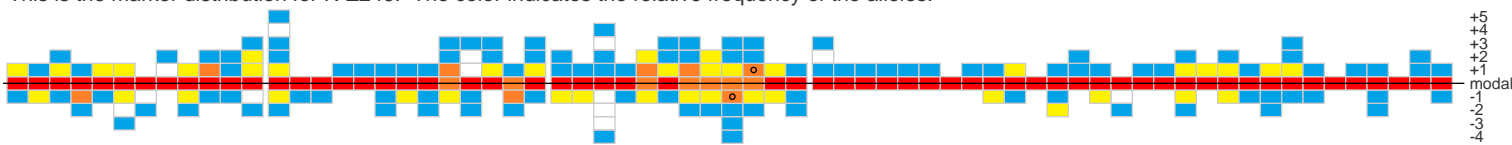
The vertical grey lines are separated 10 generations apart.

# R-Z246

This is the modal haplotype for R-Z246. The coloration is with respect to the modal haplotype of the full tree.

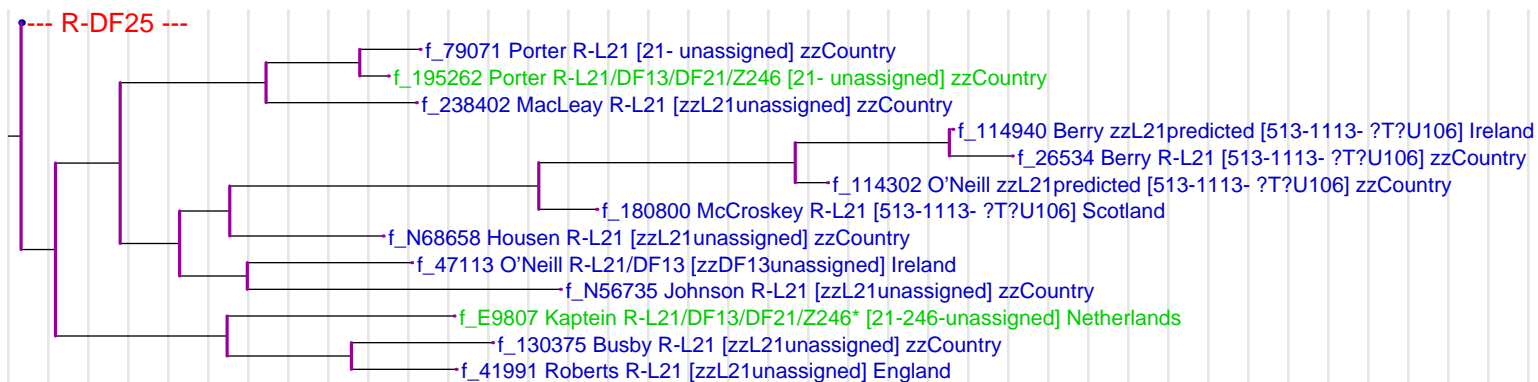


This is the marker distribution for R-Z246. The color indicates the relative frequency of the alleles.



## Age Analysis

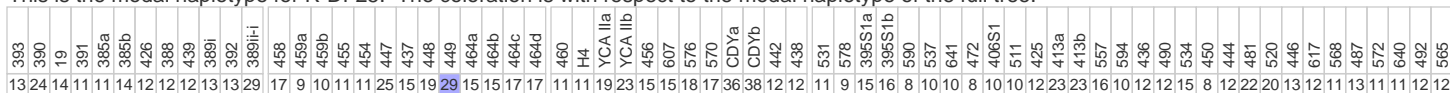
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
130	8710	1838	21.10%	117.91±11.87	2947.63±418.318



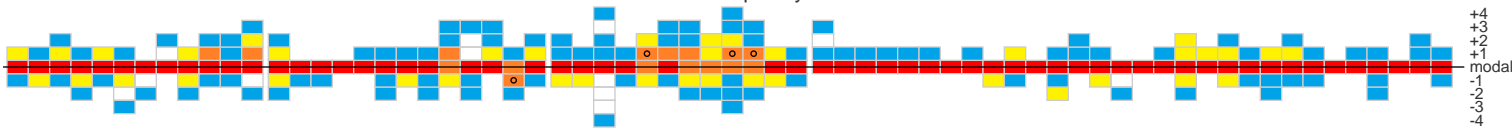
The vertical grey lines are separated 10 generations apart.

# R-DF25

This is the modal haplotype for R-DF25. The coloration is with respect to the modal haplotype of the full tree.

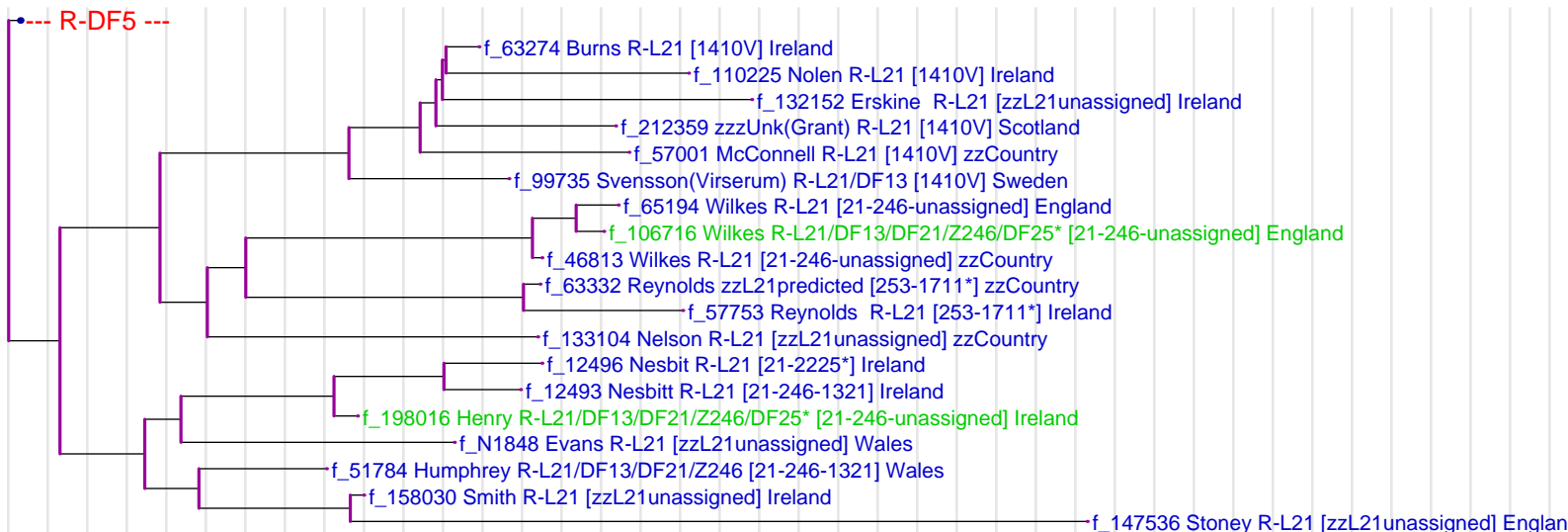


This is the marker distribution for R-DF25. The color indicates the relative frequency of the alleles.



## Age Analysis

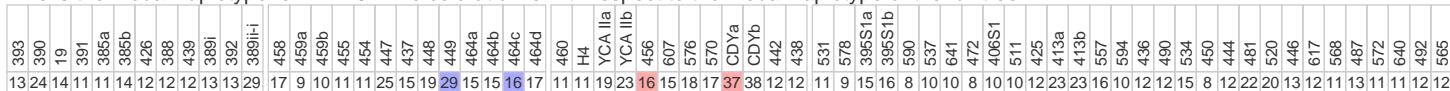
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
117	7839	1659	21.16%	118.29±11.92	2957.18±419.837



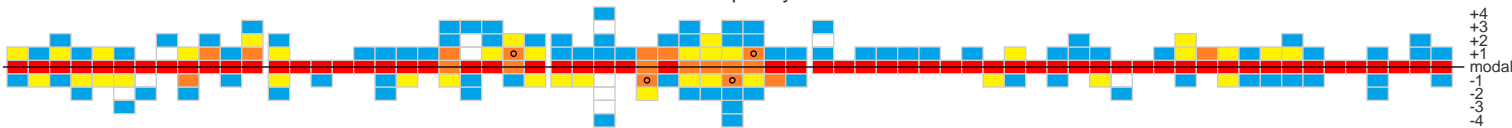
The vertical grey lines are separated 10 generations apart.

# R-DF5

This is the modal haplotype for R-DF5. The coloration is with respect to the modal haplotype of the full tree.

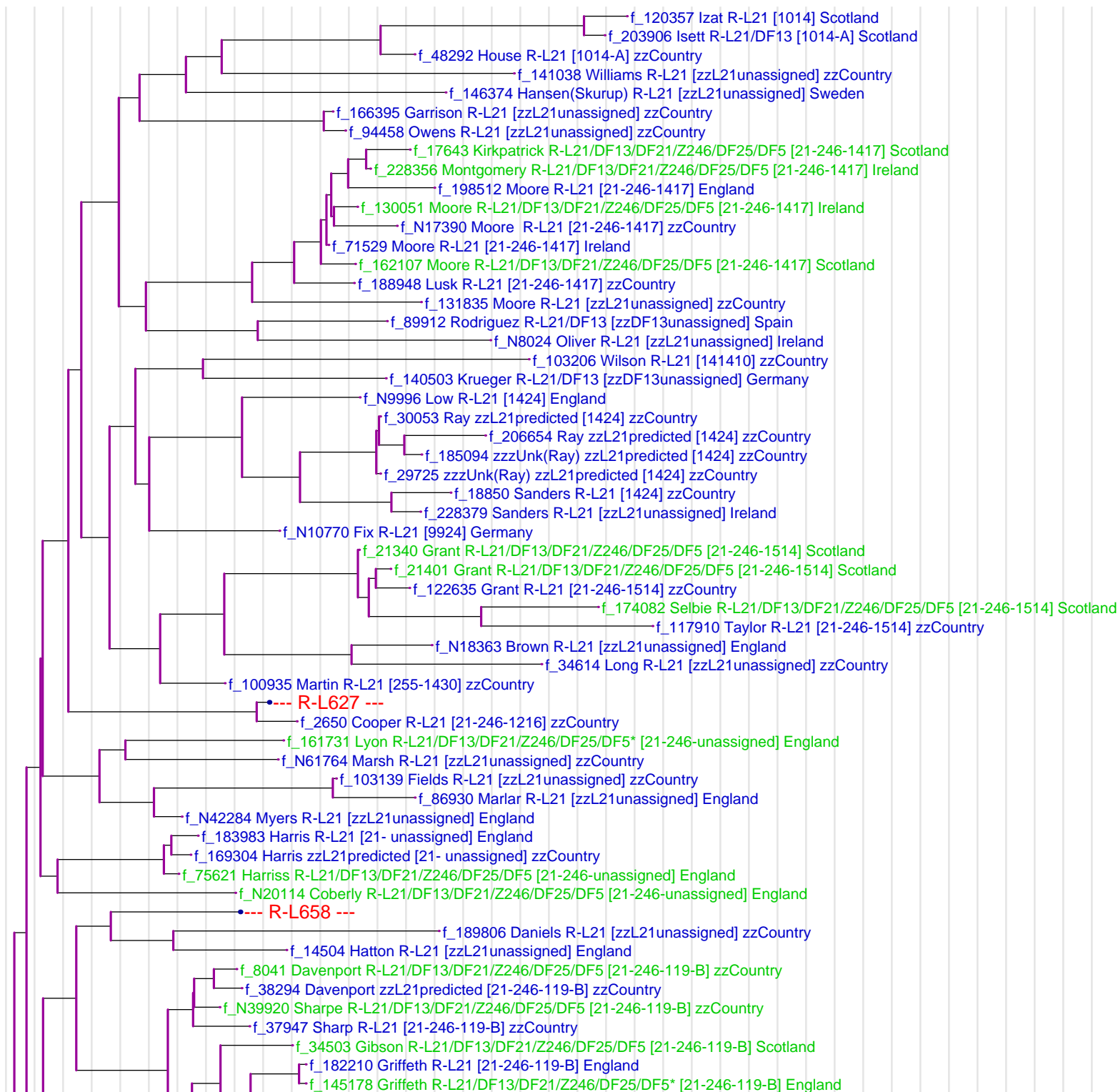


This is the marker distribution for R-DF5. The color indicates the relative frequency of the alleles.

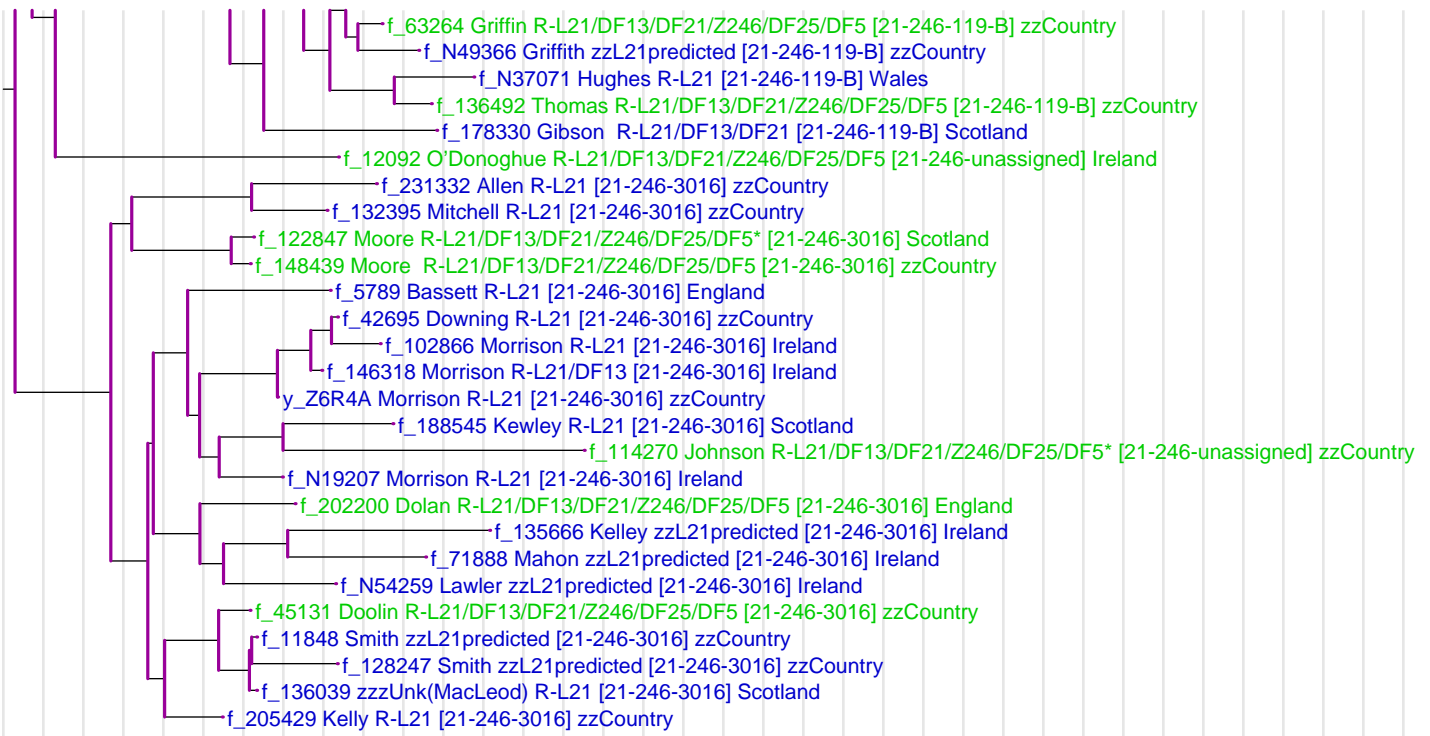


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
98	6566	1319	20.09%	111.61±11.26	2790.37±396.434



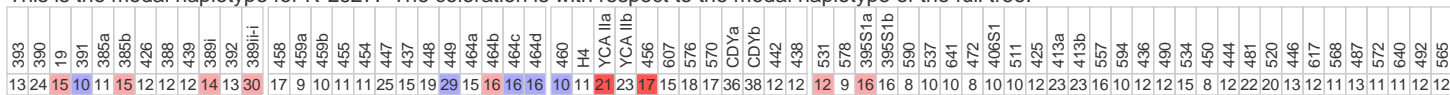
The vertical grey lines are separated 10 generations apart.



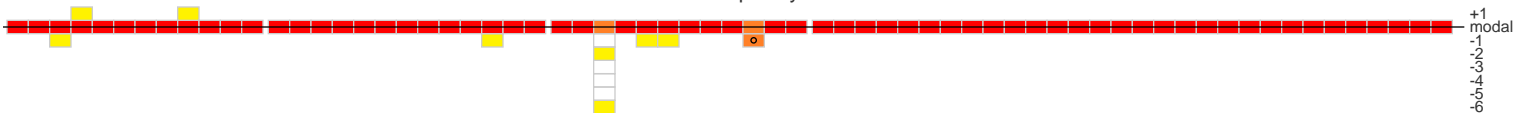
The vertical grey lines are separated 10 generations apart.

# R-L627

This is the modal haplotype for R-L627. The coloration is with respect to the modal haplotype of the full tree.

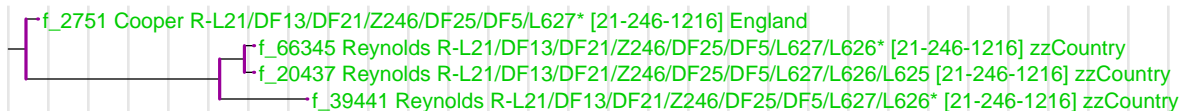


This is the marker distribution for R-L627. The color indicates the relative frequency of the alleles.



## Age Analysis

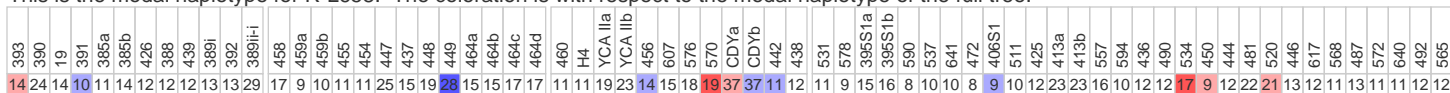
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	12	4.48%	22.90±2.70	572.517±88.5095



The vertical grey lines are separated 10 generations apart.

# R-L658

This is the modal haplotype for R-L658. The coloration is with respect to the modal haplotype of the full tree.

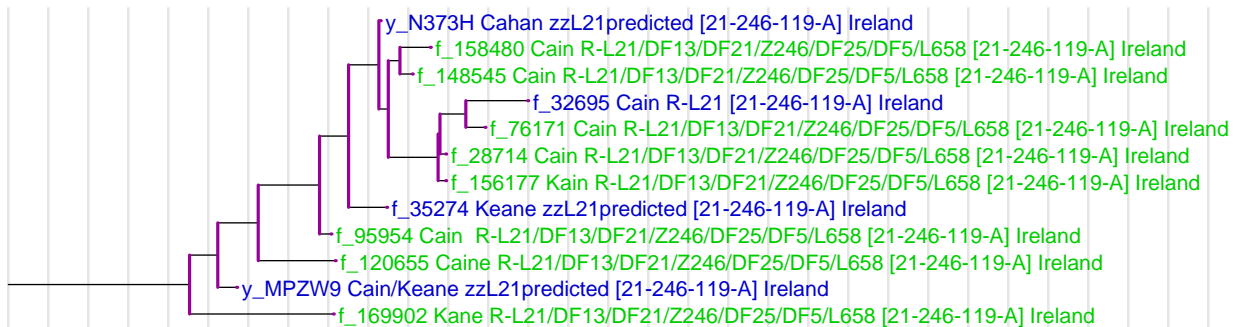


This is the marker distribution for R-L658. The color indicates the relative frequency of the alleles.



## Age Analysis

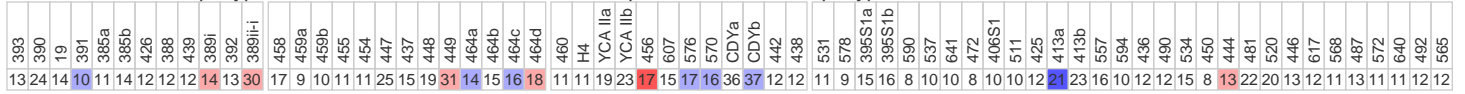
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
12	804	33	4.10%	20.95±2.23	523.808±76.4389



The vertical grey lines are separated 10 generations apart.

# R-L720

This is the modal haplotype for R-L720. The coloration is with respect to the modal haplotype of the full tree.



This is the marker distribution for R-L720. 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	29	8.66%	45.24±5.21	1131.01±172.453

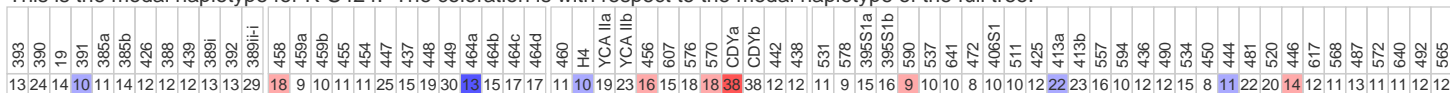


The vertical grey lines are separated 10 generations apart.

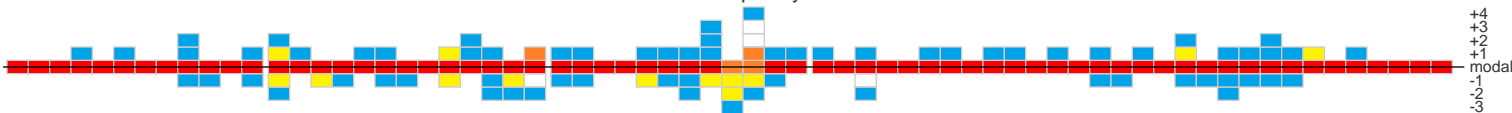


# R-S424

This is the modal haplotype for R-S424. The coloration is with respect to the modal haplotype of the full tree.

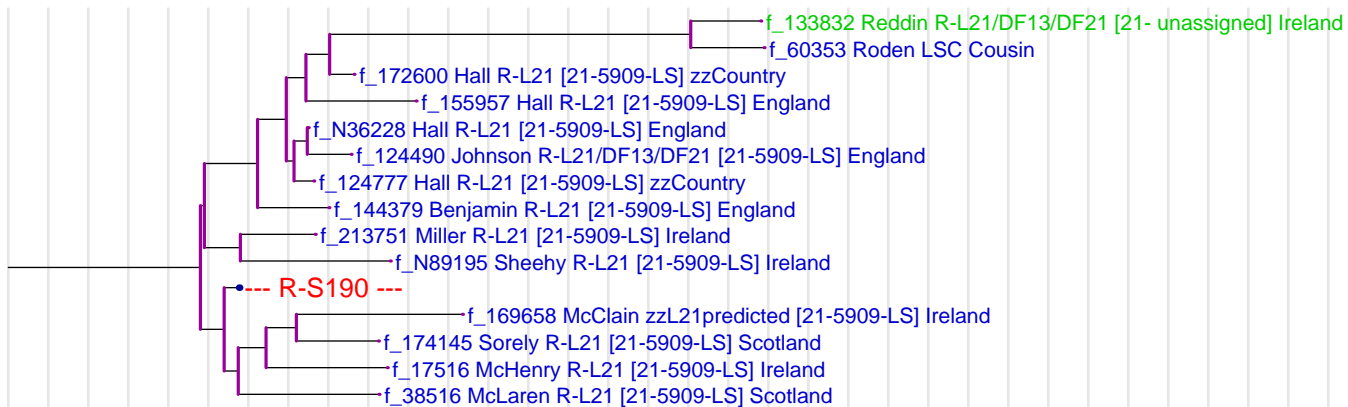


This is the marker distribution for R-S424. The color indicates the relative frequency of the alleles.



## Age Analysis

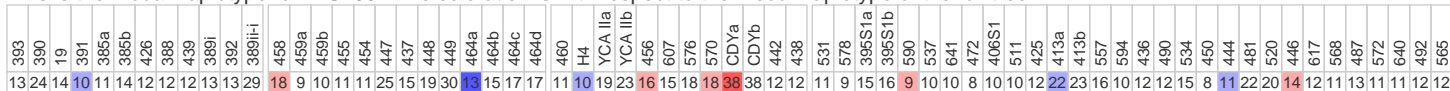
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
45	3015	287	9.52%	49.97±5.09	1249.3±178.278



The vertical grey lines are separated 10 generations apart.

# R-S190

This is the modal haplotype for R-S190. The coloration is with respect to the modal haplotype of the full tree.

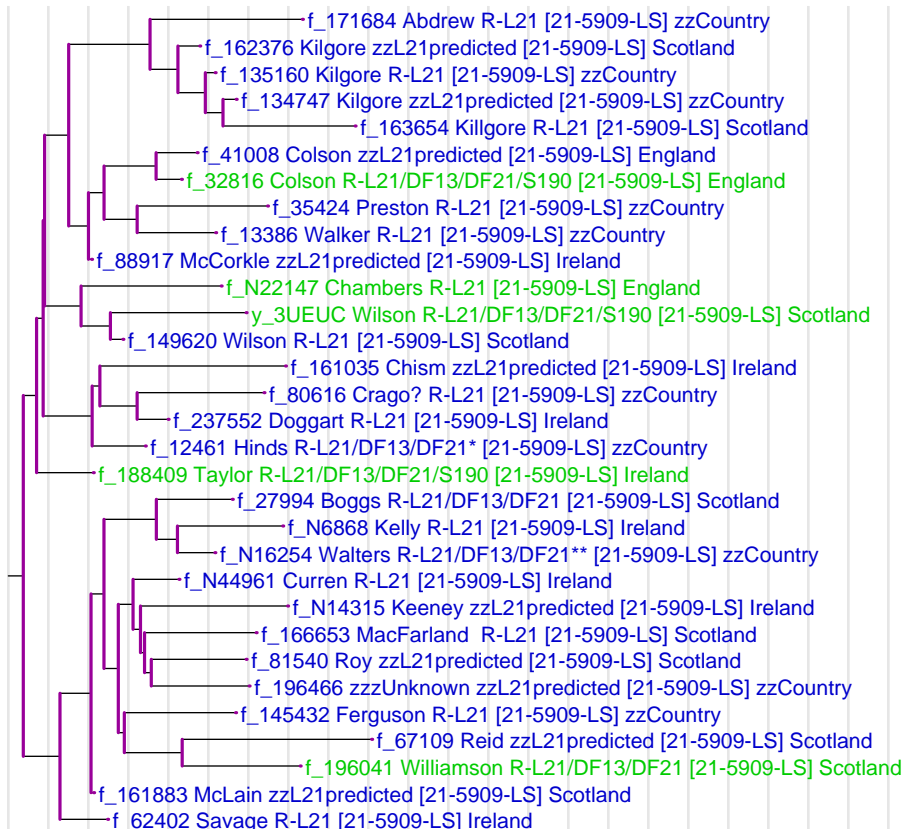


This is the marker distribution for R-S190. The color indicates the relative frequency of the alleles.



## Age Analysis

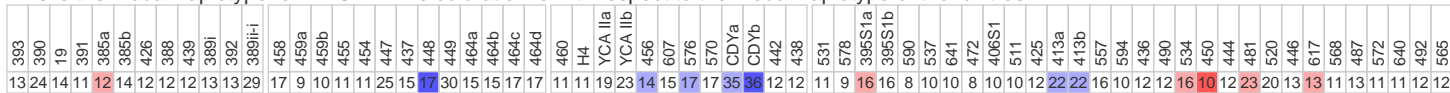
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
31	2077	176	8.47%	44.24±4.54	1106.05±158.452



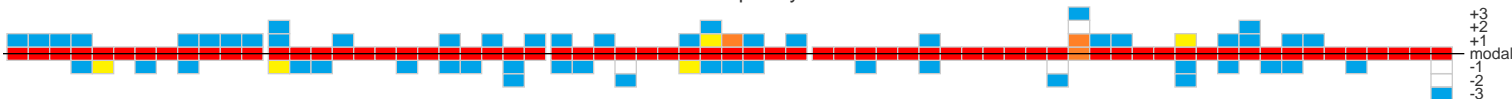
The vertical grey lines are separated 10 generations apart.

# R-L371

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

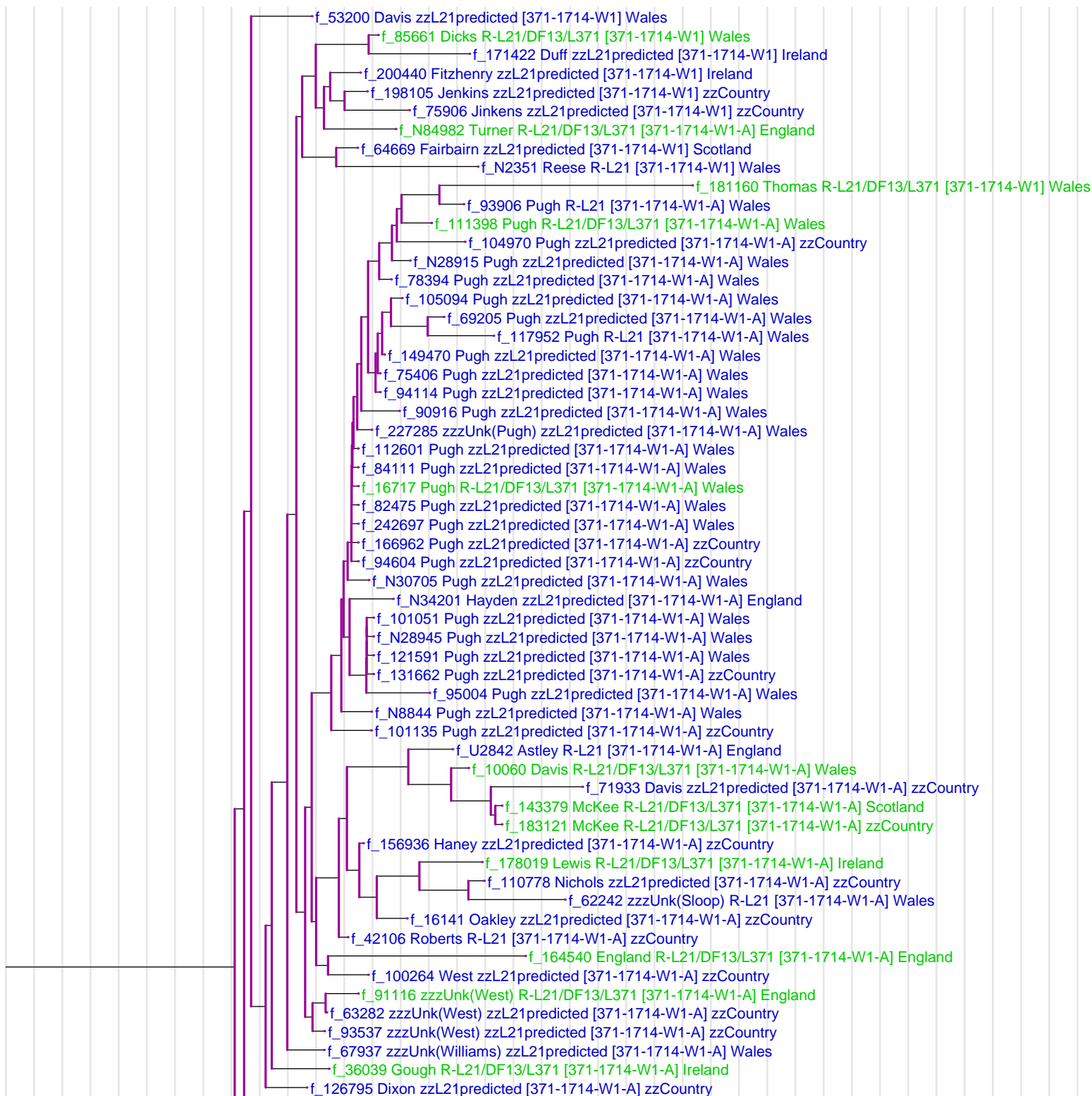


This is the marker distribution for R-L371. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
60	4020	224	5.57%	28.66±2.90	716.474±101.988

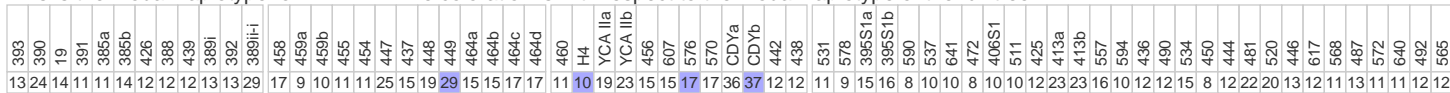


The vertical grey lines are separated 10 generations apart.

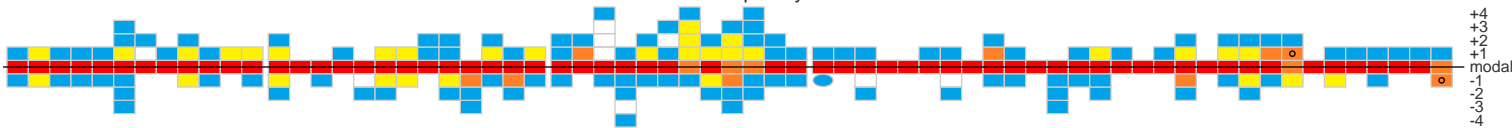
f\_190007 Griffith R-L21/DF13/L371 [371-1714-W1] zzCountry  
f\_193782 Griffith R-L21/DF13/L371 [371-1714-W1] zzCountry

# R-DF41

This is the modal haplotype for R-DF41. The coloration is with respect to the modal haplotype of the full tree.

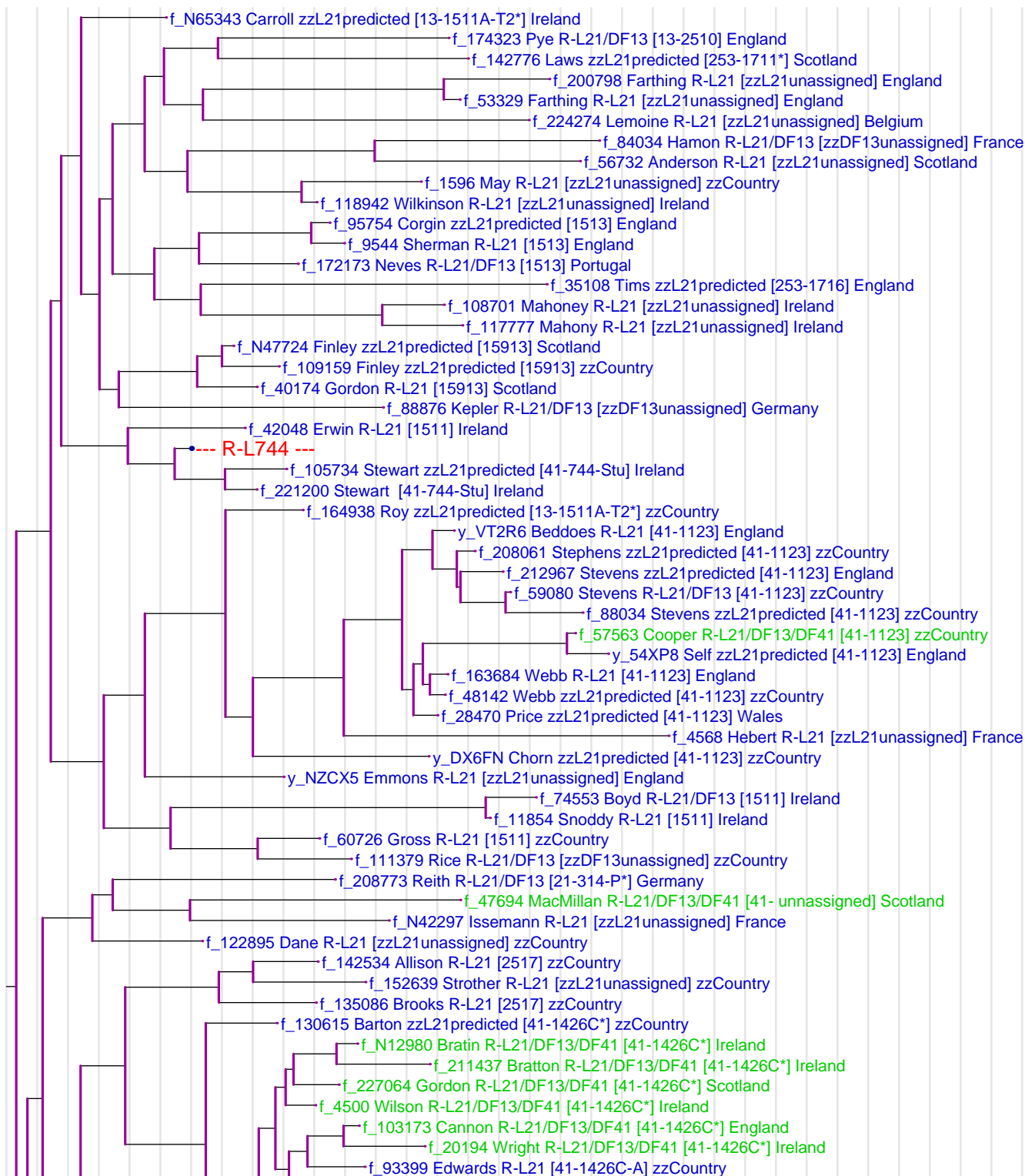


This is the marker distribution for R-DF41. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
155	10385	1981	19.08%	105.40±10.60	2635.01±373.722



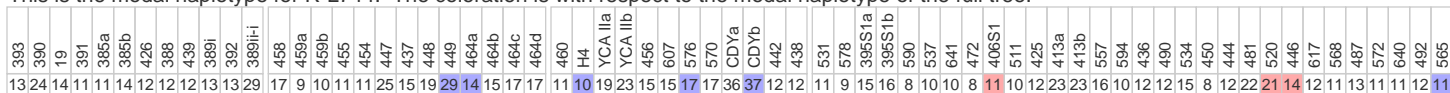
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

# R-L744

This is the modal haplotype for R-L744. The coloration is with respect to the modal haplotype of the full tree.

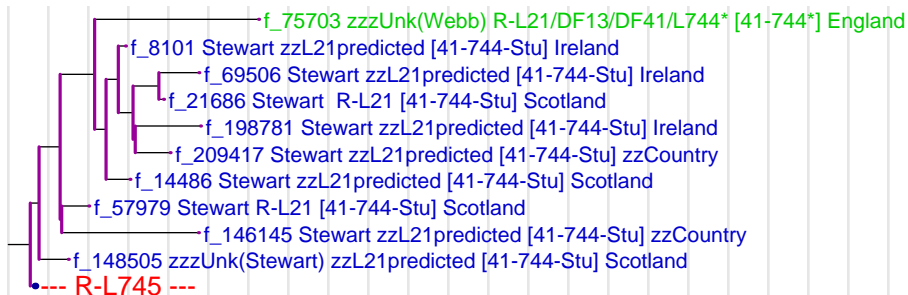


This is the marker distribution for R-L744. The color indicates the relative frequency of the alleles.



## Age Analysis

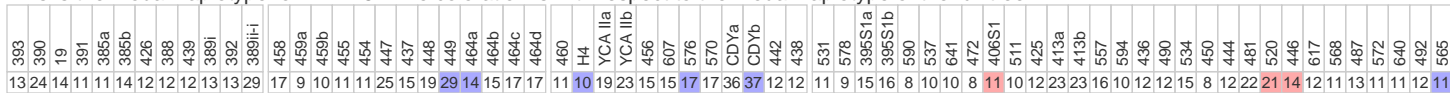
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
58	3886	186	4.79%	24.52±2.48	612.968±87.2696



The vertical grey lines are separated 10 generations apart.

# R-L745

This is the modal haplotype for R-L745. The coloration is with respect to the modal haplotype of the full tree.

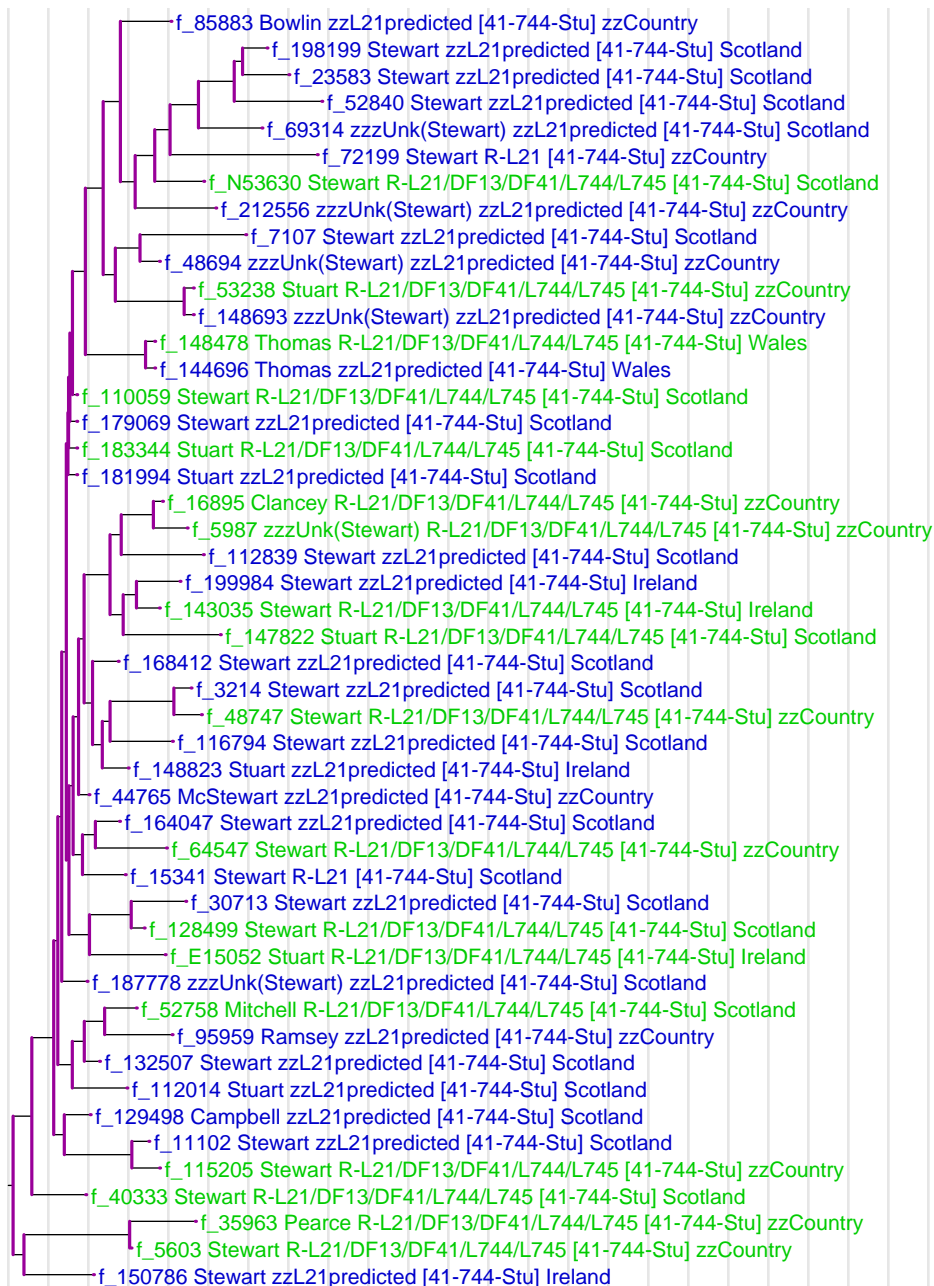


This is the marker distribution for R-L745. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
48	3216	158	4.91%	25.18±2.56	629.579±89.7596

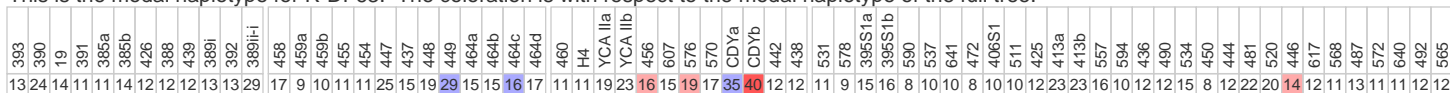


The vertical grey lines are separated 10 generations apart.

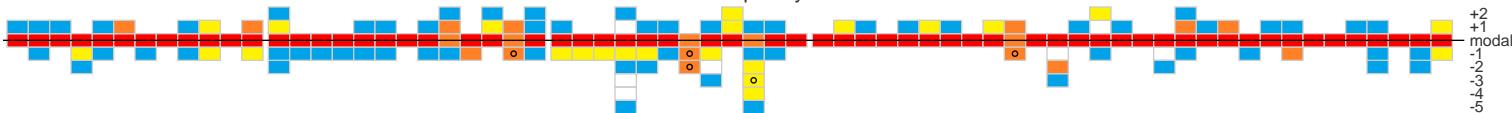


# R-DF63

This is the modal haplotype for R-DF63. The coloration is with respect to the modal haplotype of the full tree.

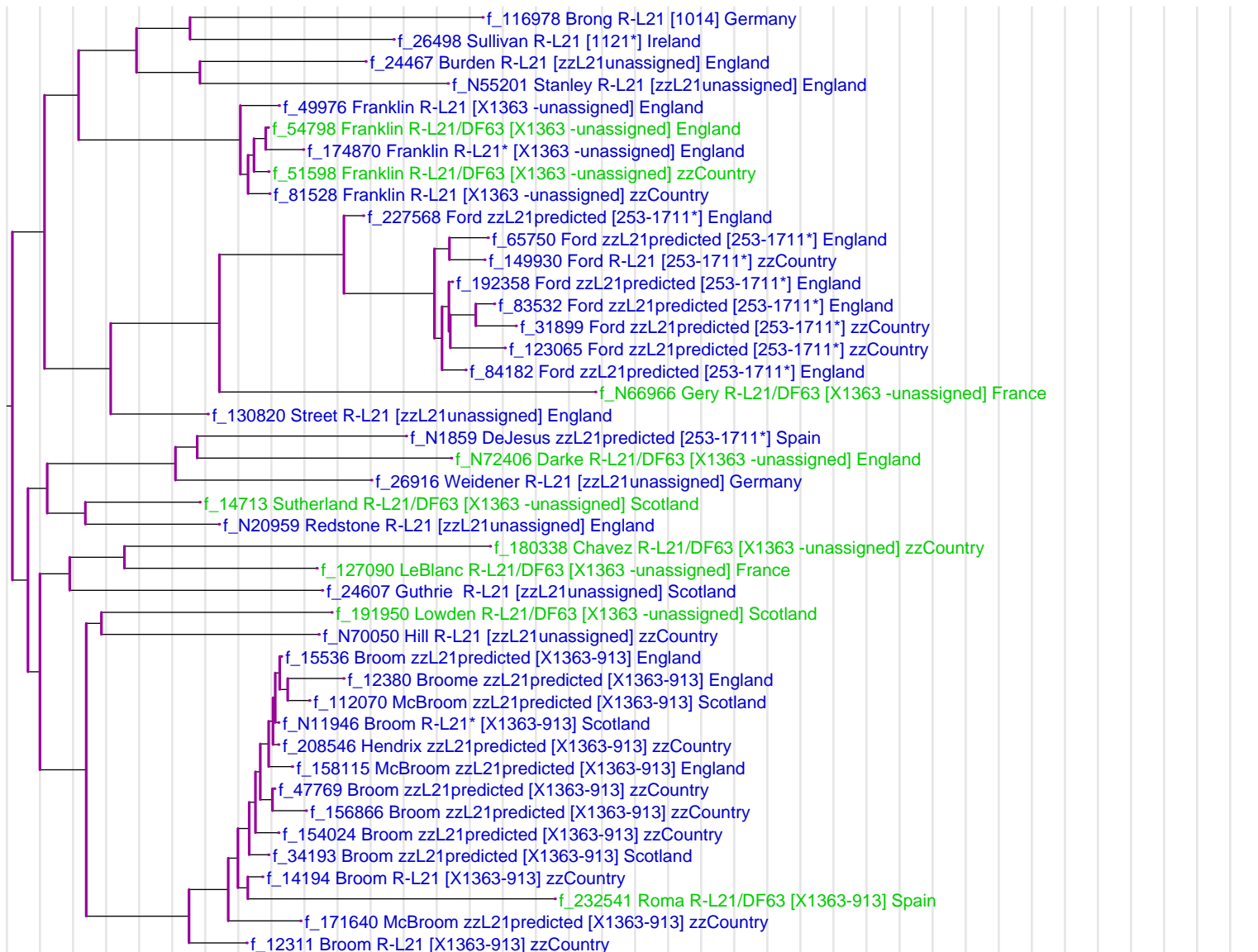


This is the marker distribution for R-DF63. The color indicates the relative frequency of the alleles.



## Age Analysis

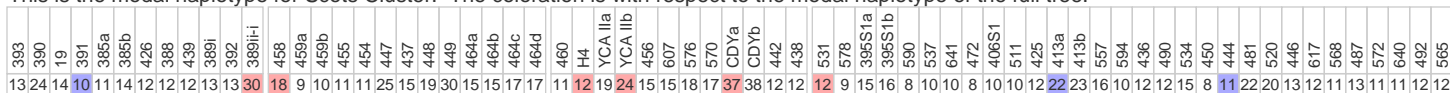
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
43	2881	578	20.06%	111.46±11.38	2786.38±398.173



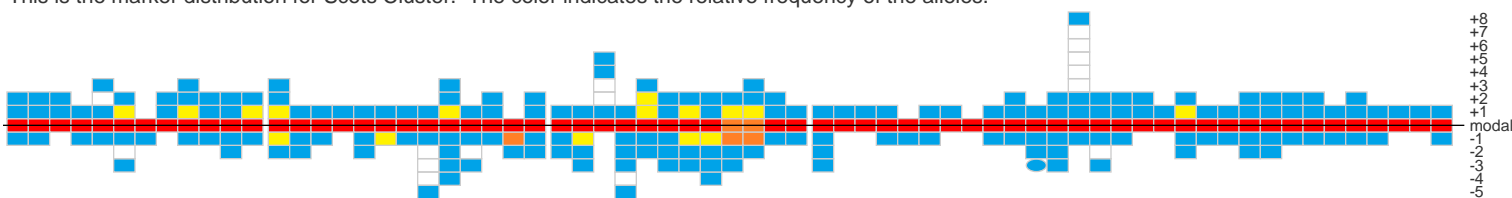
The vertical grey lines are separated 10 generations apart.

# Scots Cluster

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

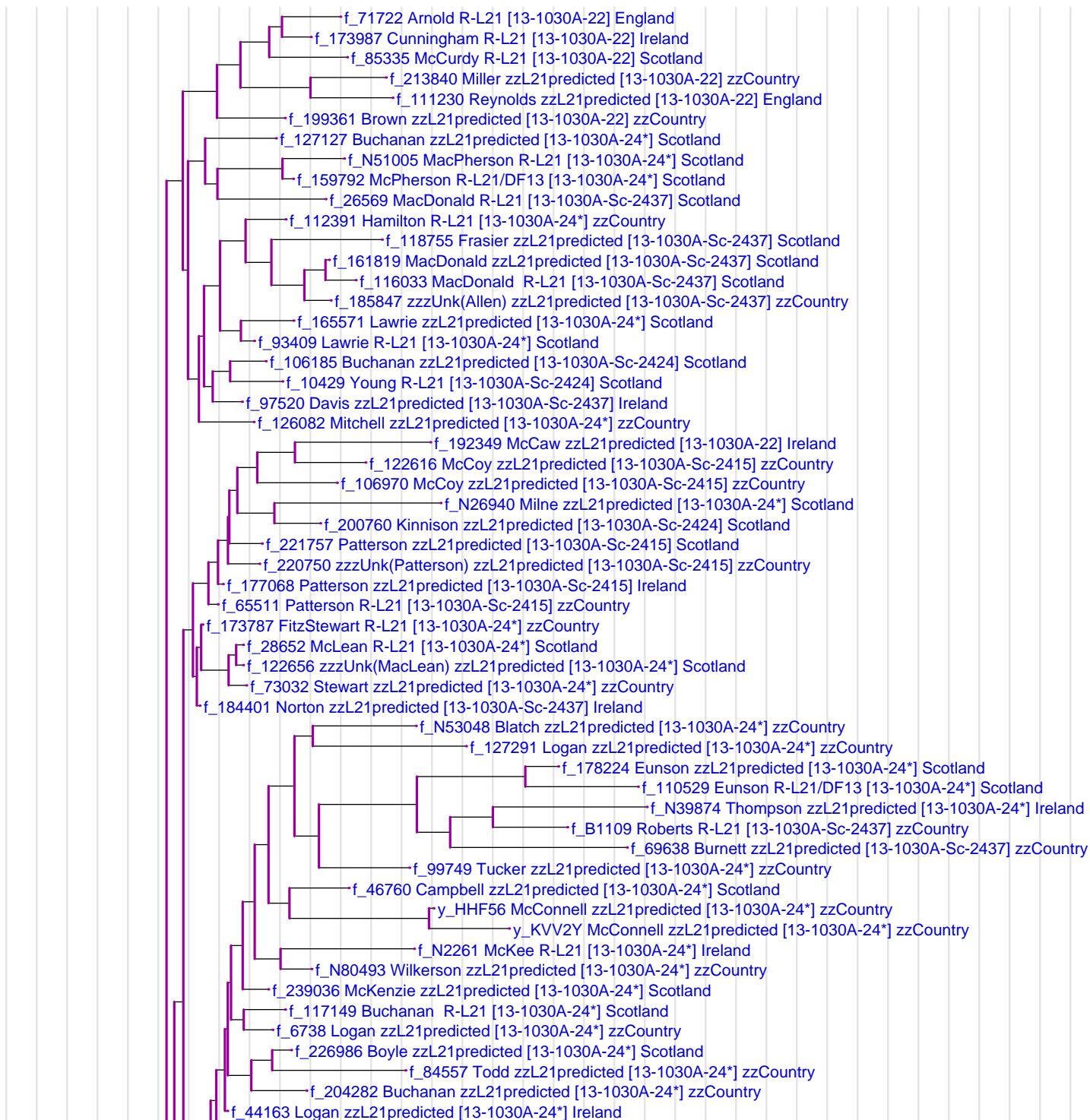


This is the marker distribution for Scots Cluster. The color indicates the relative frequency of the alleles.

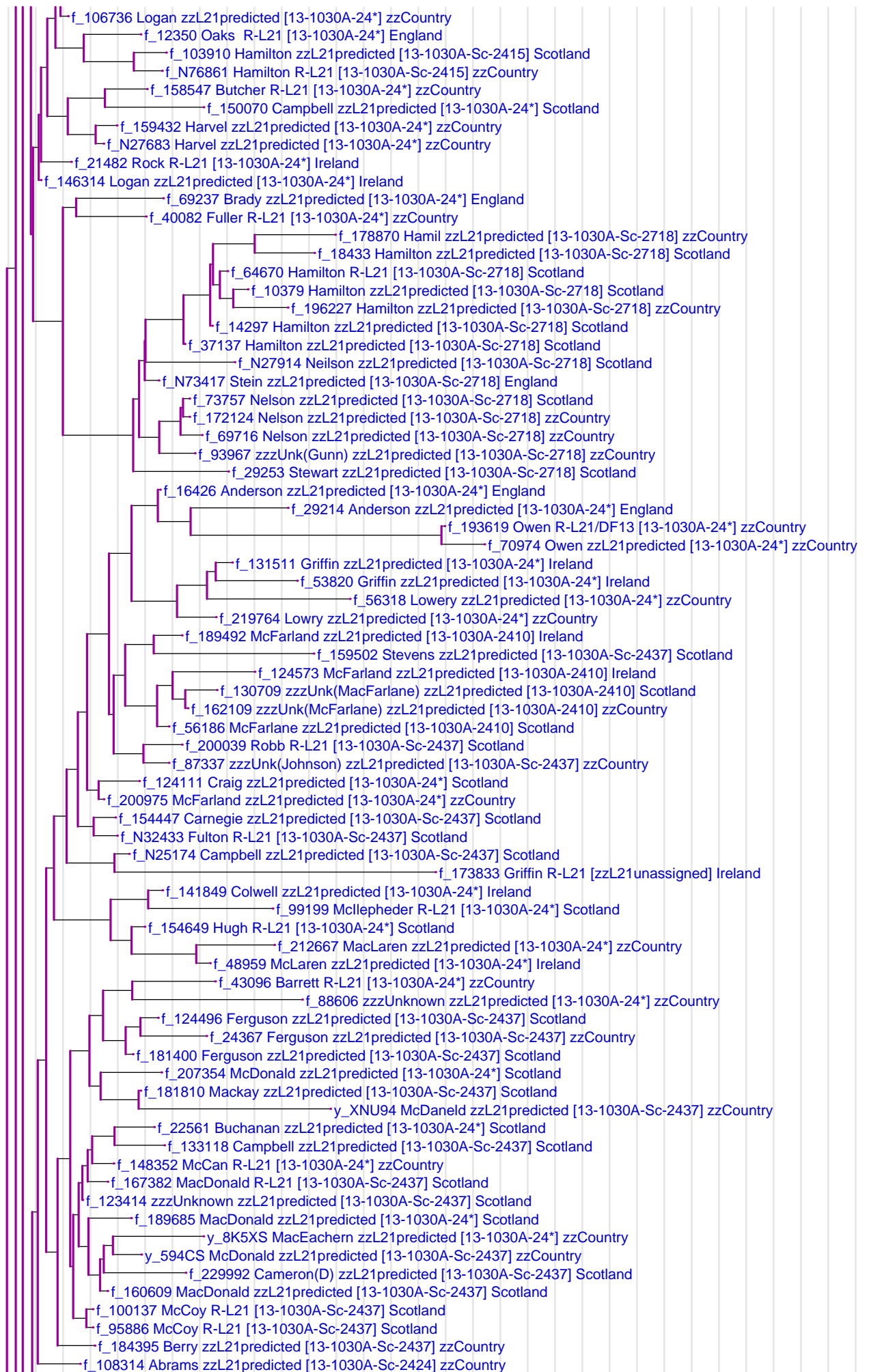


## Age Analysis

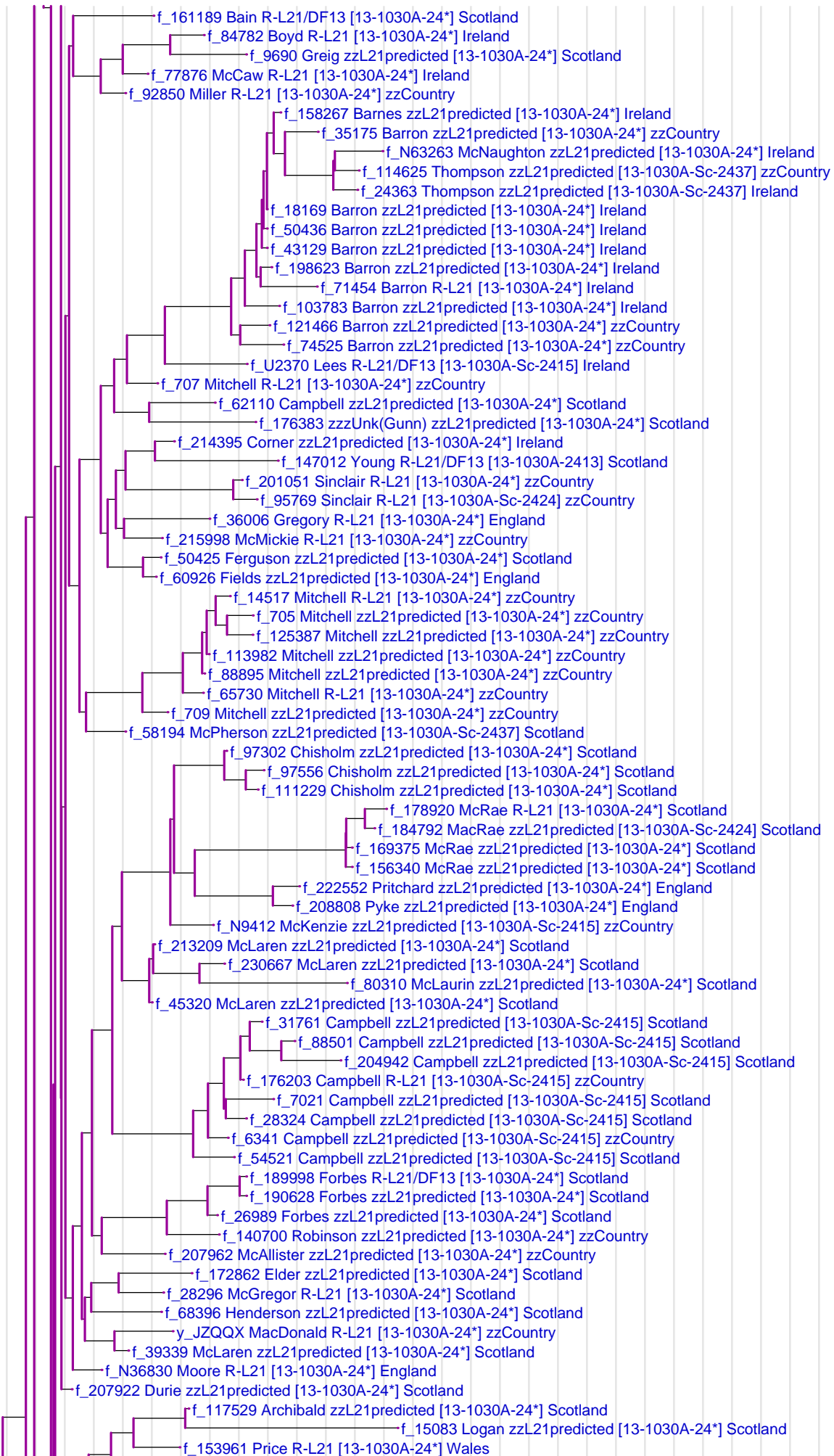
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
746	49982	5672	11.35%	60.15±6.02	1503.74±212.78



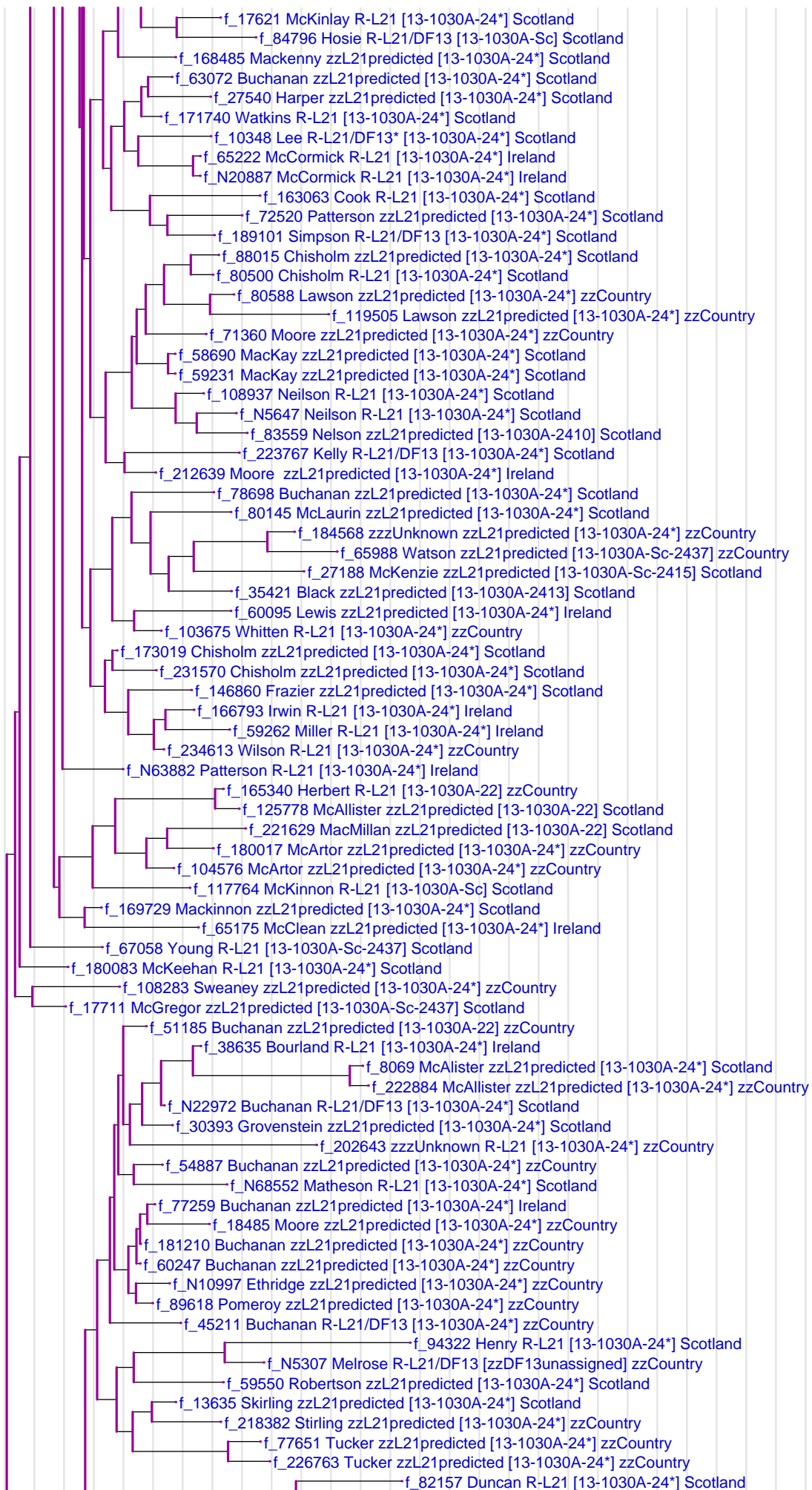
The vertical grey lines are separated 10 generations apart.



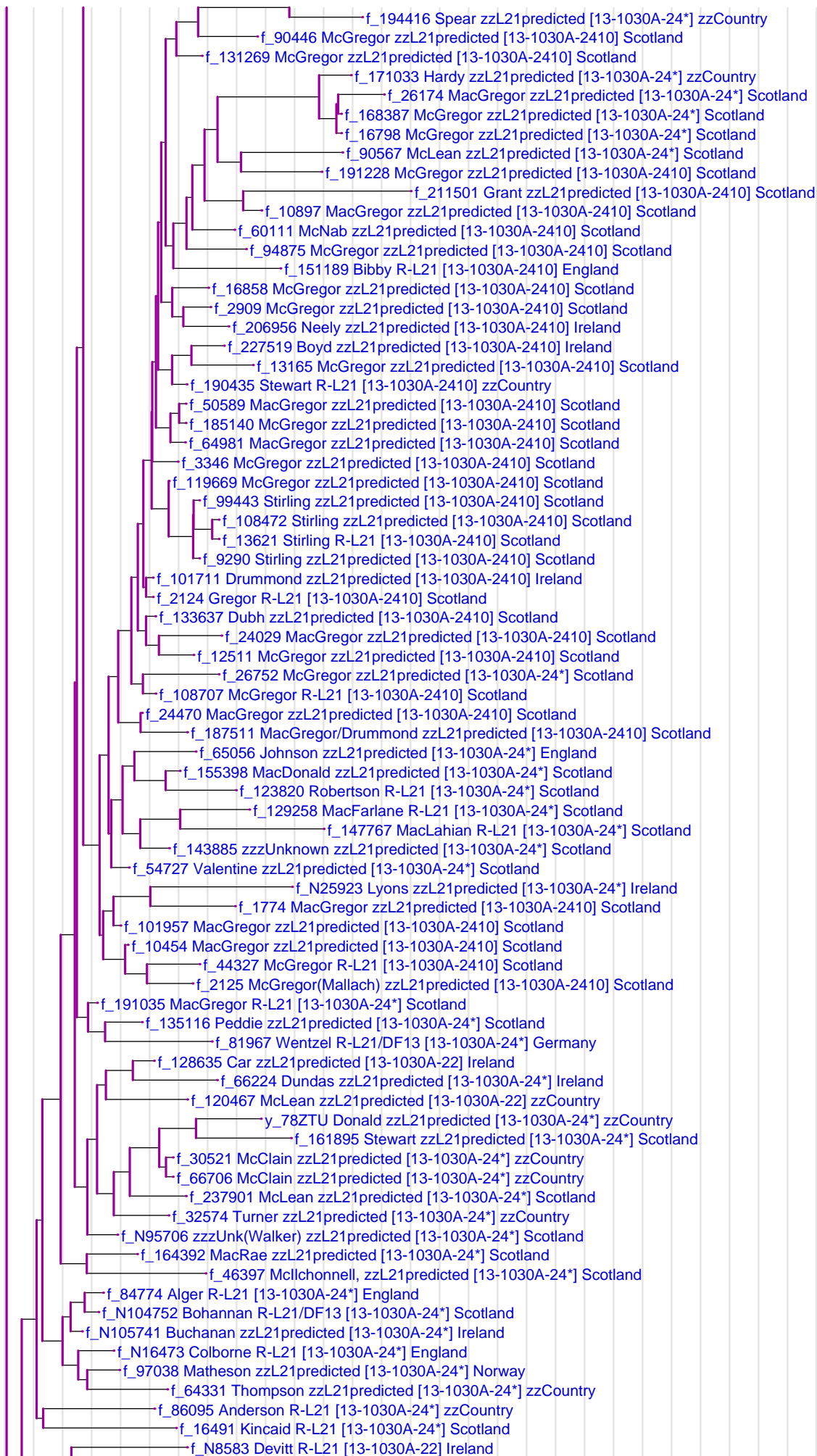
The vertical grey lines are separated 10 generations apart.



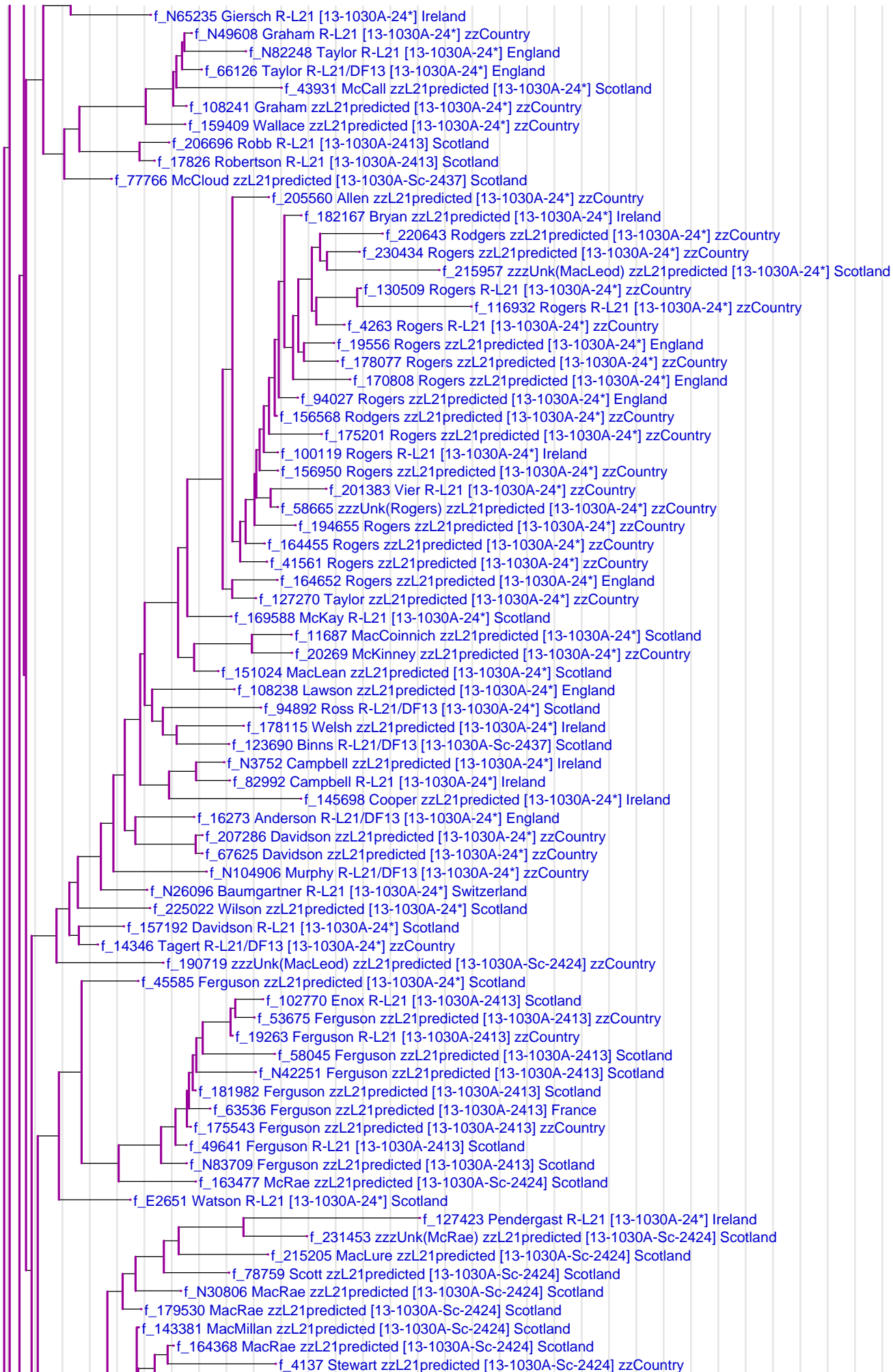
The vertical grey lines are separated 10 generations apart.



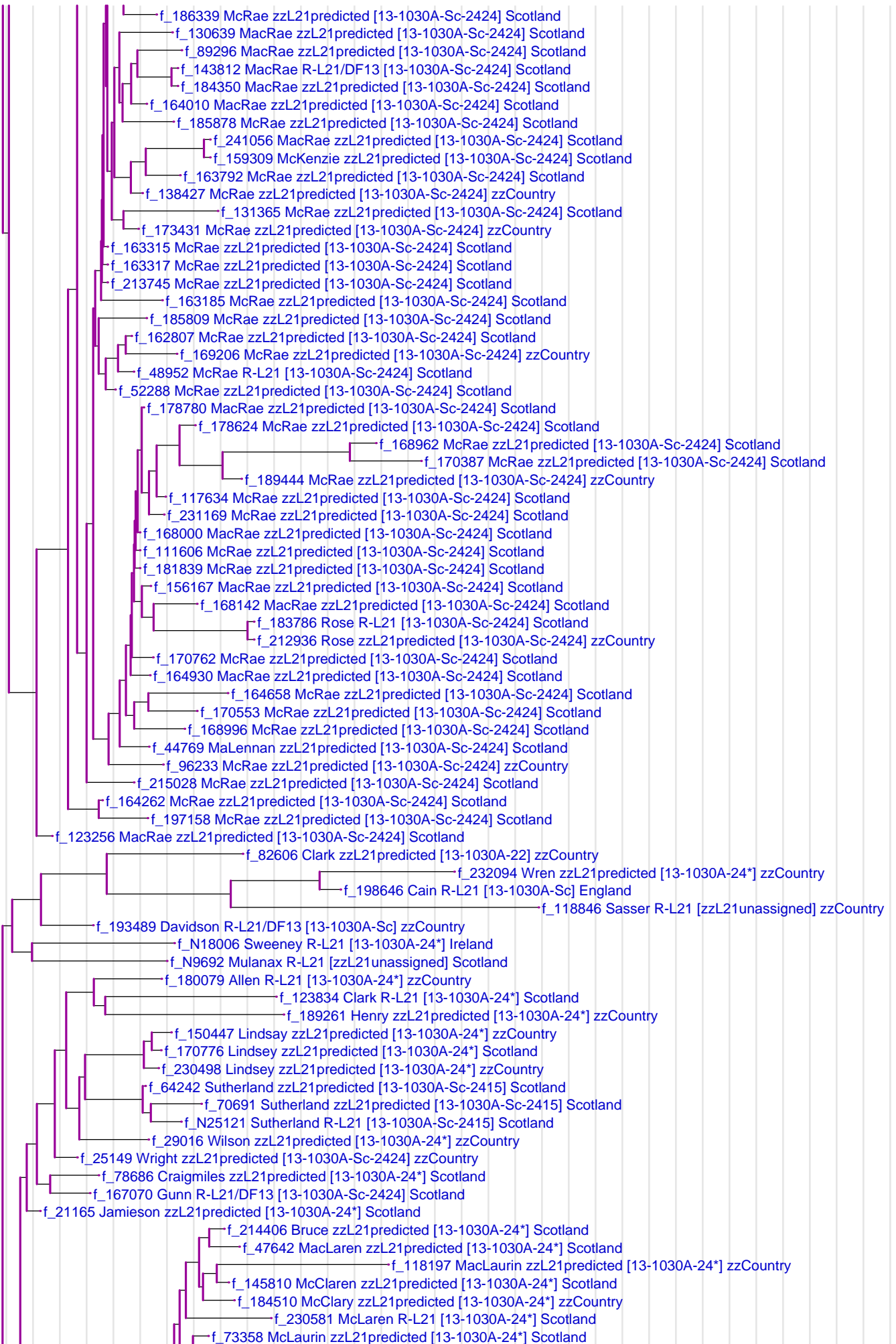
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

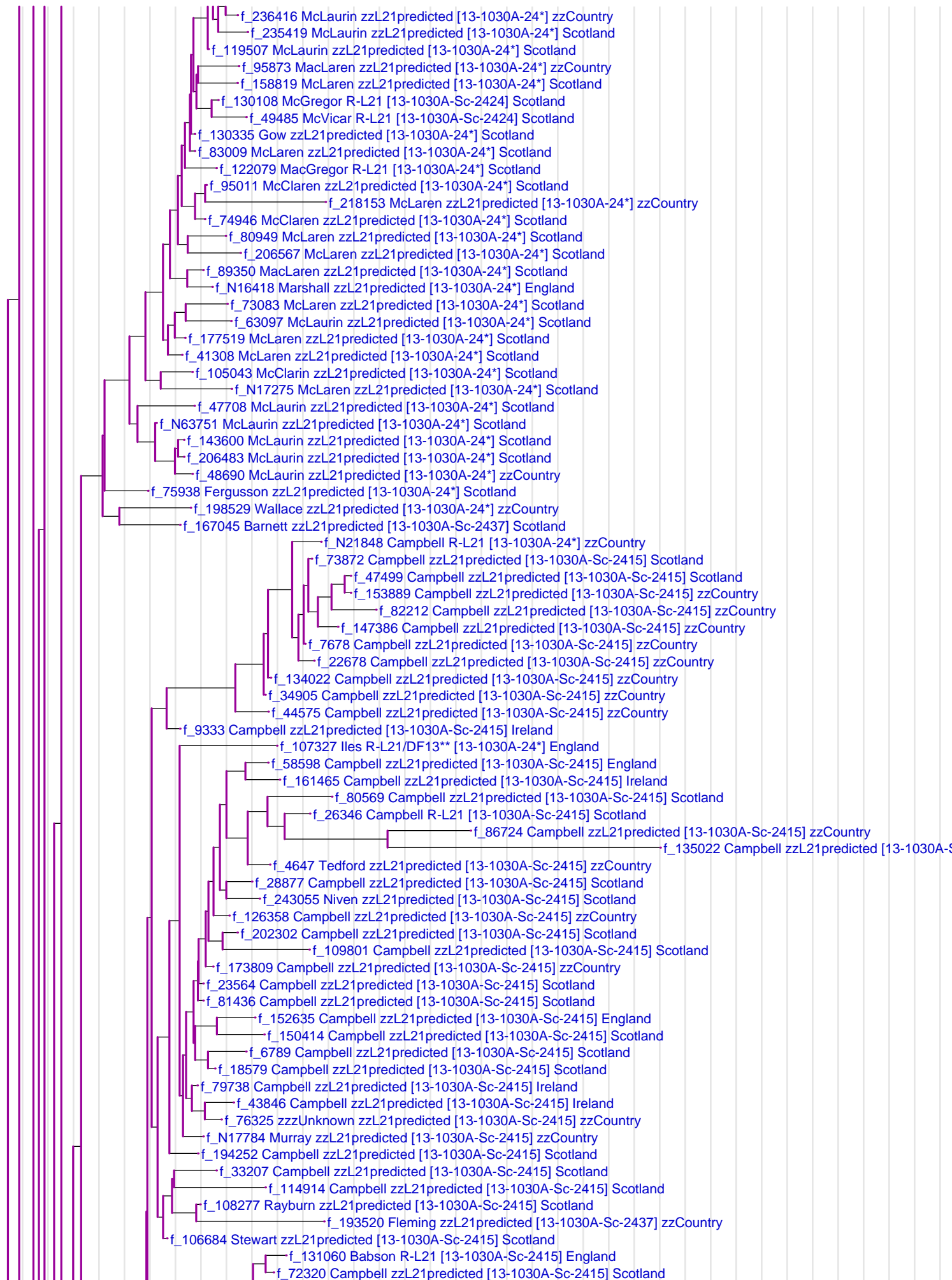


The vertical grey lines are separated 10 generations apart.

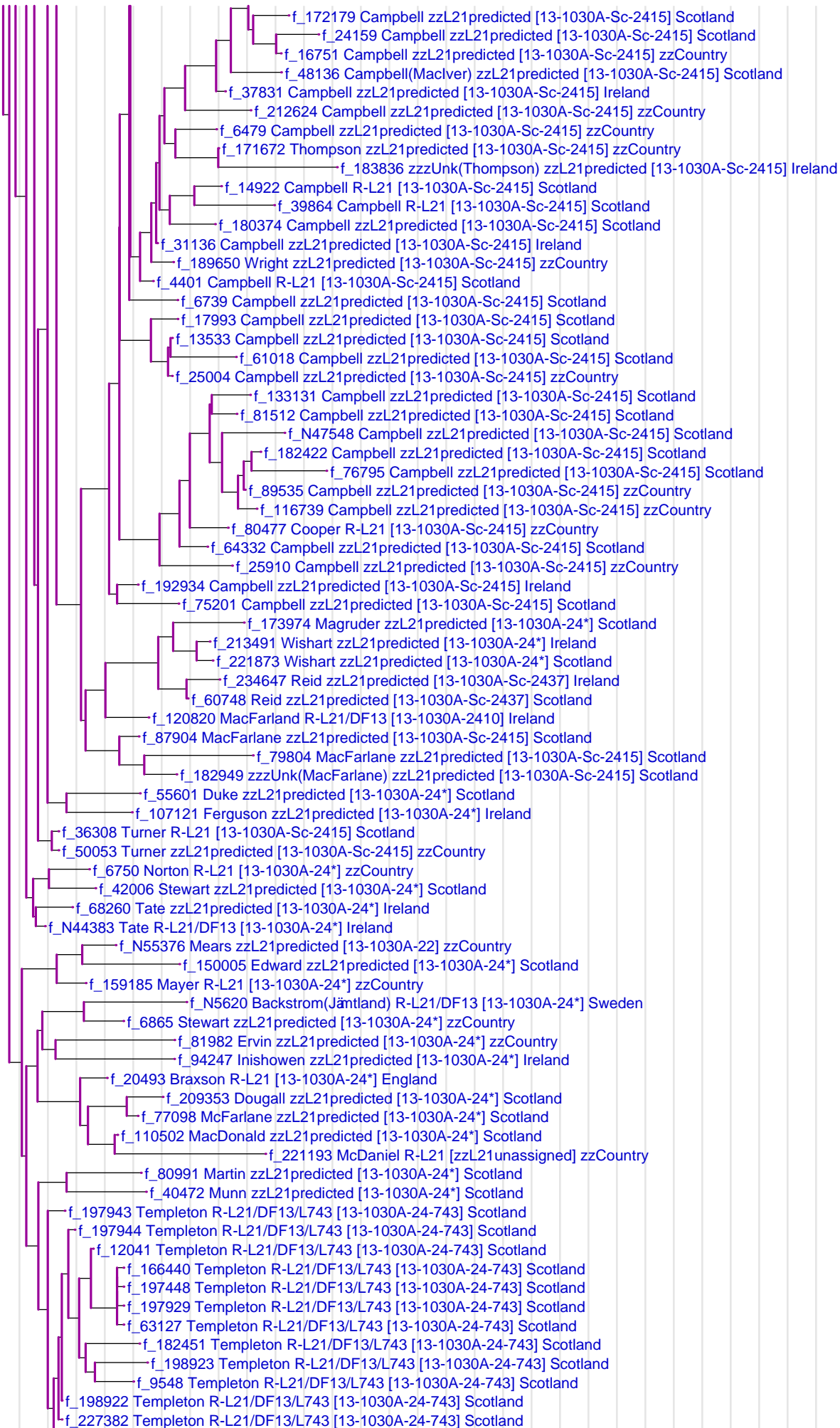


The vertical grey lines are separated 10 generations apart.

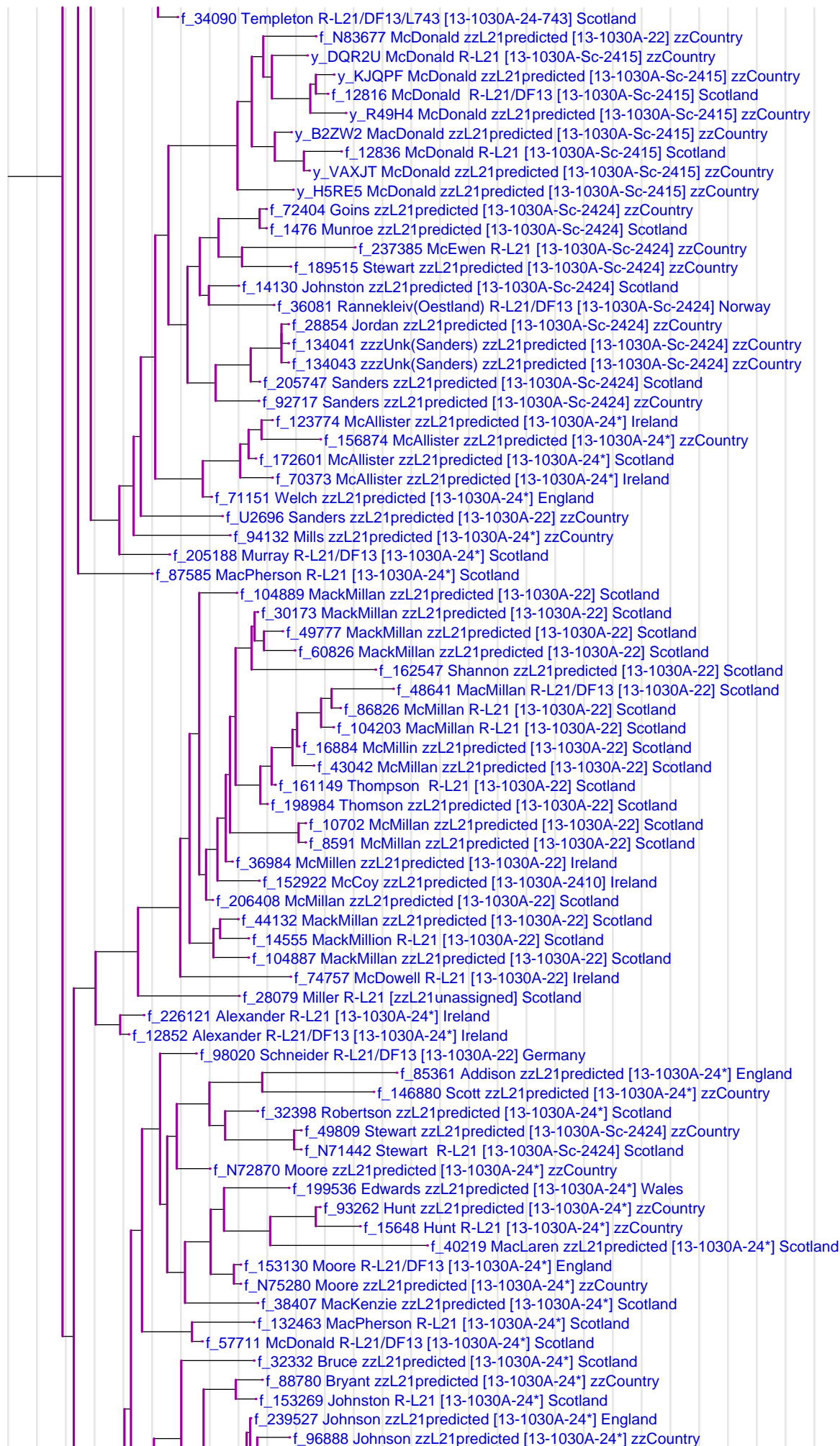




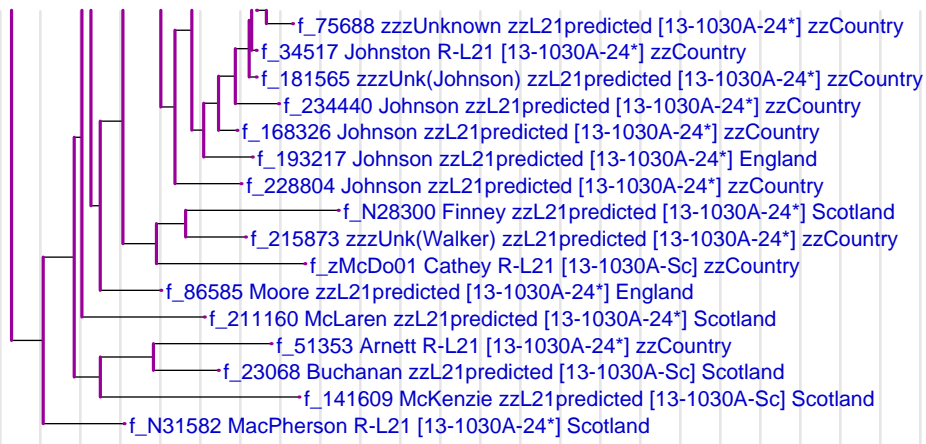
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

# Cluster Modals

Full Tree (R-L21)

Age: 3497.9±494.72 years

393	390	19	391	385a	385b	426	388	439	389i	392	389iH	458	459a	459b	455	454	447	437	448	449	464a	464c	464d	480	H4	YCA Ila	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	567	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565		
13	24	14	11	11	14	12	12	13	13	29	17	9	10	11	11	25	15	19	30	15	15	17	17	11	11	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12		
R-DF13																																																				Age: 3504.12±495.601 years															
R-DF49																																																				Age: 2333.14±330.111 years															
13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17	11	11	19	23	17	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-DF23																																																				Age: 2057.42±291.109 years															
13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17	11	11	19	23	17	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-M222																																																				Age: 1543.32±218.384 years															
13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17	11	11	19	23	17	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-L513																																																				Age: 3034.94±429.437 years															
13	24	14	11	11	14	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	15	18	17	38	37	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	11	11	12	12		
R-P66																																																				Age: 187.97±29.7502 years															
13	25	14	11	11	14	12	12	12	13	13	29	15	9	10	11	11	25	16	18	29	15	16	17	18	11	11	19	23	18	15	17	17	35	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	24	20	13	13	11	13	11	12	12		
R-L193																																																				Age: 1424.03±201.691 years															
13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	12	12			
R-L706.2																																																				Age: 1235.88±176.264 years															
13	24	15	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	18	23	16	15	18	18	37	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12	
R-L705.2																																																				Age: 1240.16±176.973 years															
13	24	15	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	18	23	16	15	18	18	37	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12	
R-L555																																																				Age: 452.363±64.2984 years															
13	24	14	11	11	15	12	12	12	13	13	29	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	16	8	12	22	20	13	12	11	13	11	11	12	12	
R-L96																																																				Age: 1274.46±197.858 years															
13	24	14	10	11	14	12	12	12	13	13	28	17	9	10	11	11	24	15	19	29	15	15	17	17	11	11	19	23	16	15	19	19	35	39	12	12	11	9	15	16	8	11	10	8	10	10	12	23	23	17	10	12	12	15	8	12	23	21	13	12	11	13	11	11	12	12	
R-Z255																																																				Age: 1670.05±236.559 years															
13	24	14	11	11	14	12	12	12	14	13	30	17	9	10	11	11	25	15	18	30	15	15	17	17	11	11	19	23	16	15	18	18	30	40	11	12	11	9	15	16	8	10	10	8	10	10	12	23	23	17	10	12	12	15	8	12	22	20	14	12	11	13	11	11	12	12	
R-Z253																																																				Age: 3132.18±443.217 years															
13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17	11	11	19	23	15	15	18	17	36	39	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	17	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-L226																																																				Age: 1251.78±177.335 years															
13	24	14	11	11	14	12	12	11	13	13	29	17	8	9	11	11	25	15	19	29	13	13	15	17	11	11	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	15	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-L554																																																				Age: 902.049±143.558 years															
13	25	14	11	11	14	12	12	11	14	13	30	17	9	10	11	11	25	14	19	29	15	15	15	17	17	10	11	19	23	15	15	18	17	36	40	13	12	11	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	17	8	12	22	20	13	12	11	14	11	11	12	12
R-L1066																																																				Age: 3130.94±444.247 years															
13	24	14	10	11	15	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17	17	10	10	19	23	16	15	17	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-DF21																																																				Age: 2930.38±414.707 years															
13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	28	15	15	17	17	11	11	19	23	16	15	18	18	36	37	12	12	11	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-P314.2																																																				Age: 1923.4±274.159 years															
13	23	14	11	11	14	12	13	13	13	28	17	9	10	11	11	25	15	19	29	15	15	16	17	17	10	11	19	23	16	15	18	18	37	38	12	12	11	9	16	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	12	22	20	13	13	11	13	11	11	12	12	
R-L362																																																				Age: 1065.96±153.167 years															
13	23	14	11	11	14	12	13	13	13	28	17	9	10	11	11	25	15	19	29	15	15	16	17	17	10	11	19	23	16	15	18	18	37	38	12	12	11	9	16	16	8	10	10	8	11	10	12	23	23	17	10	12	12	15	8	12	22	20	13	13	11	13	11	11	12	12	
R-Z246																																																				Age: 2947.63±418.318 years															
13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	15	15	18	17	37	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-DF25																																																				Age: 2957.18±419.837 years															
13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12	
R-DF5																																																				Age: 2790.37±396.434 years															
13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17	17	11	11	19	23	16	15	18	17	37	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L627																																																				Age: 572.517±88.5095 years															
13	24	15	10	11	15	12	12	12	14	13	30	17	9	10	11	11	25	15	19	29	15	16	16	16	17	10	11	21	23																																						

# Notes

## The Tree

The tree was generated using a custom neighbor-joining algorithm which takes into account constraints imposed by SNP results. The STR data came from the 2012-08-30 version of Mike Walsh's Excel spreadsheet, while the SNP data came primarily from the L21+, Scottish, and Irish FTDNA projects. Only members with 67 FTDNA markers, and who were supposedly L21+ were used.

Only those SNPs which appear on the ISOGG tree have been included in the analysis. Those men whose entries are colored green have tested positive for the SNP corresponding to the branch on which they're located. Those men whose names are blue are positioned only by virtue of their STR results.

## Modal Values

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 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%	

