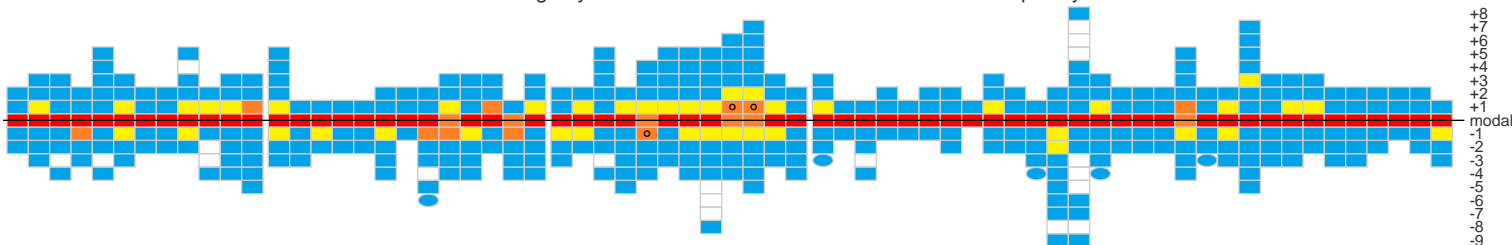


# R-L21

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

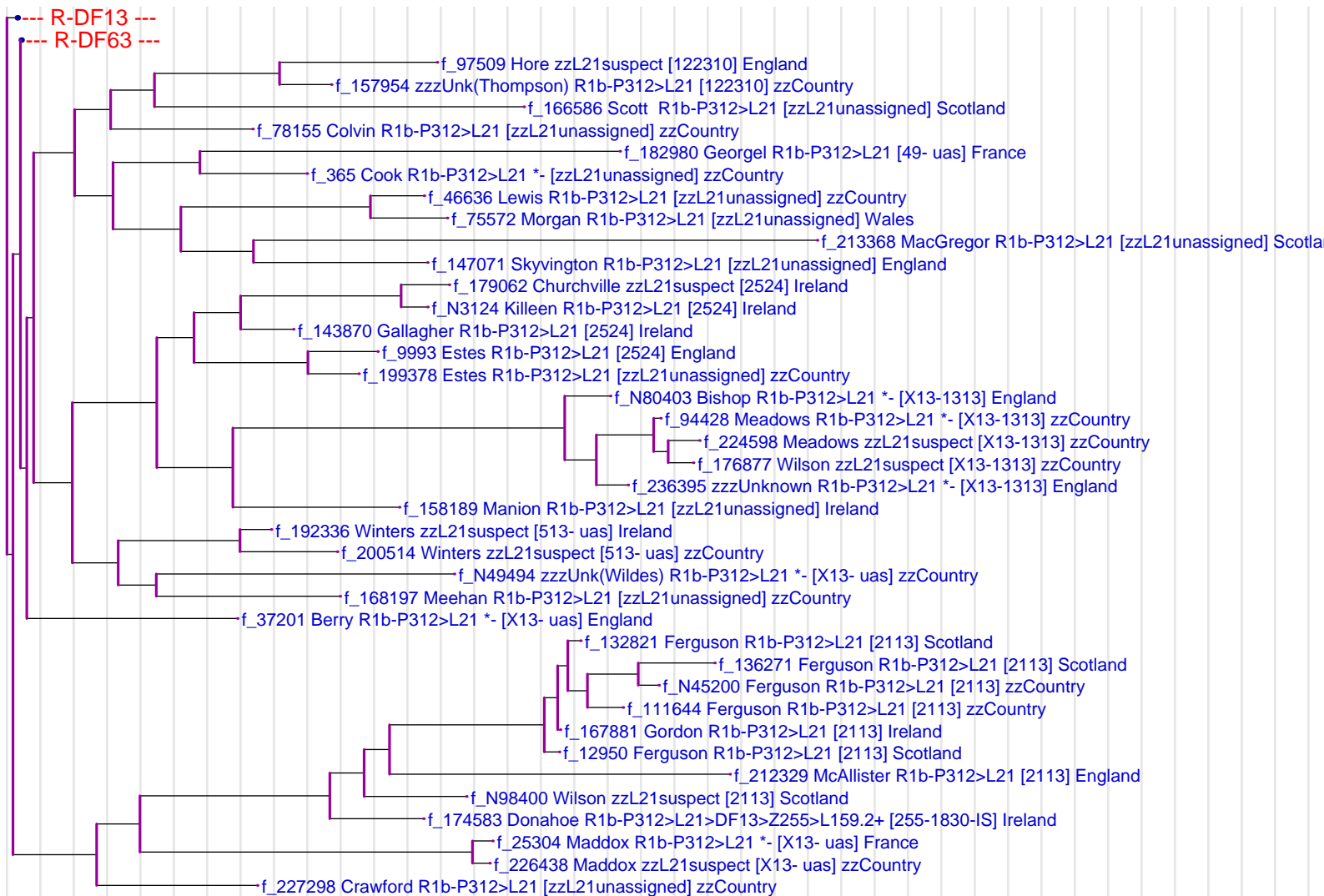
393	390	19	391	385a	385b	426	388	439	389i	392	389i-1	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	466	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	11	14	12	12	13	13	29	17	9	10	10	11	11	25	15	19	30	15	15	17	17	11	11	19	23	16	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

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



## Age Analysis

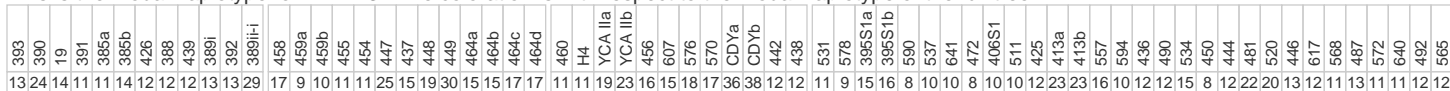
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6817	456739	113056	24.75%	141.14±14.12	3528.61±499.055



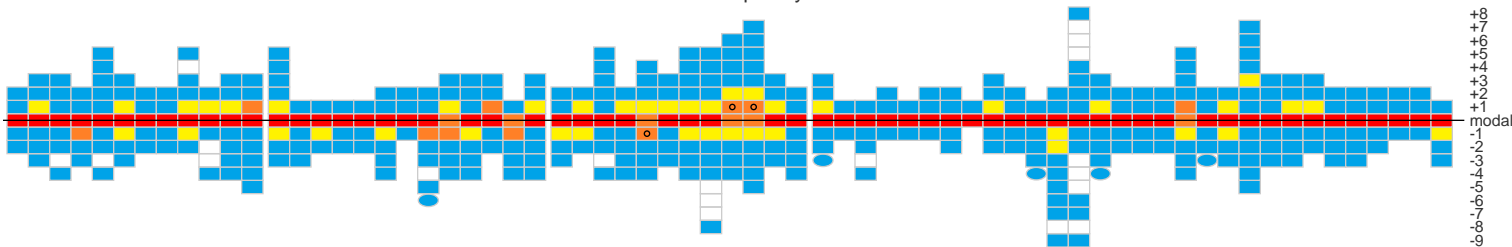
The vertical grey lines are separated 10 generations apart.

# R-DF13

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

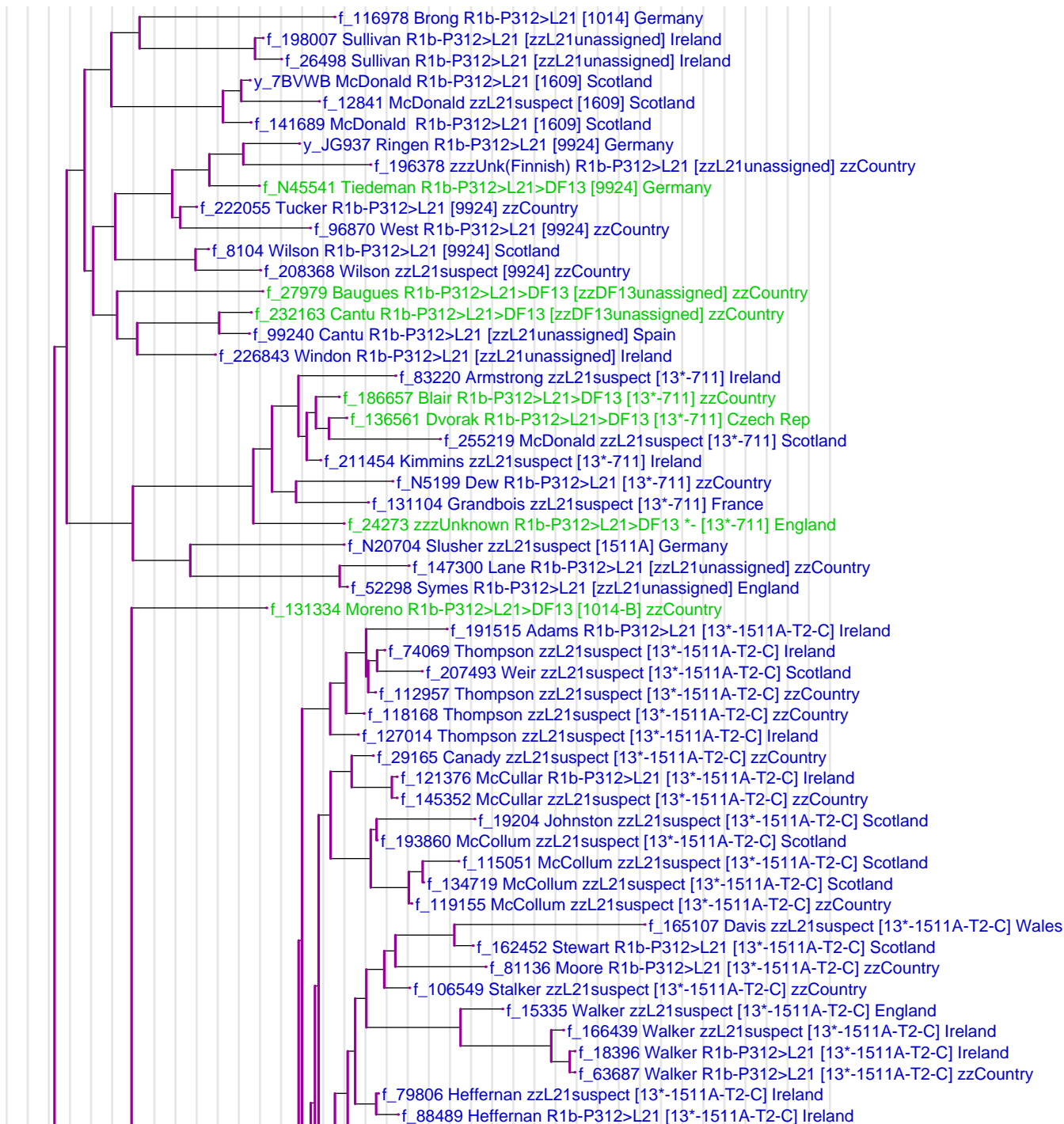


This is the marker distribution for R-DF13. The color indicates the relative frequency of the alleles.

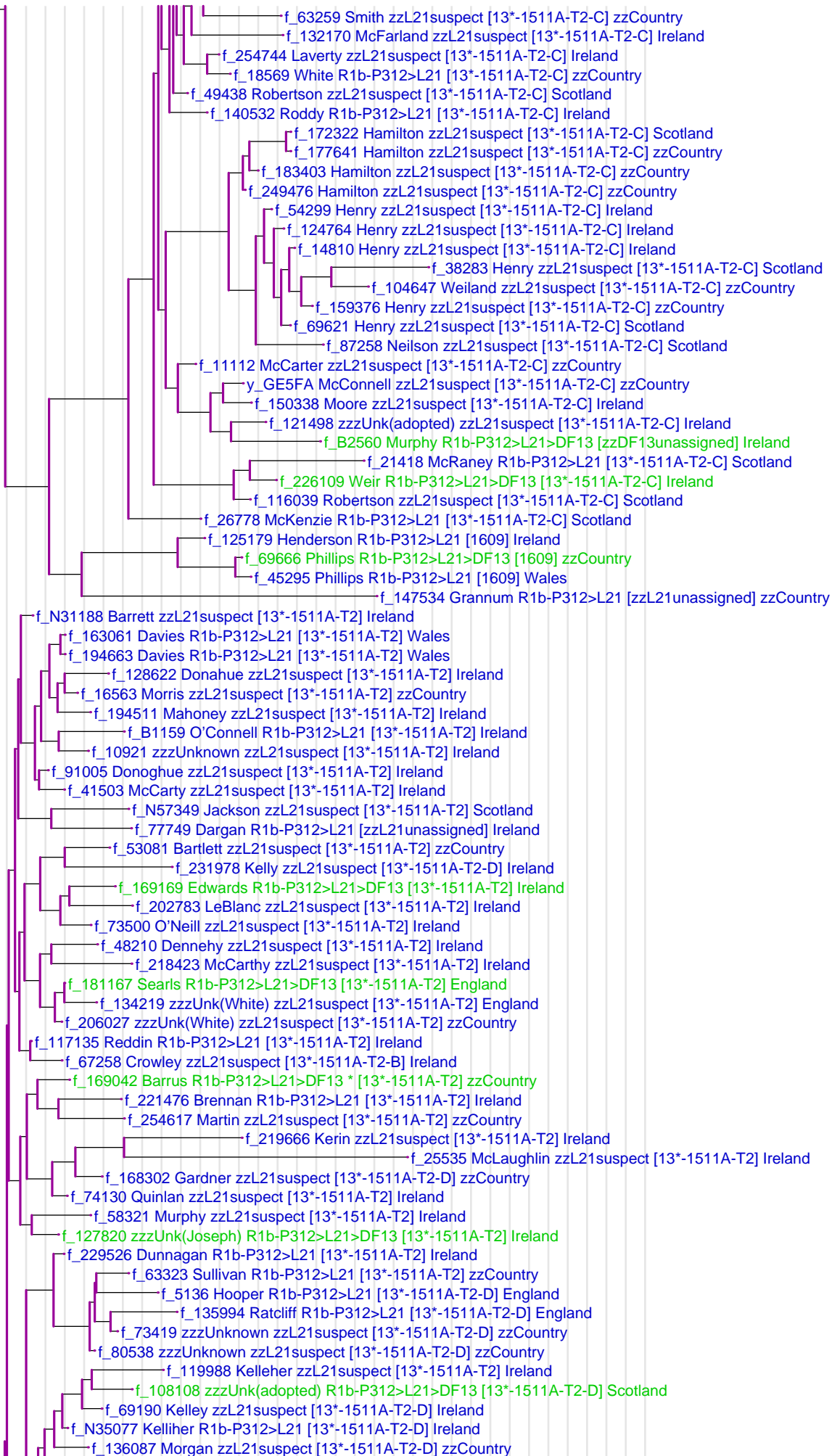


## Age Analysis

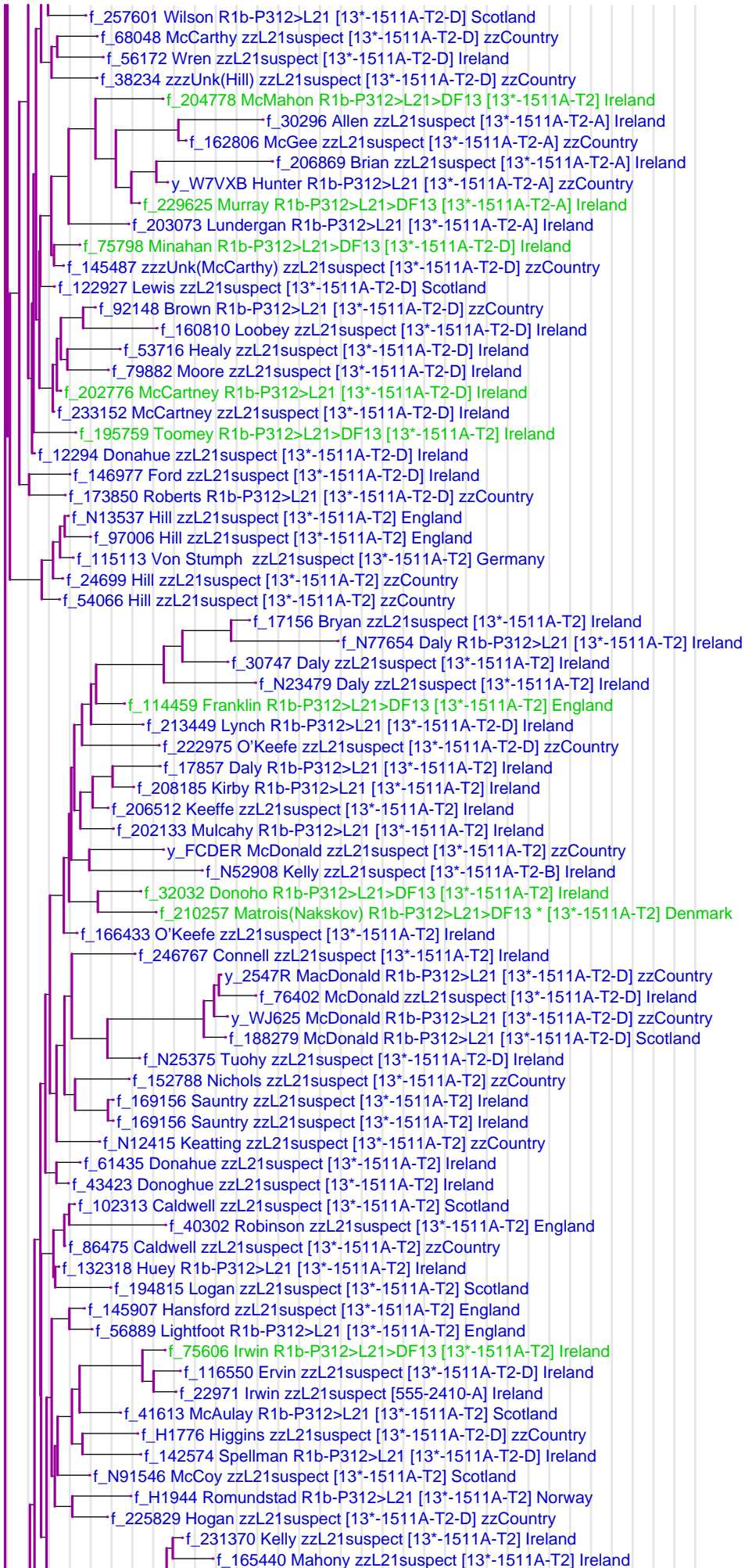
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6641	444947	110264	24.78%	141.33±14.13	3533.24±499.711



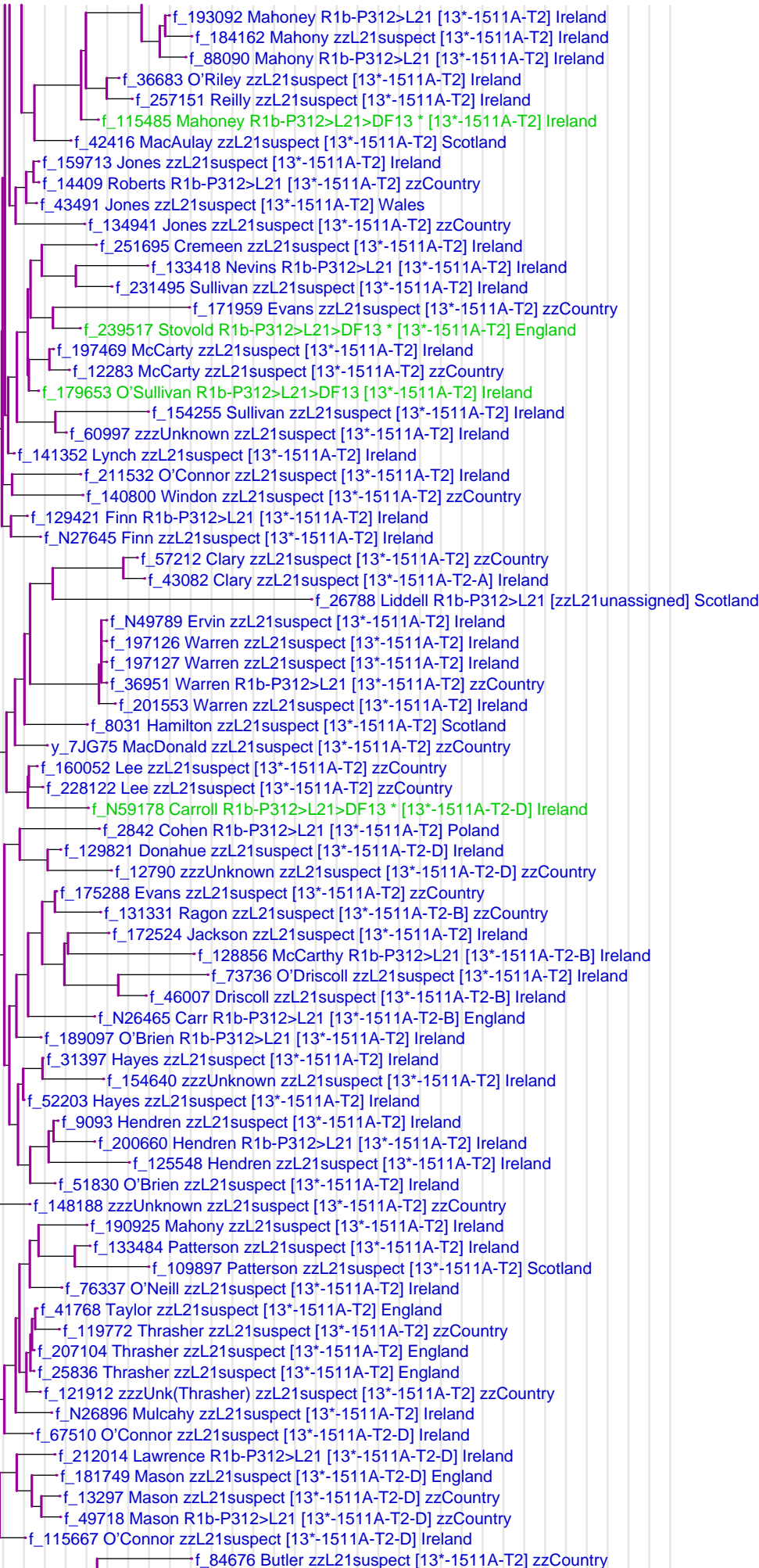
The vertical grey lines are separated 10 generations apart.



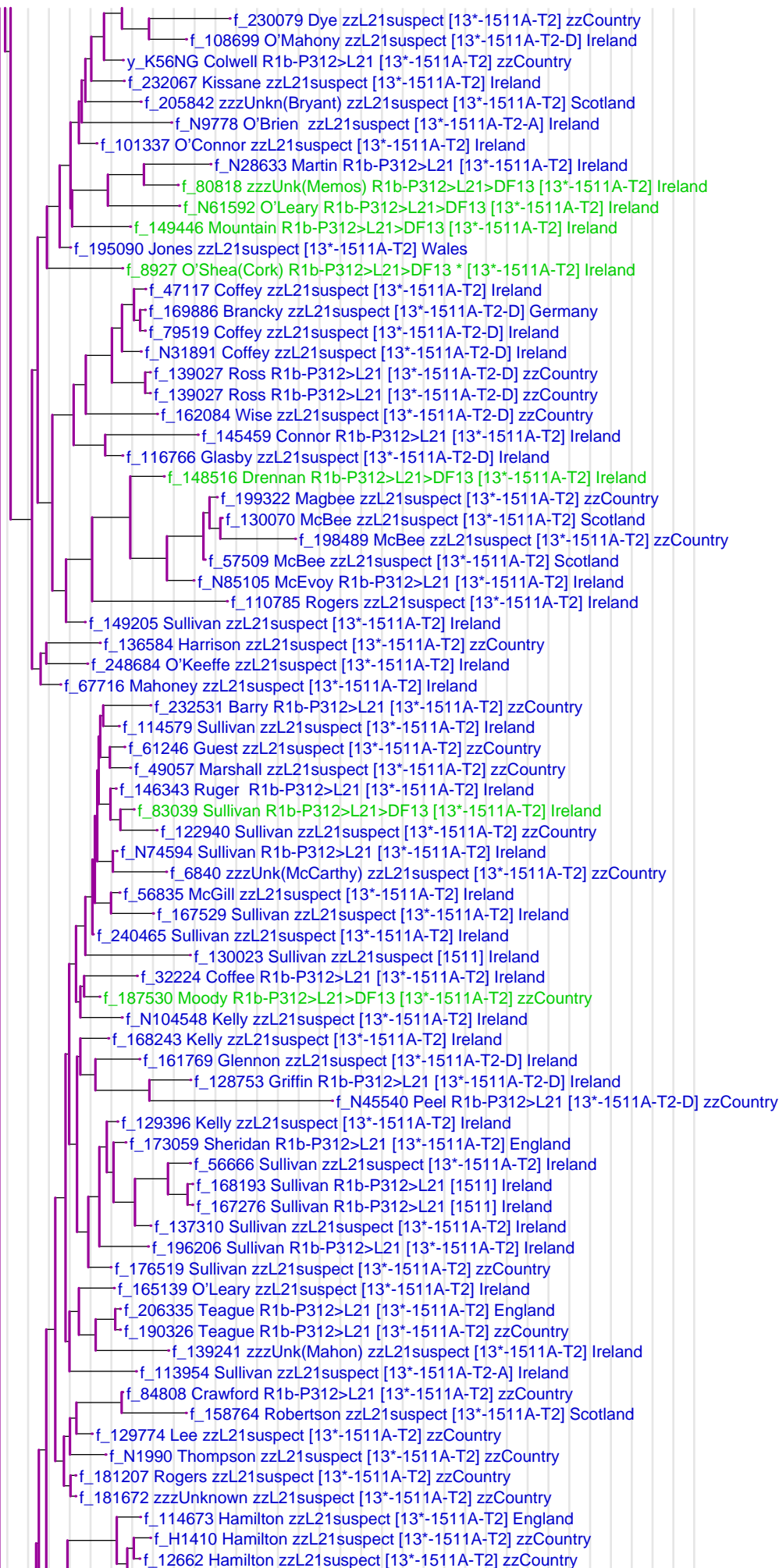
The vertical grey lines are separated 10 generations apart.



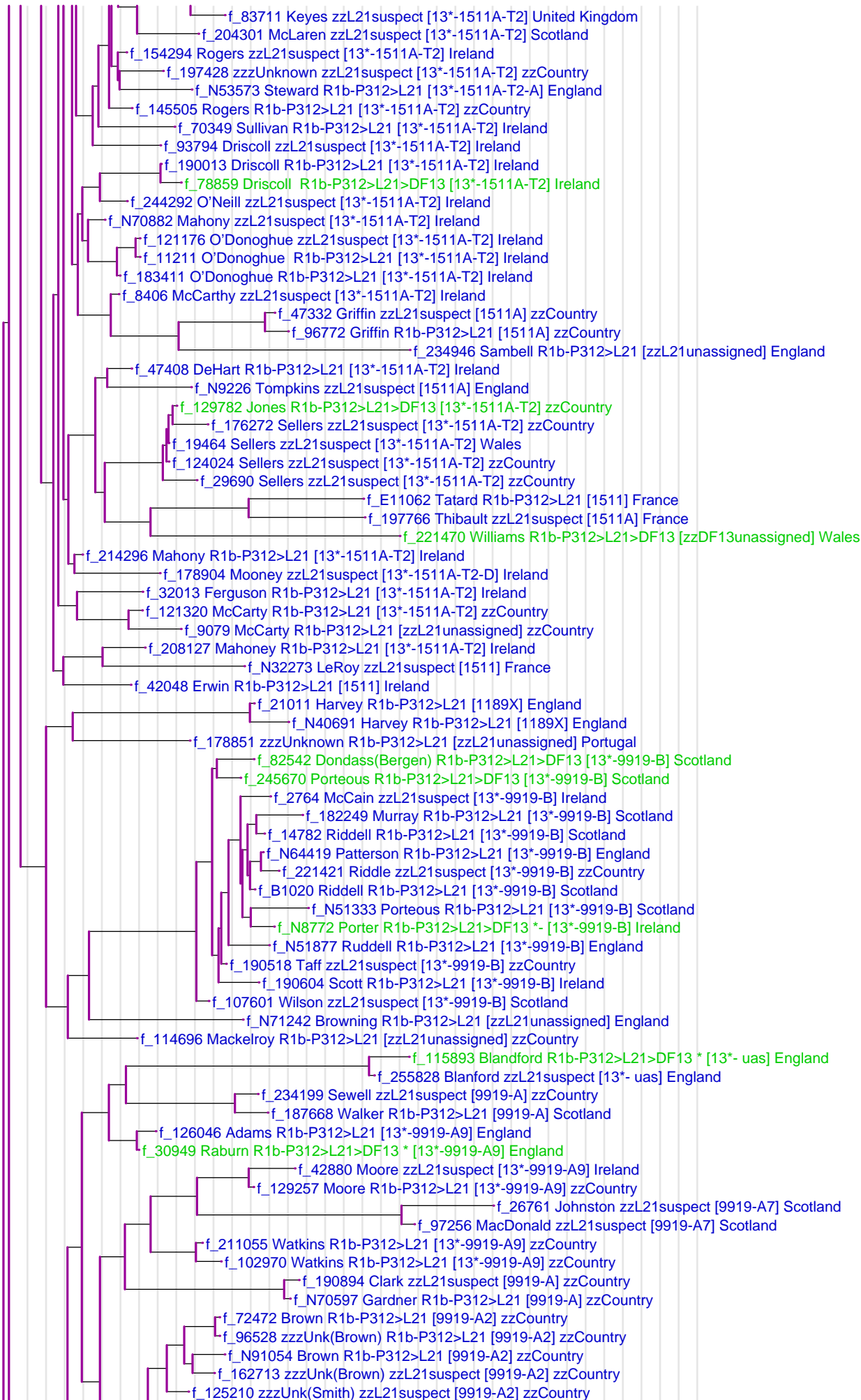
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

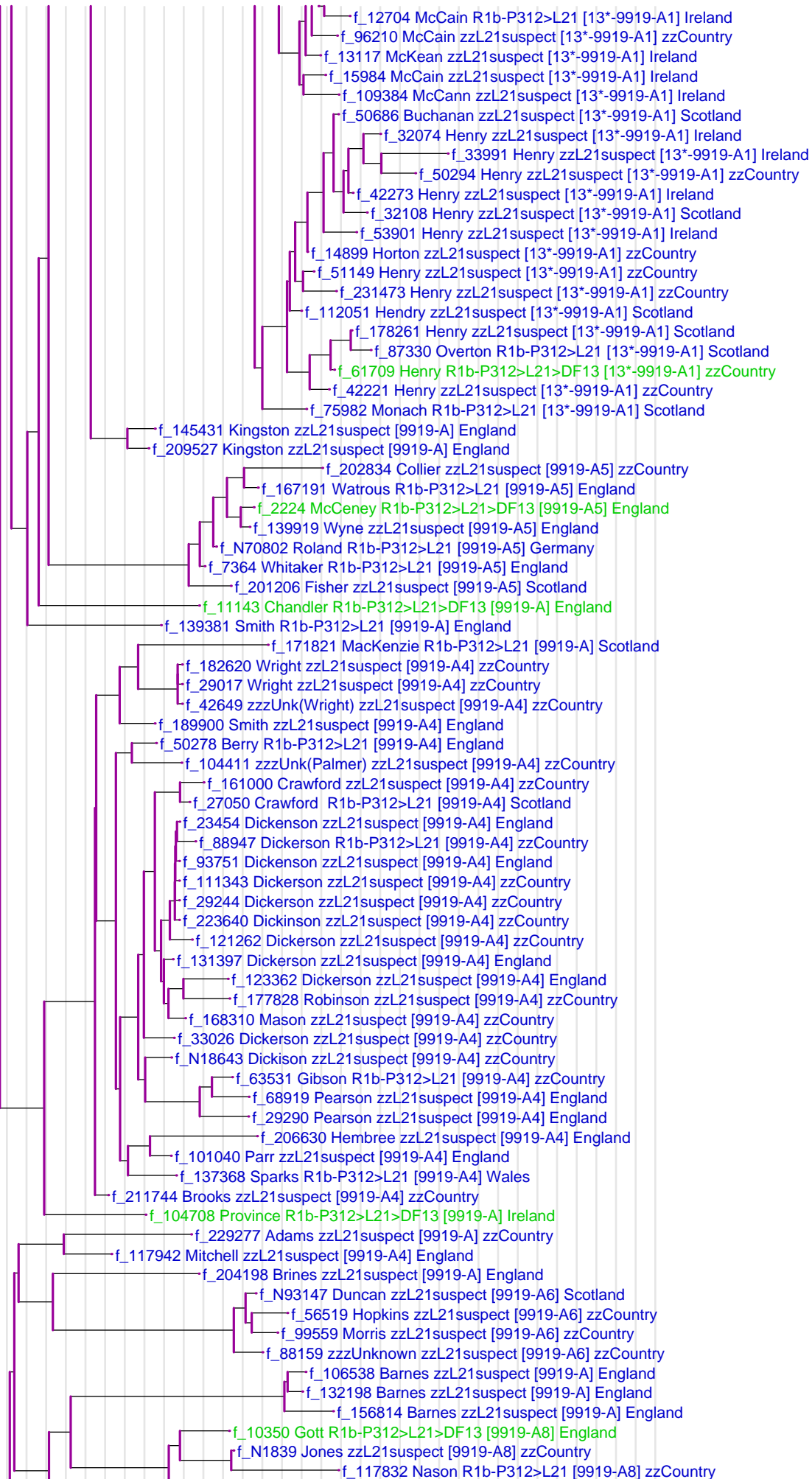


The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

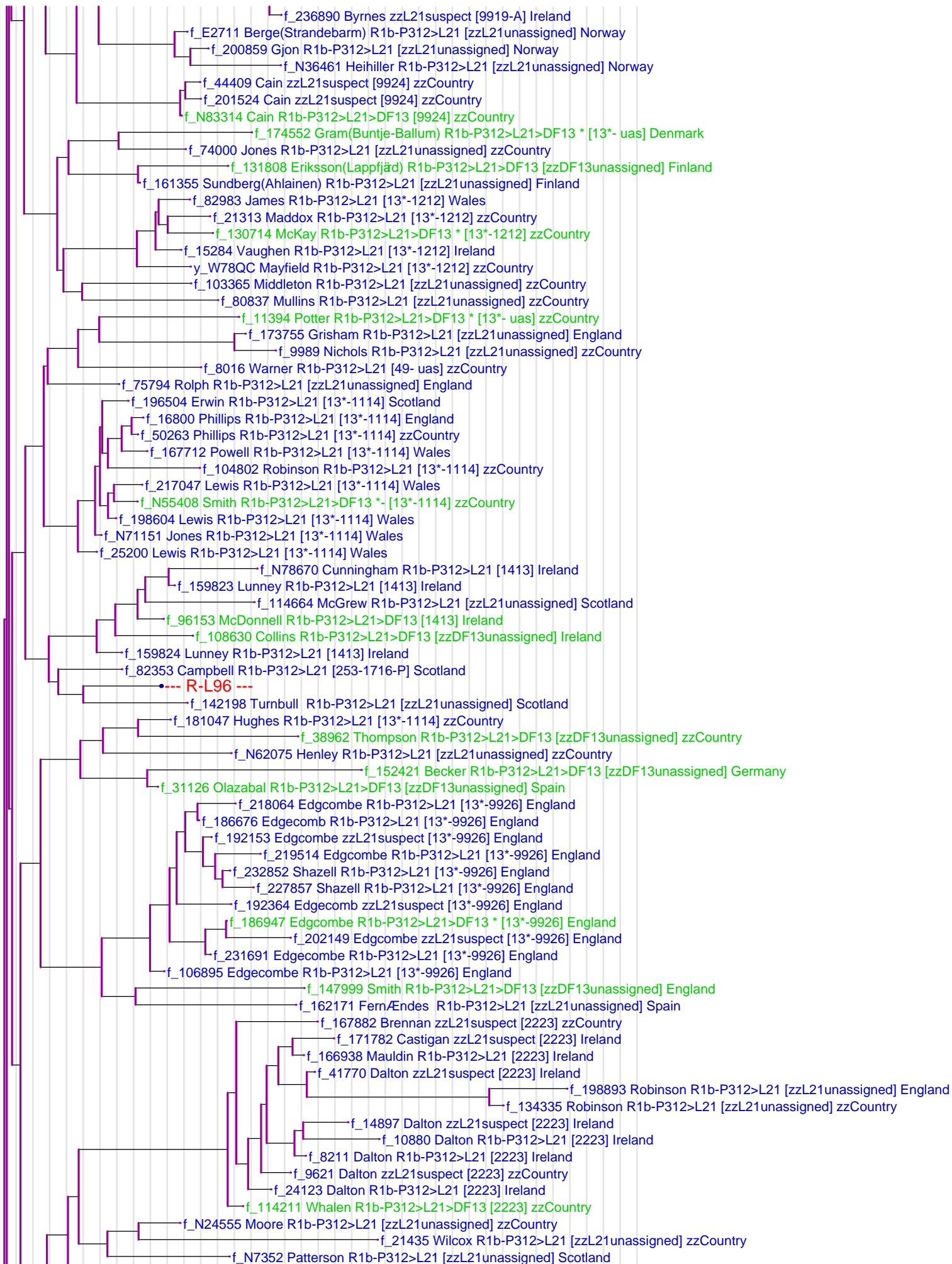




The vertical grey lines are separated 10 generations apart.



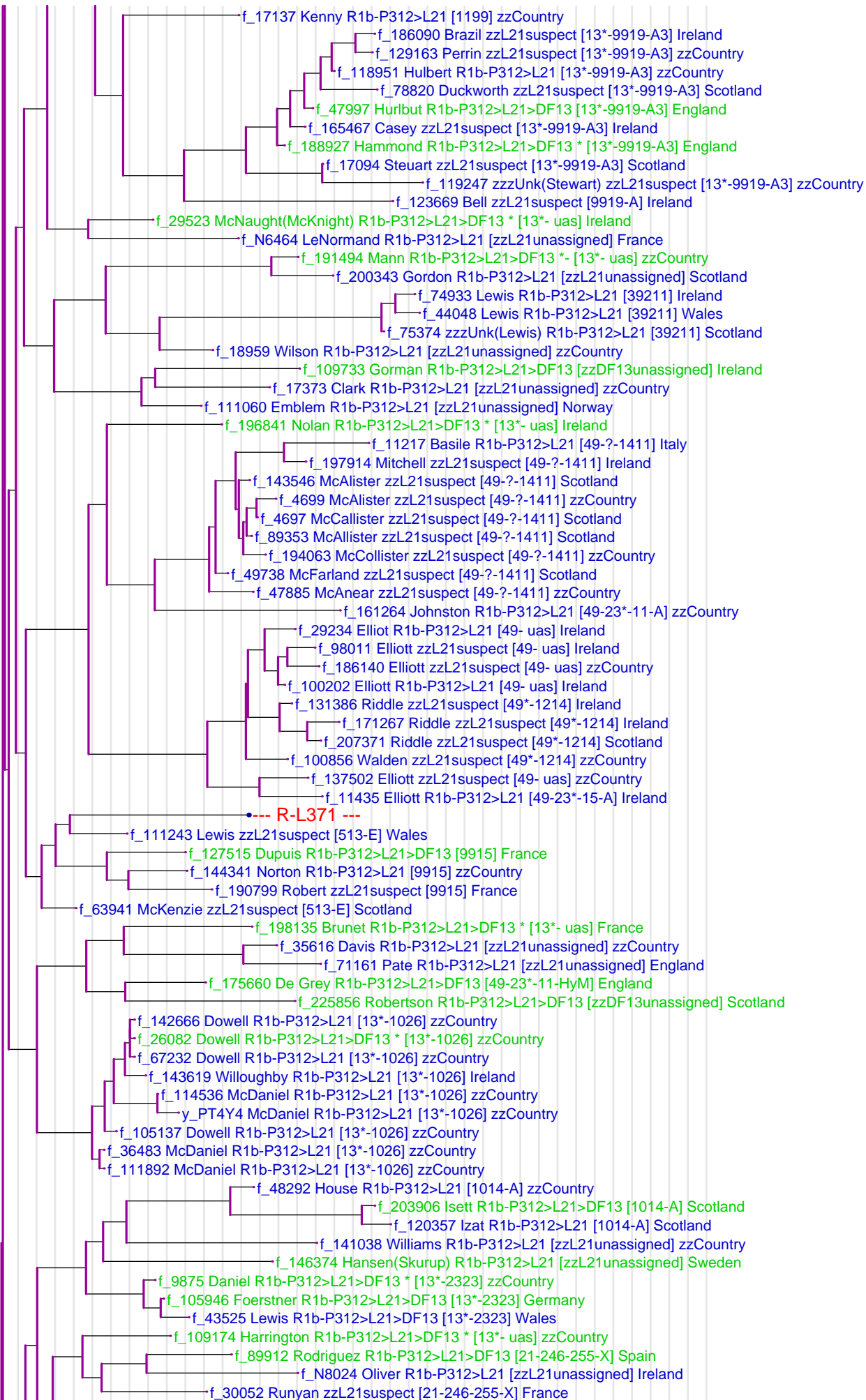
The vertical grey lines are separated 10 generations apart.



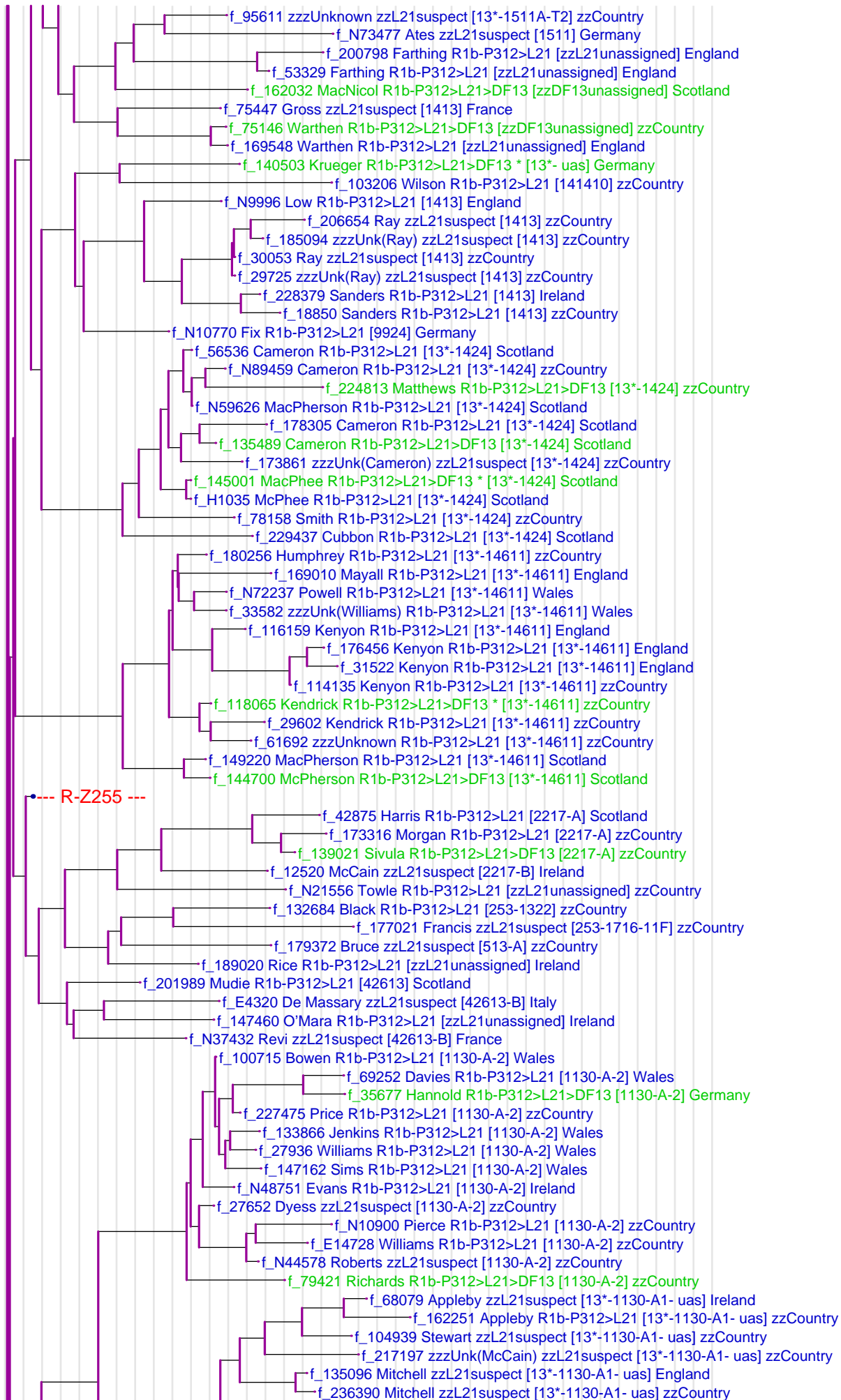
The vertical grey lines are separated 10 generations apart.



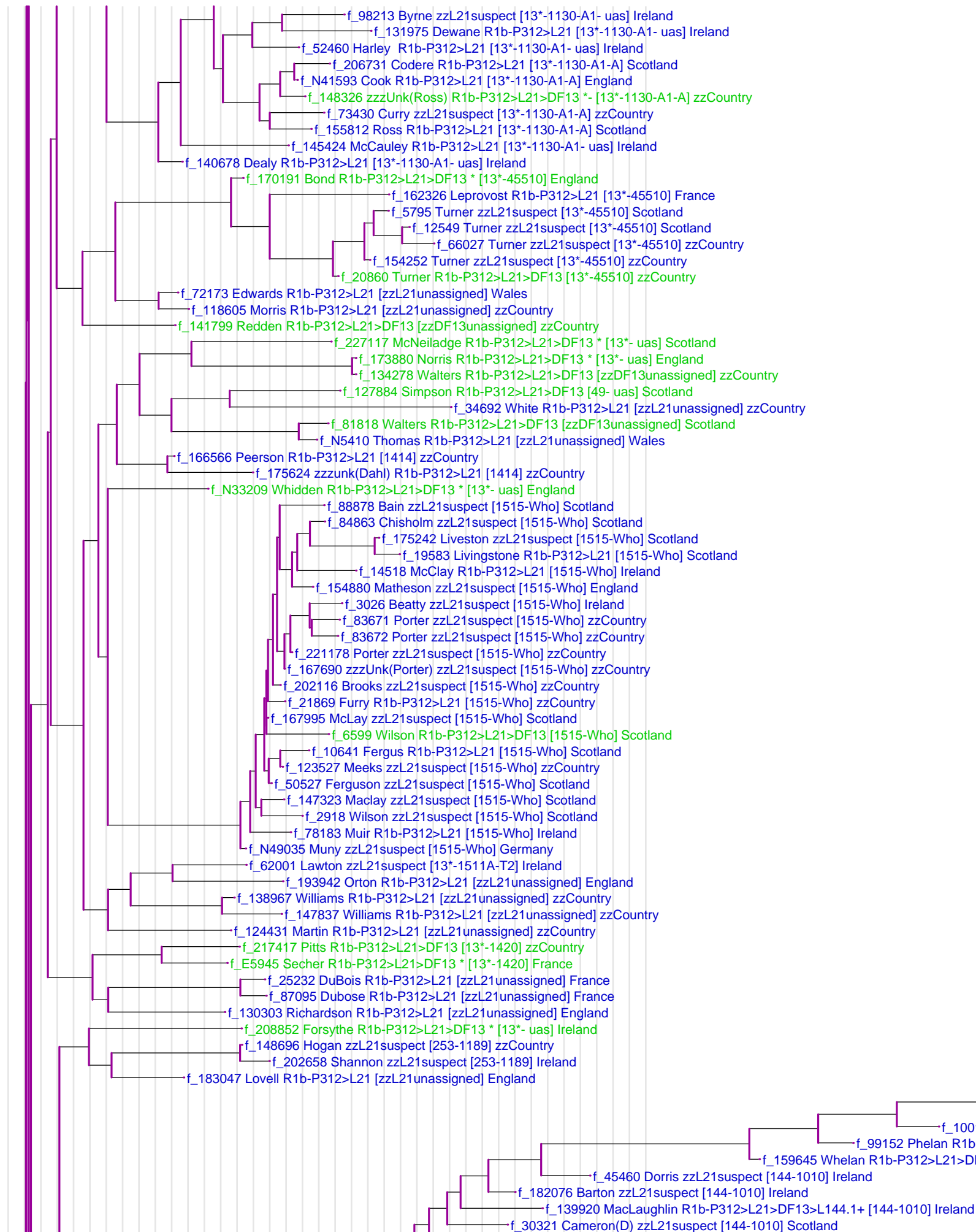
The vertical grey lines are separated 10 generations apart.



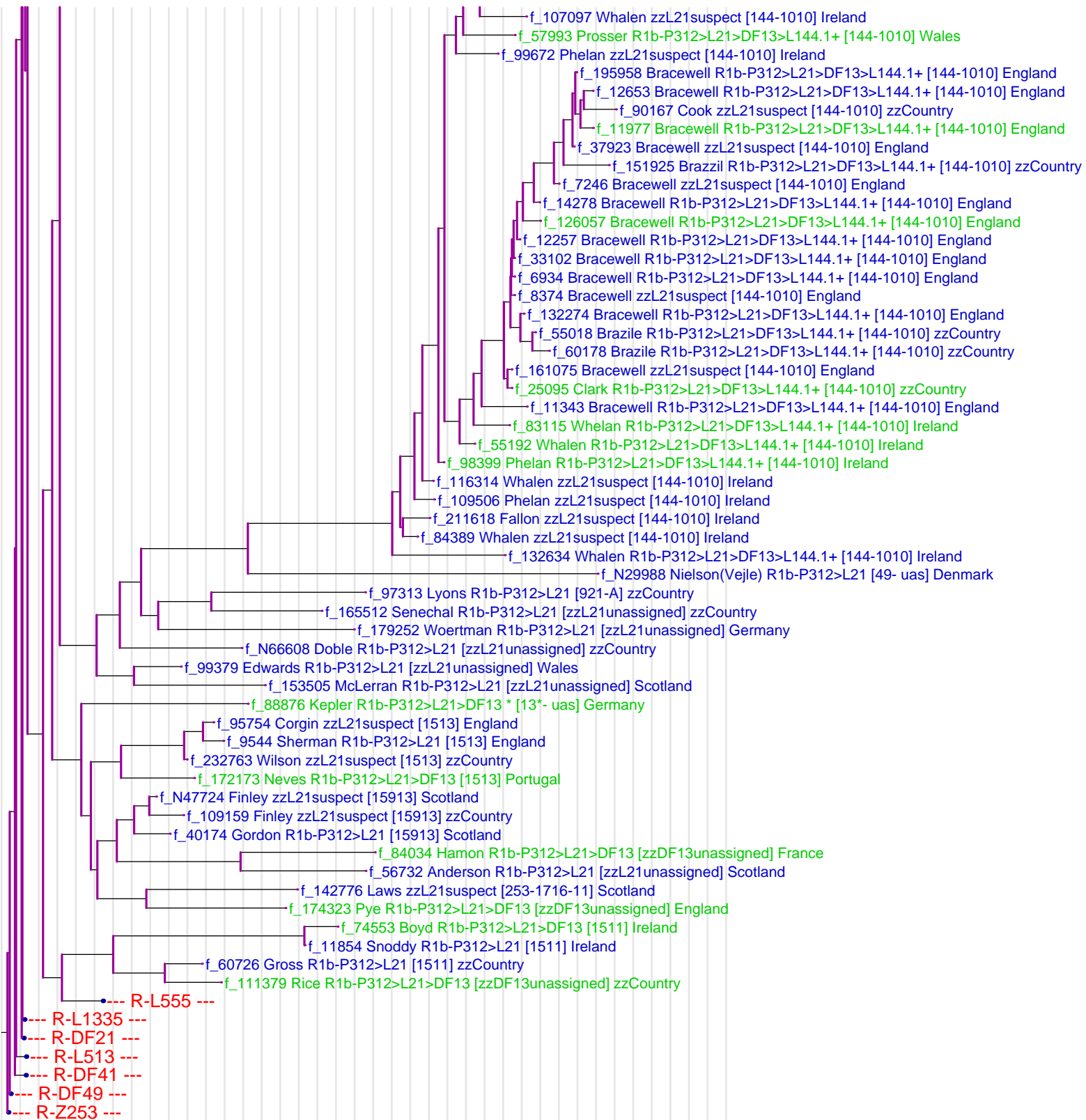
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

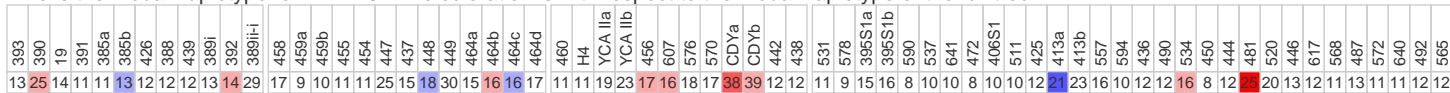


The vertical grey lines are separated 10 generations apart.

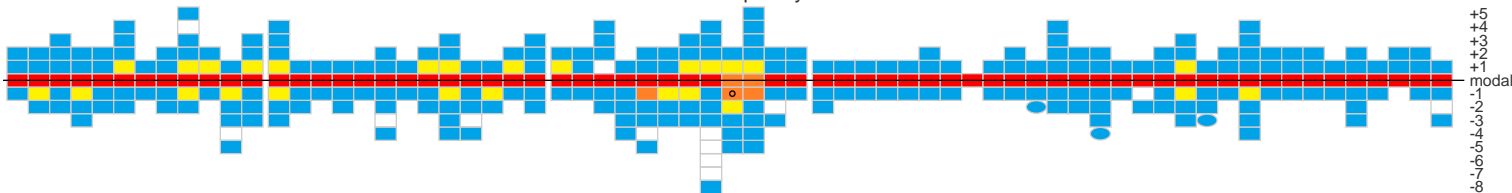


# R-DF49

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

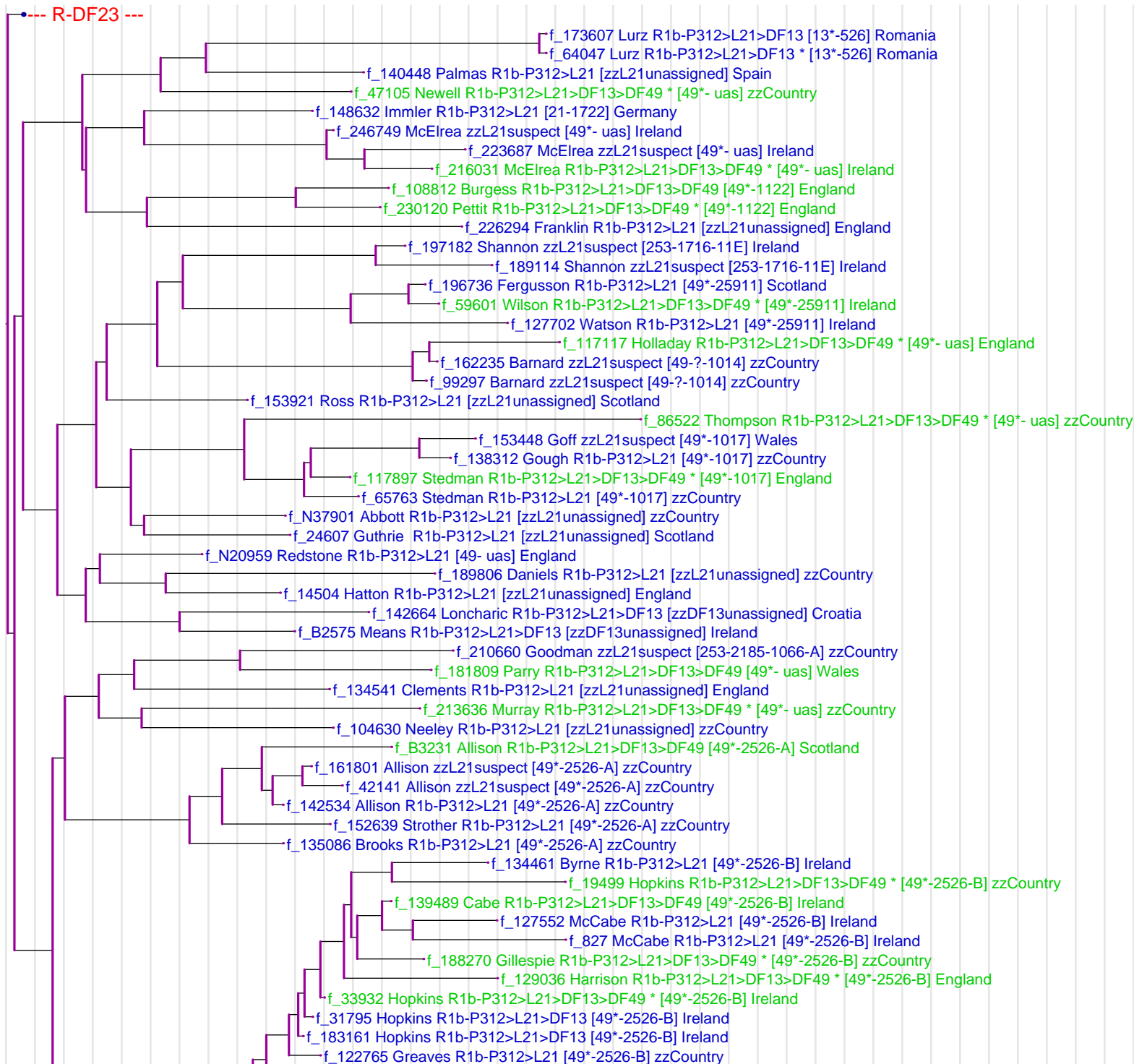


This is the marker distribution for R-DF49. The color indicates the relative frequency of the alleles.

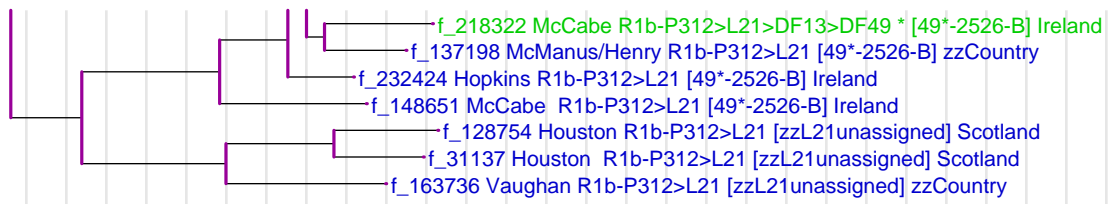


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
1529	102443	16106	15.72%	85.30±8.53	2132.53±301.671



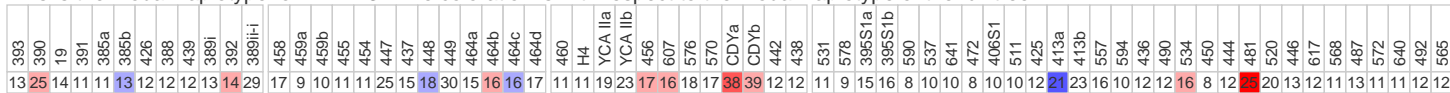
The vertical grey lines are separated 10 generations apart.



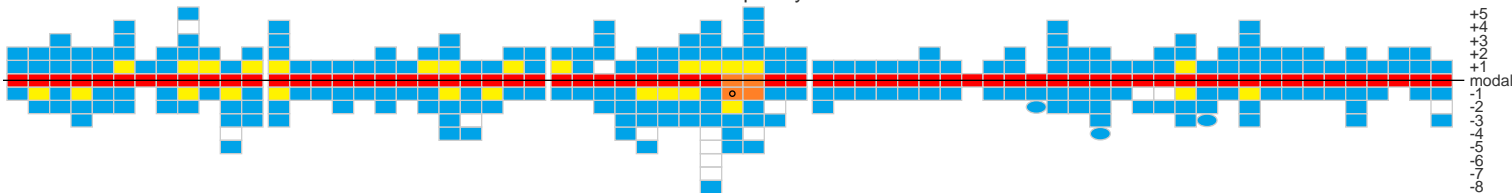
The vertical grey lines are separated 10 generations apart.

# R-DF23

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

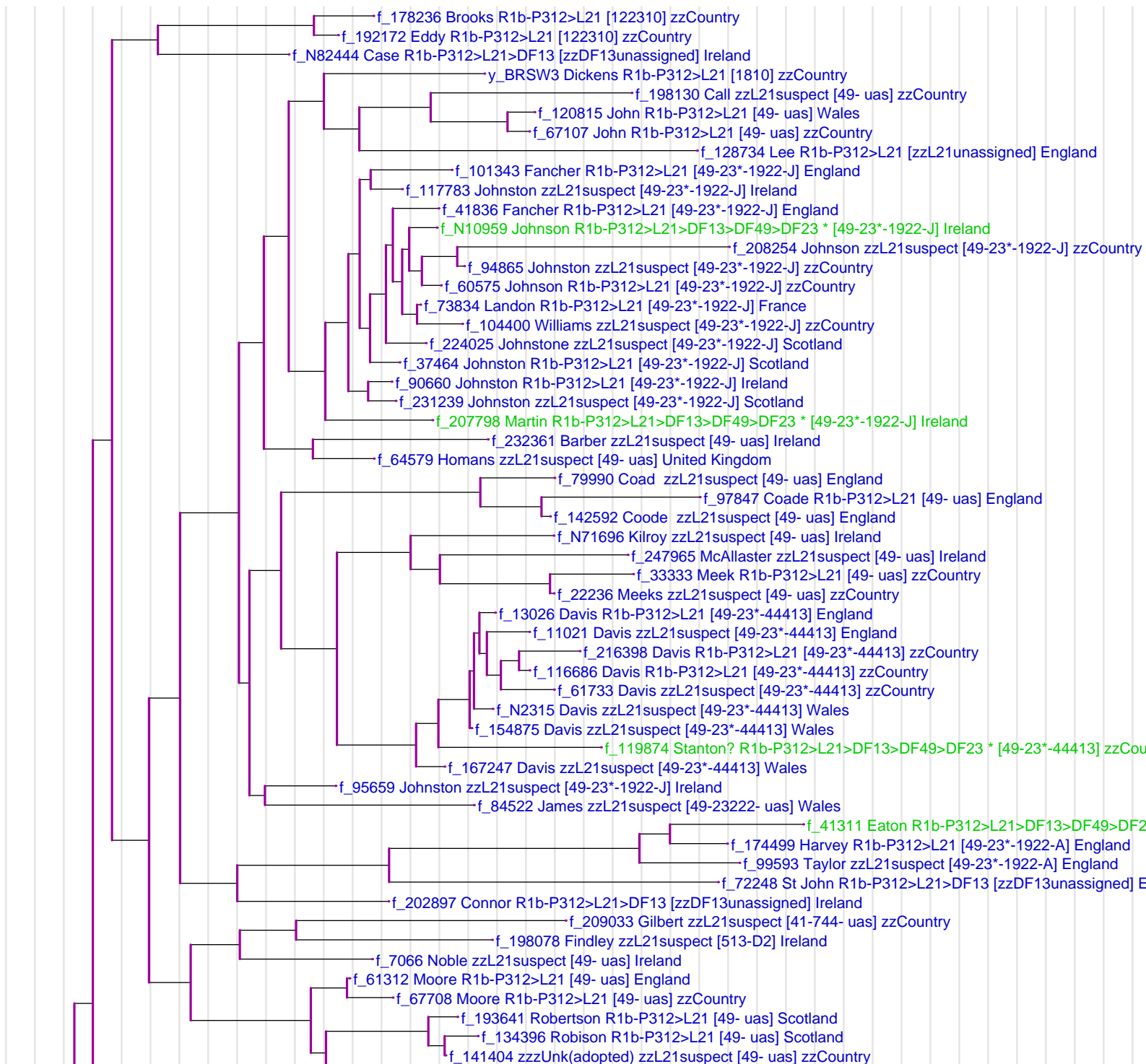


This is the marker distribution for R-DF23. The color indicates the relative frequency of the alleles.

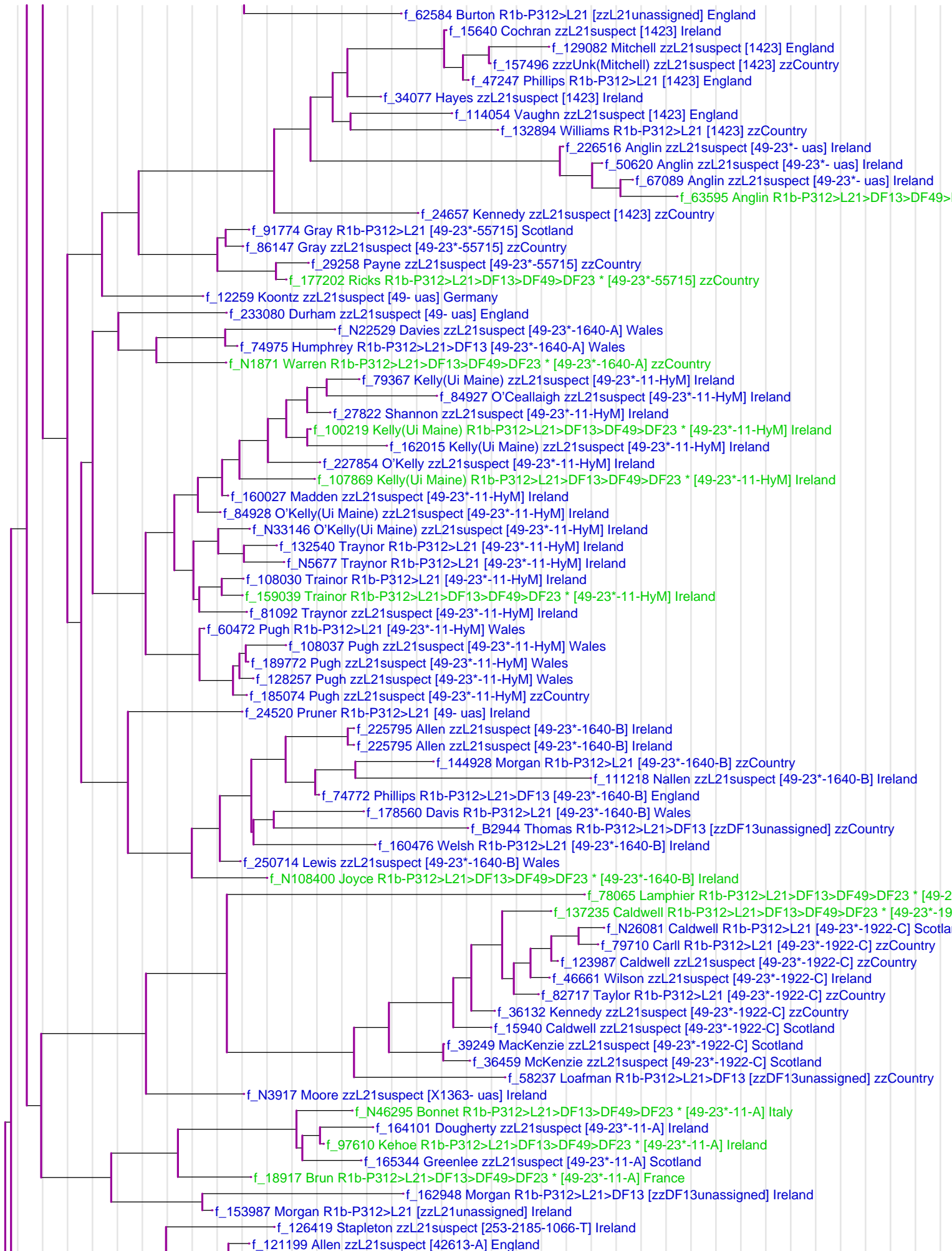


## Age Analysis

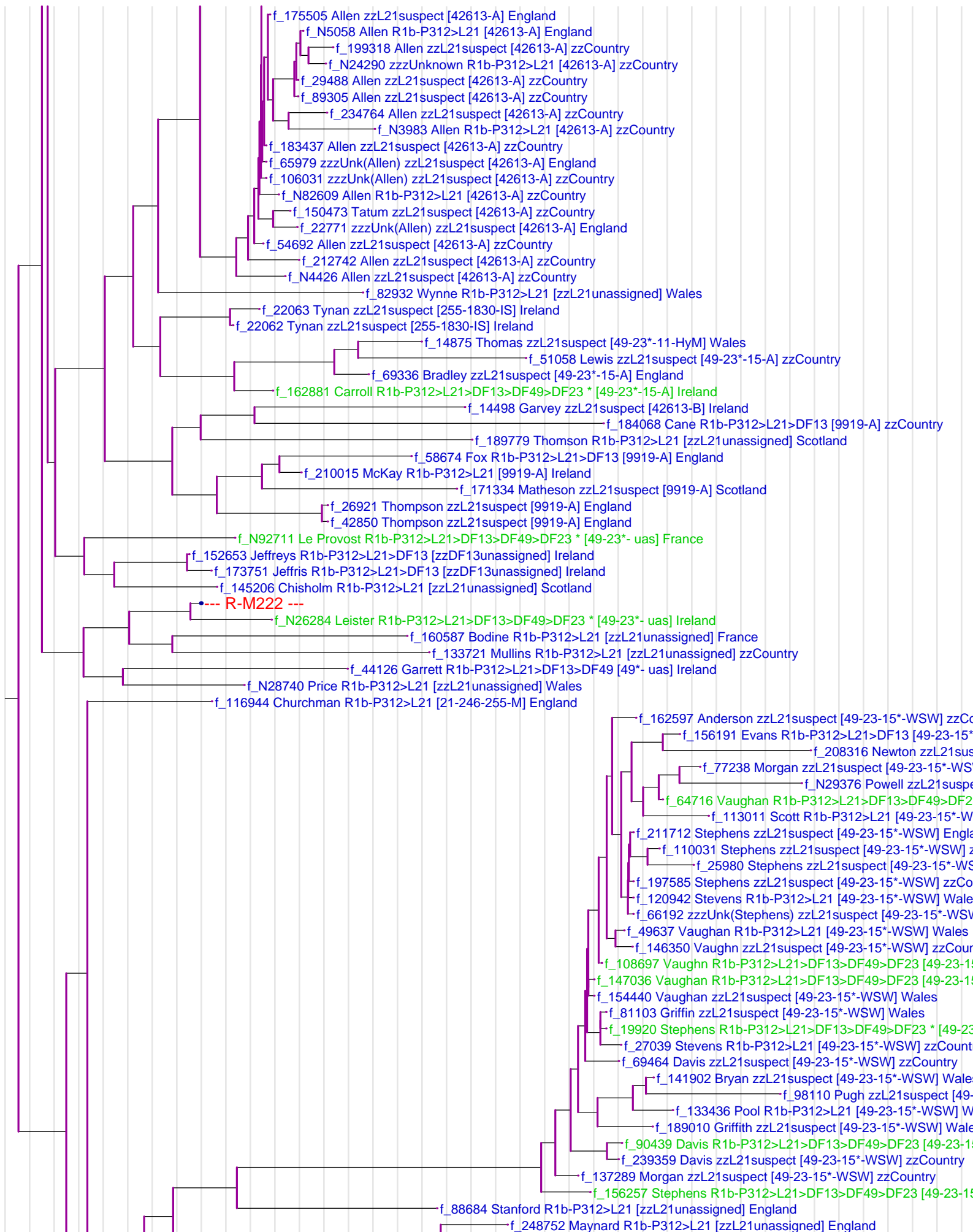
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
1468	98356	14449	14.69%	79.26±7.93	1981.61±280.324



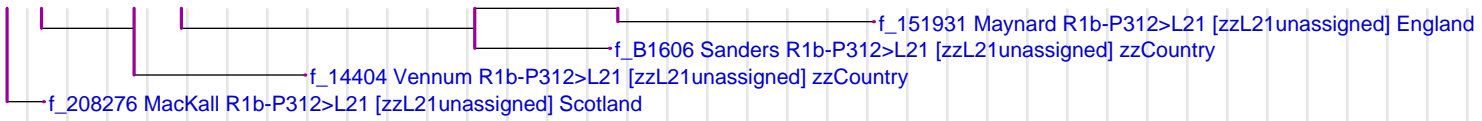
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



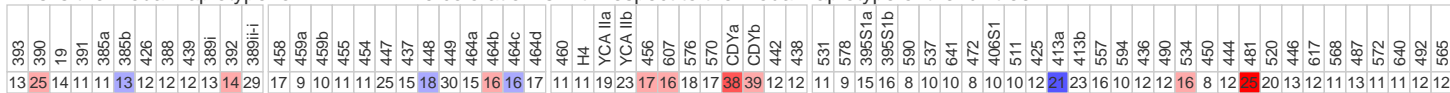
The vertical grey lines are separated 10 generations apart.



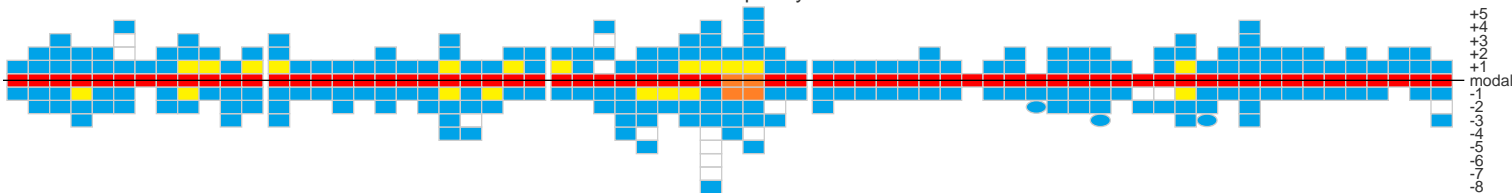
The vertical grey lines are separated 10 generations apart.

# R-M222

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

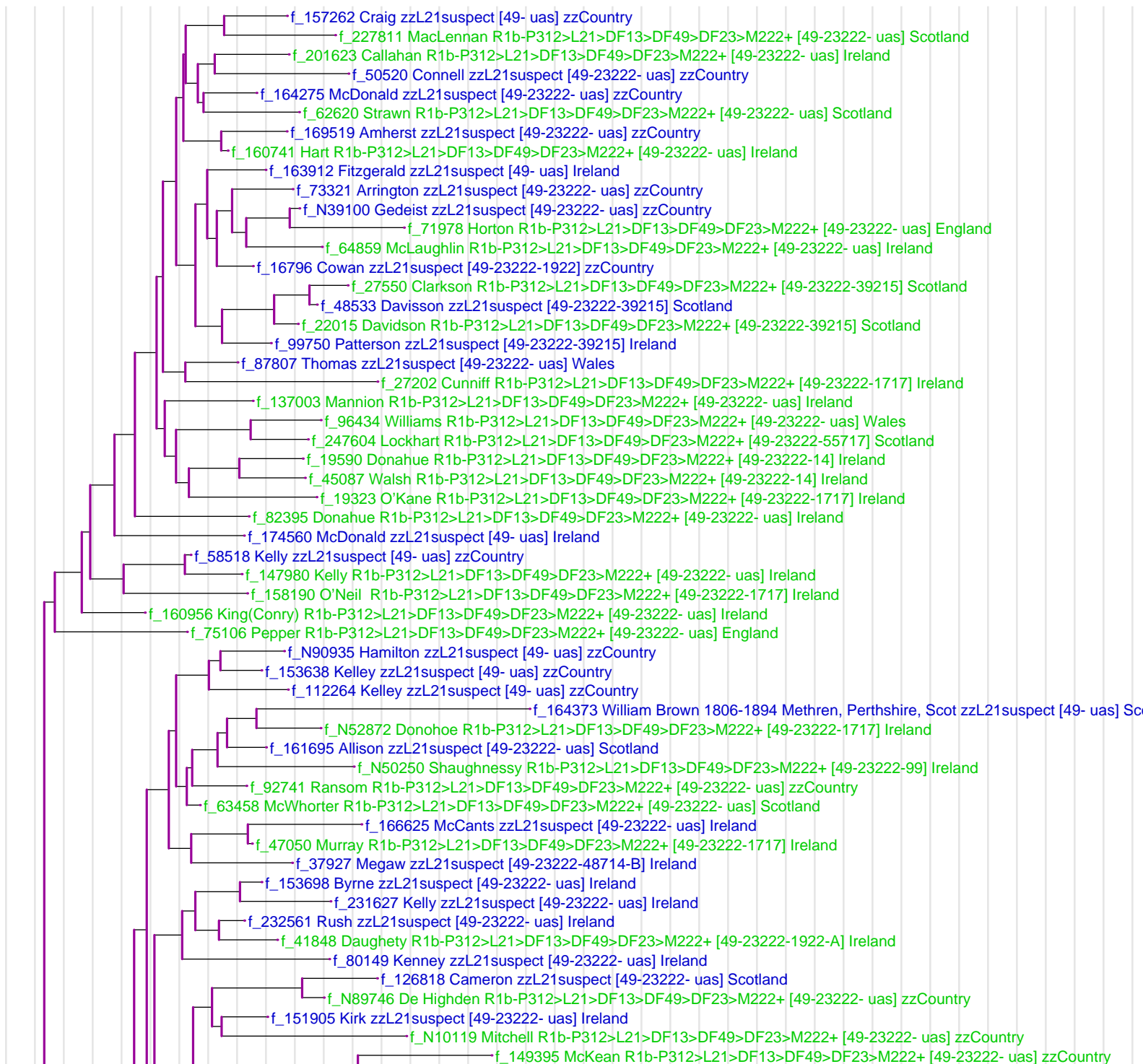


This is the marker distribution for R-M222. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
1260	84420	9679	11.47%	60.81±6.08	1520.21±215.062



The vertical grey lines are separated 10 generations apart.

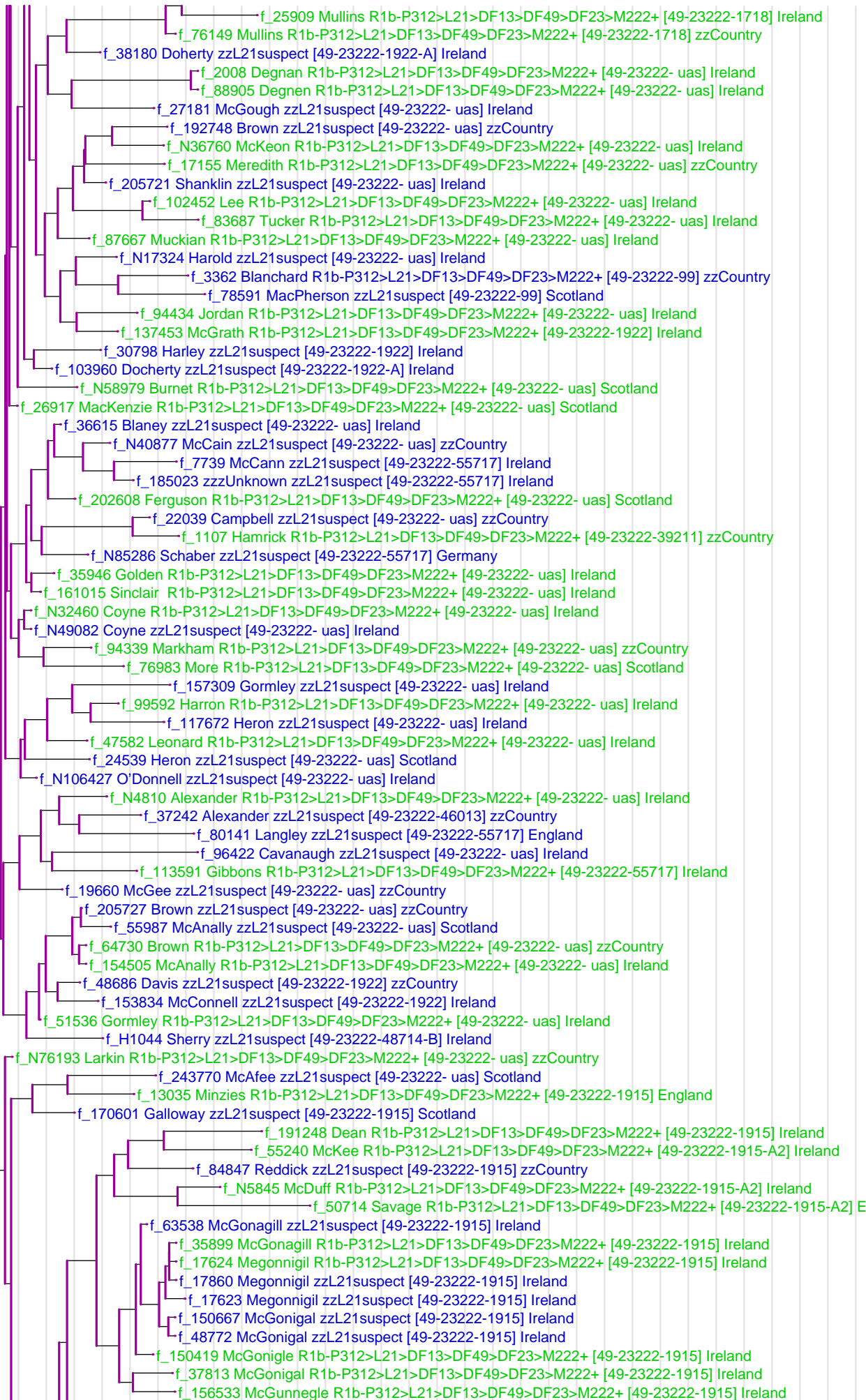


The vertical grey lines are separated 10 generations apart.





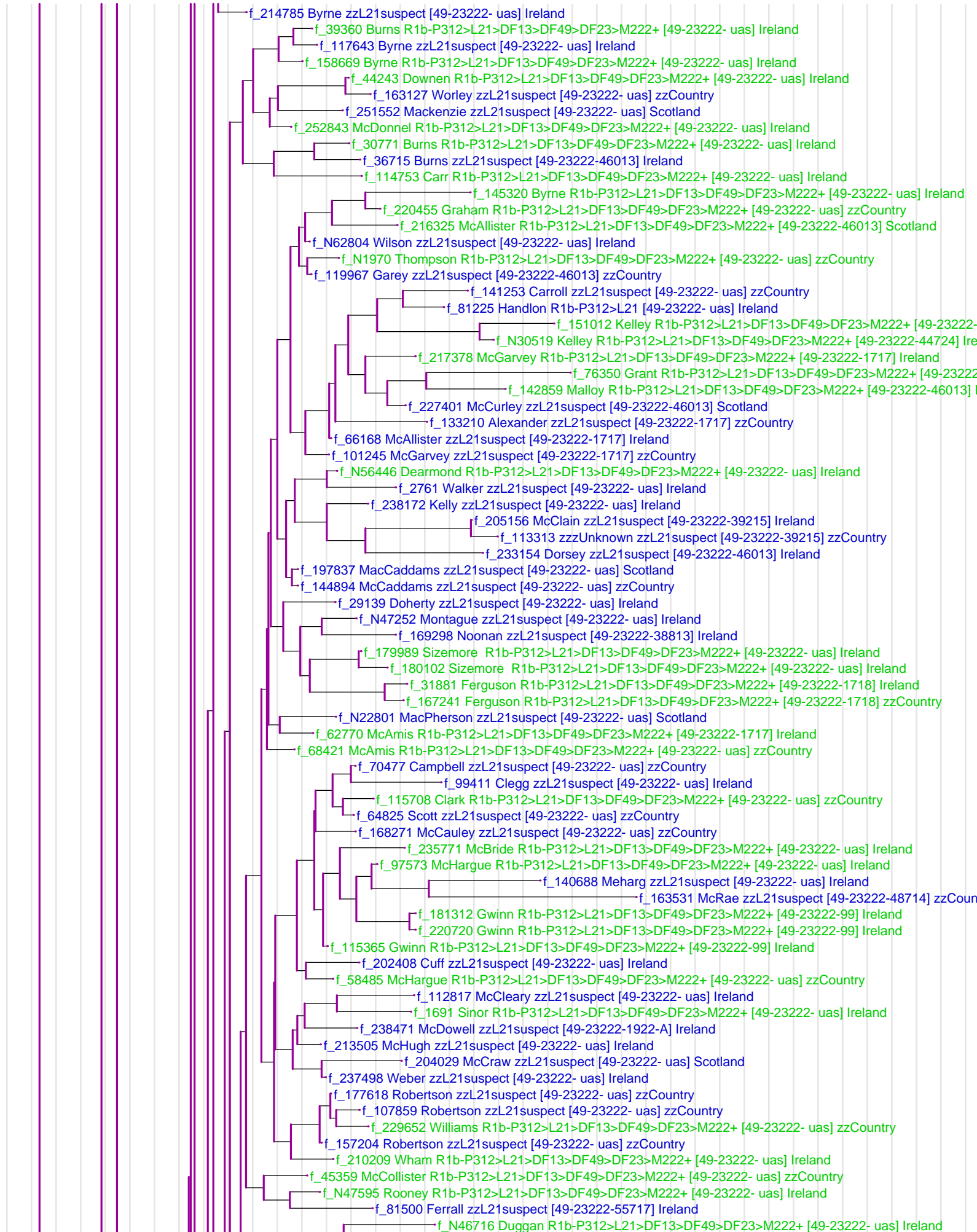
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



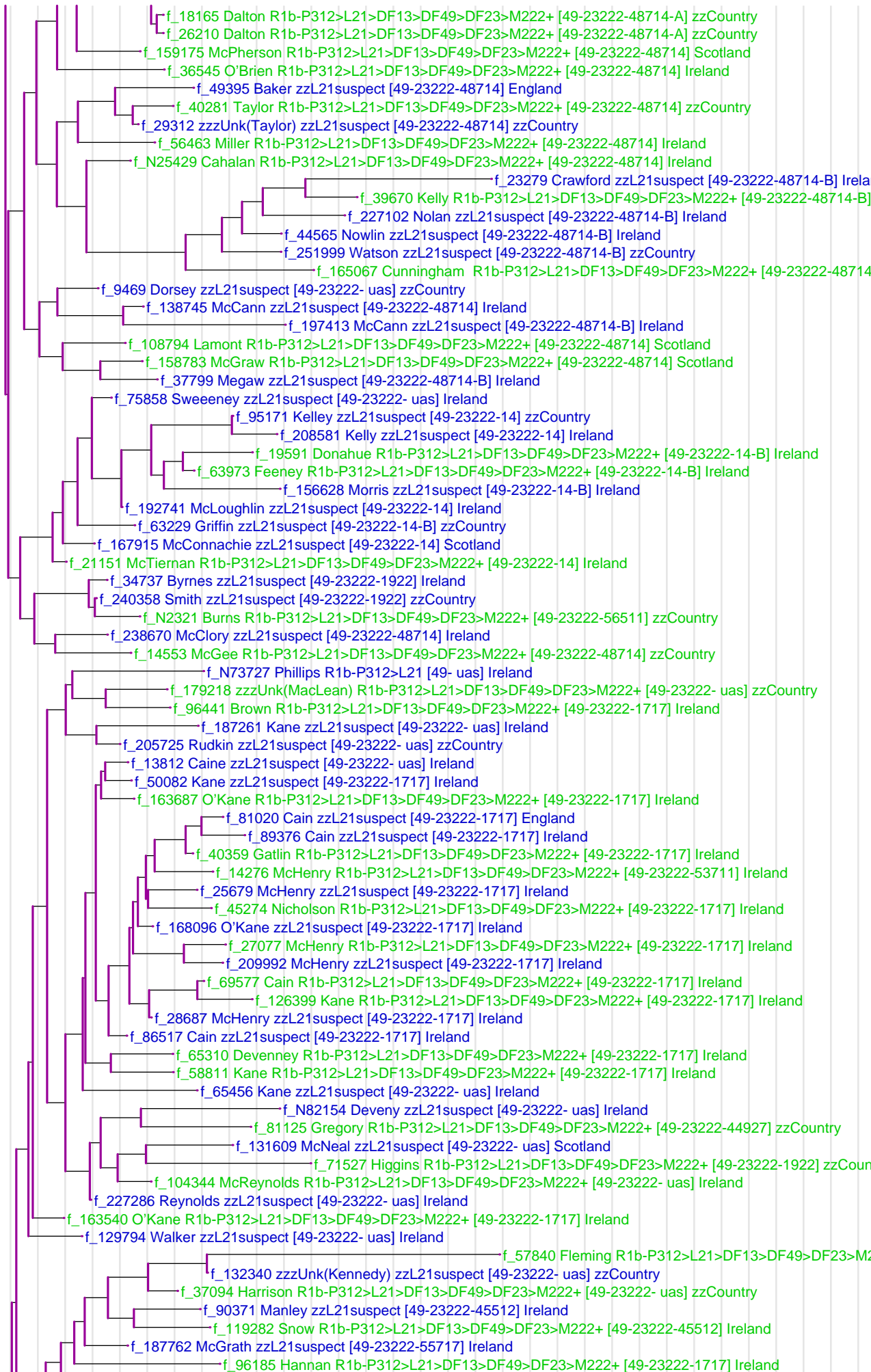
The vertical grey lines are separated 10 generations apart.



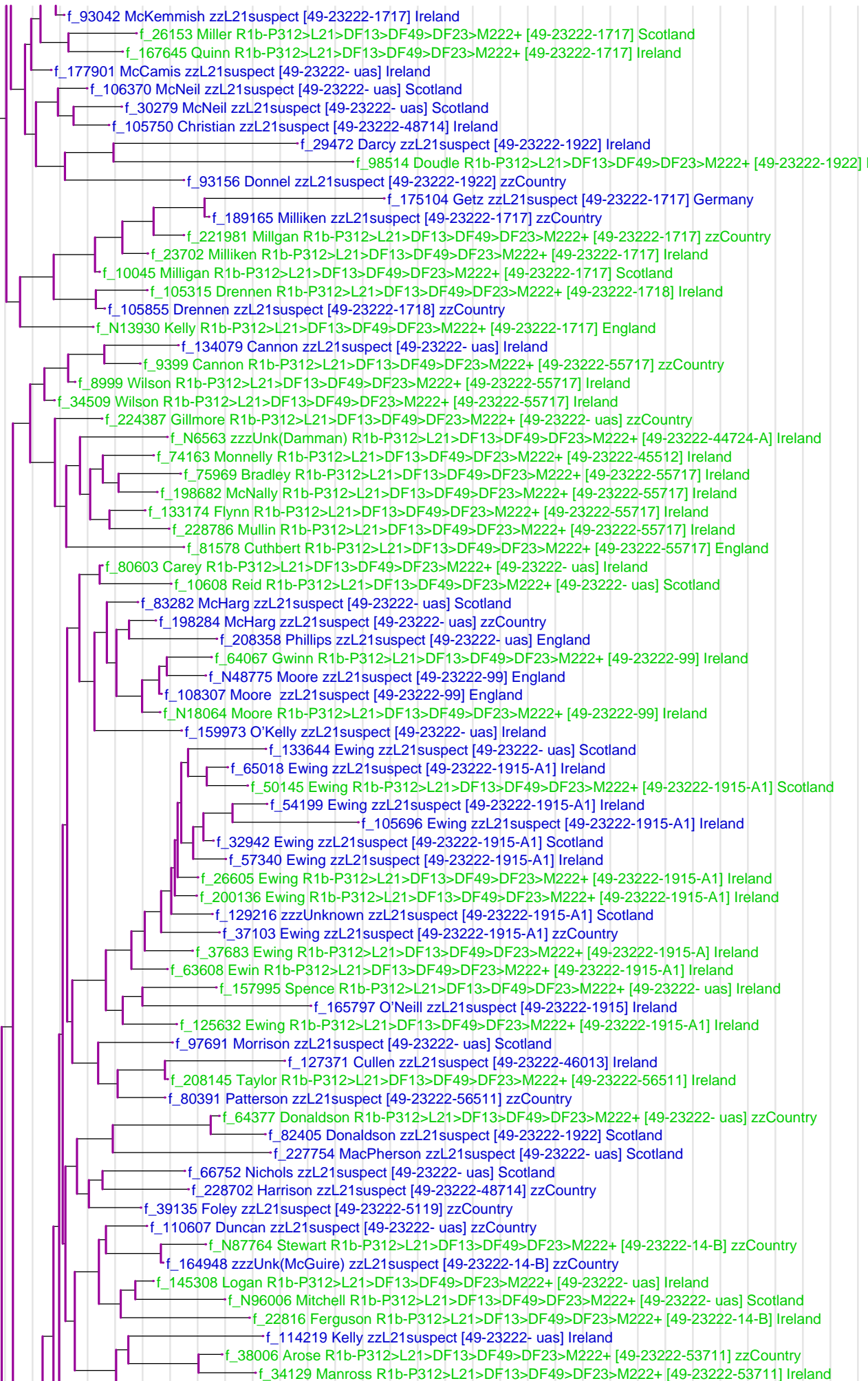
The vertical grey lines are separated 10 generations apart.



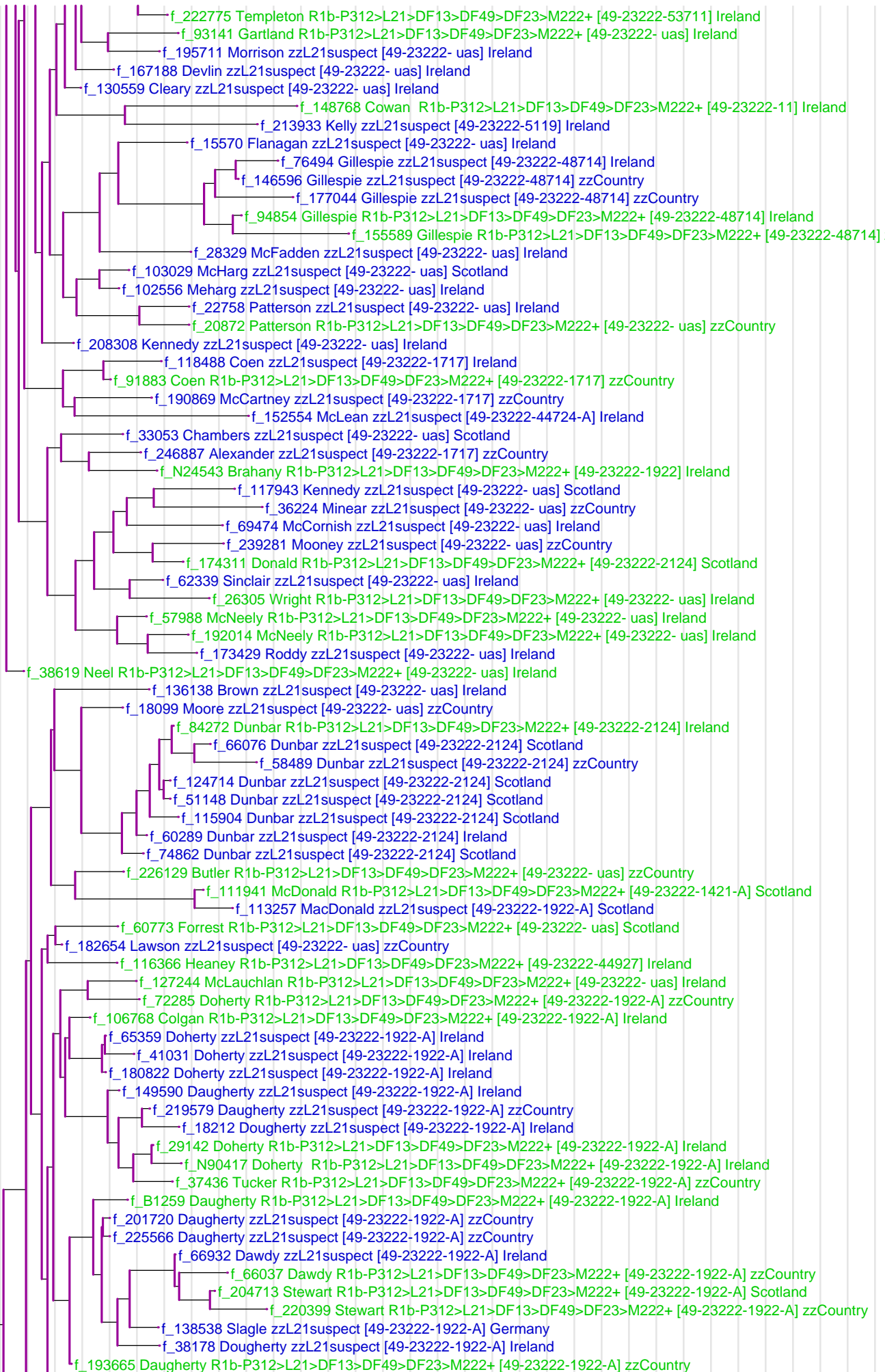
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

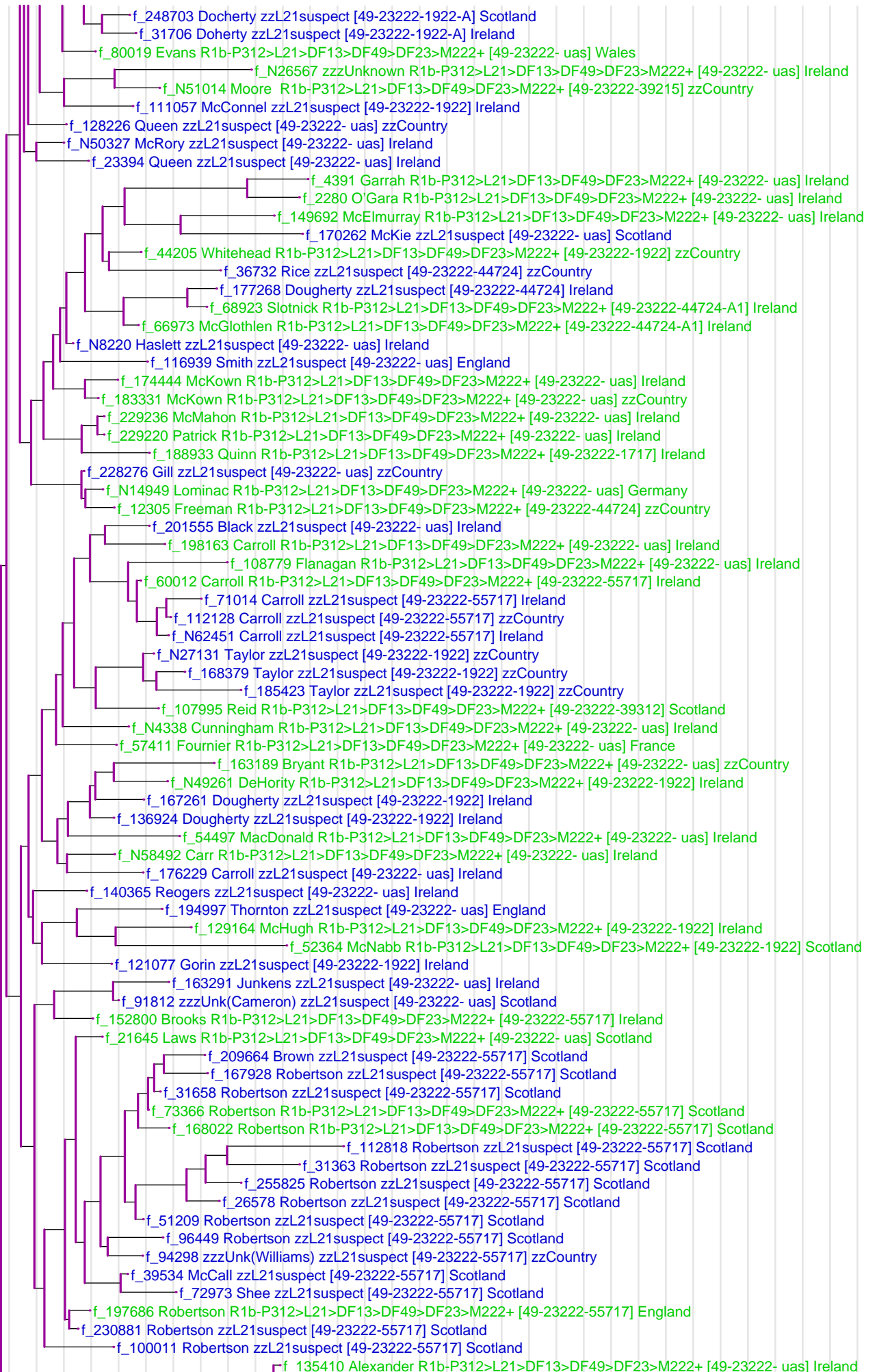


The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

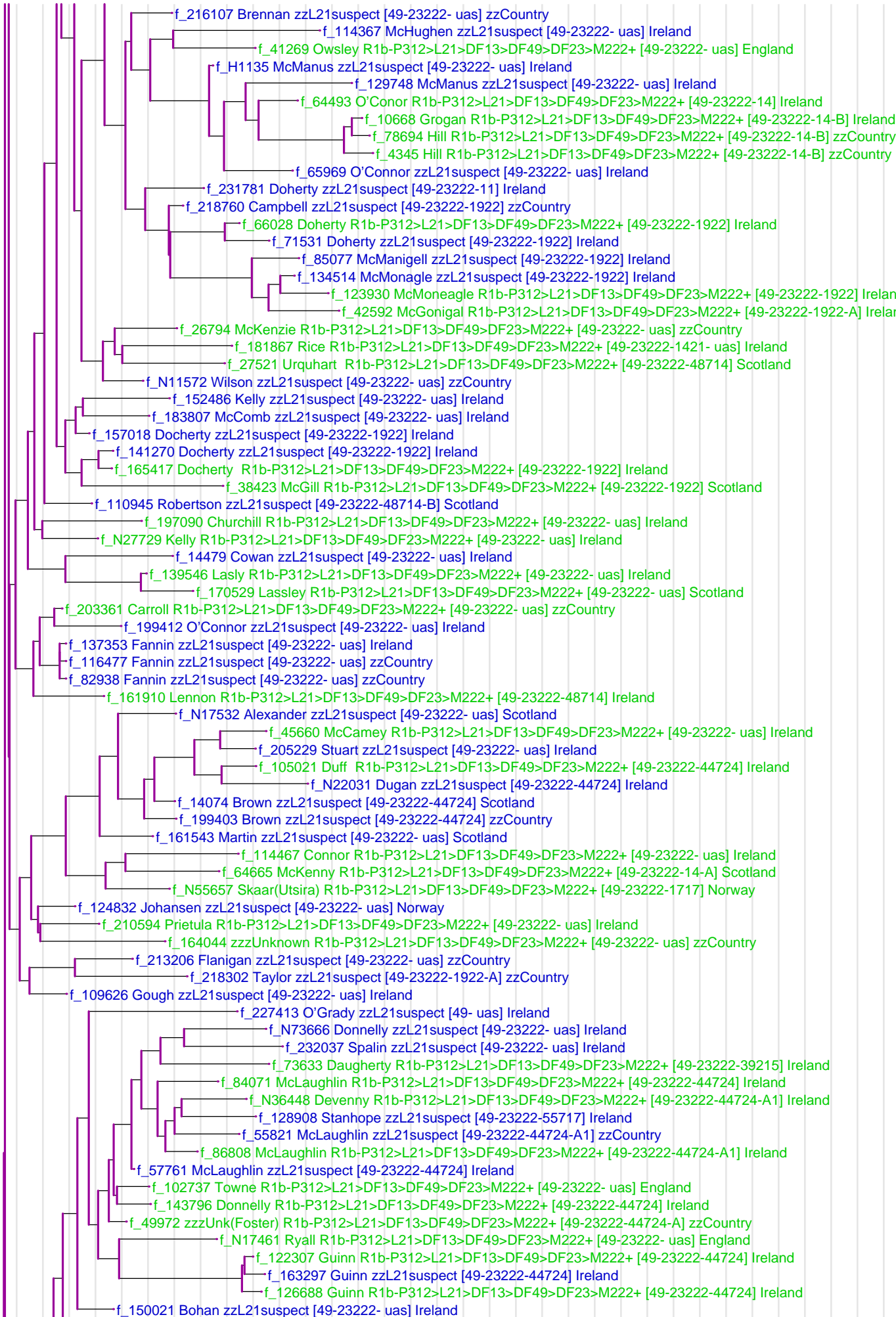




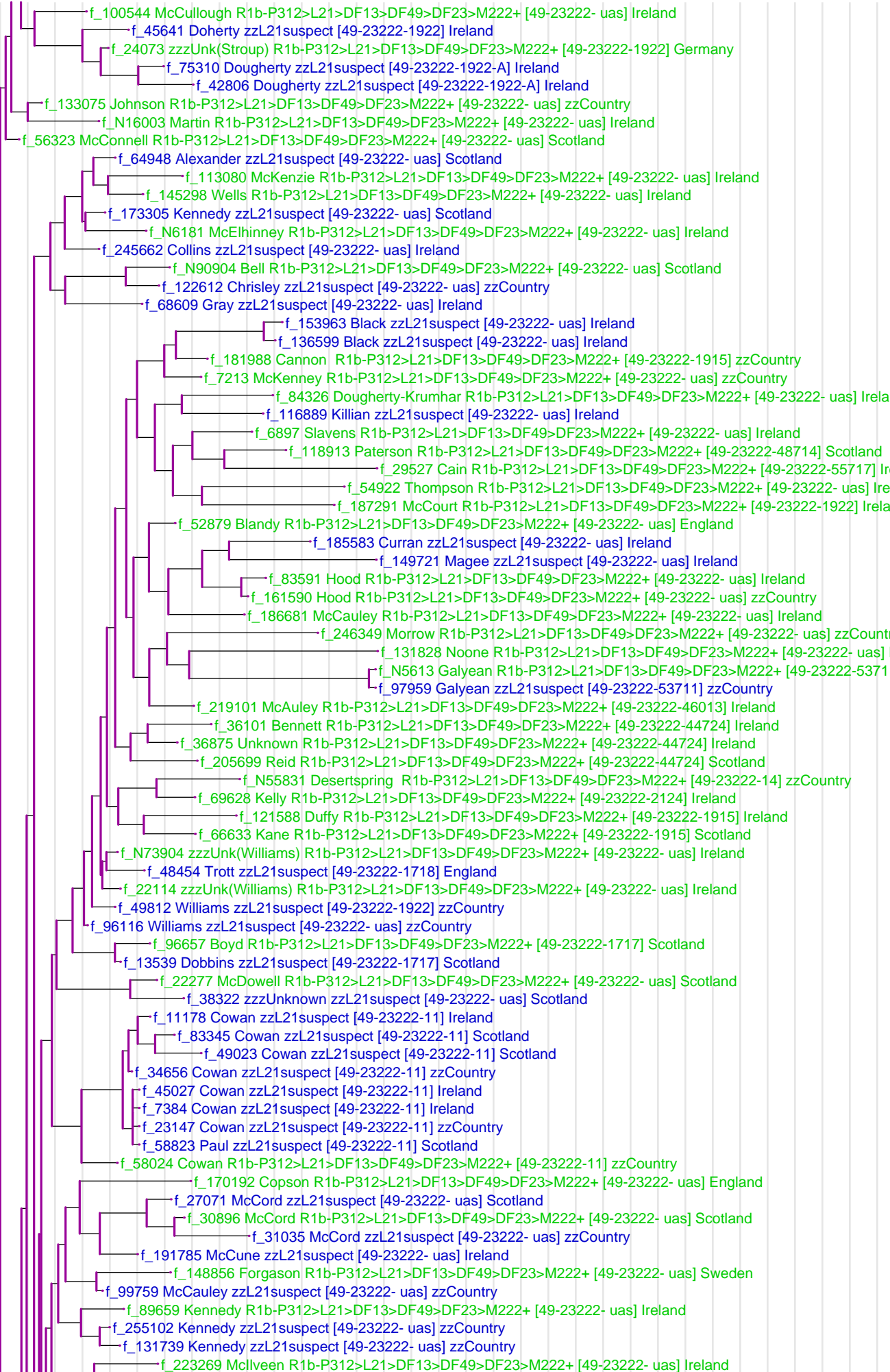
The vertical grey lines are separated 10 generations apart.



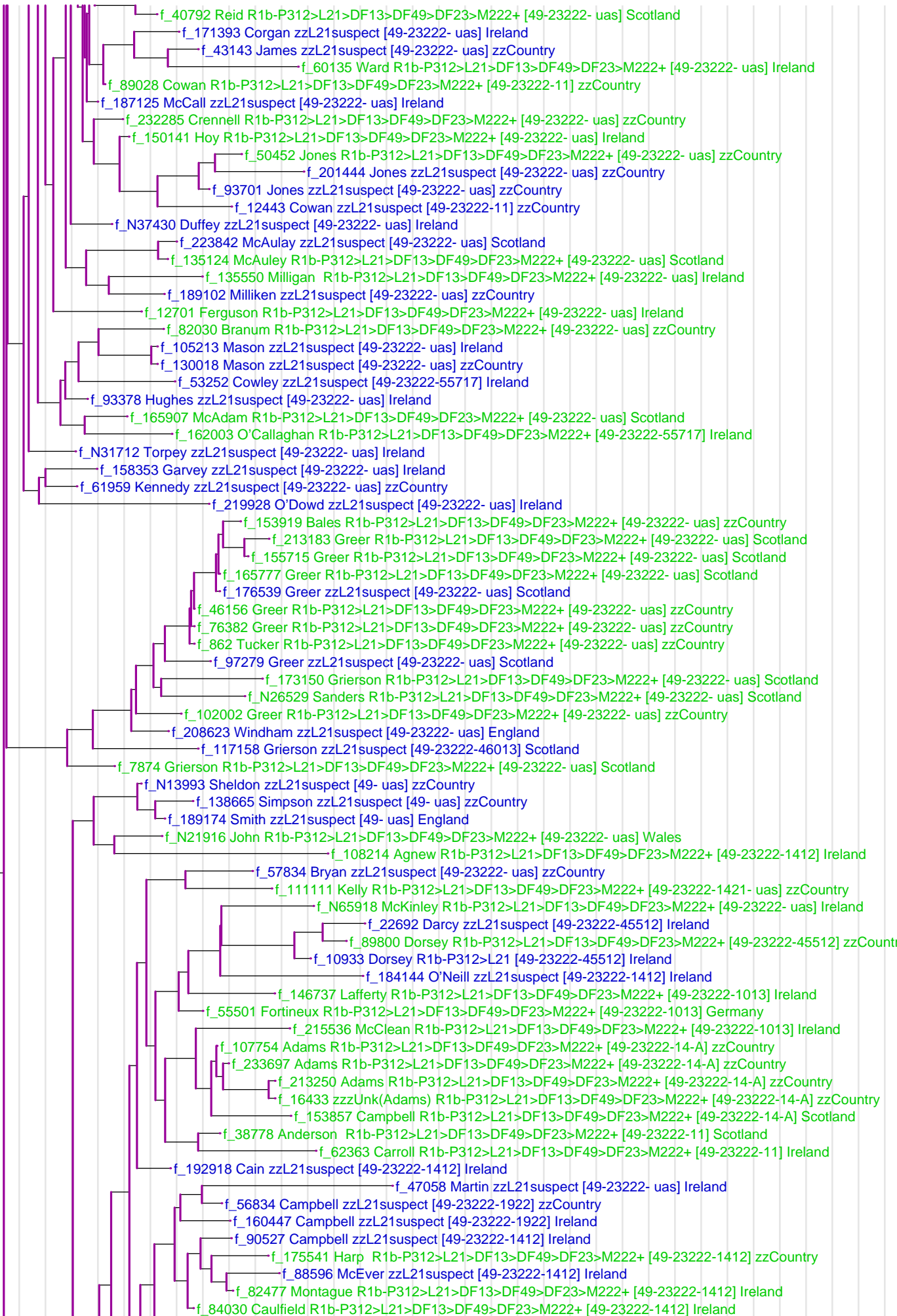
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



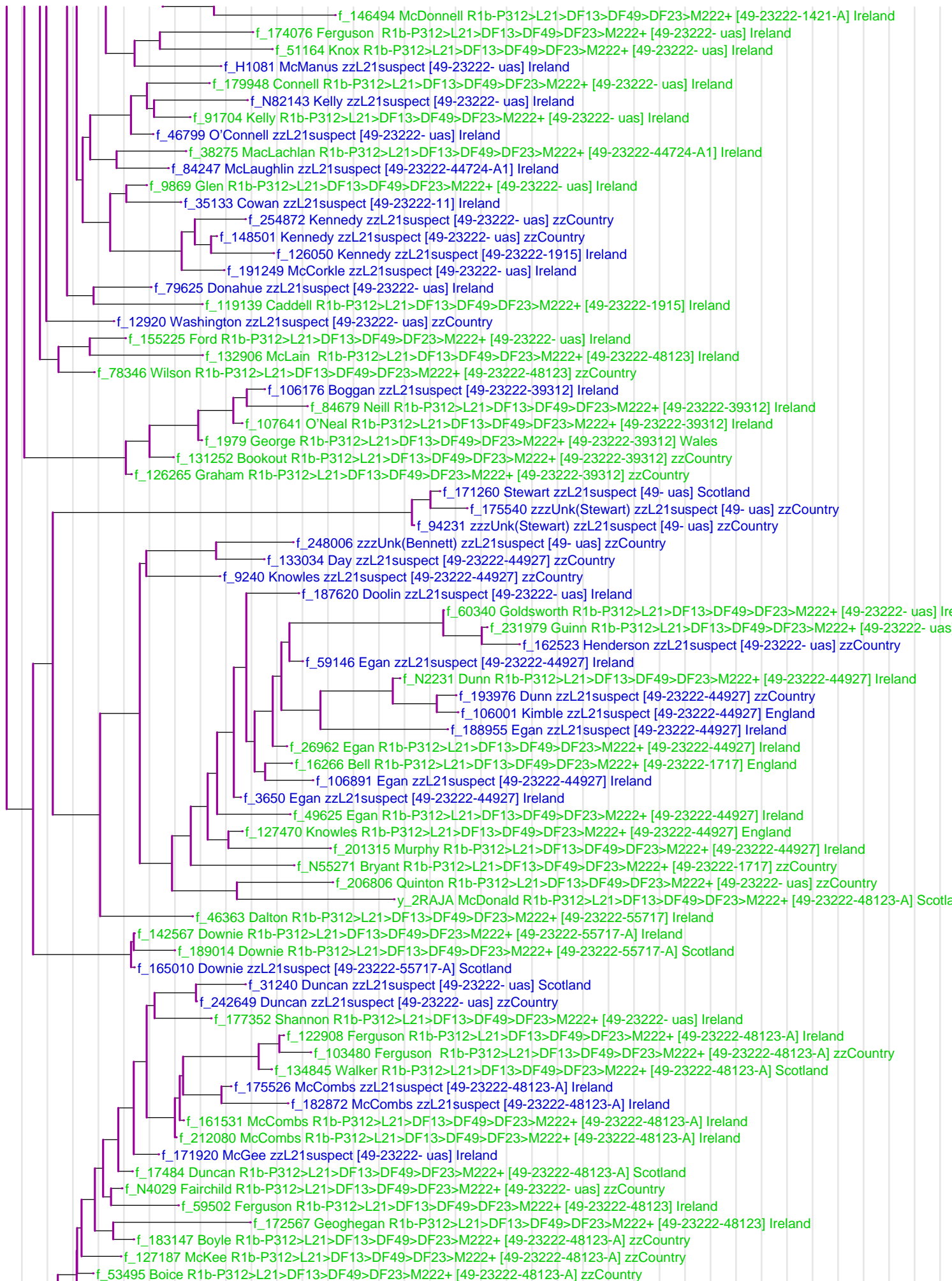
The vertical grey lines are separated 10 generations apart.



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.

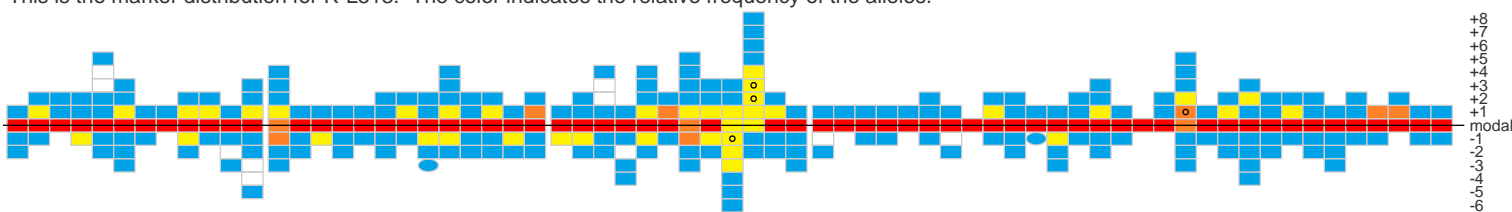


# R-L513

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

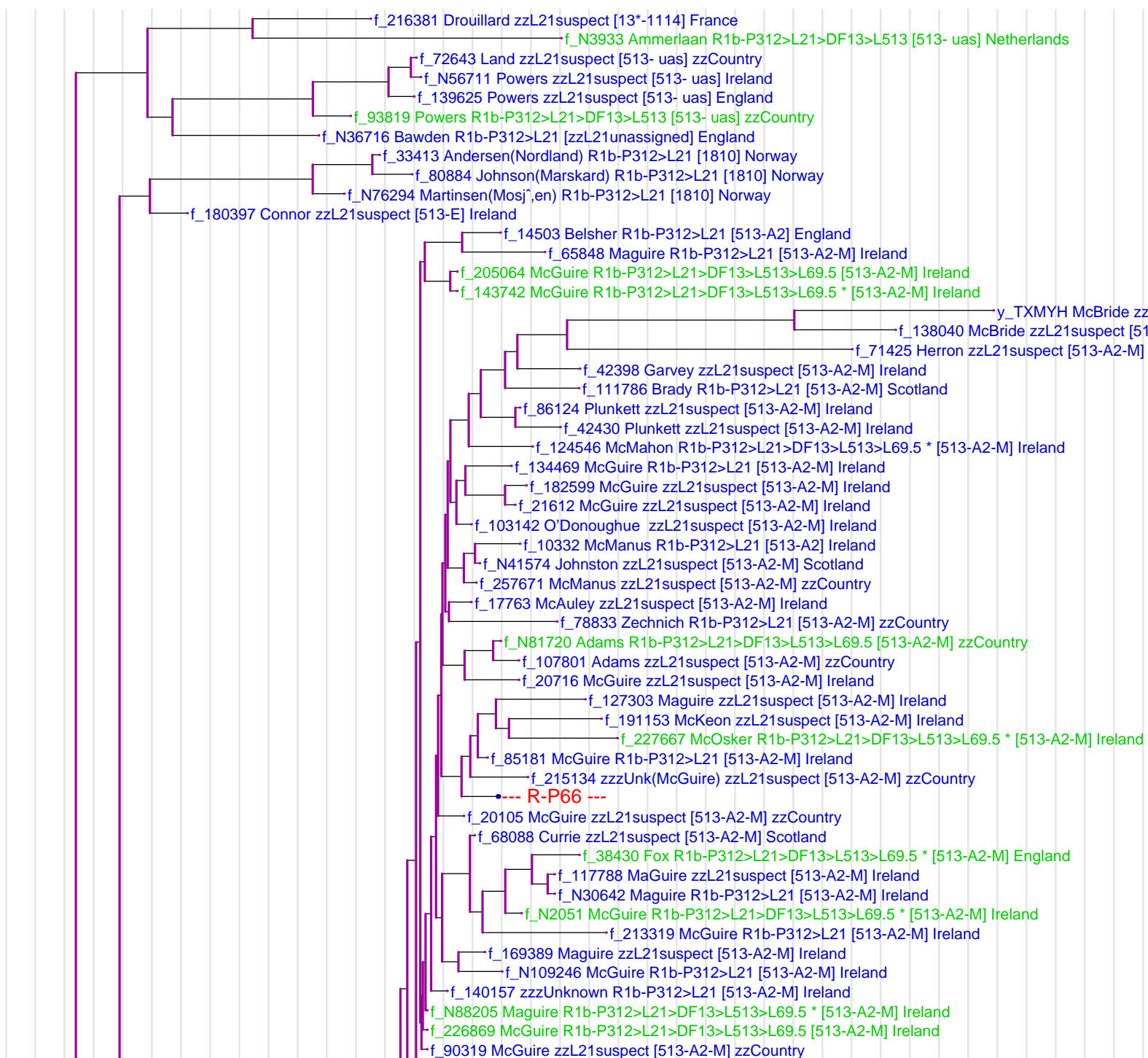
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	466	607	576	570	CDY <sub>a</sub>	CDY <sub>b</sub>	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	11	14	12	12	13	13	29	17	9	10	11	11	25	15	19	15	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

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

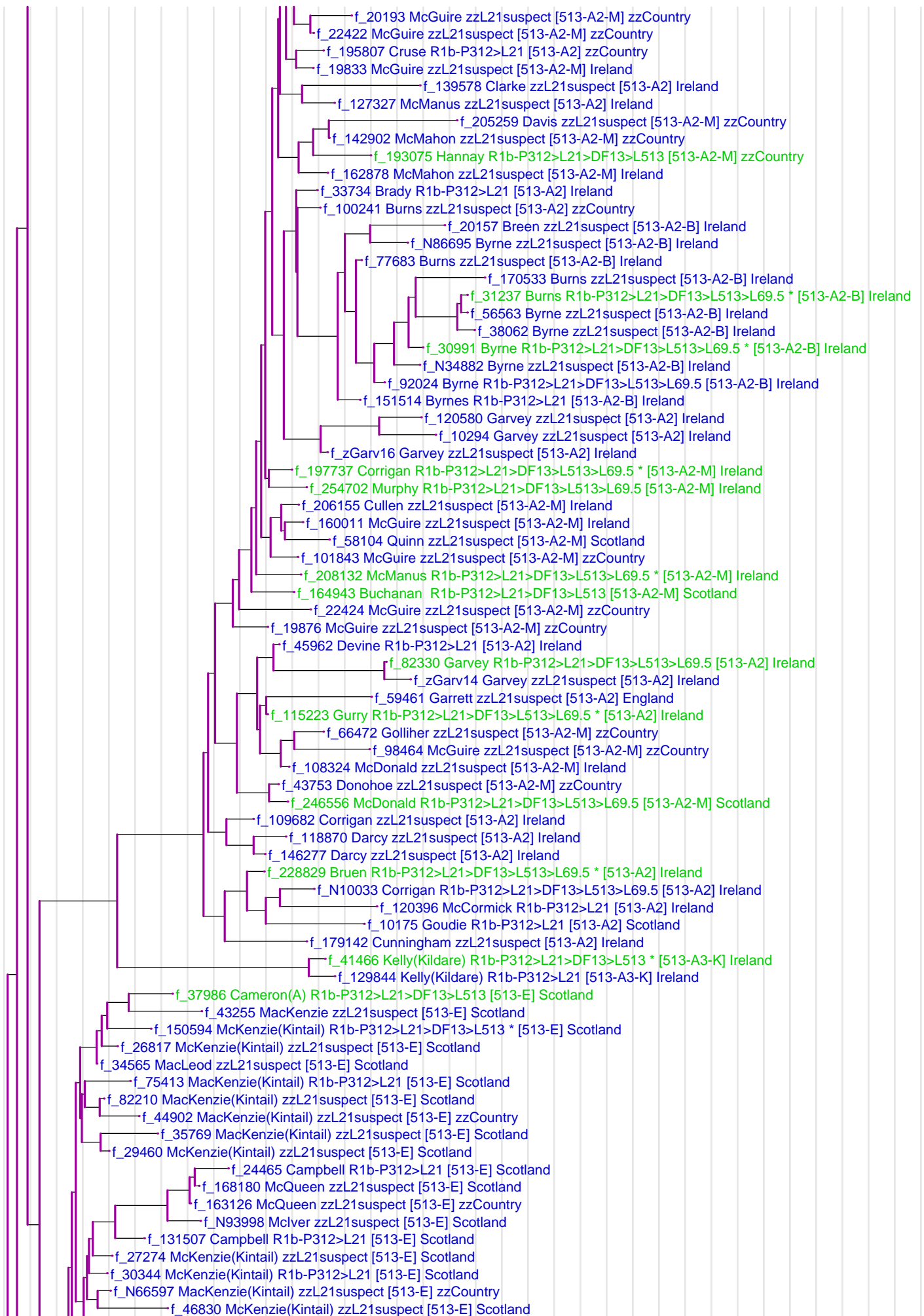


## Age Analysis

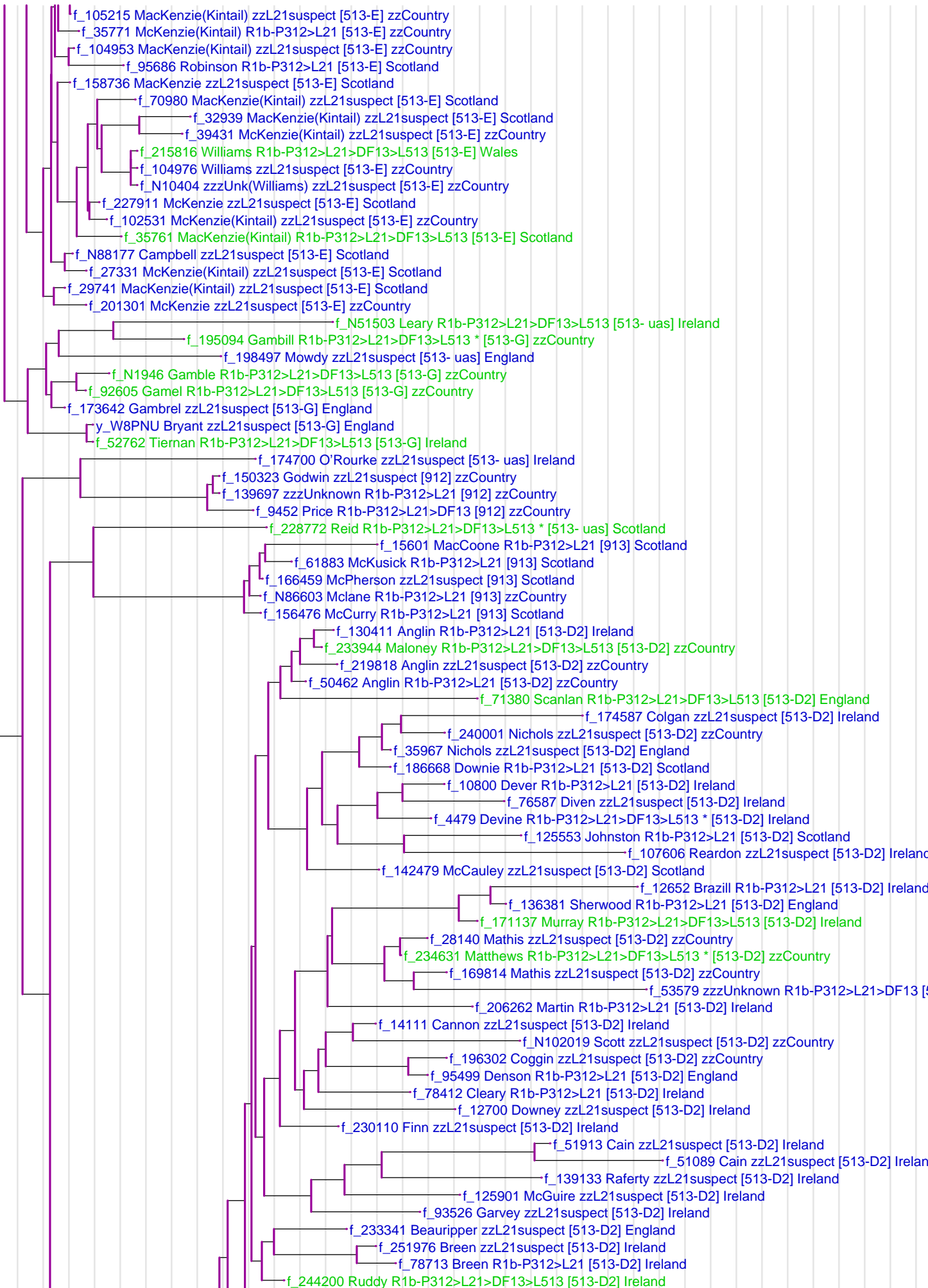
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
918	61506	13335	21.68%	121.53±12.16	3038.17±429.876



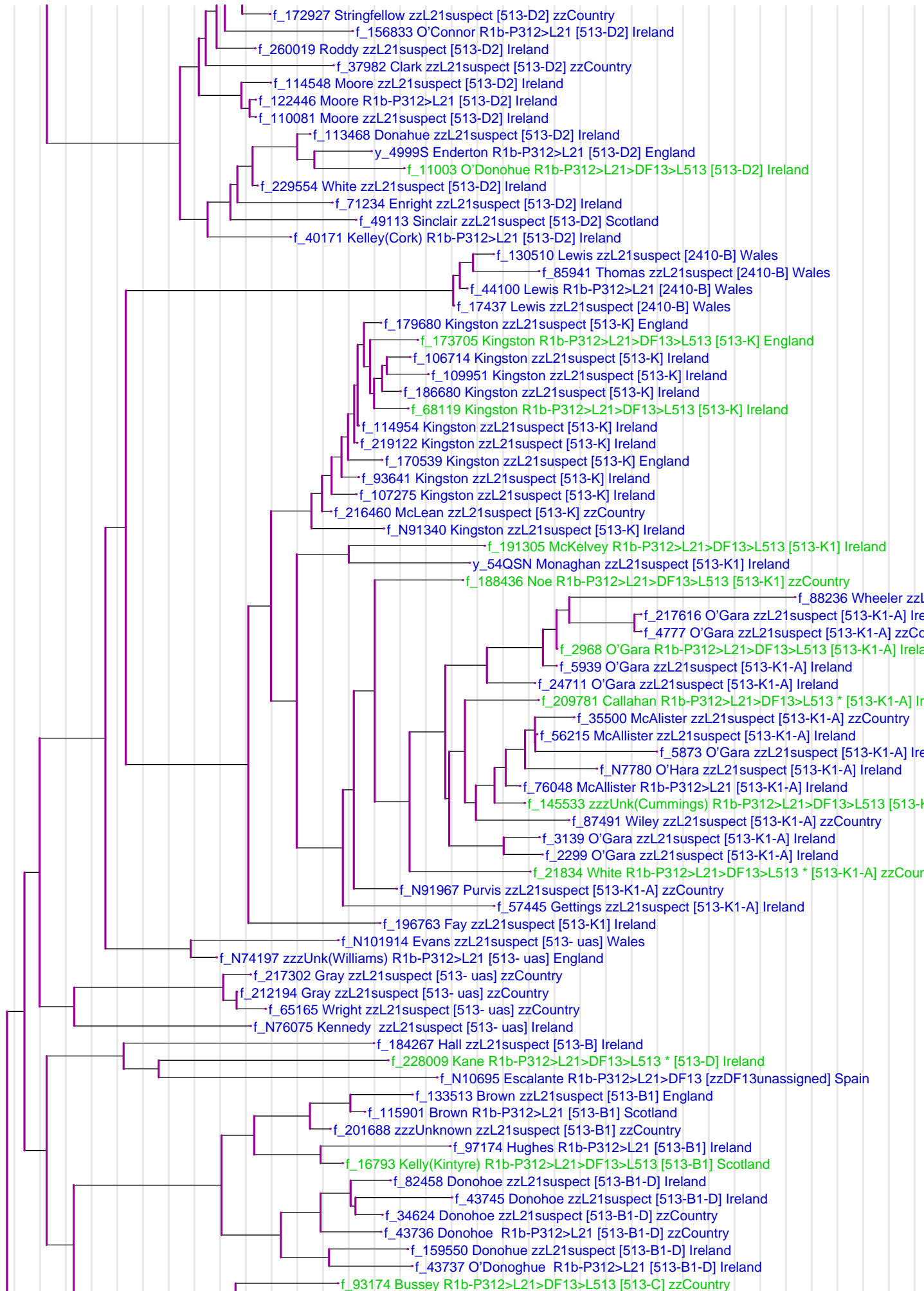
The vertical grey lines are separated 10 generations apart.



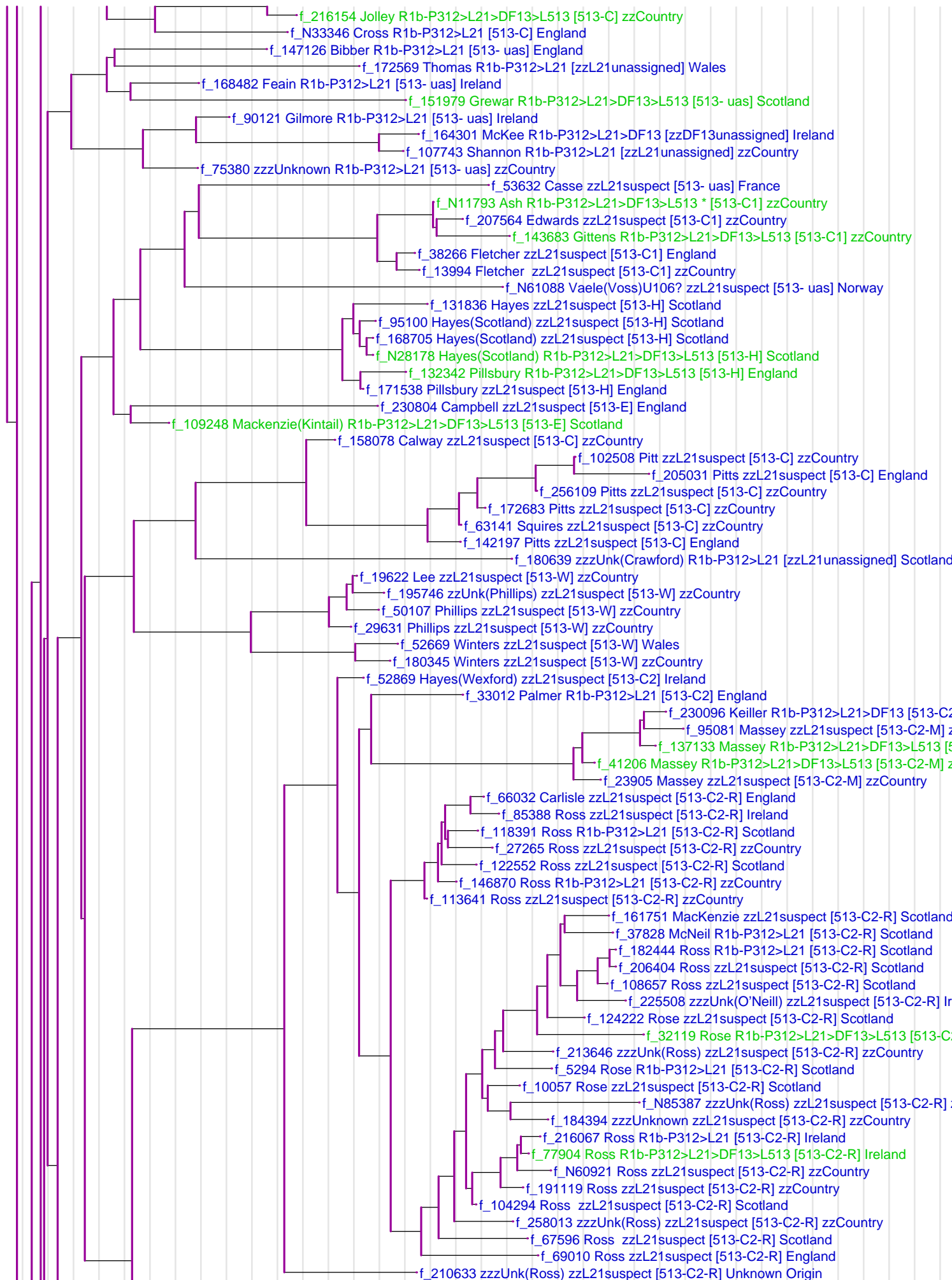
The vertical grey lines are separated 10 generations apart.



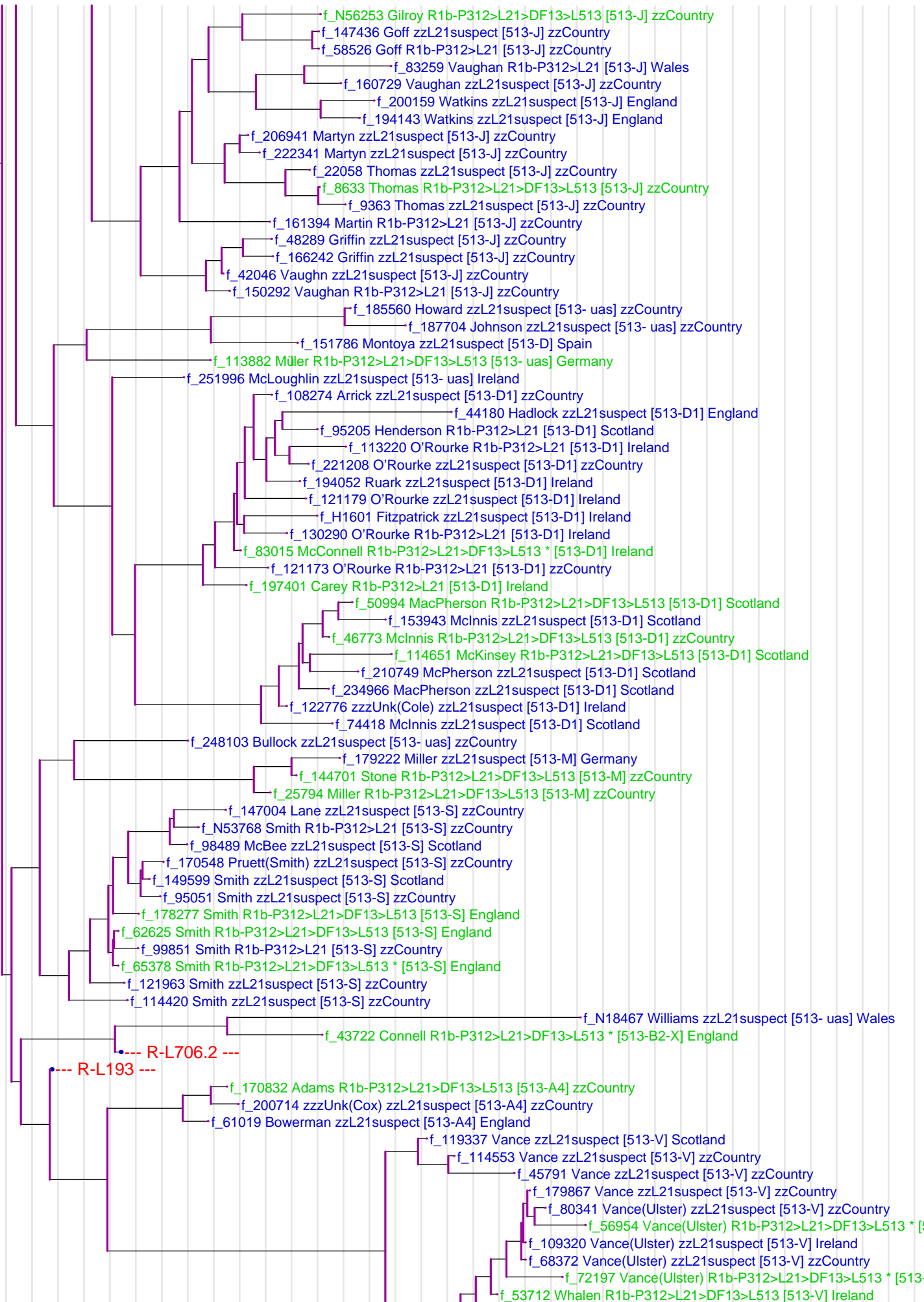
The vertical grey lines are separated 10 generations apart.



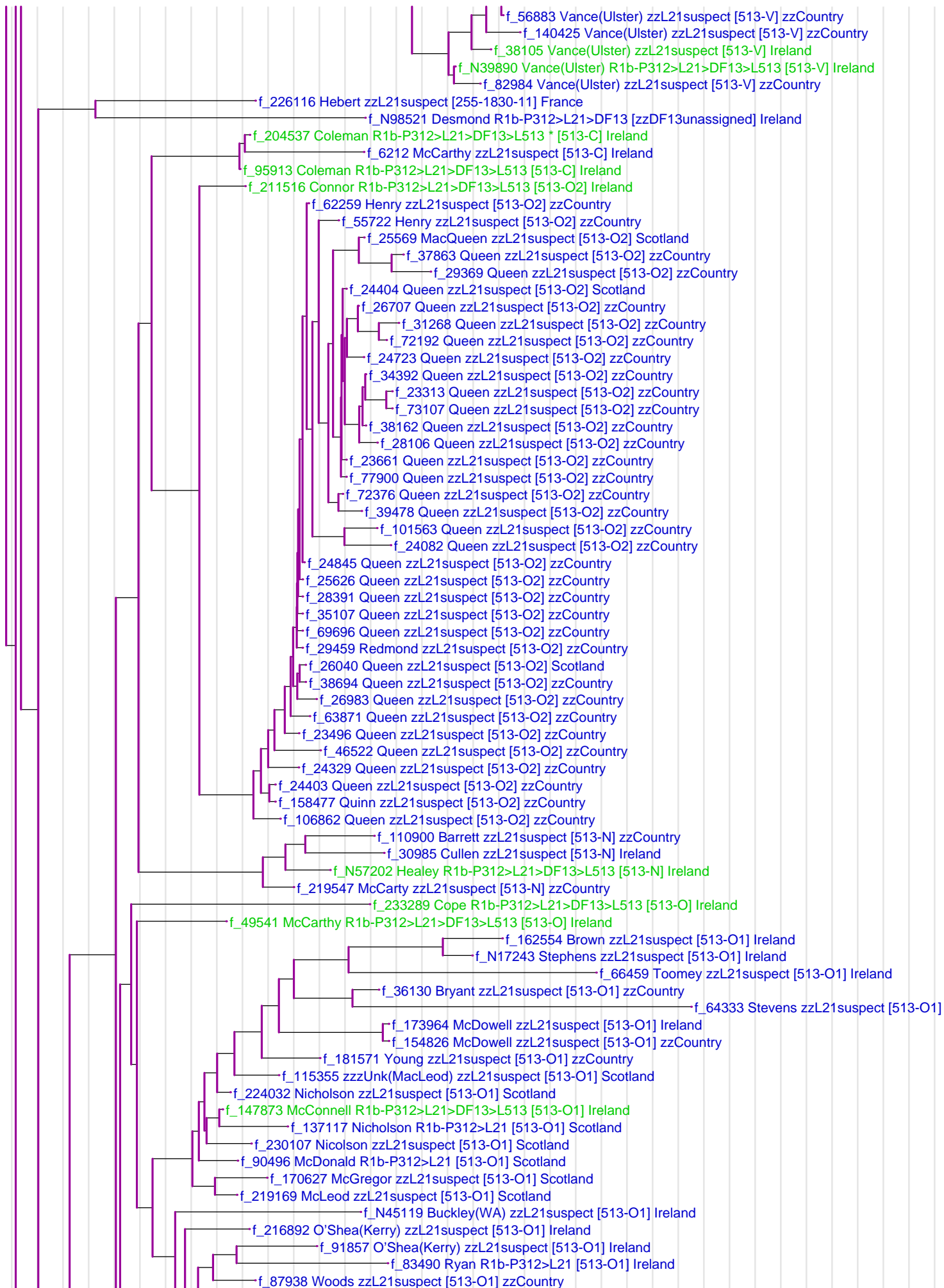
The vertical grey lines are separated 10 generations apart.



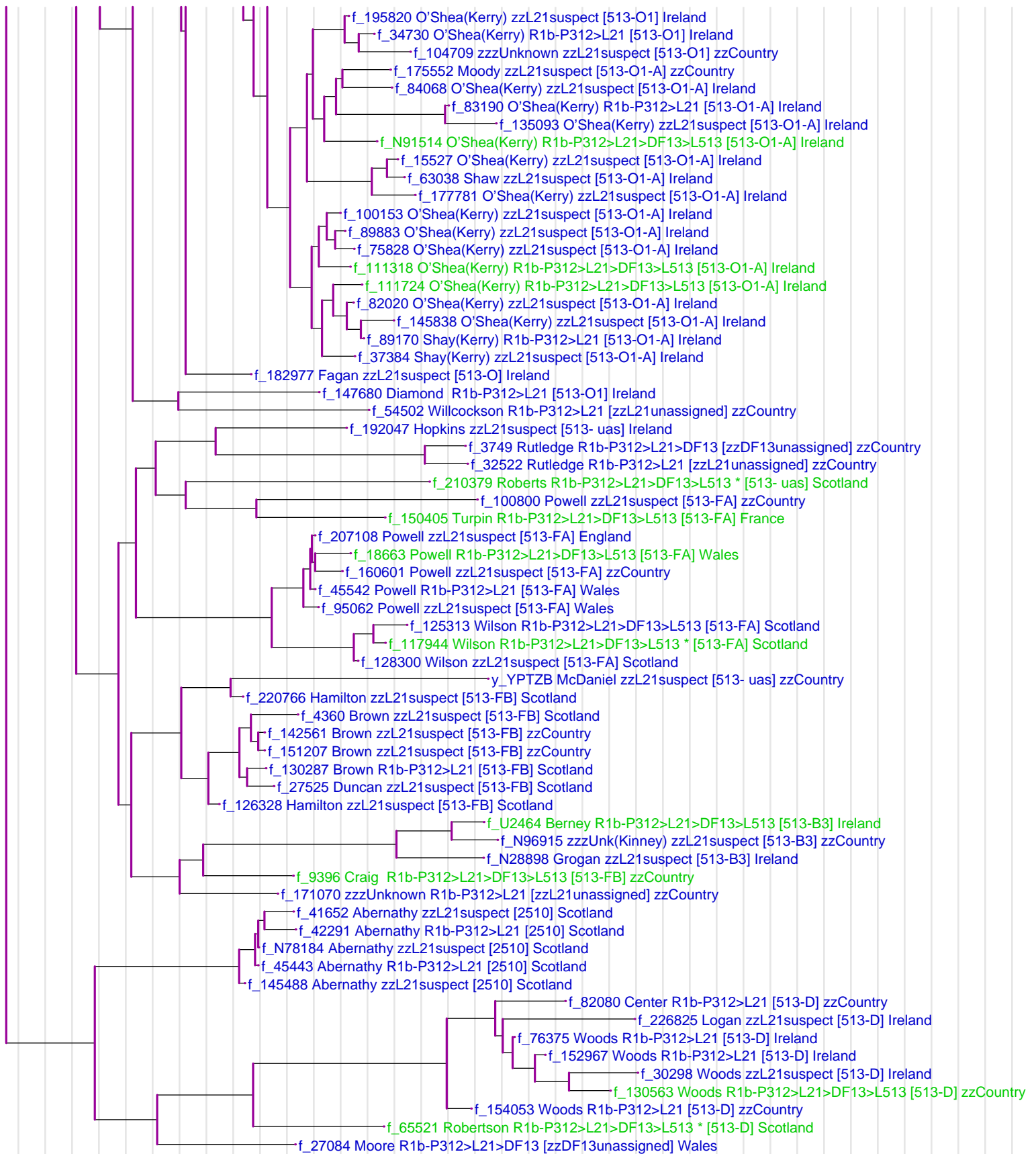
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

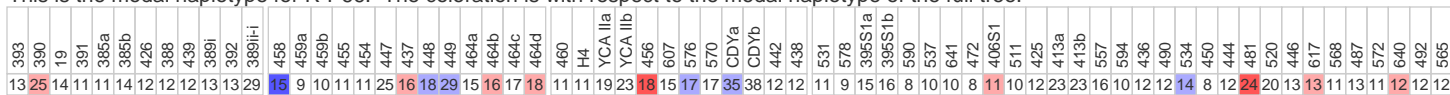


The vertical grey lines are separated 10 generations apart.



# R-P66

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

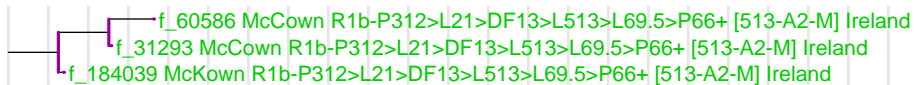


This is the marker distribution for R-P66. The color indicates the relative frequency of the alleles.



## Age Analysis

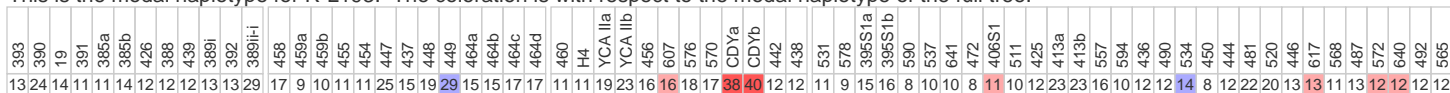
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	3	1.49%	7.52±0.92	187.97±29.7502



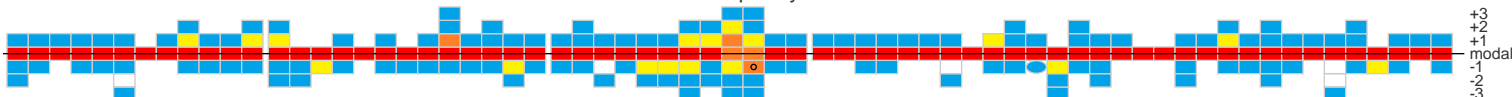
The vertical grey lines are separated 10 generations apart.

# R-L193

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

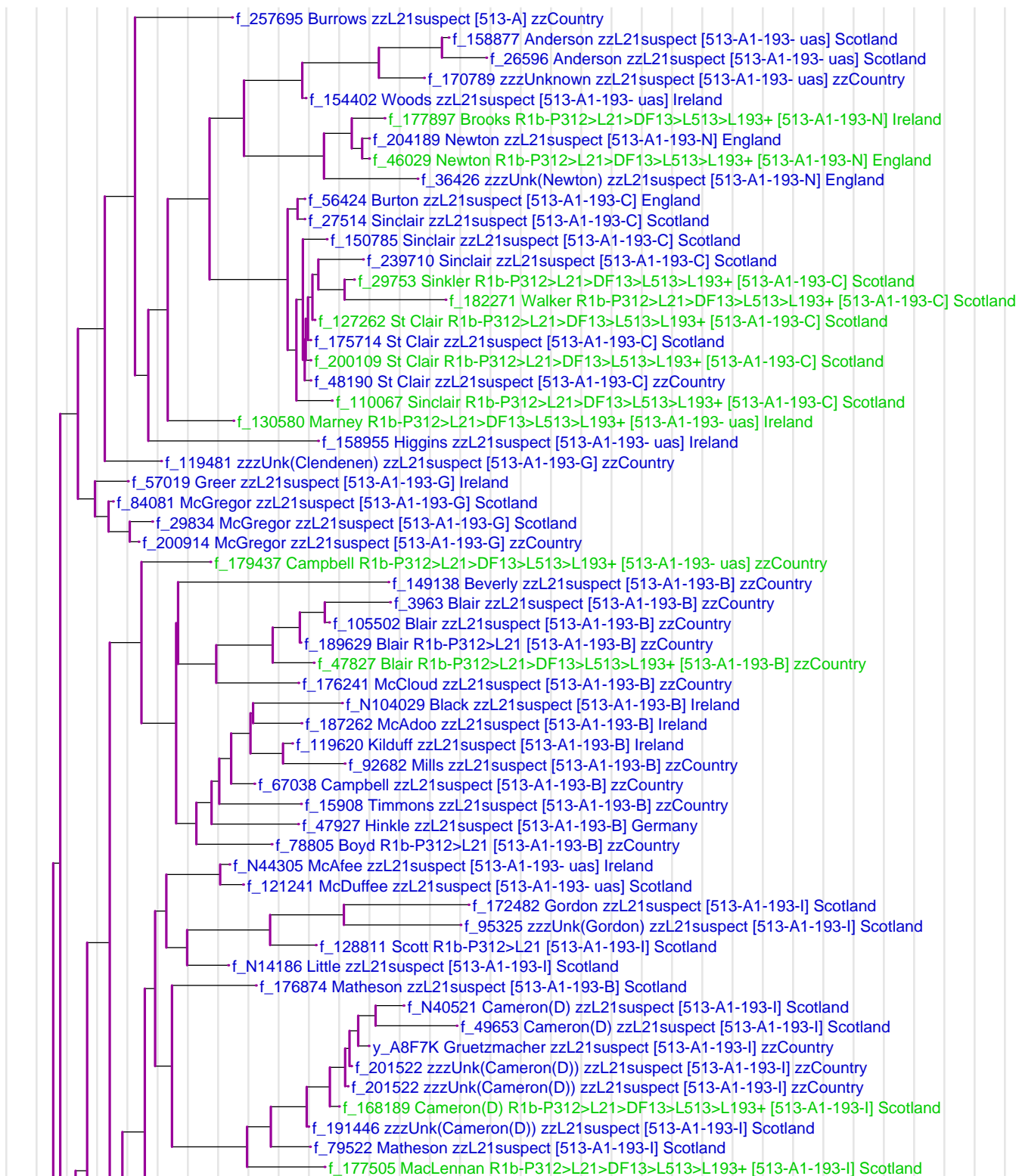


This is the marker distribution for R-L193. The color indicates the relative frequency of the alleles.

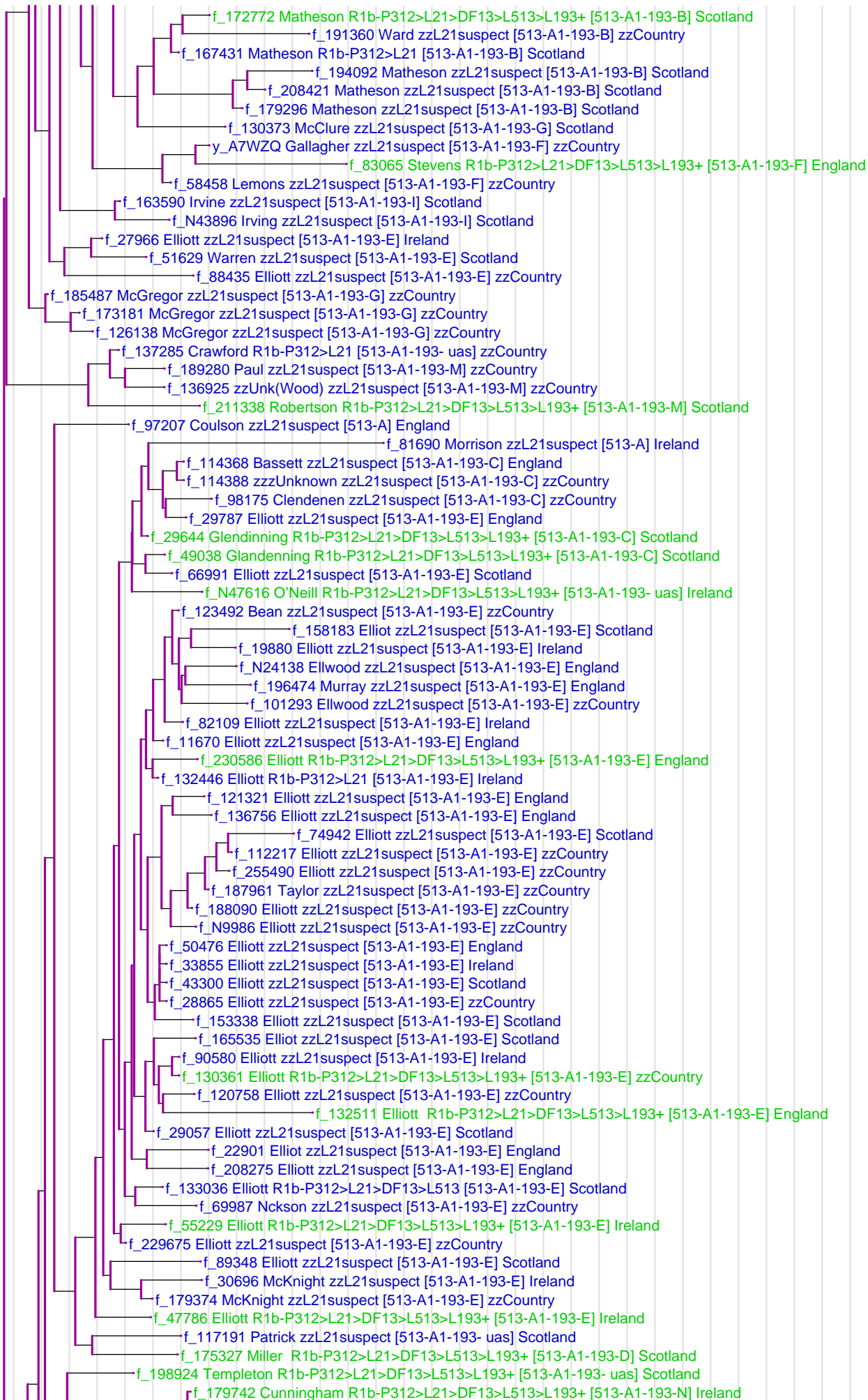


## Age Analysis

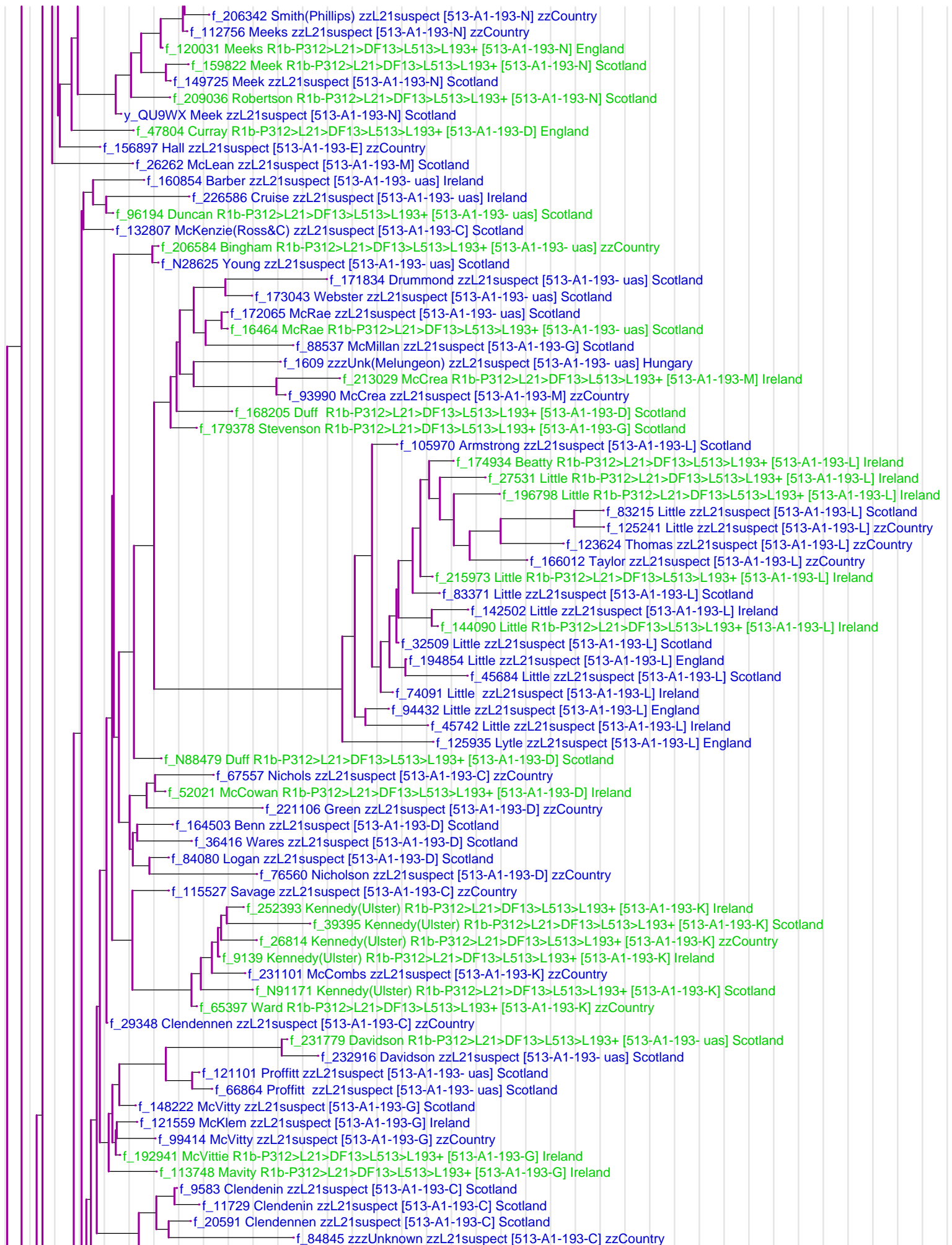
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
299	20033	2108	10.52%	55.53±5.57	1388.31±196.607



The vertical grey lines are separated 10 generations apart.



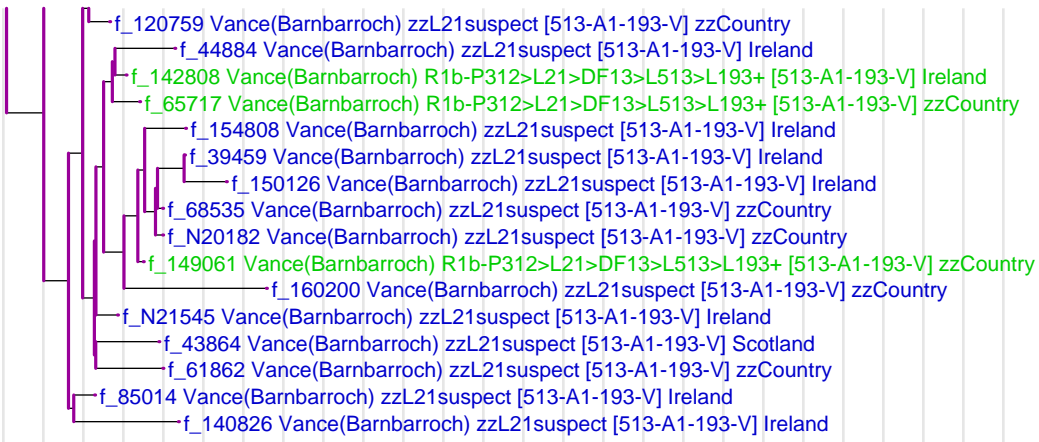
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



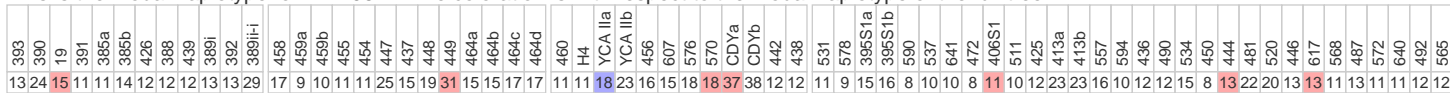
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

# R-L706.2

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

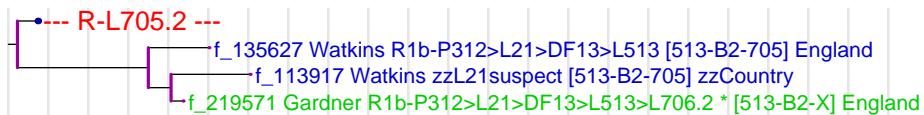


This is the marker distribution for R-L706.2. The color indicates the relative frequency of the alleles.



## Age Analysis

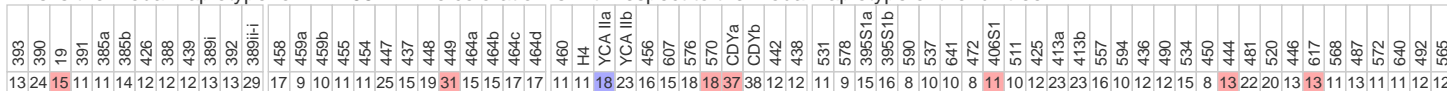
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
51	3417	310	9.07%	47.52±4.83	1187.88±169.33



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.

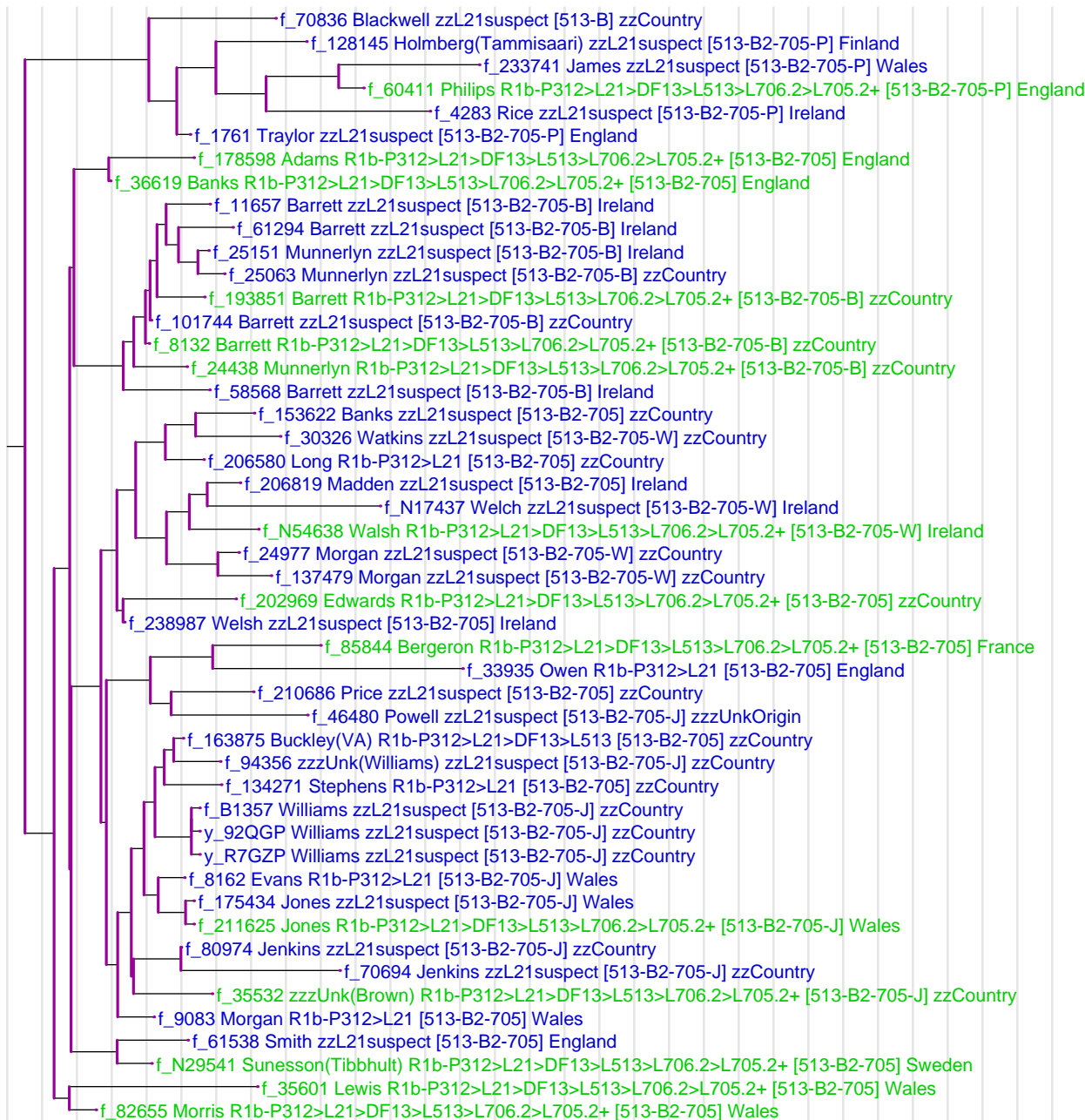


This is the marker distribution for R-L705.2. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
48	3216	298	9.27%	48.58±4.94	1214.5±173.212

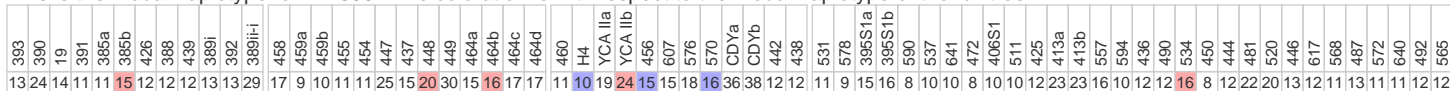


The vertical grey lines are separated 10 generations apart.



# R-L555

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

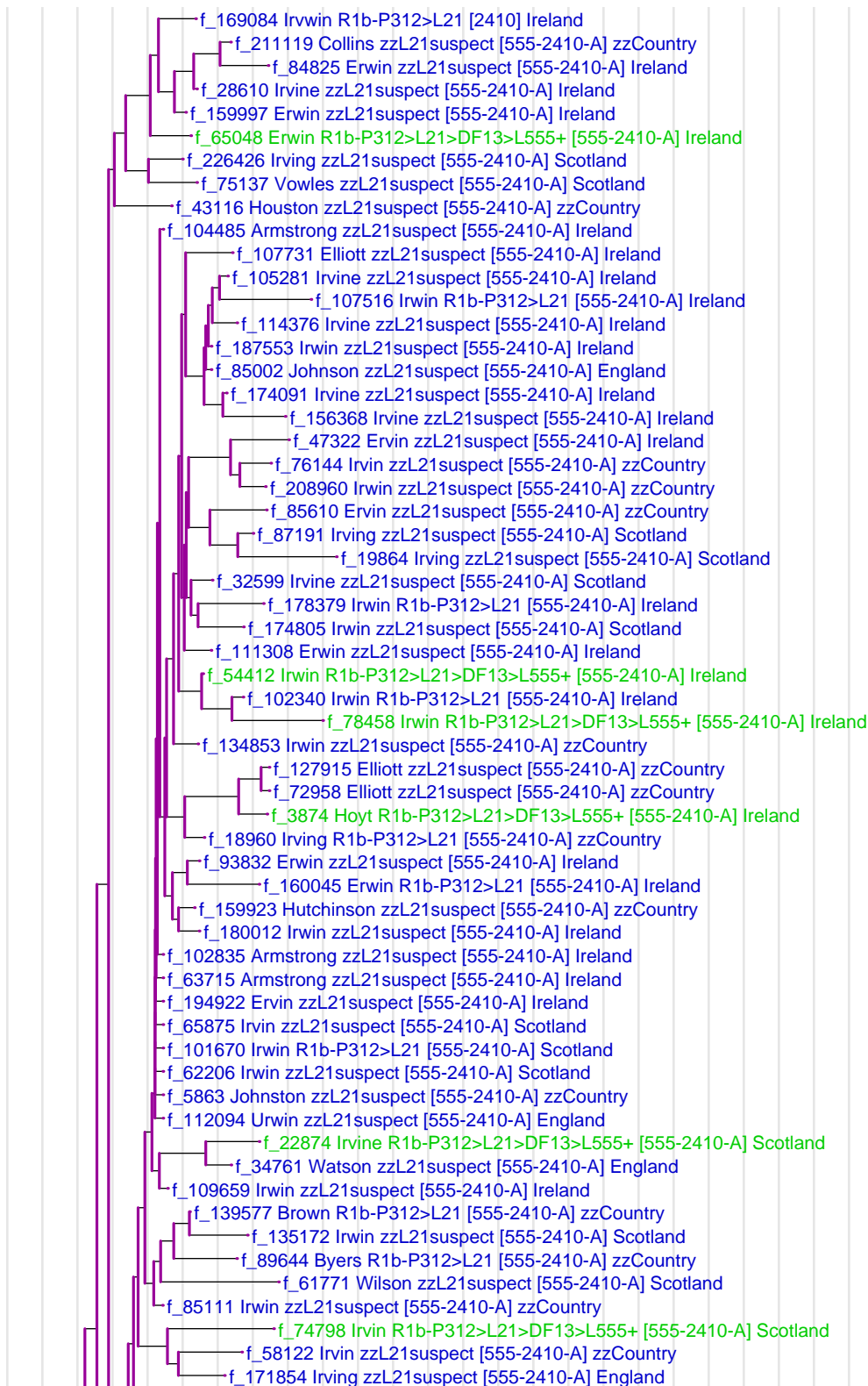


This is the marker distribution for R-L555. The color indicates the relative frequency of the alleles.

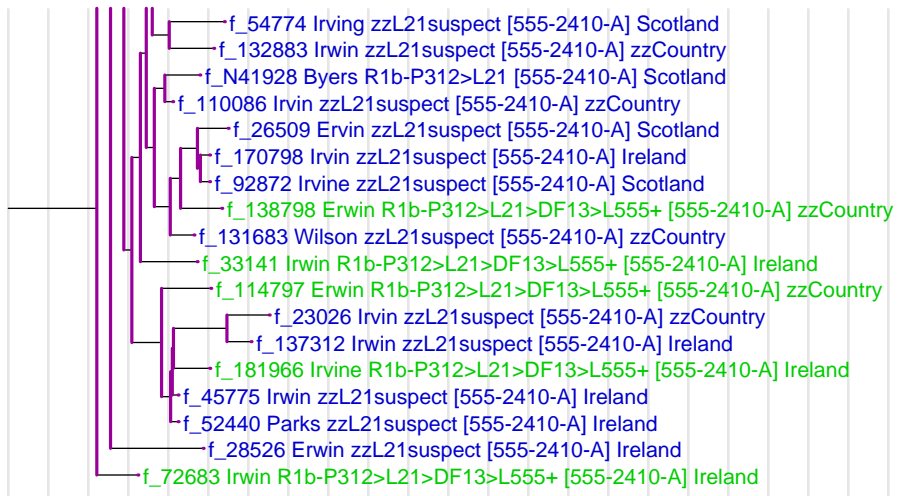


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
77	5159	188	3.64%	18.56±1.87	463.967±65.9437



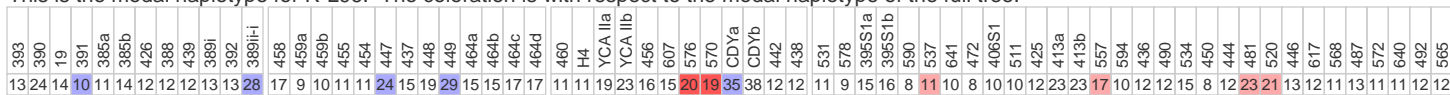
The vertical grey lines are separated 10 generations apart.



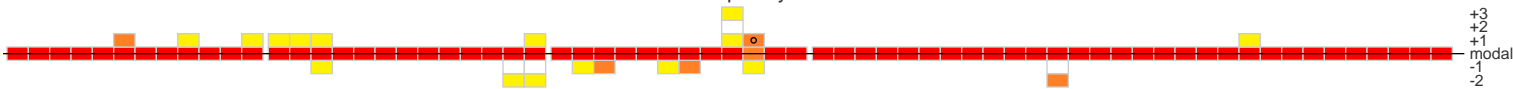
The vertical grey lines are separated 10 generations apart.

# R-L96

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



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



## Age Analysis

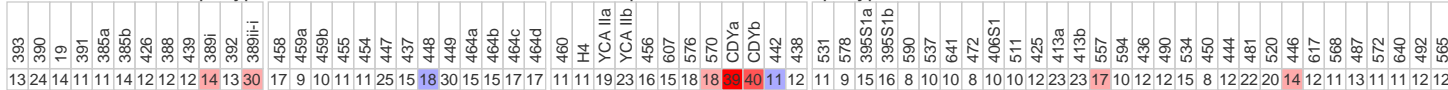
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	31	9.25%	48.51±5.59	1212.79±184.996



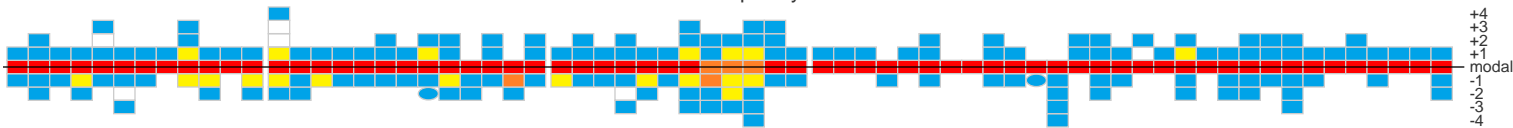
The vertical grey lines are separated 10 generations apart.

# R-Z255

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

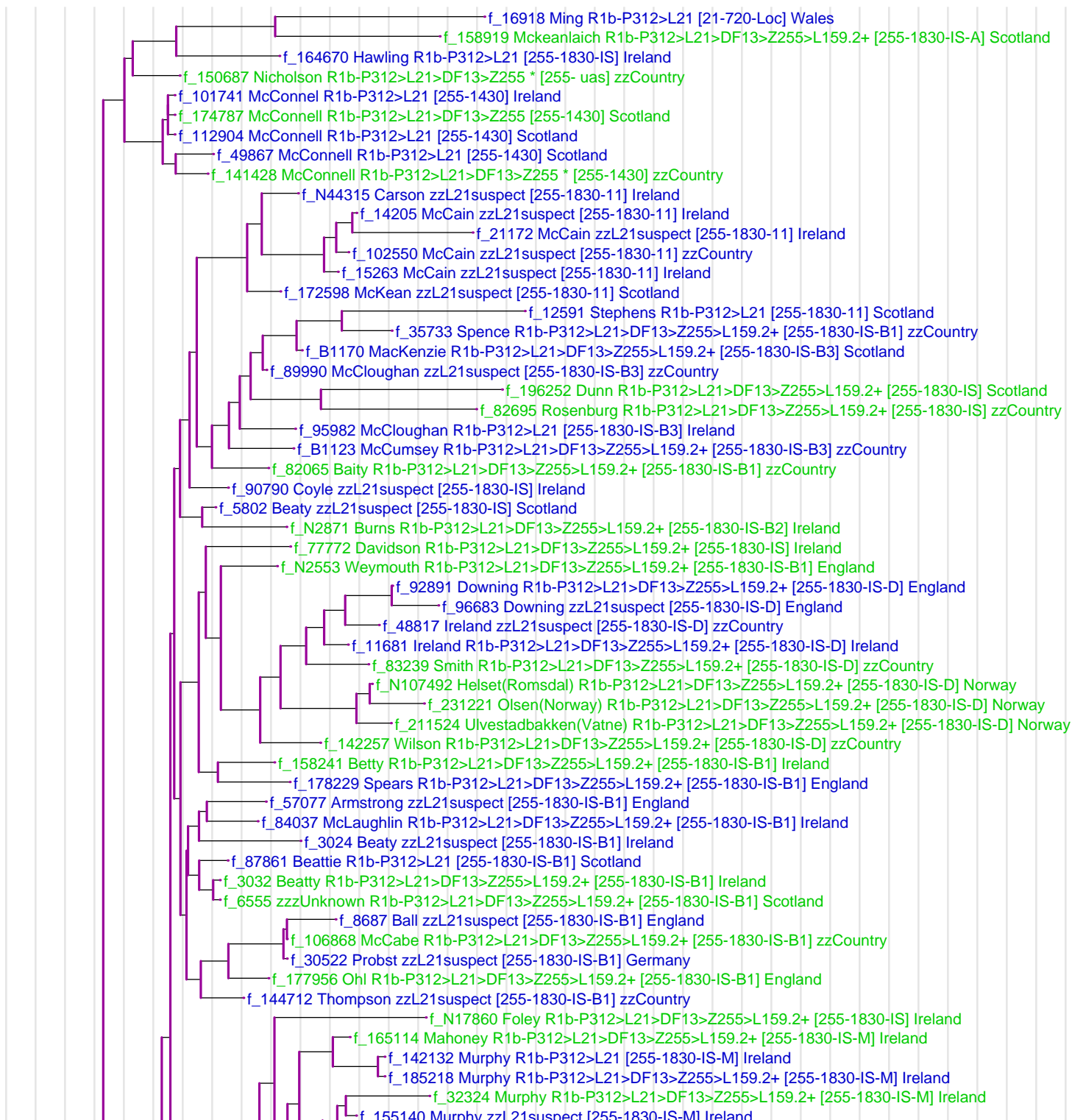


This is the marker distribution for R-Z255. The color indicates the relative frequency of the alleles.

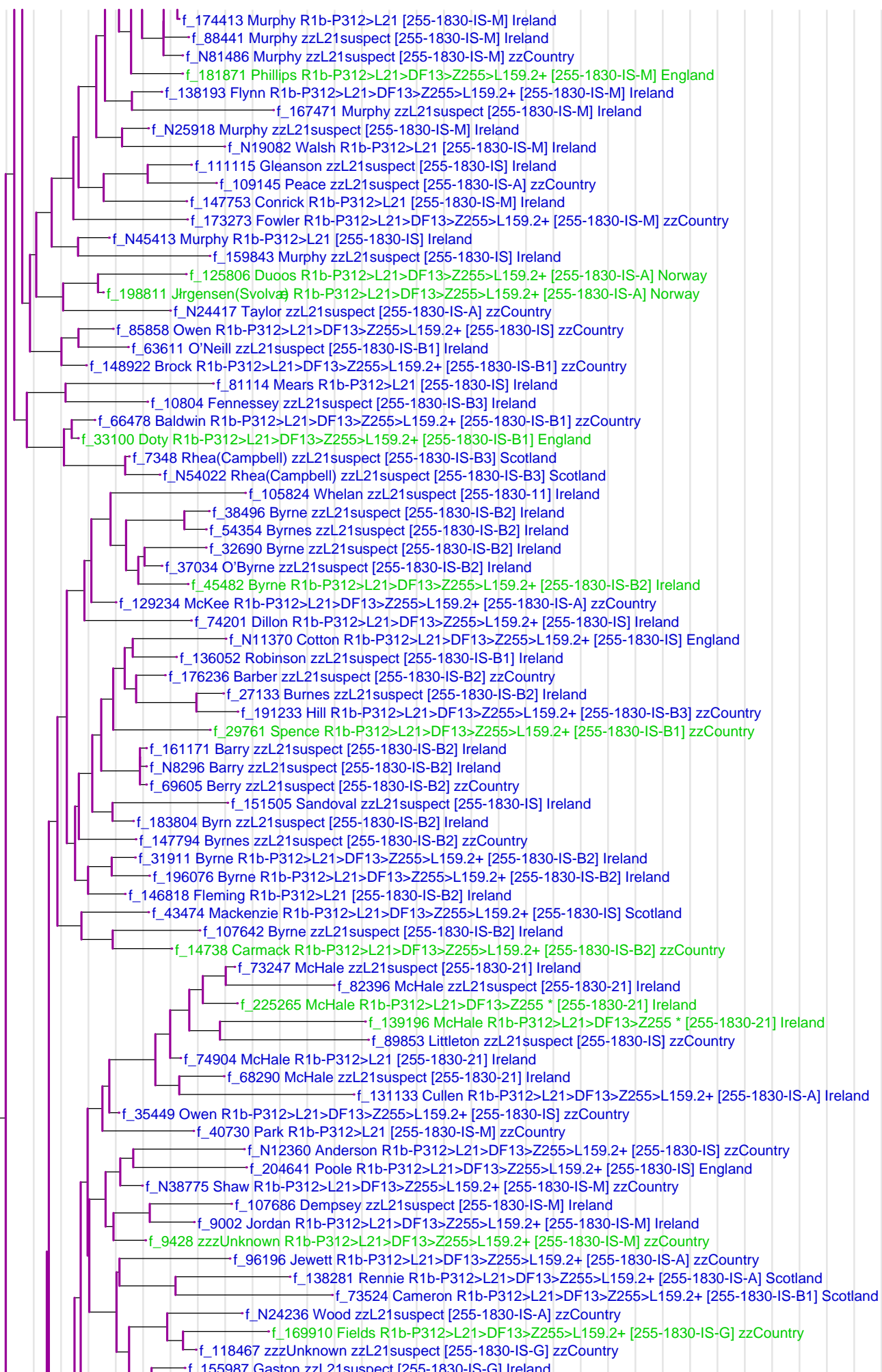


## Age Analysis

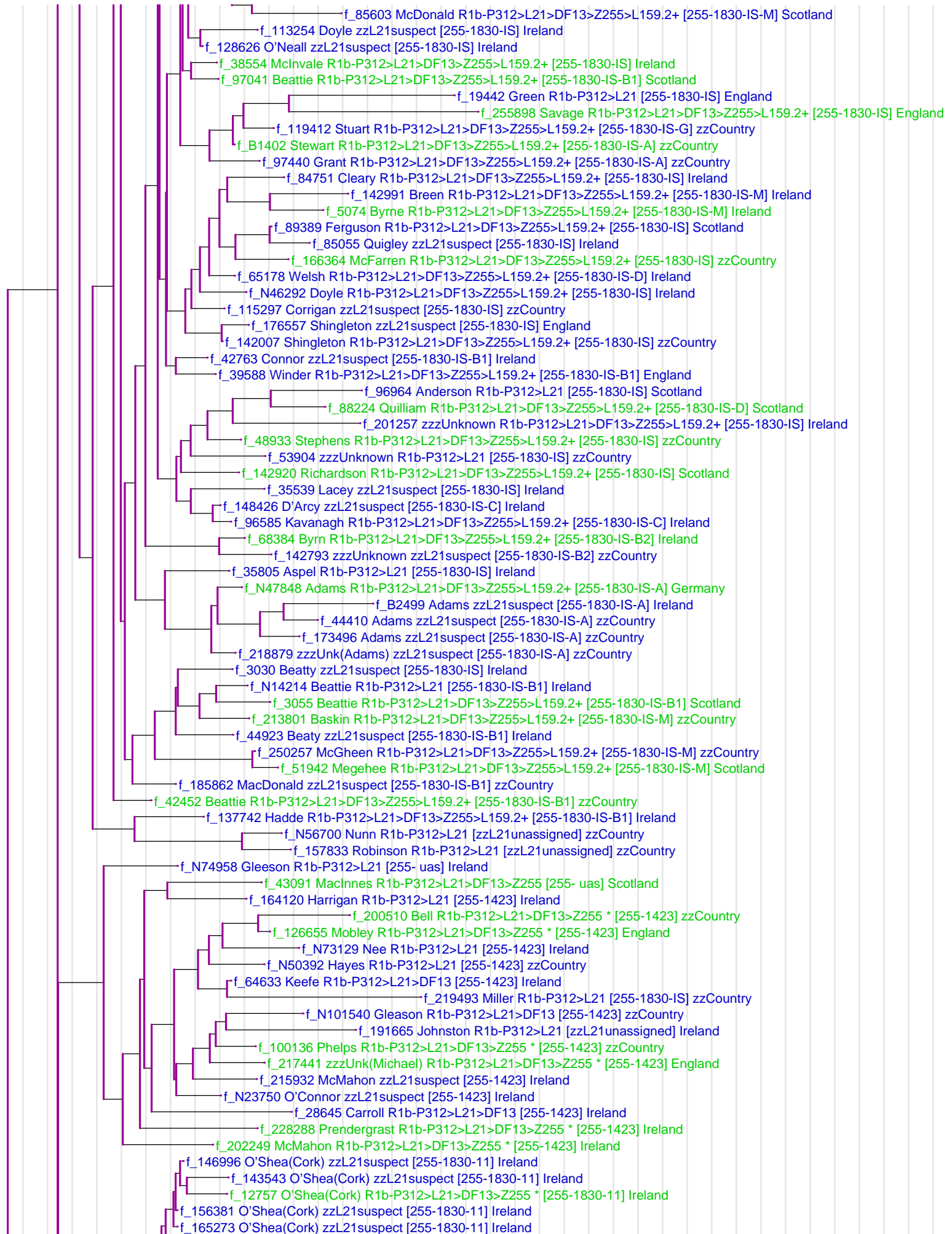
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
281	18827	2406	12.78%	68.25±6.85	1706.32±241.673



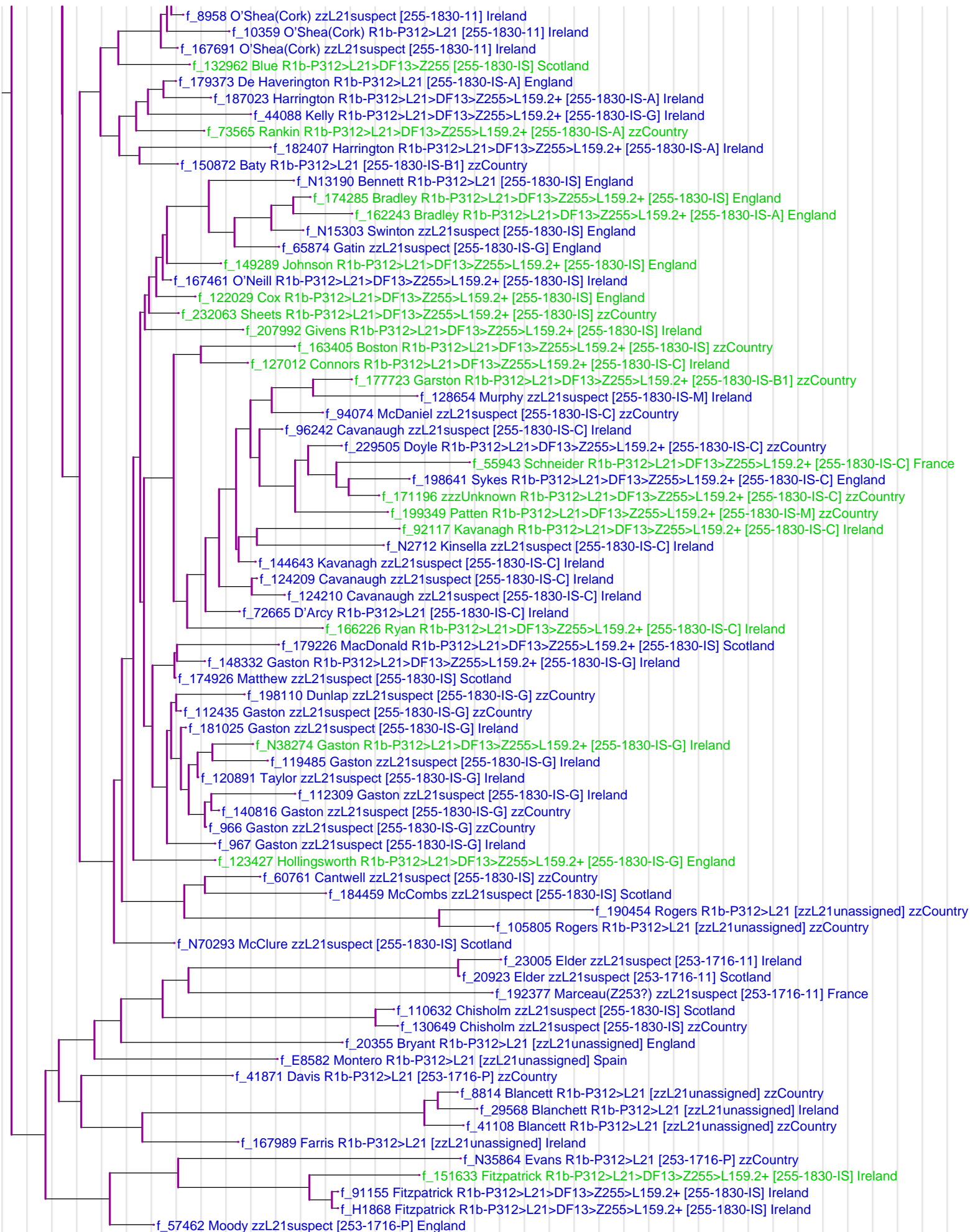
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



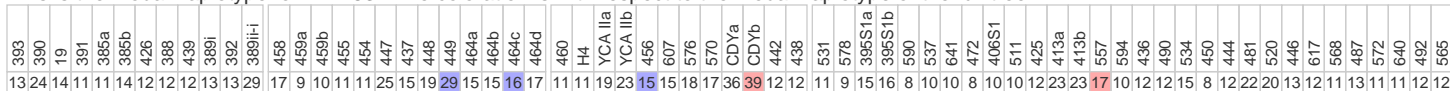
The vertical grey lines are separated 10 generations apart.



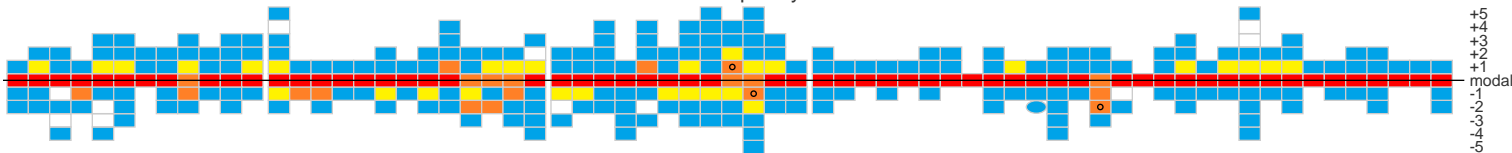
The vertical grey lines are separated 10 generations apart.

# R-Z253

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

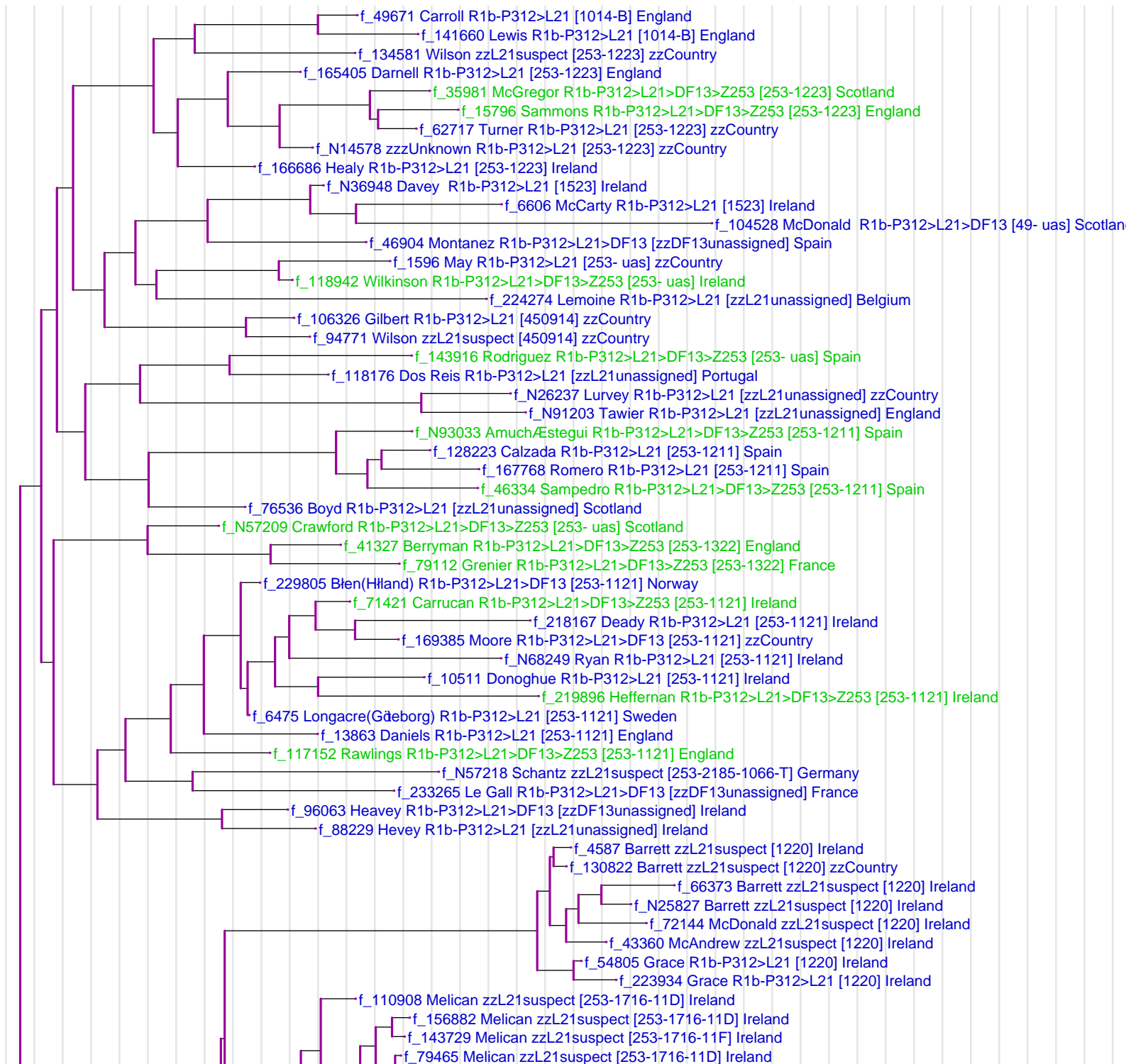


This is the marker distribution for R-Z253. The color indicates the relative frequency of the alleles.



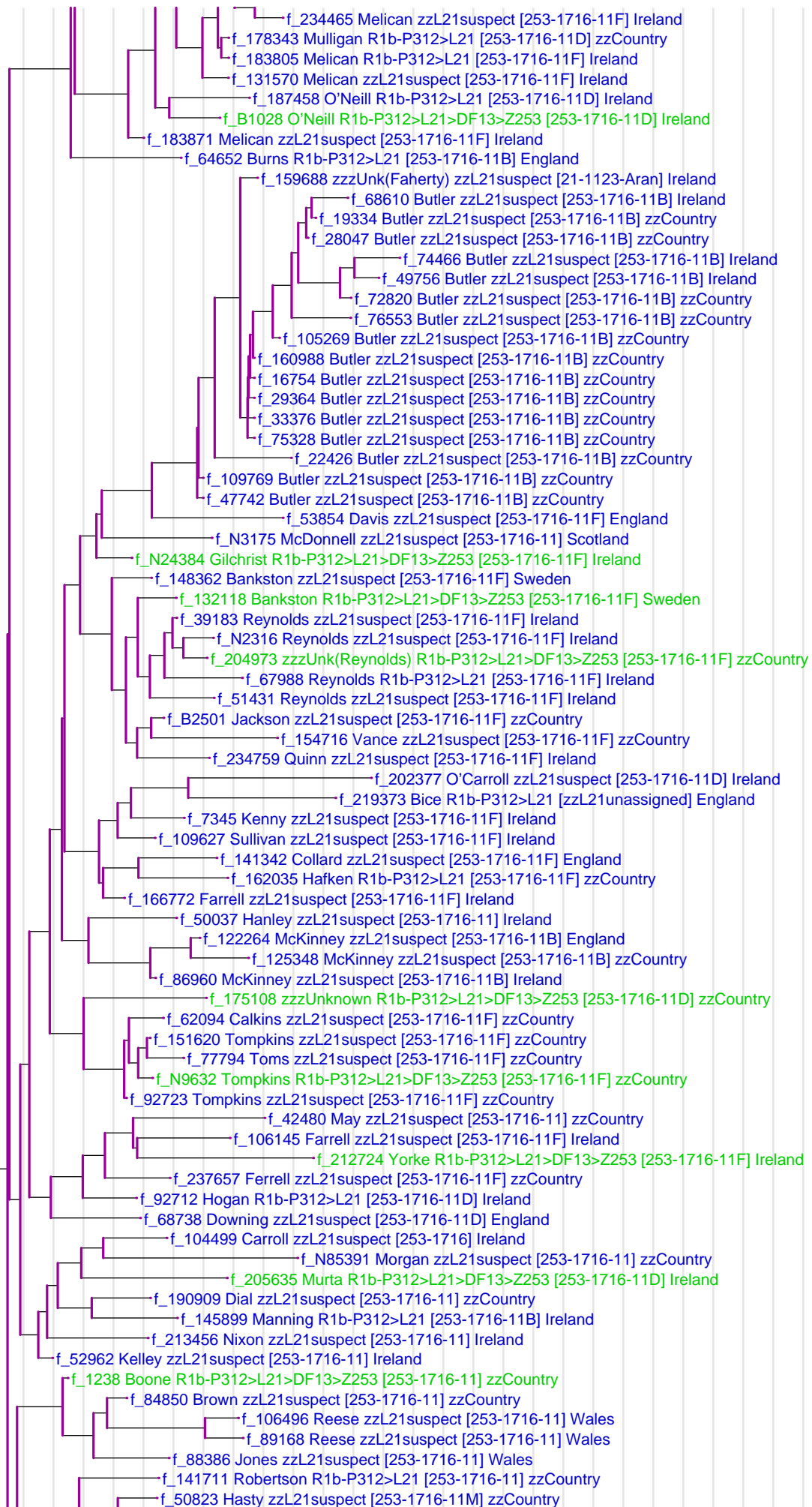
## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
833	55811	12248	21.95%	123.19±12.33	3079.77±435.786

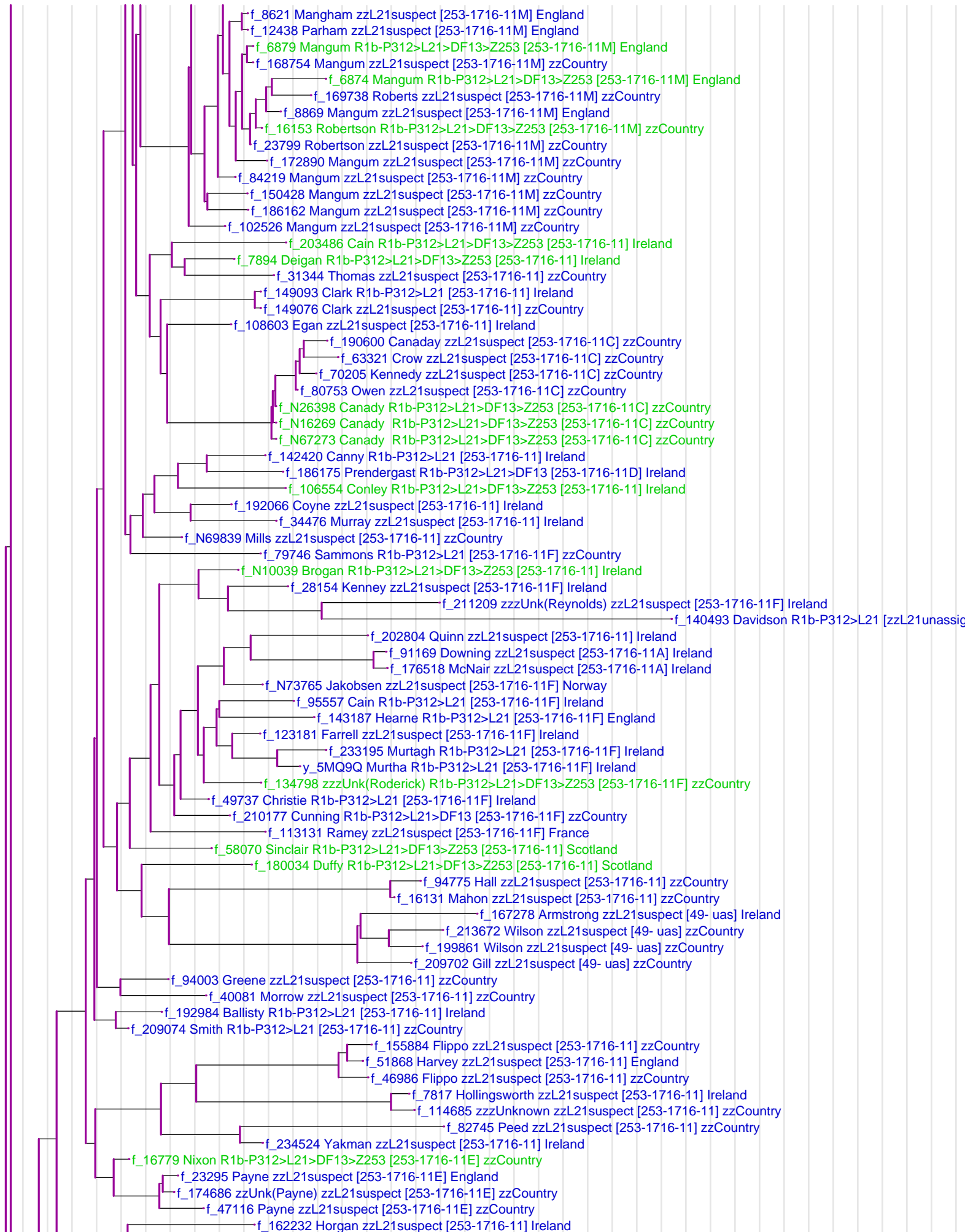


The vertical grey lines are separated 10 generations apart.

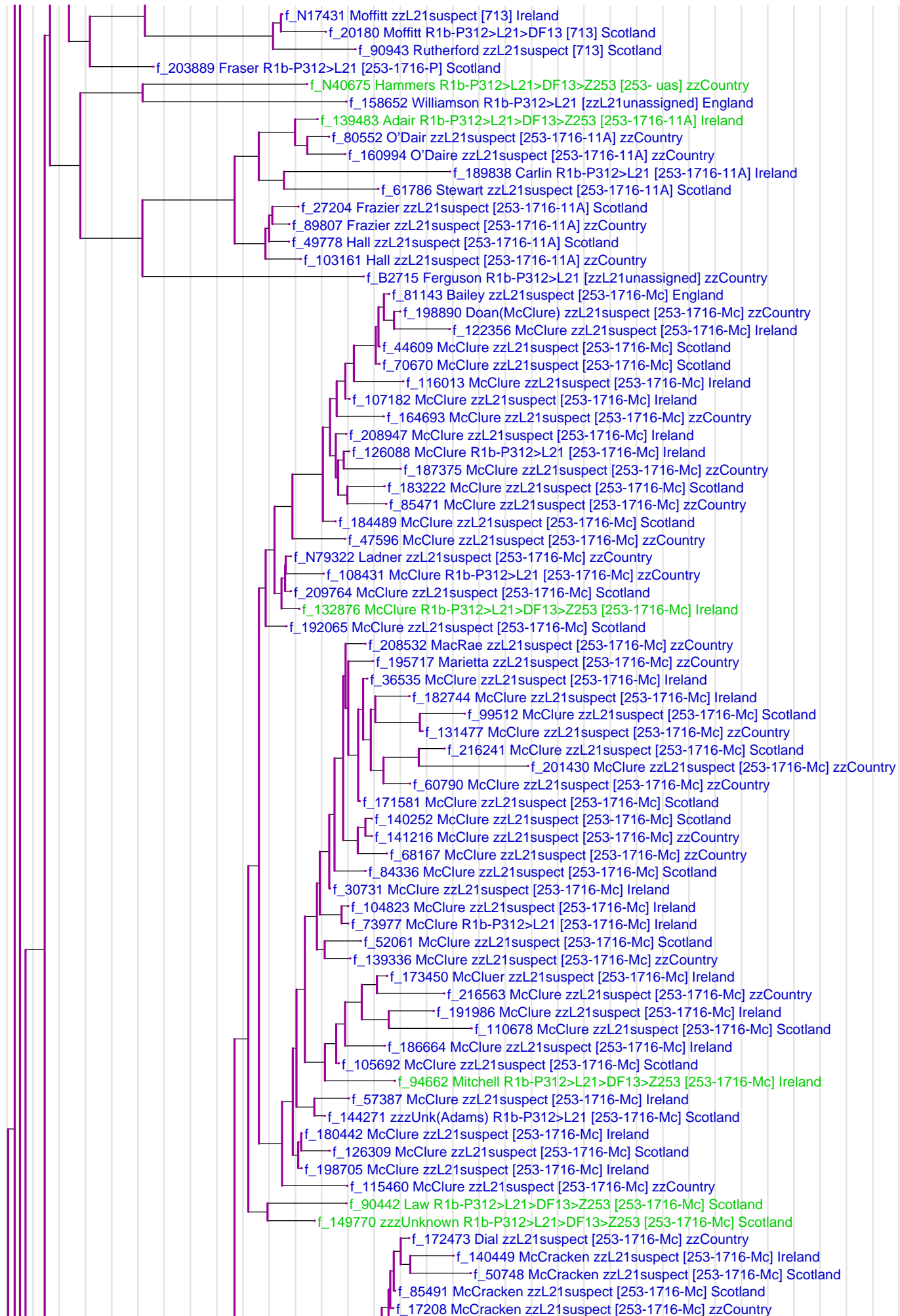




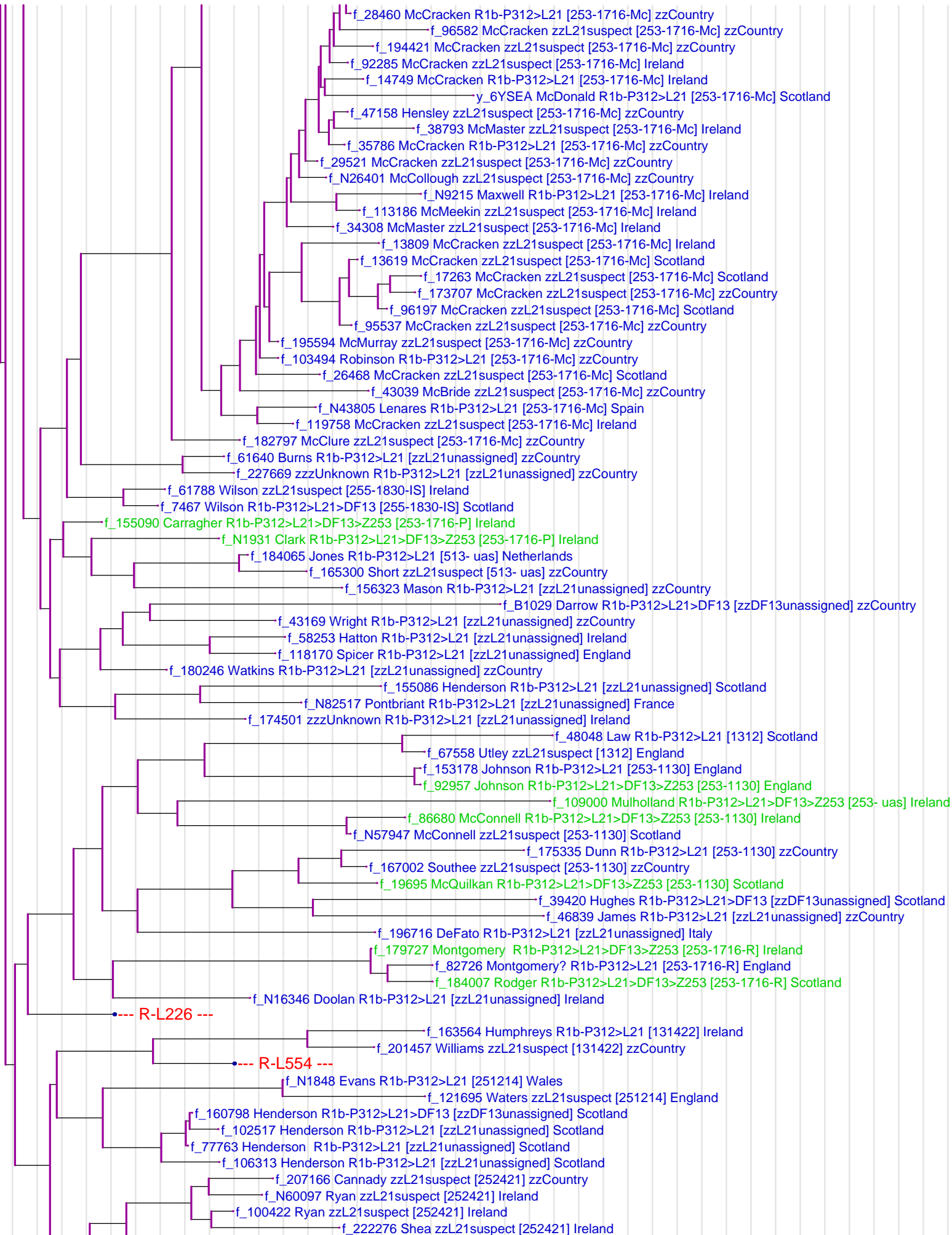
The vertical grey lines are separated 10 generations apart.



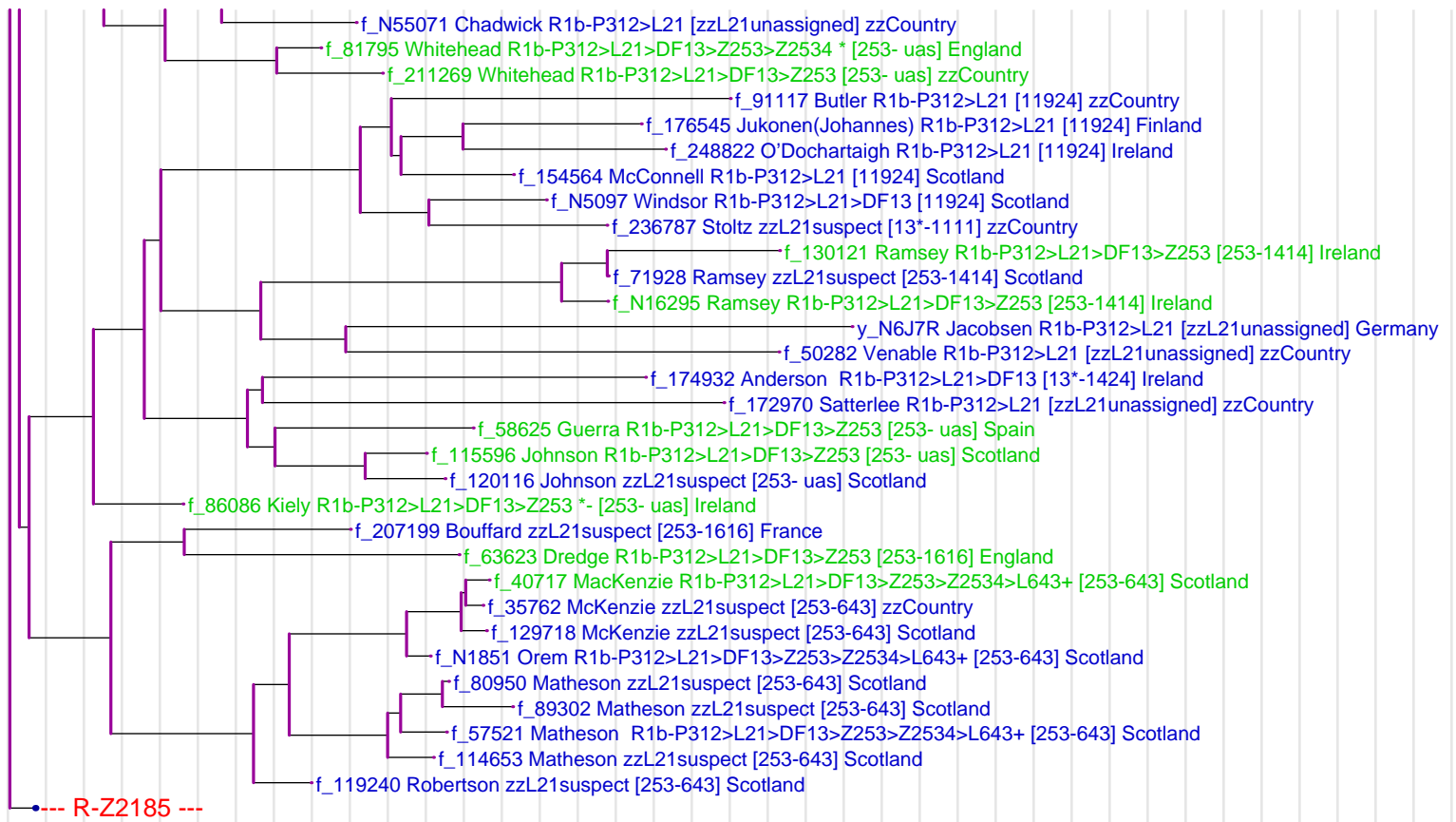
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



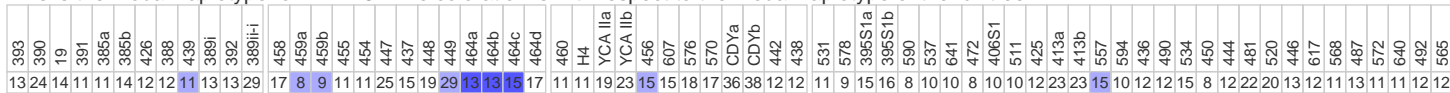
The vertical grey lines are separated 10 generations apart.



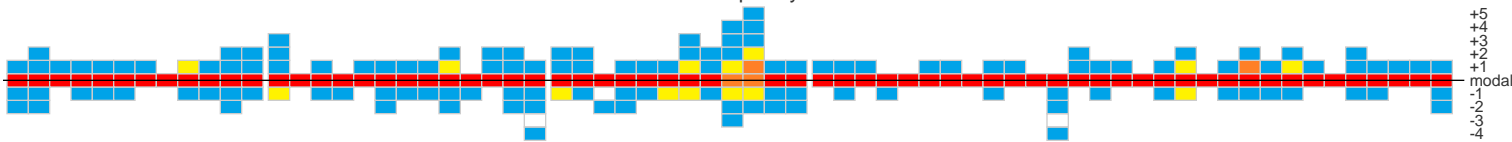
The vertical grey lines are separated 10 generations apart.

# R-L226

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

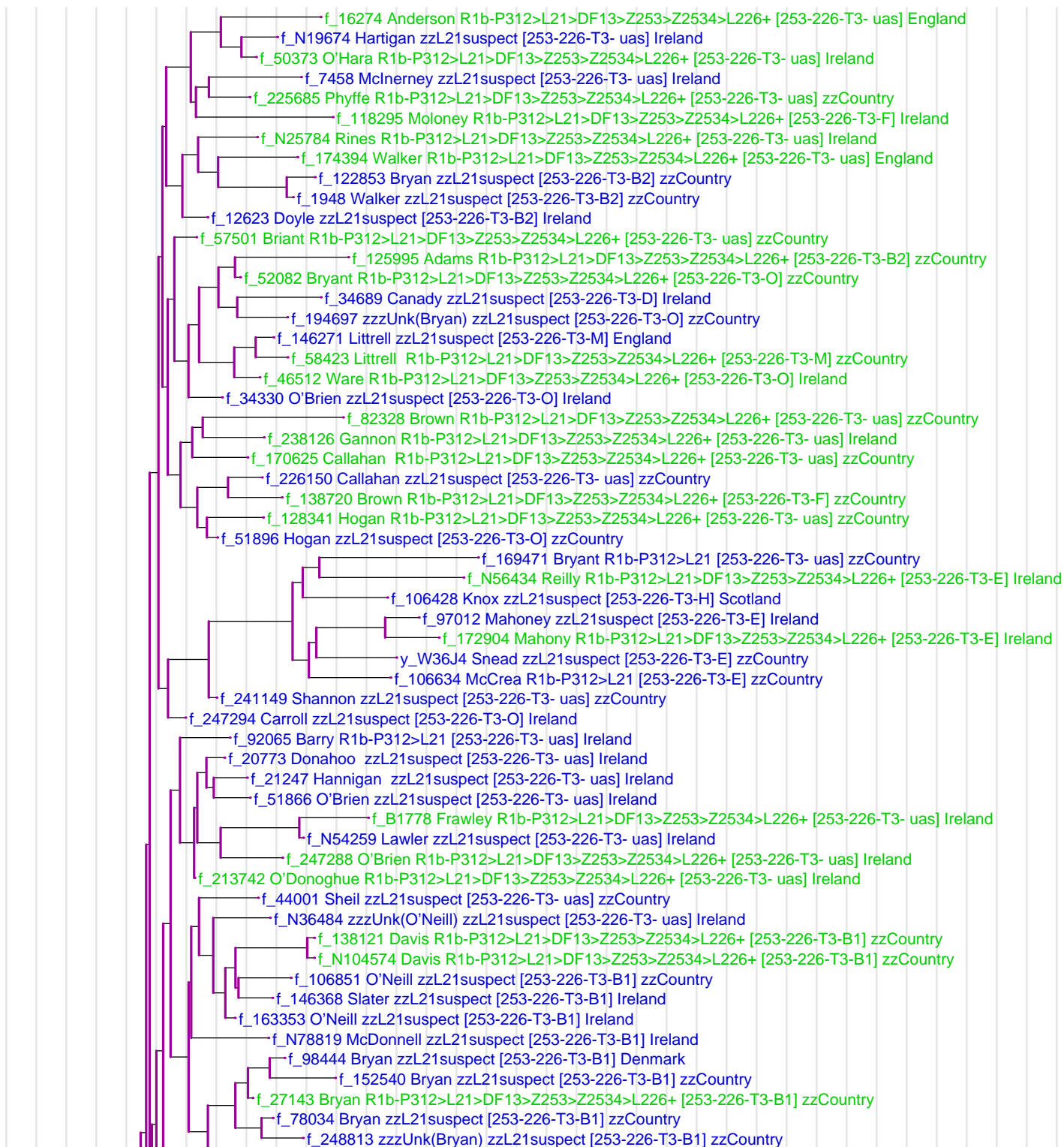


This is the marker distribution for R-L226. The color indicates the relative frequency of the alleles.

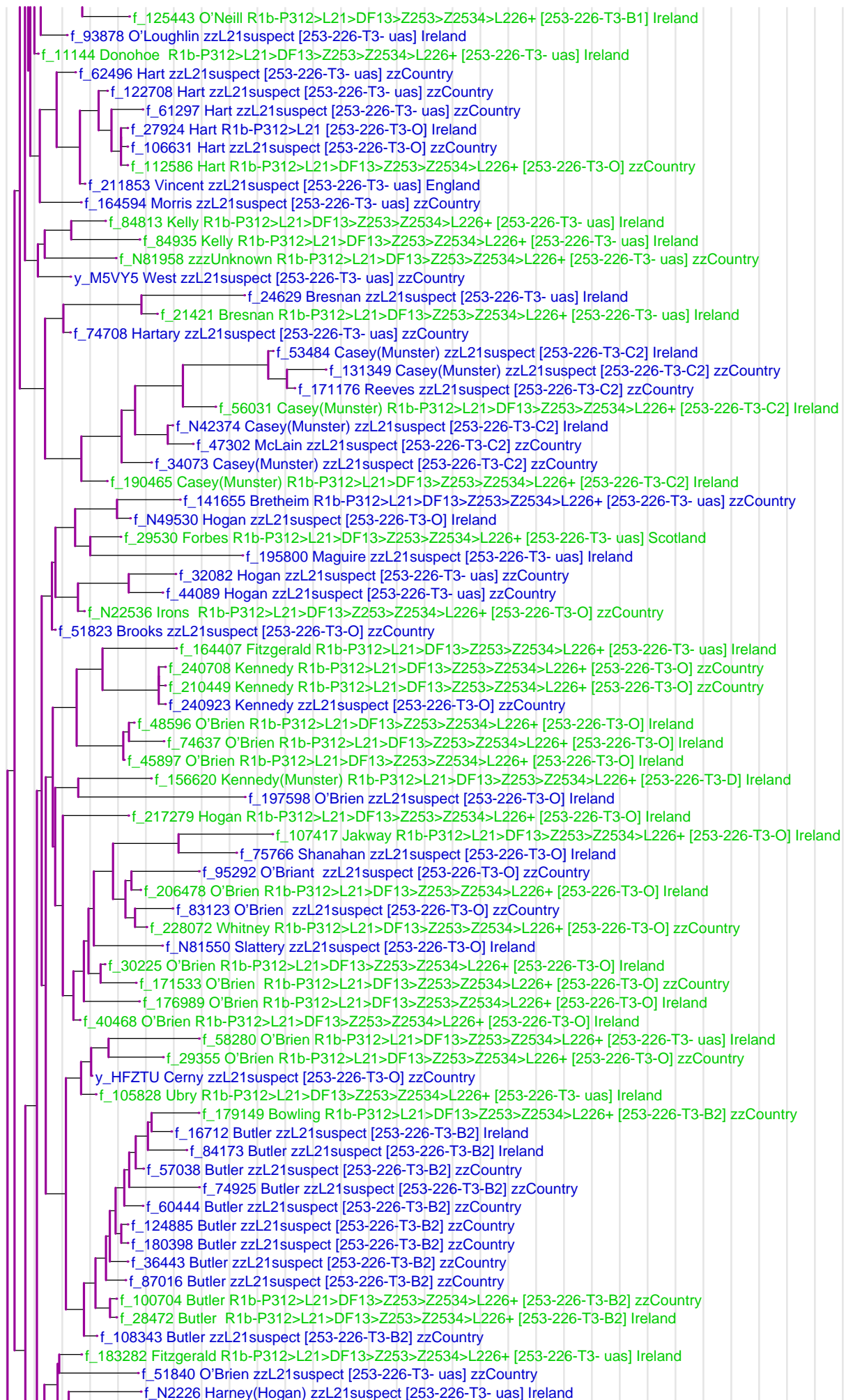


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
249	16683	1588	9.52%	49.97±5.01	1249.24±176.96



The vertical grey lines are separated 10 generations apart.

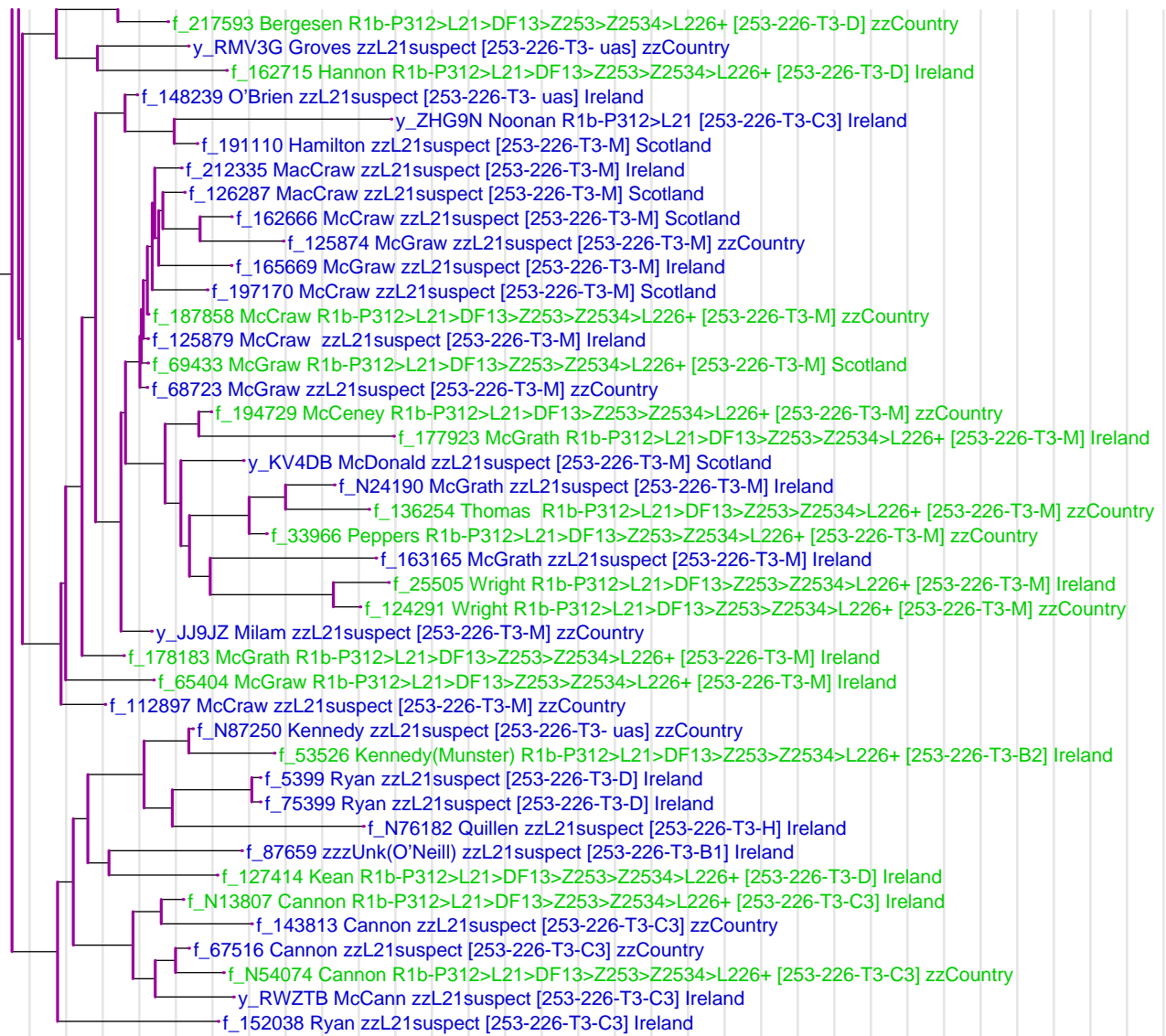


The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.





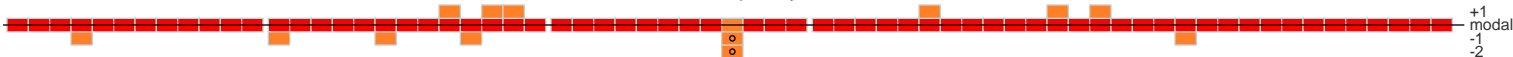
The vertical grey lines are separated 10 generations apart.

# R-L554

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

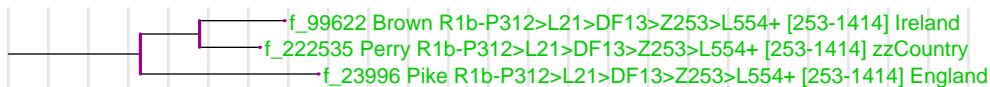
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565		
13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

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



## Age Analysis

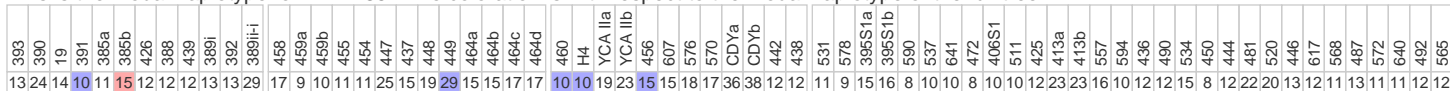
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	14	6.97%	36.08±4.47	902.049±143.558



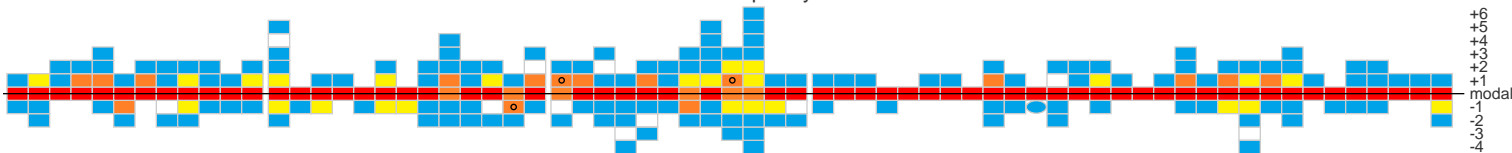
The vertical grey lines are separated 10 generations apart.

# R-Z2185

This is the modal haplotype for R-Z2185. The coloration is with respect to the modal haplotype of the full tree.



This is the marker distribution for R-Z2185. The color indicates the relative frequency of the alleles.



## Age Analysis

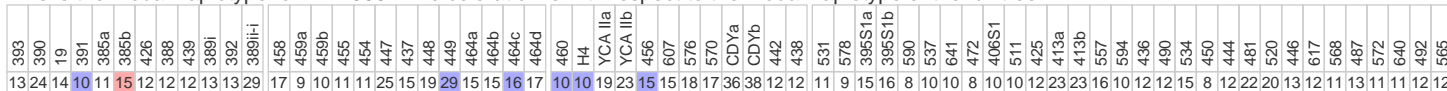
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
196	13132	2930	22.31%	125.50±12.61	3137.57±444.762



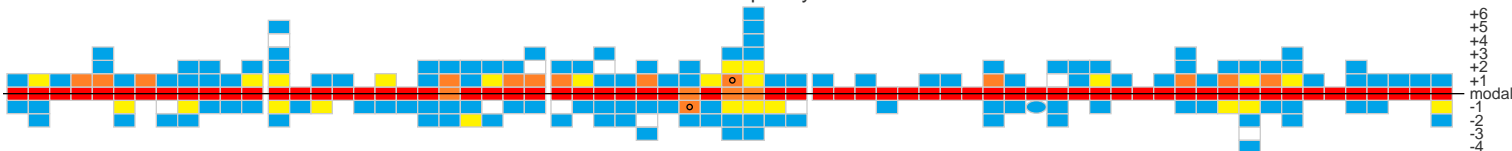
The vertical grey lines are separated 10 generations apart.

# R-L1066

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

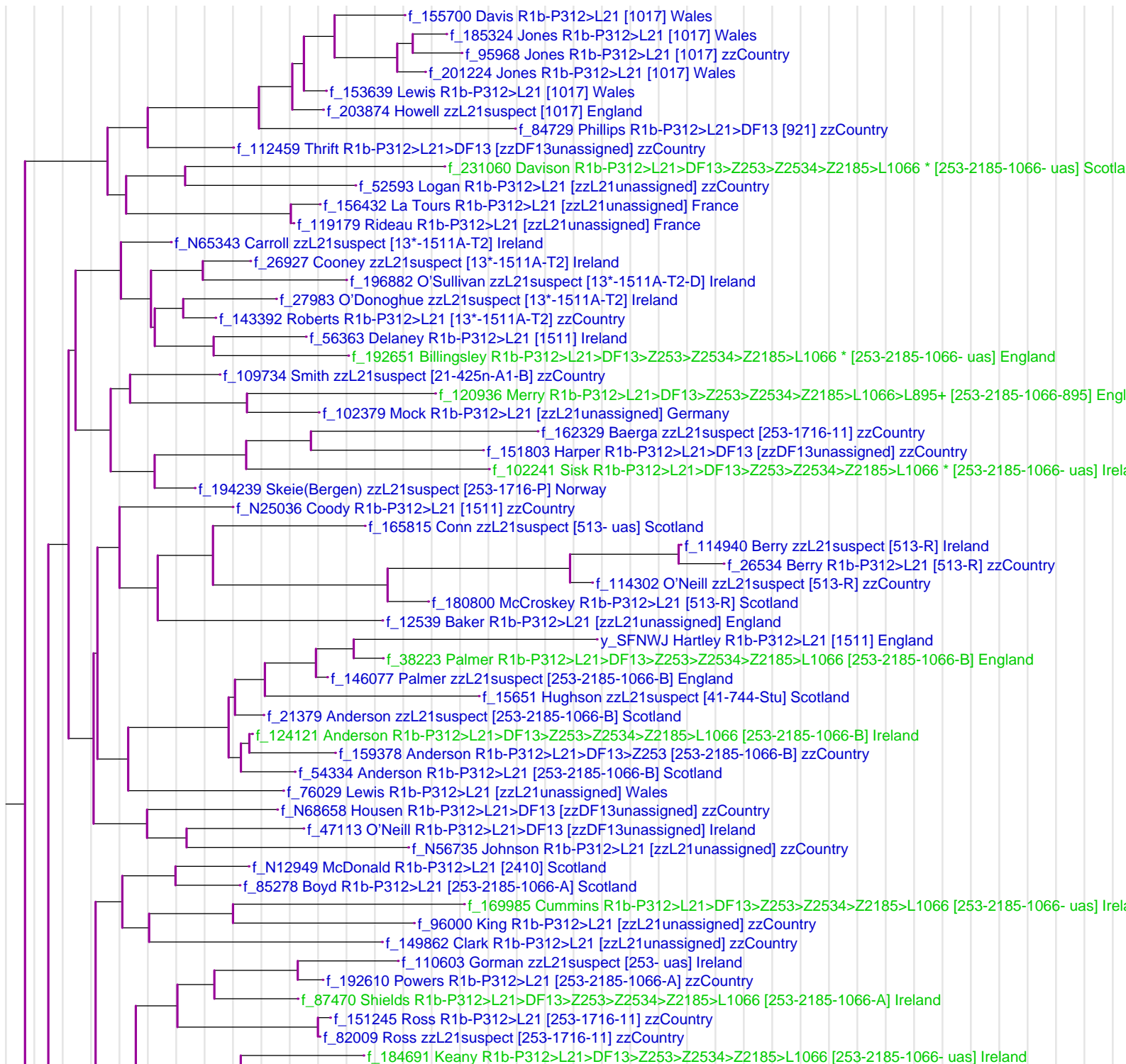


This is the marker distribution for R-L1066. The color indicates the relative frequency of the alleles.

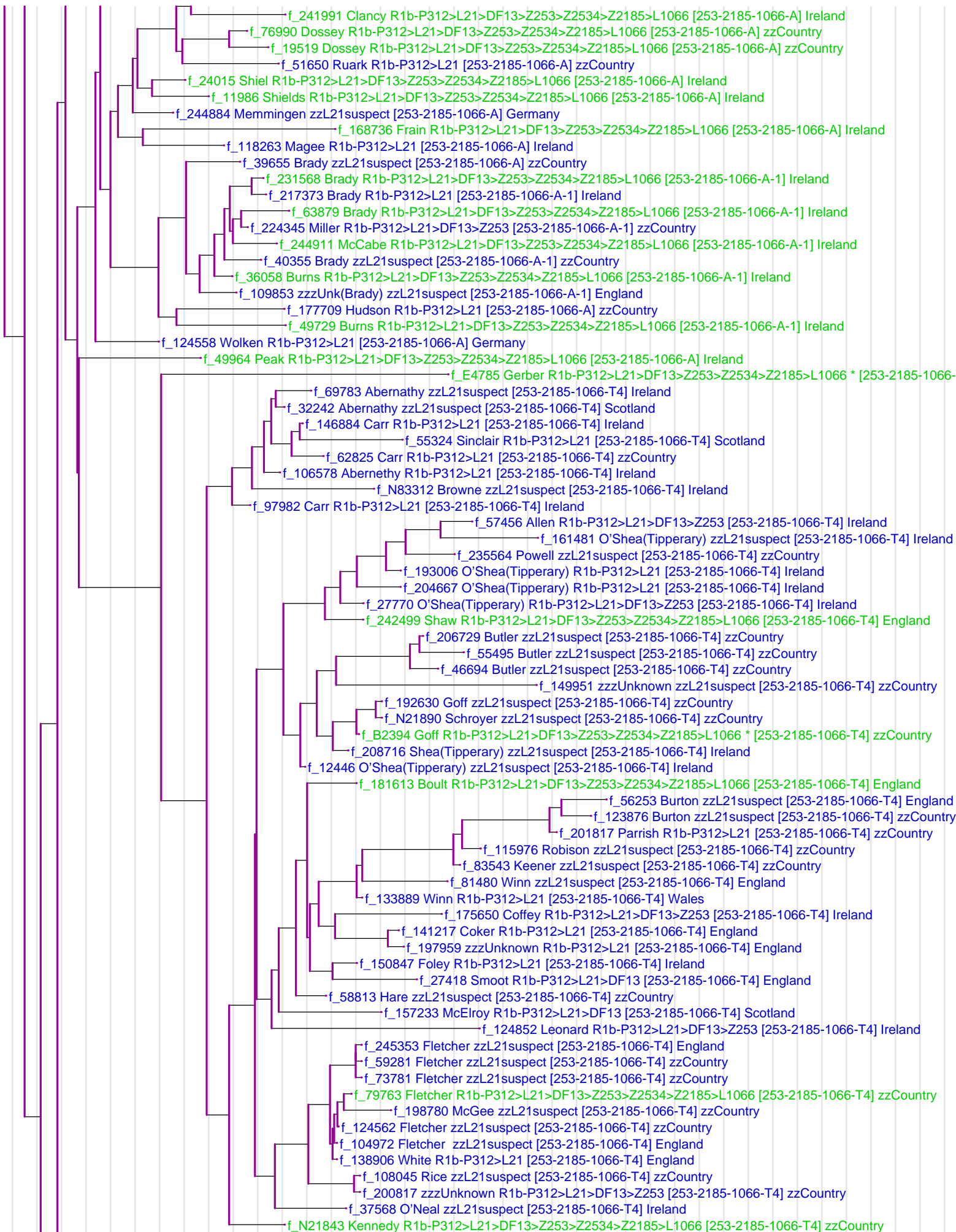


## Age Analysis

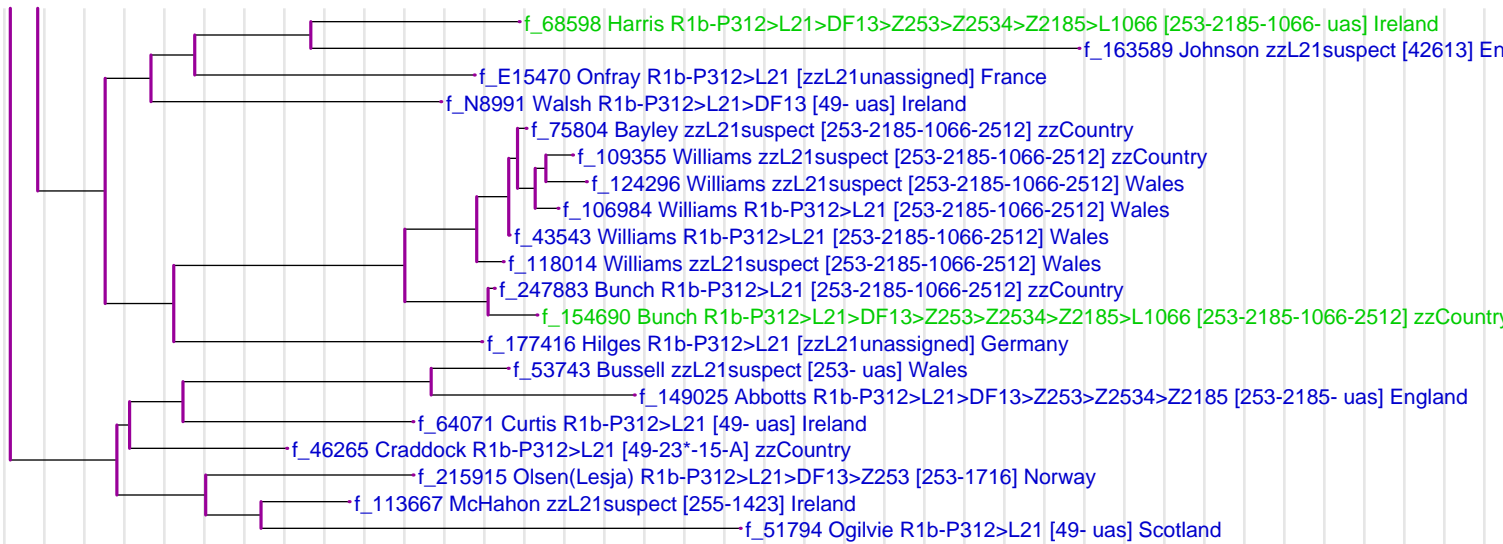
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
151	10117	2101	20.77%	115.82±11.65	2895.45±410.71



The vertical grey lines are separated 10 generations apart.



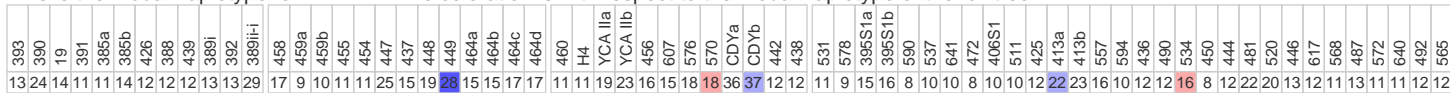
The vertical grey lines are separated 10 generations apart.



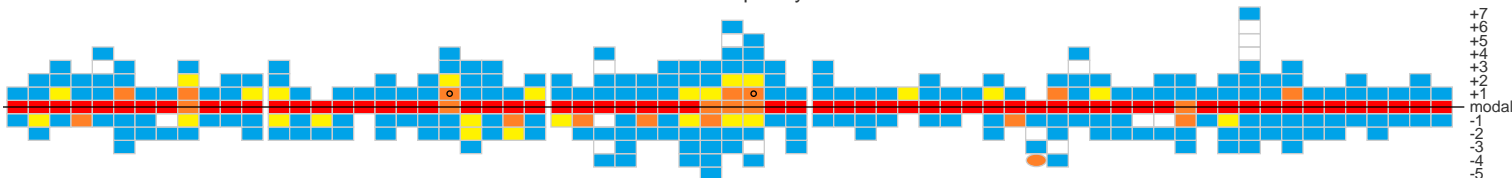
The vertical grey lines are separated 10 generations apart.

# R-DF21

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



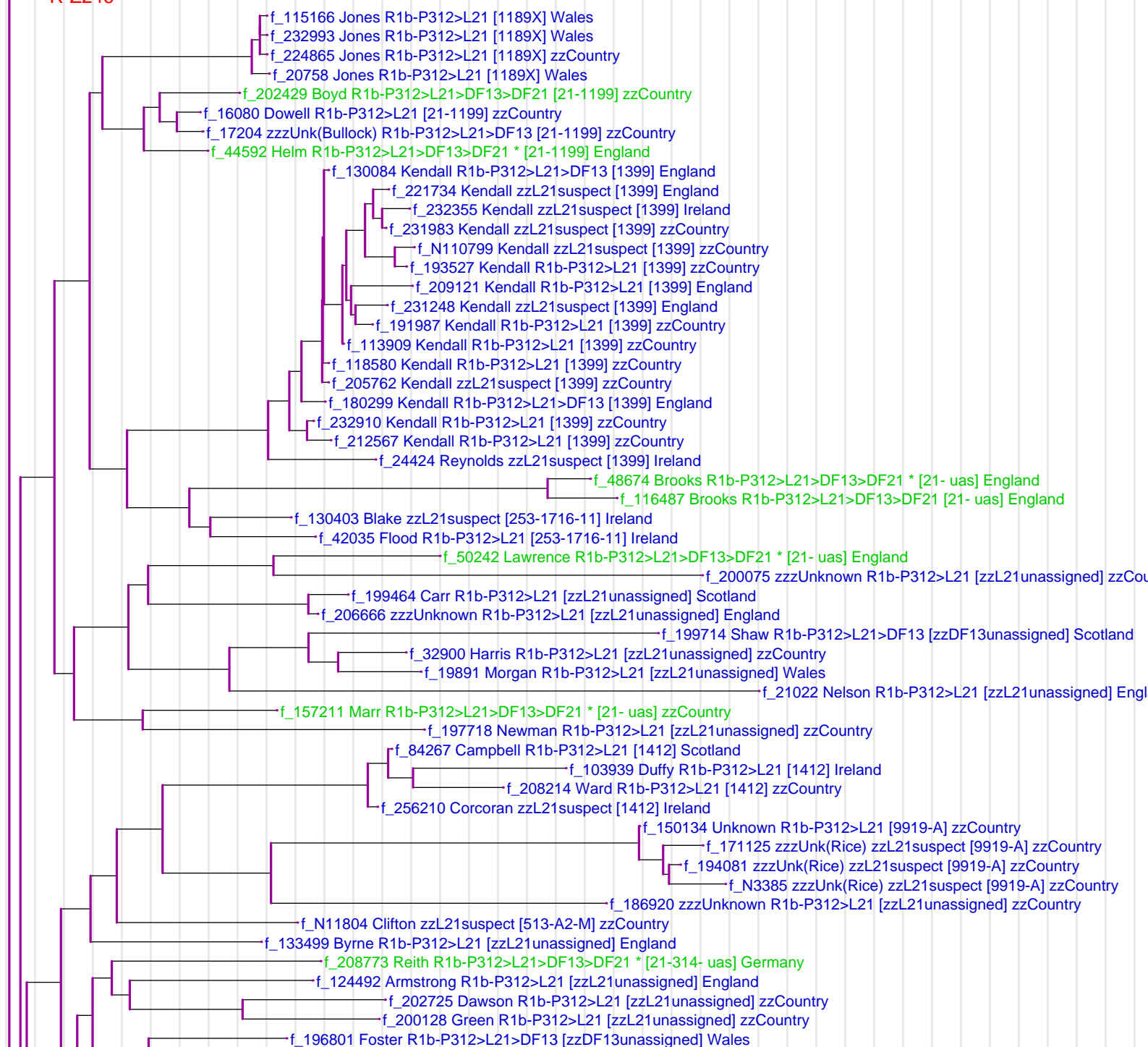
This is the marker distribution for R-DF21. The color indicates the relative frequency of the alleles.



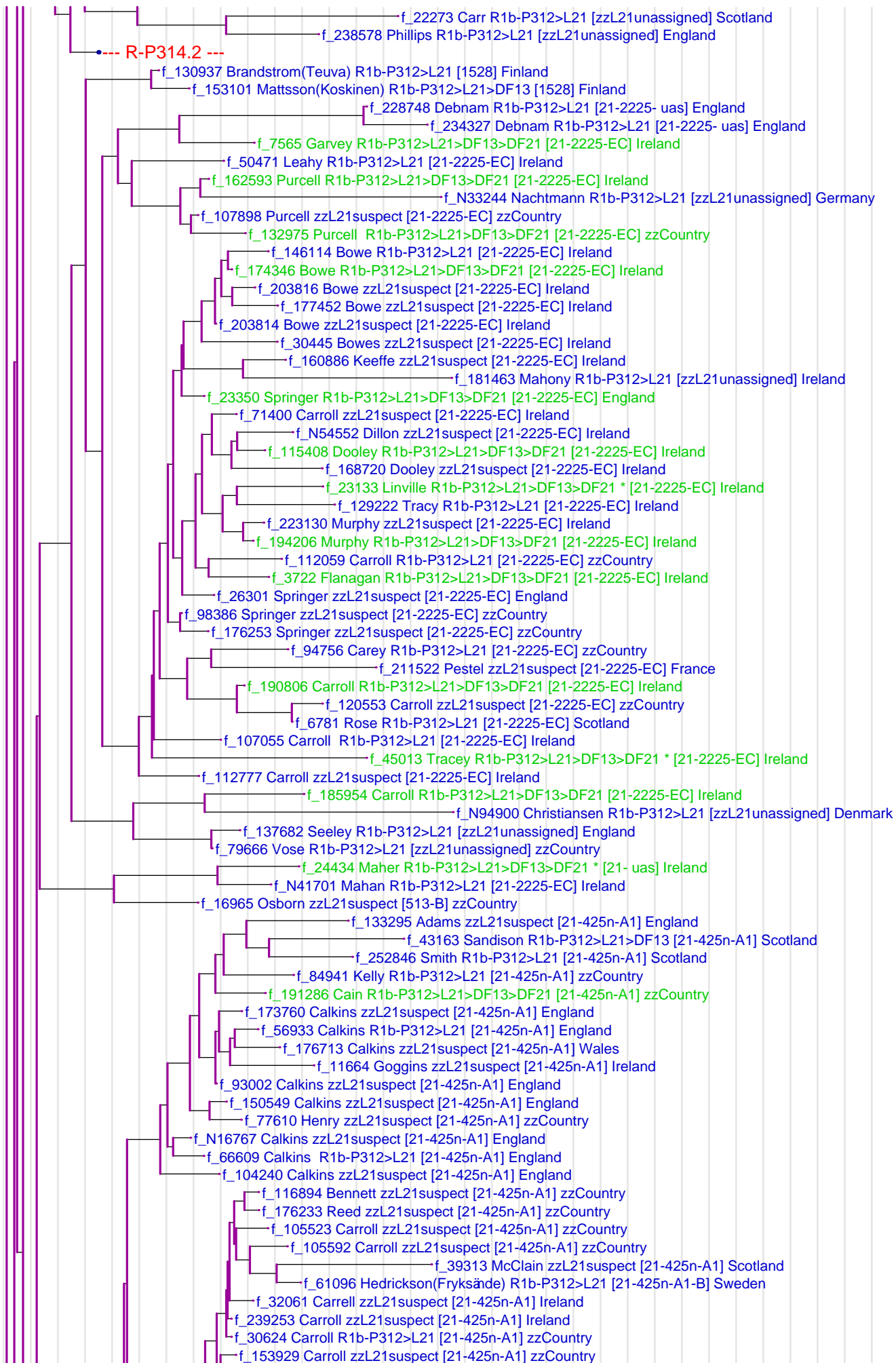
## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
864	57888	12485	21.57%	120.82±12.09	3020.39±427.375

## R-Z246 ---

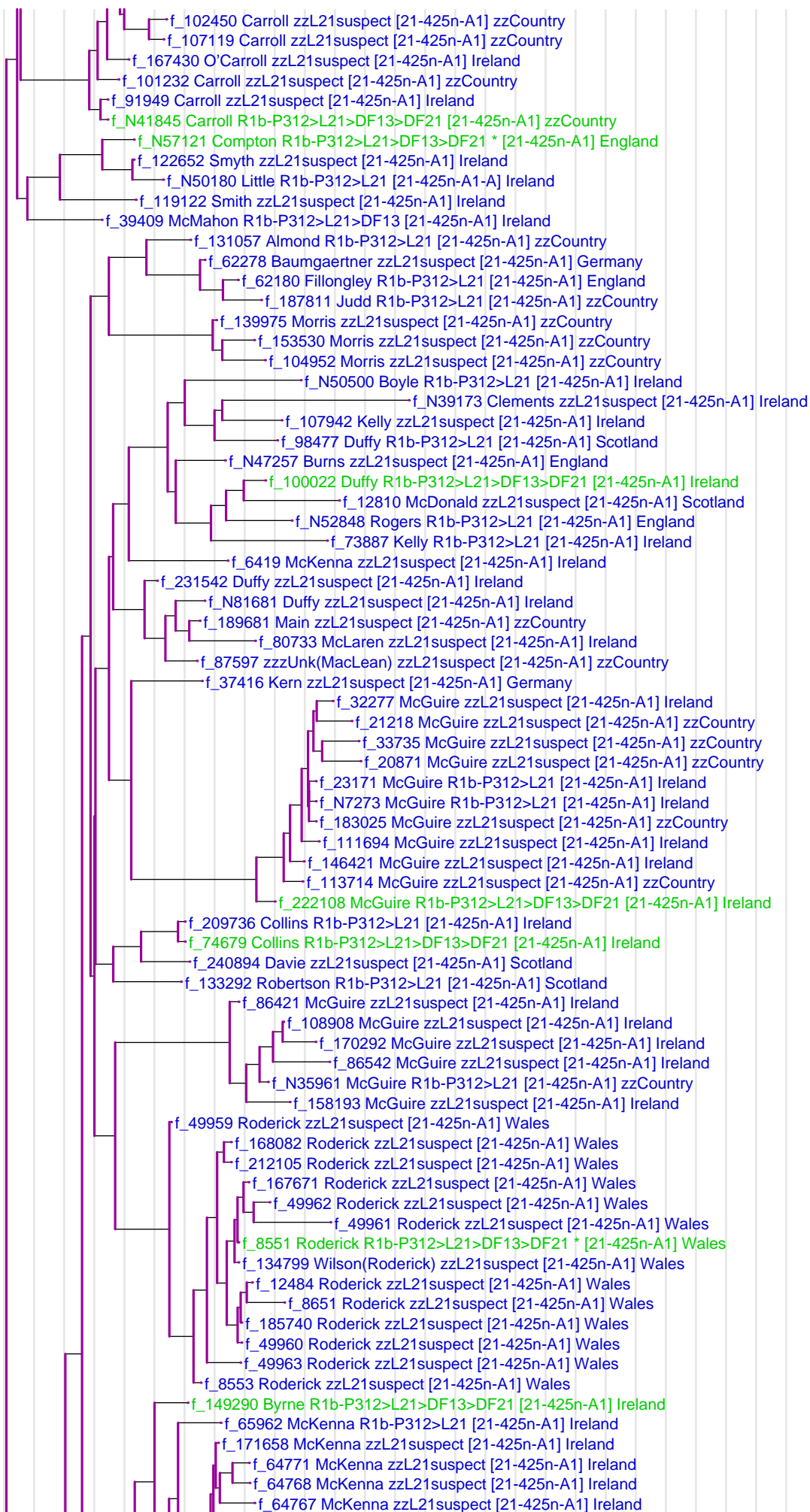


The vertical grey lines are separated 10 generations apart.

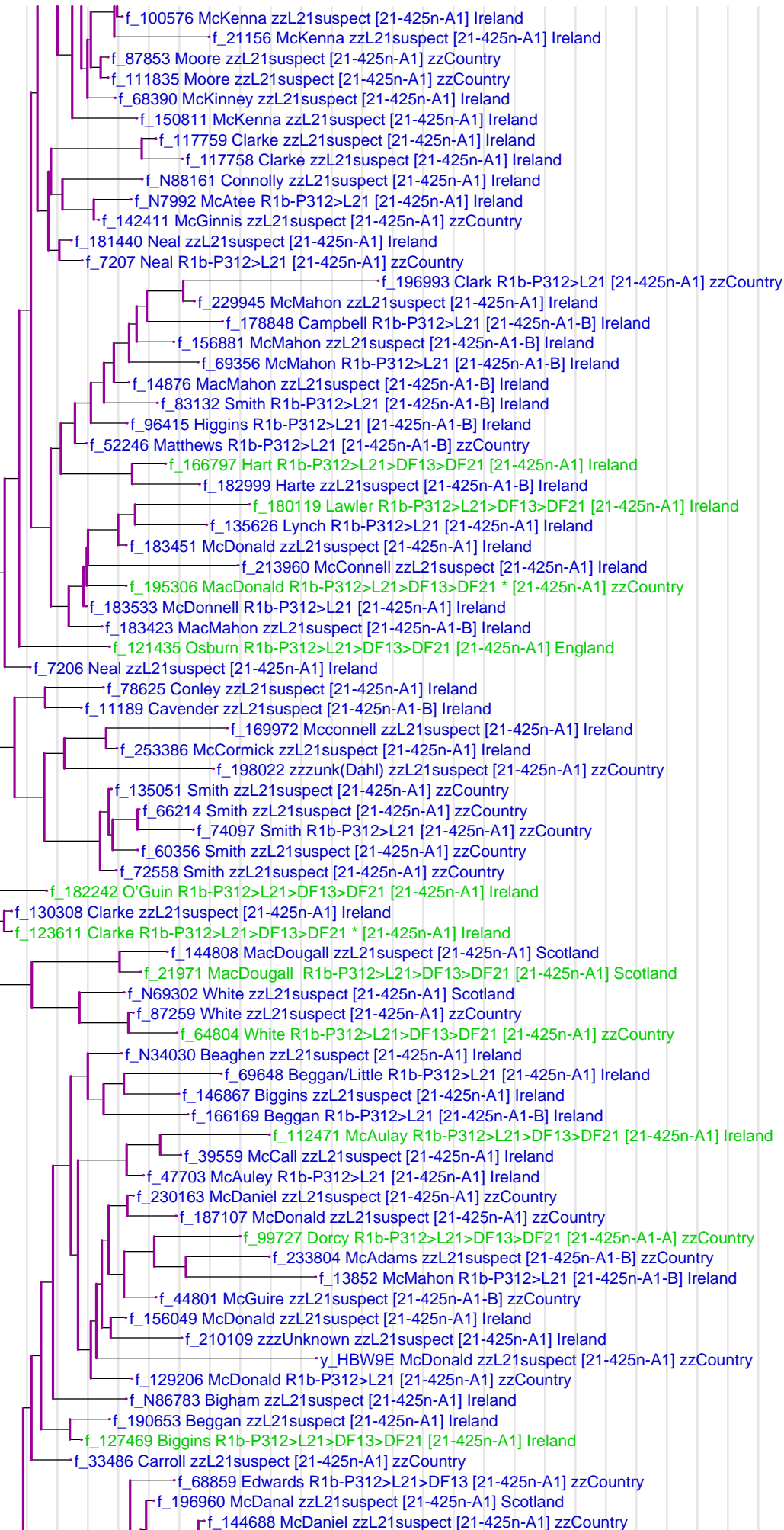


The vertical grey lines are separated 10 generations apart.

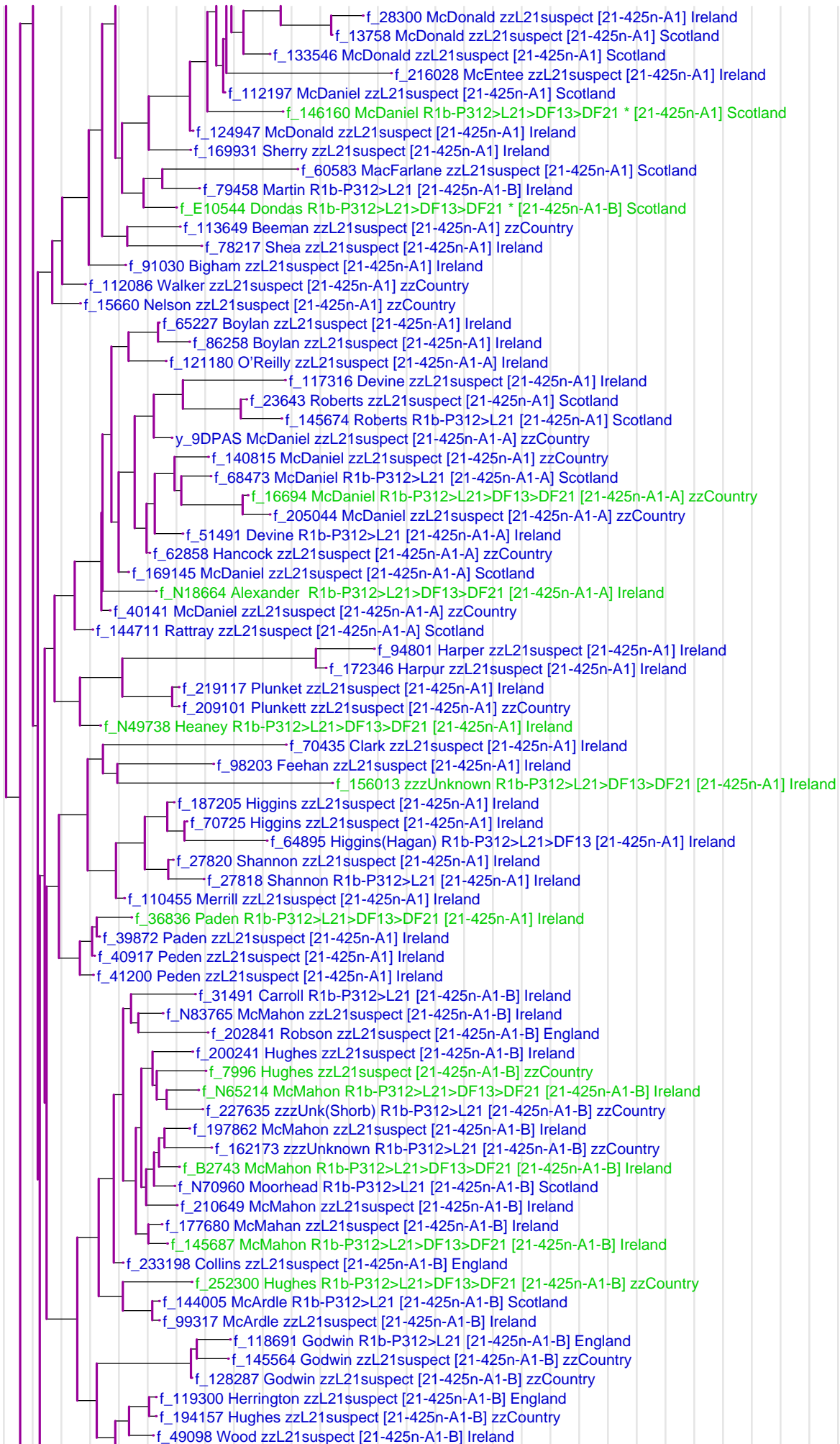




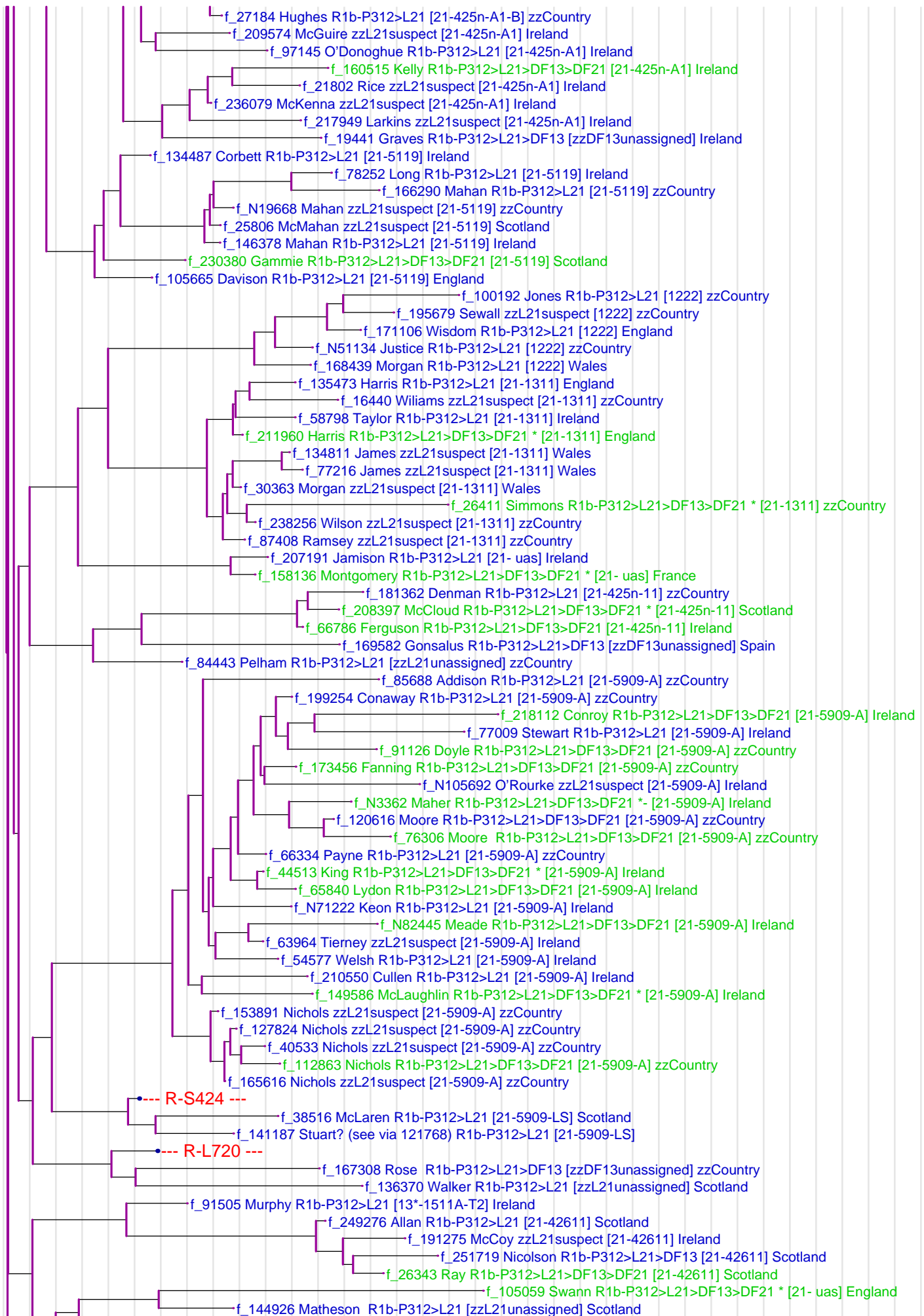
The vertical grey lines are separated 10 generations apart.



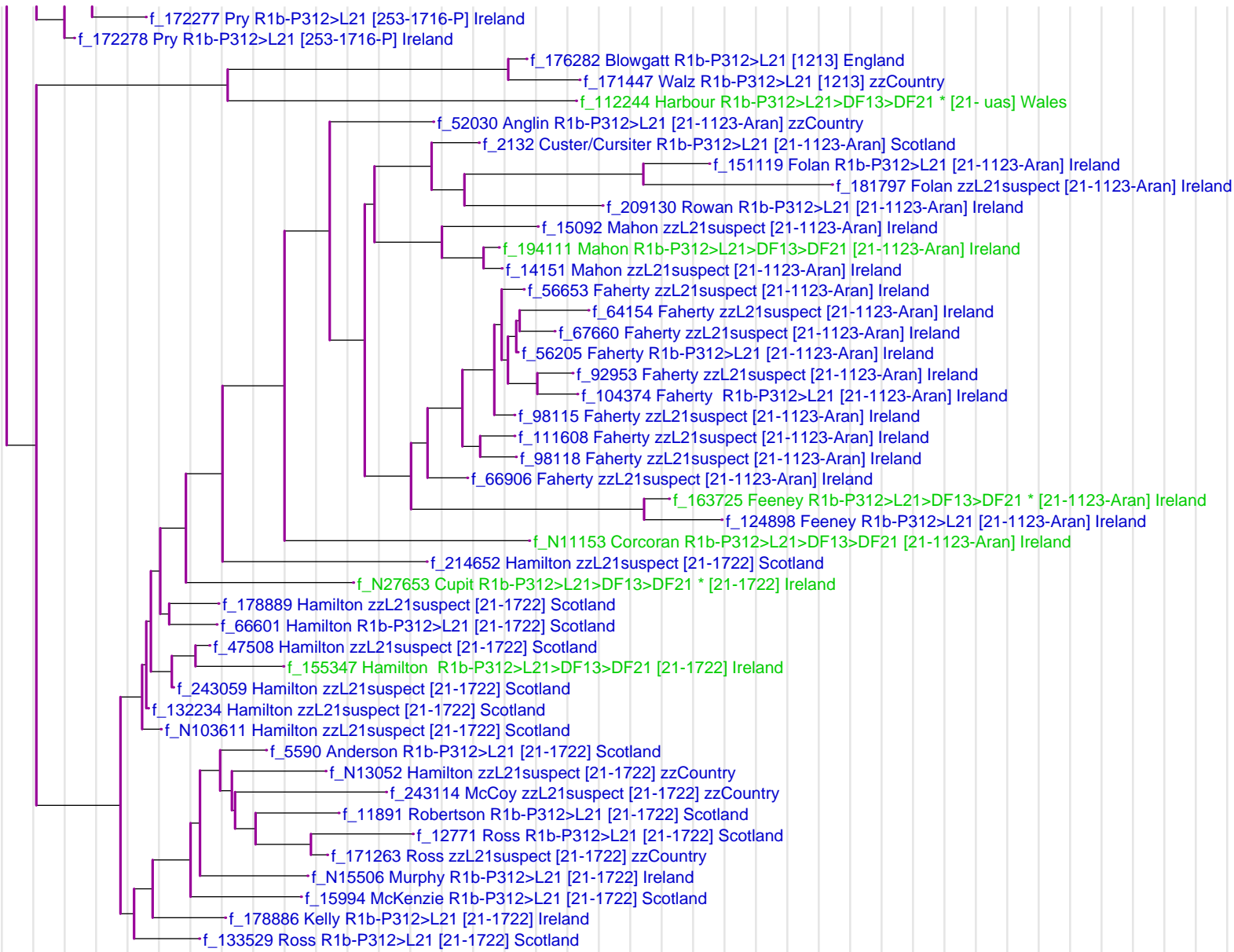
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



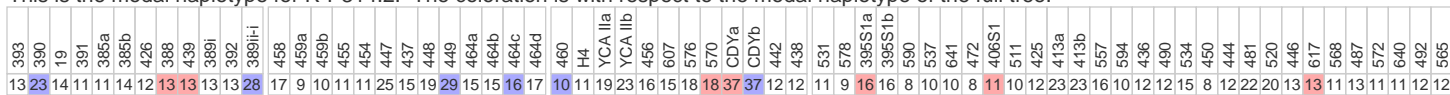
The vertical grey lines are separated 10 generations apart.



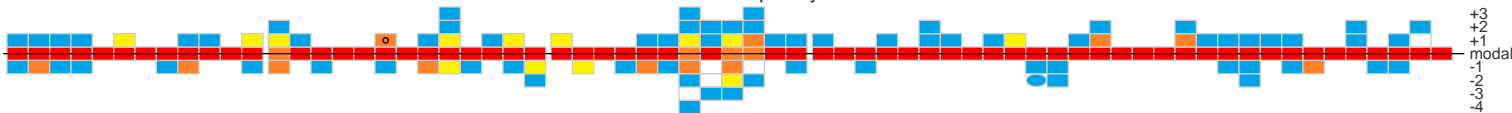
The vertical grey lines are separated 10 generations apart.

# R-P314.2

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

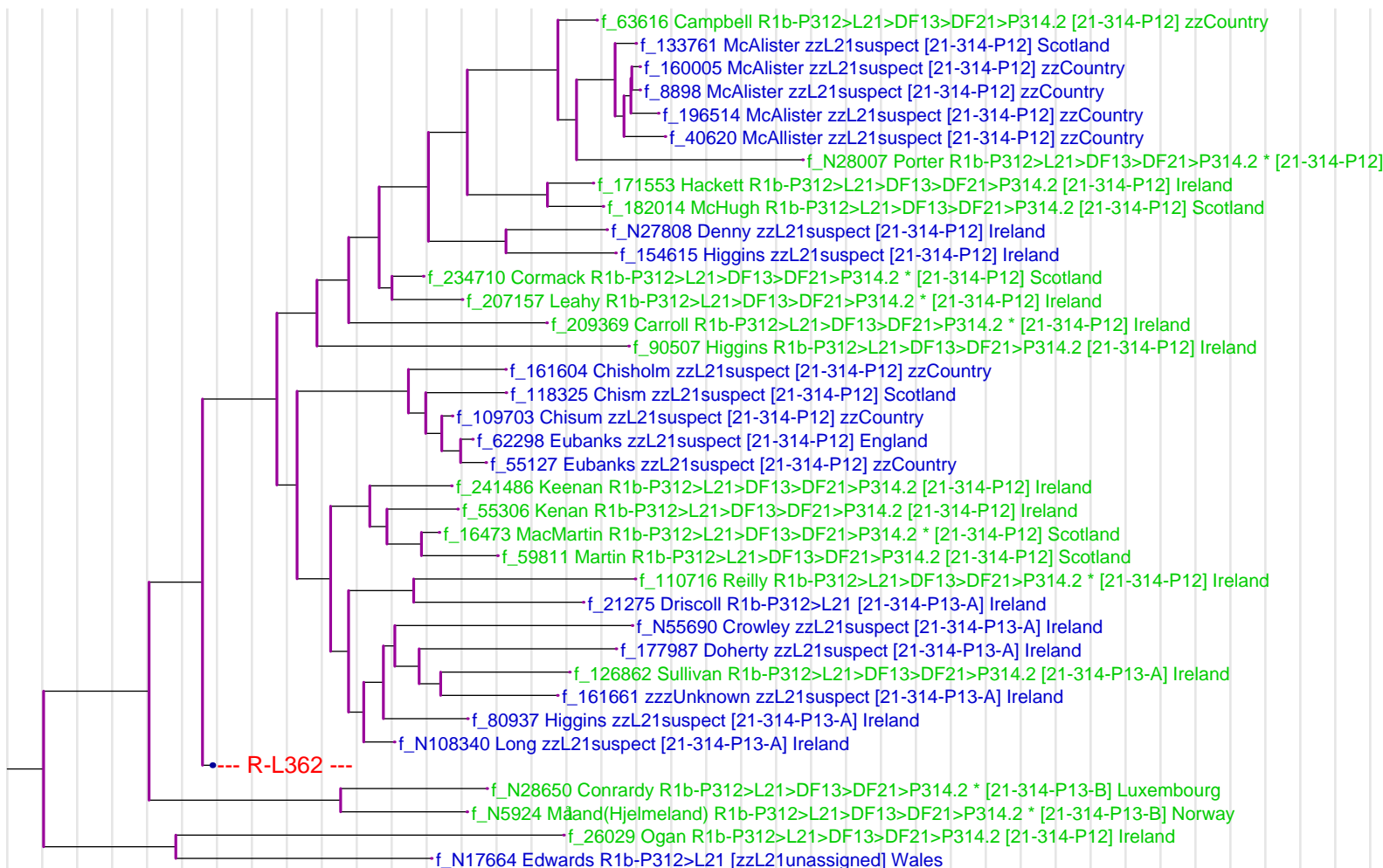


This is the marker distribution for R-P314.2. The color indicates the relative frequency of the alleles.



## Age Analysis

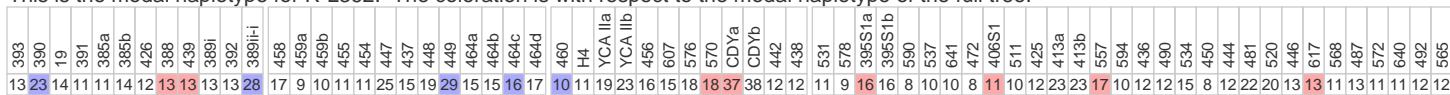
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
59	3953	560	14.17%	76.22±7.73	1905.56±271.434



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)
23	1541	121	7.85%	40.86±4.23	1021.59±146.985



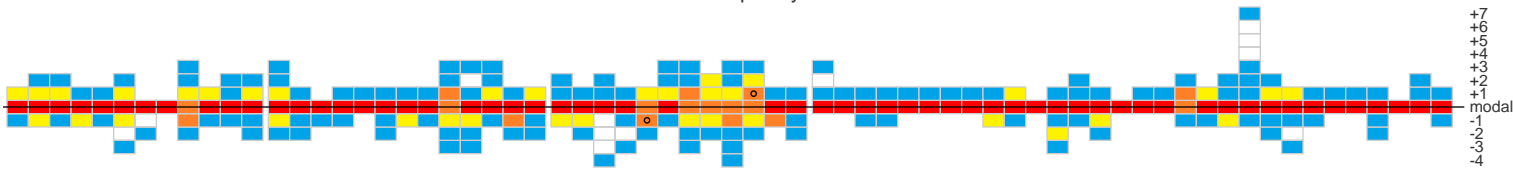
The vertical grey lines are separated 10 generations apart.

# R-Z246

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

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	13	13	29	17	9	10	11	11	25	15	19	19	29	15	15	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	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

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)
164	10988	2280	20.75%	115.71±11.64	2892.79±410.235

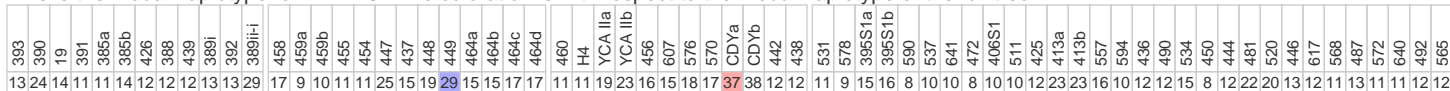


The vertical grey lines are separated 10 generations apart.

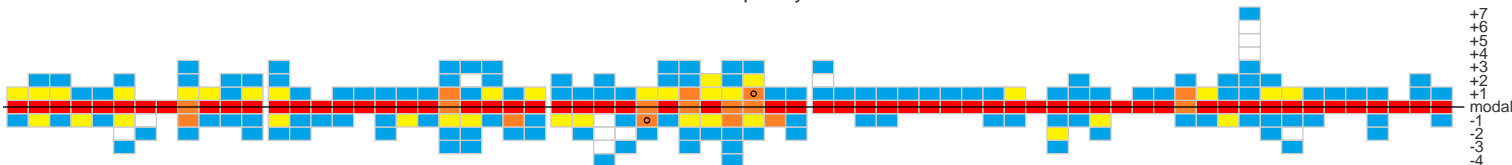


# R-DF25

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

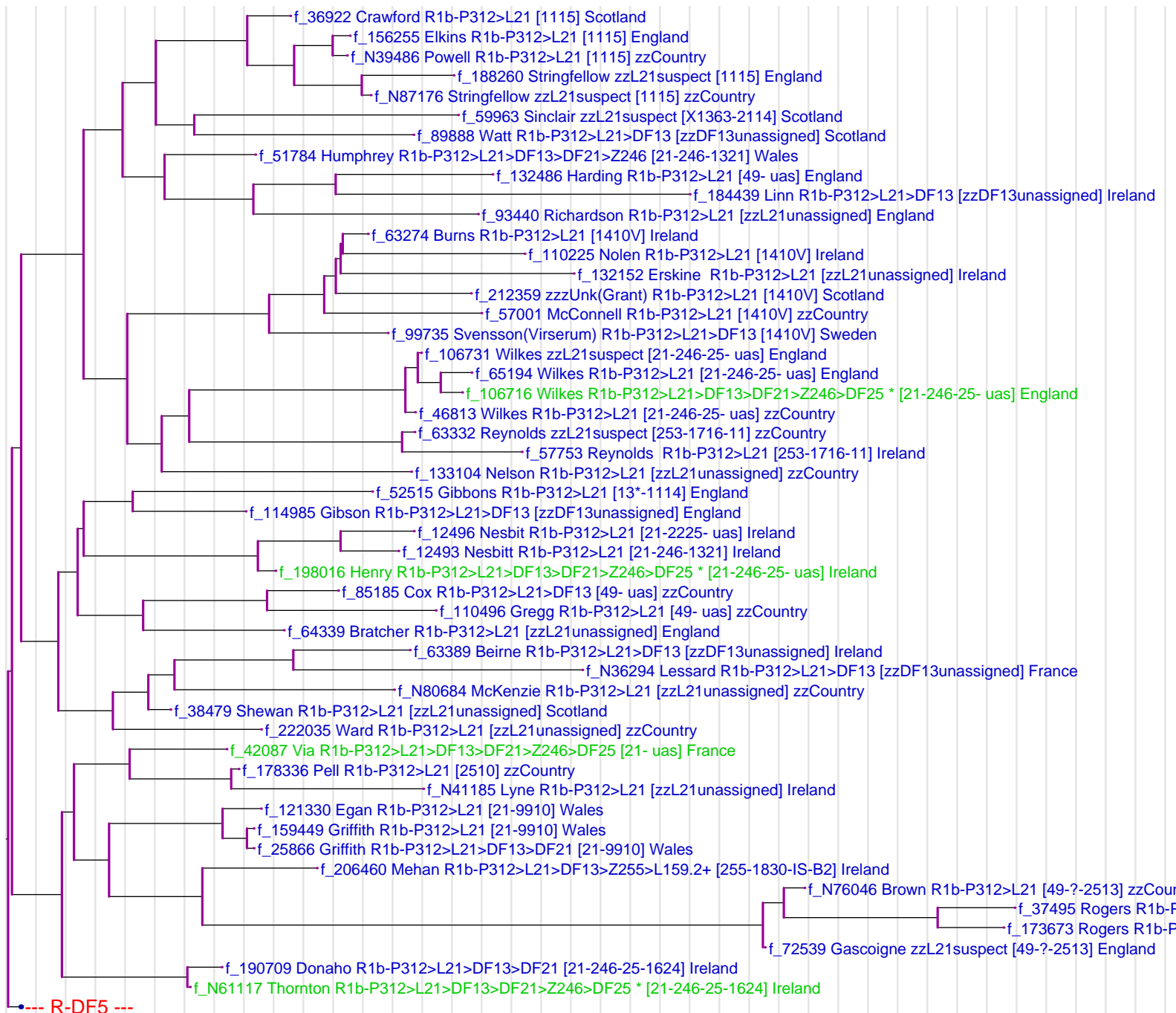


This is the marker distribution for R-DF25. The color indicates the relative frequency of the alleles.



## Age Analysis

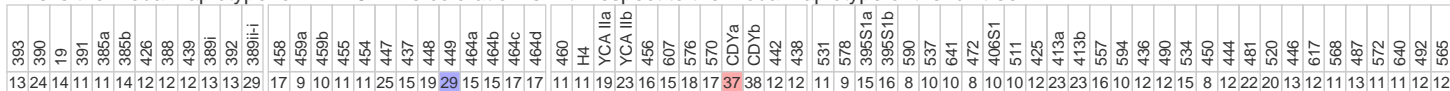
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
161	10787	2239	20.76%	115.75±11.64	2893.81±410.401



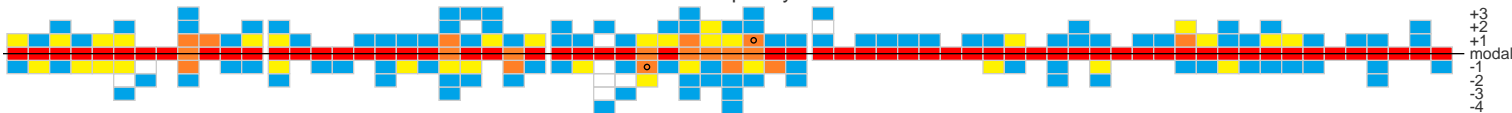
The vertical grey lines are separated 10 generations apart.

# R-DF5

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

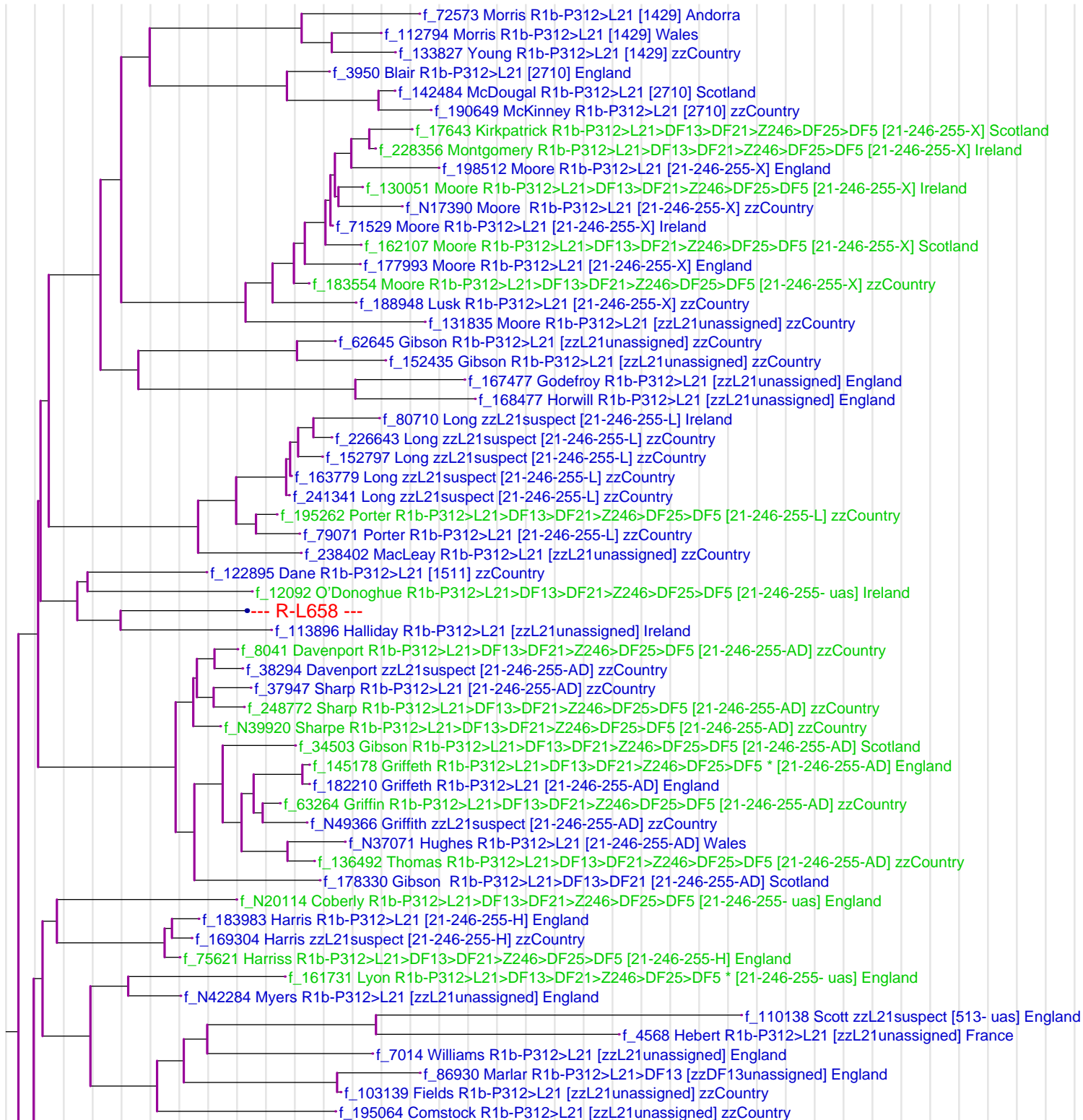


This is the marker distribution for R-DF5. The color indicates the relative frequency of the alleles.

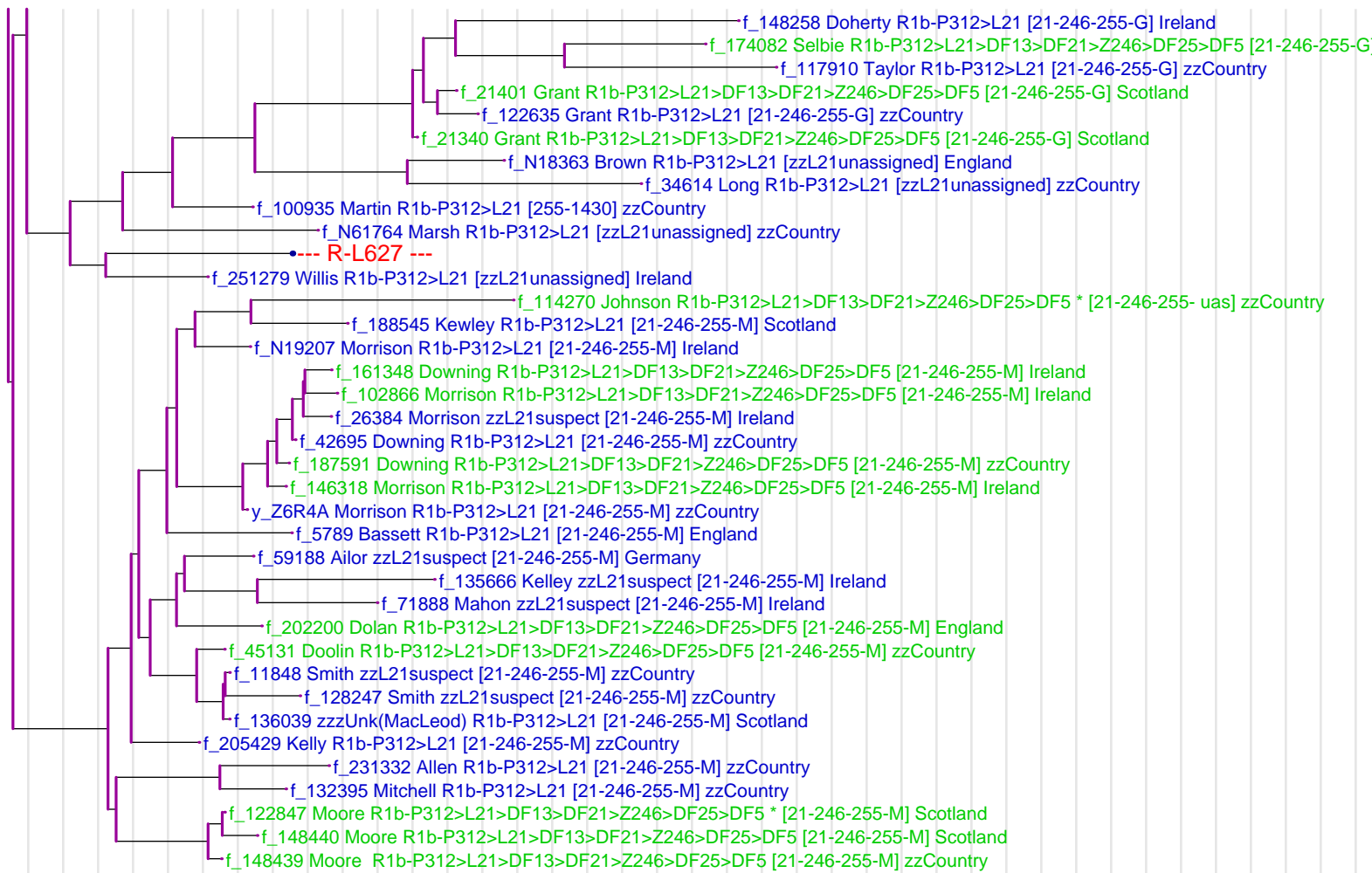


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
111	7437	1468	19.74%	109.46±11.03	2736.61±388.582



The vertical grey lines are separated 10 generations apart.



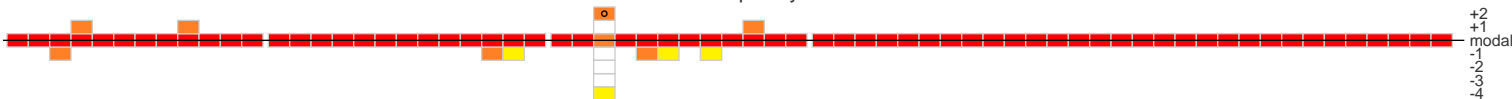
The vertical grey lines are separated 10 generations apart.

# R-L627

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

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	15	10	11	15	12	12	12	14	13	30	17	9	10	11	11	25	15	19	29	15	16	16	16	10	11	19	23	17	15	18	17	36	37	12	12	12	9	16	16	8	8	10	10	8	10	10	10	12	23	23	16	10	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

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



## Age Analysis

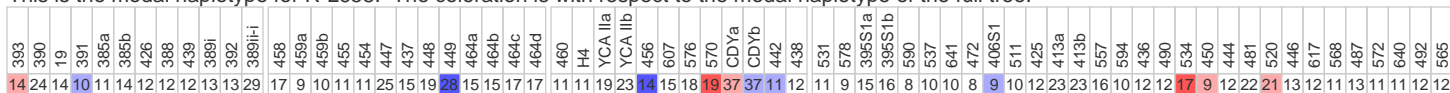
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	21	6.27%	32.36±3.71	808.928±123.146



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

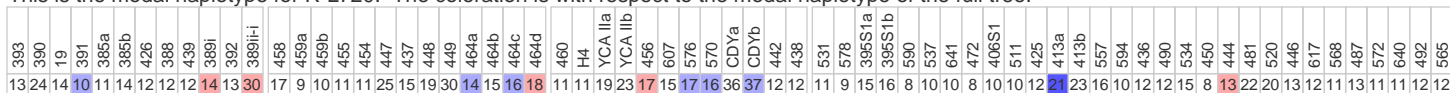
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
13	871	41	4.71%	24.10±2.55	602.584±87.7433



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

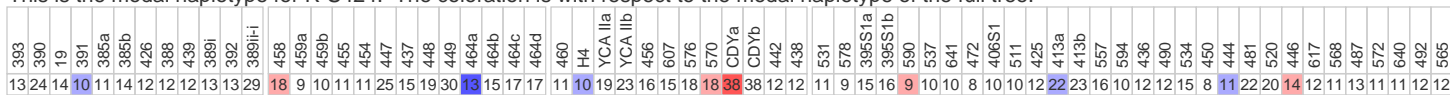
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	36	8.96%	46.87±5.29	1171.84±176.615



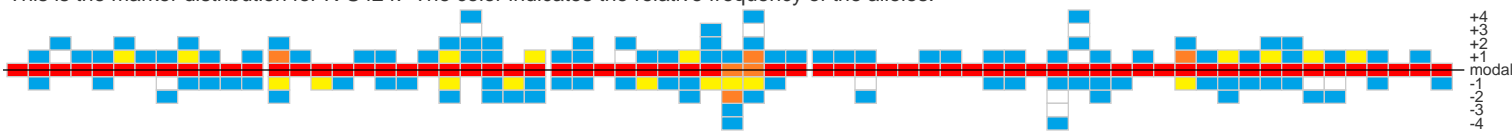
The vertical grey lines are separated 10 generations apart.

# R-S424

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

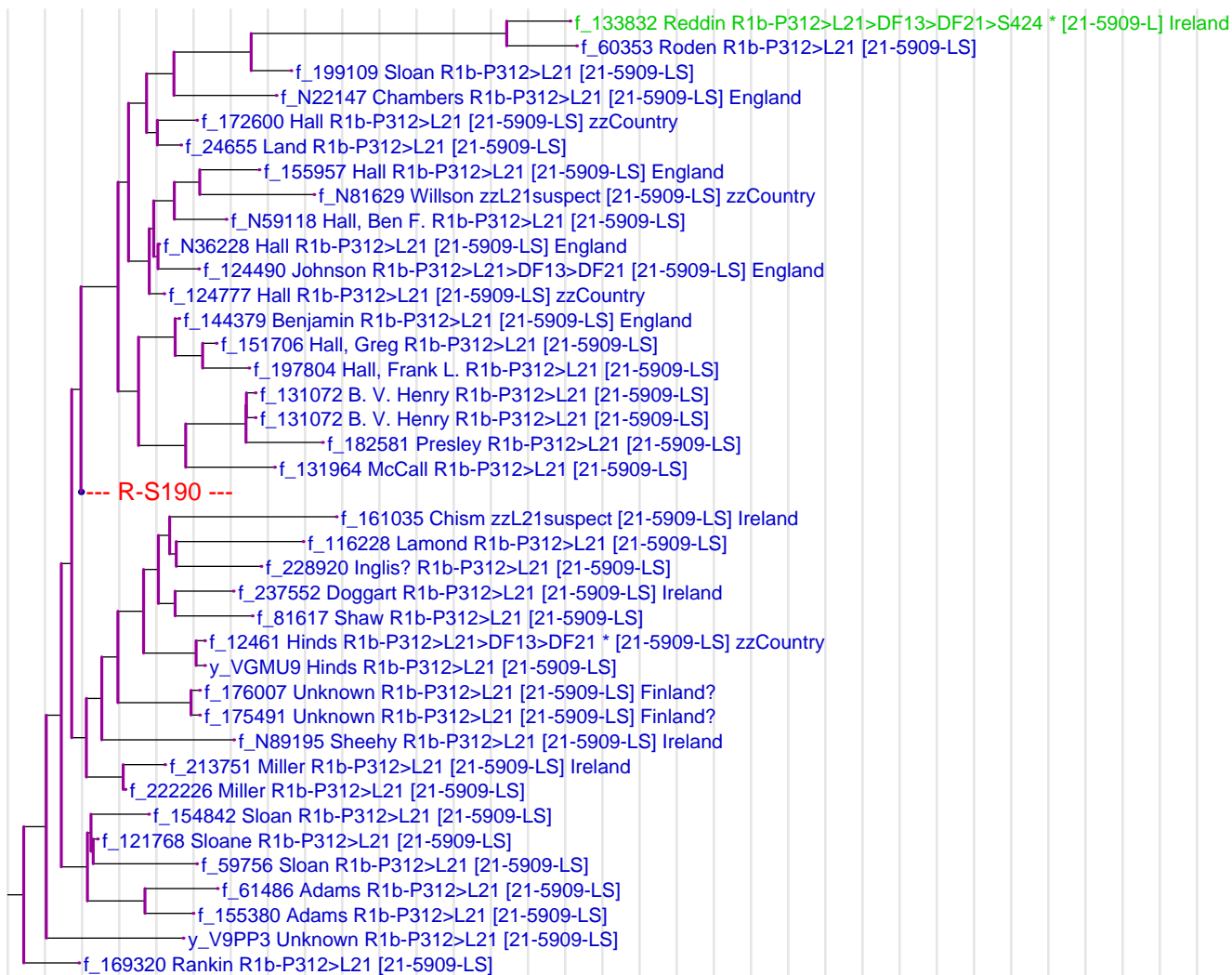


This is the marker distribution for R-S424. The color indicates the relative frequency of the alleles.



## Age Analysis

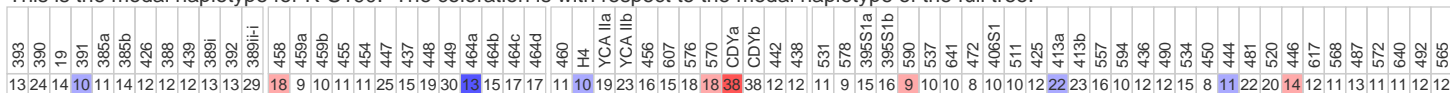
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
164	10988	1095	9.97%	52.44±5.27	1310.94±185.86



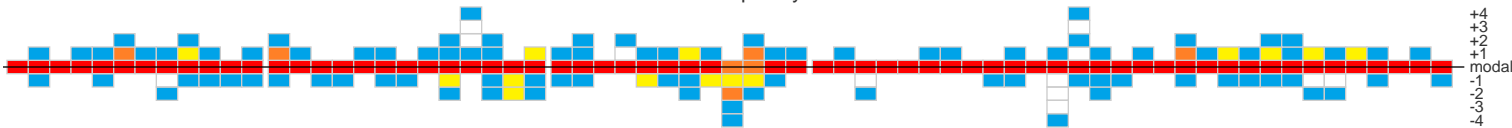
The vertical grey lines are separated 10 generations apart.

# R-S190

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

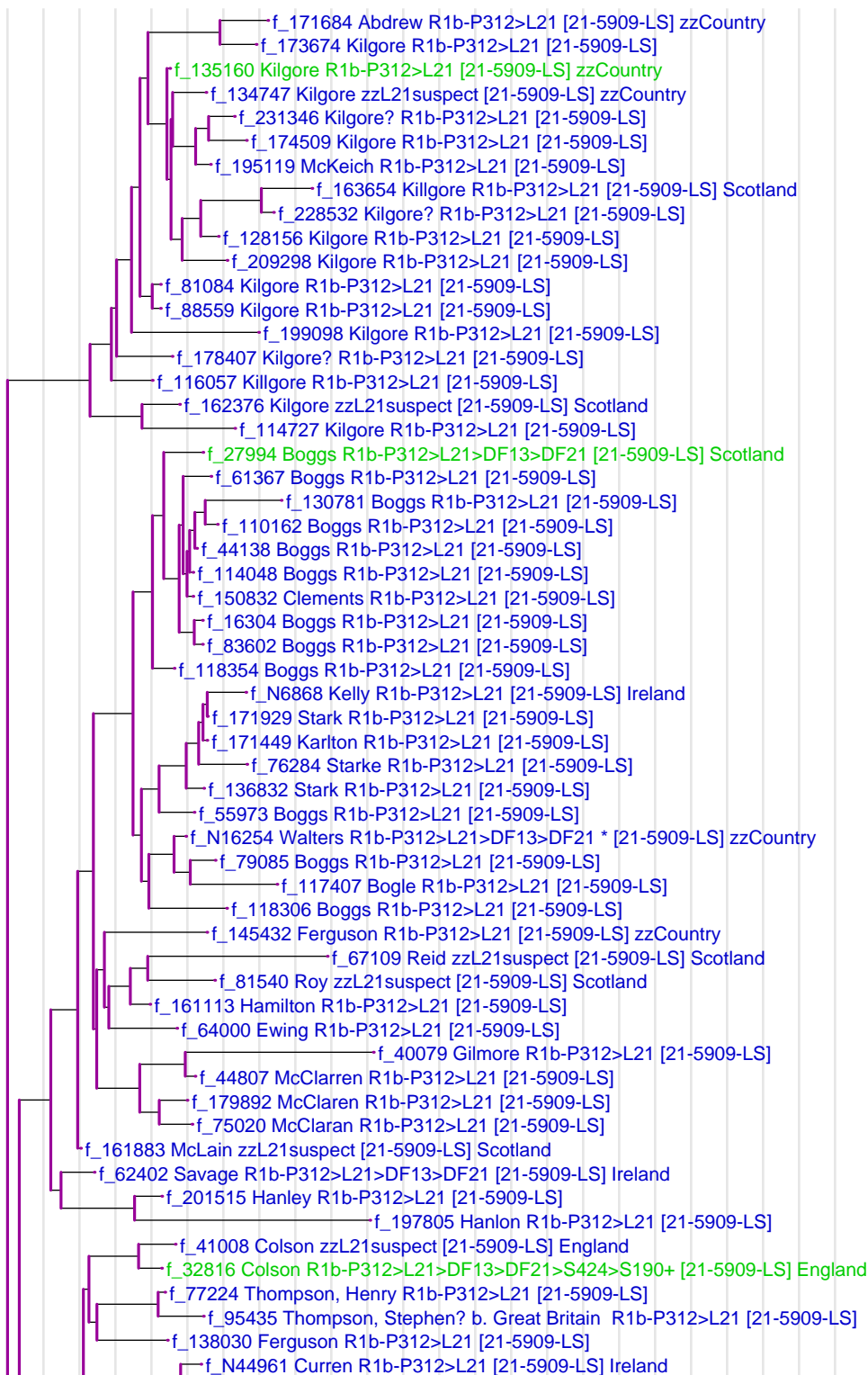


This is the marker distribution for R-S190. The color indicates the relative frequency of the alleles.



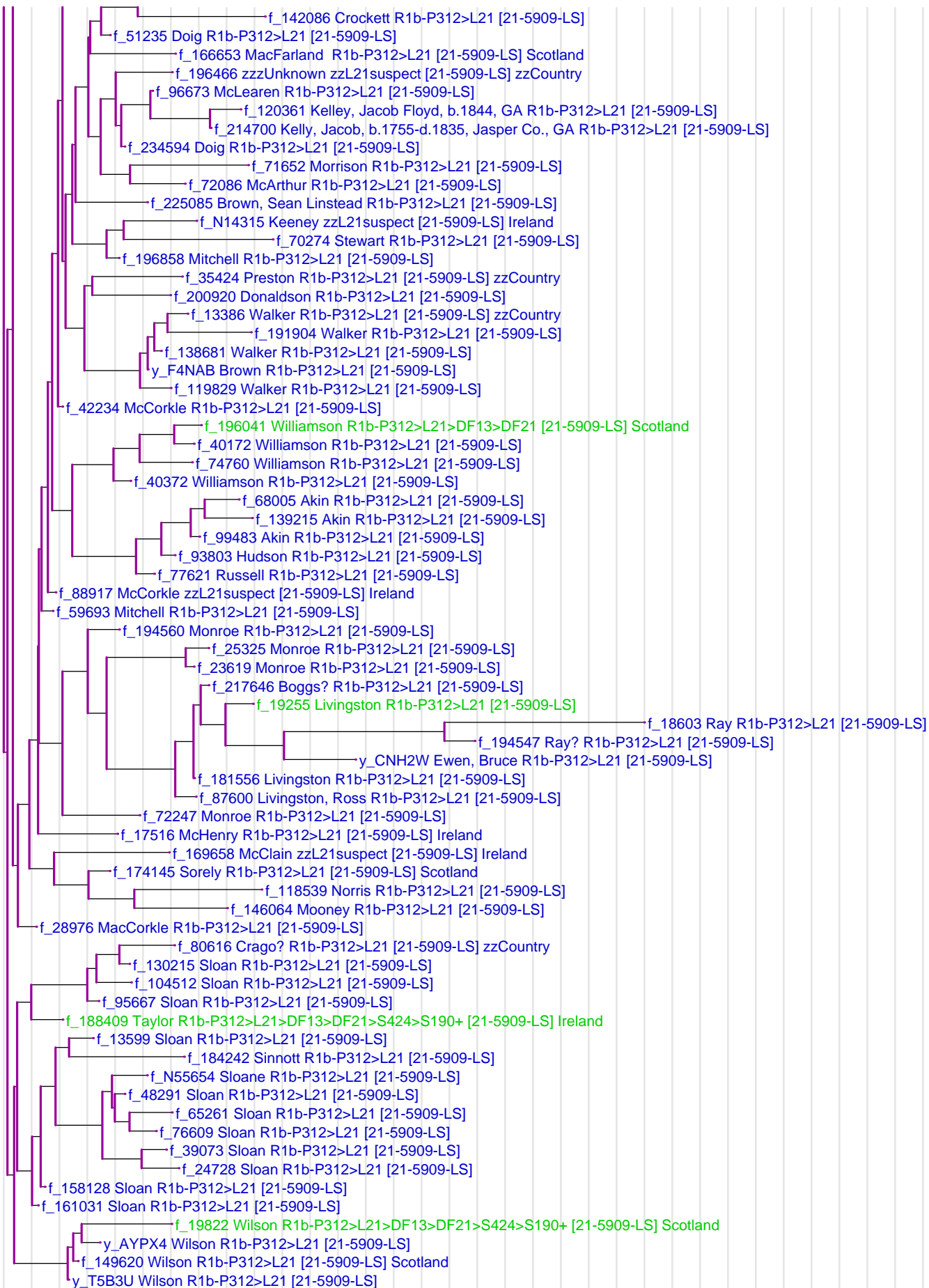
## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
126	8442	844	10.00%	52.62±5.30	1315.4±186.633



The vertical grey lines are separated 10 generations apart.

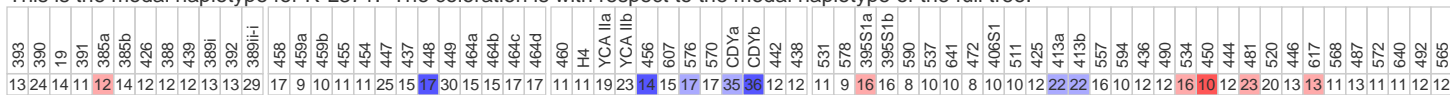




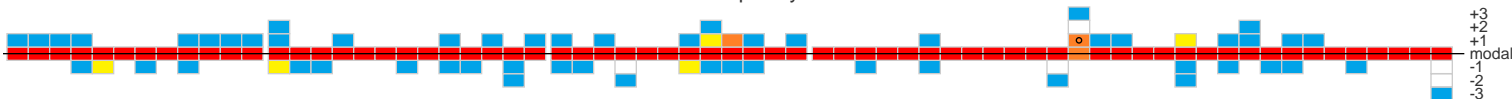
The vertical grey lines are separated 10 generations apart.

# R-L371

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

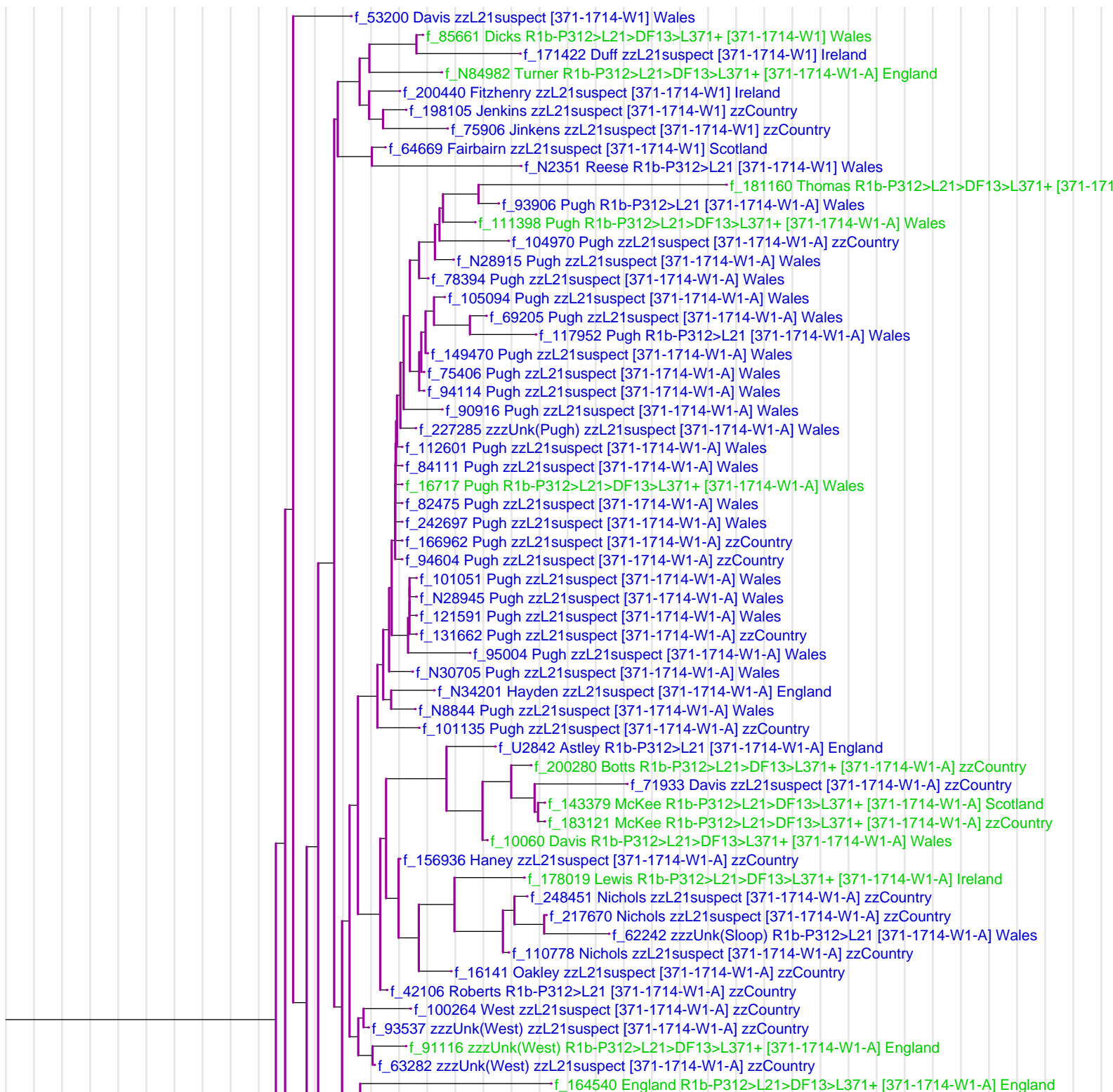


This is the marker distribution for R-L371. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
64	4288	247	5.76%	29.66±3.00	741.379±105.492

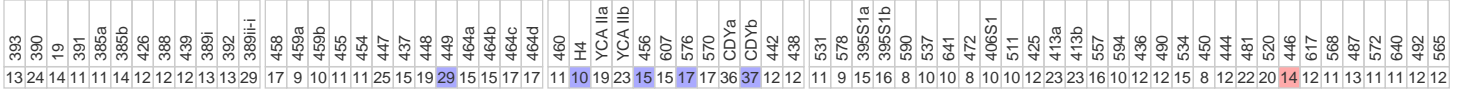


The vertical grey lines are separated 10 generations apart.

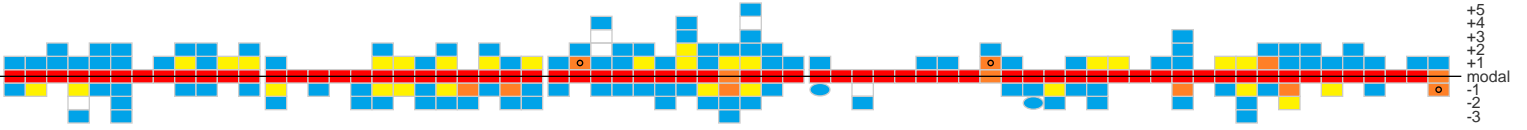
f\_67937 zzzUnk(Williams) zzL21suspect [371-1714-W1-A] Wales  
f\_126795 Dixon zzL21suspect [371-1714-W1-A] zzCountry  
f\_39814 Matthews zzL21suspect [371-1714-W1-A] zzCountry  
f\_36039 Gough R1b-P312>L21>DF13>L371+ [371-1714-W1-A] Ireland  
f\_190007 Griffith R1b-P312>L21>DF13>L371+ [371-1714-W1] zzCountry  
f\_193782 Griffith R1b-P312>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.

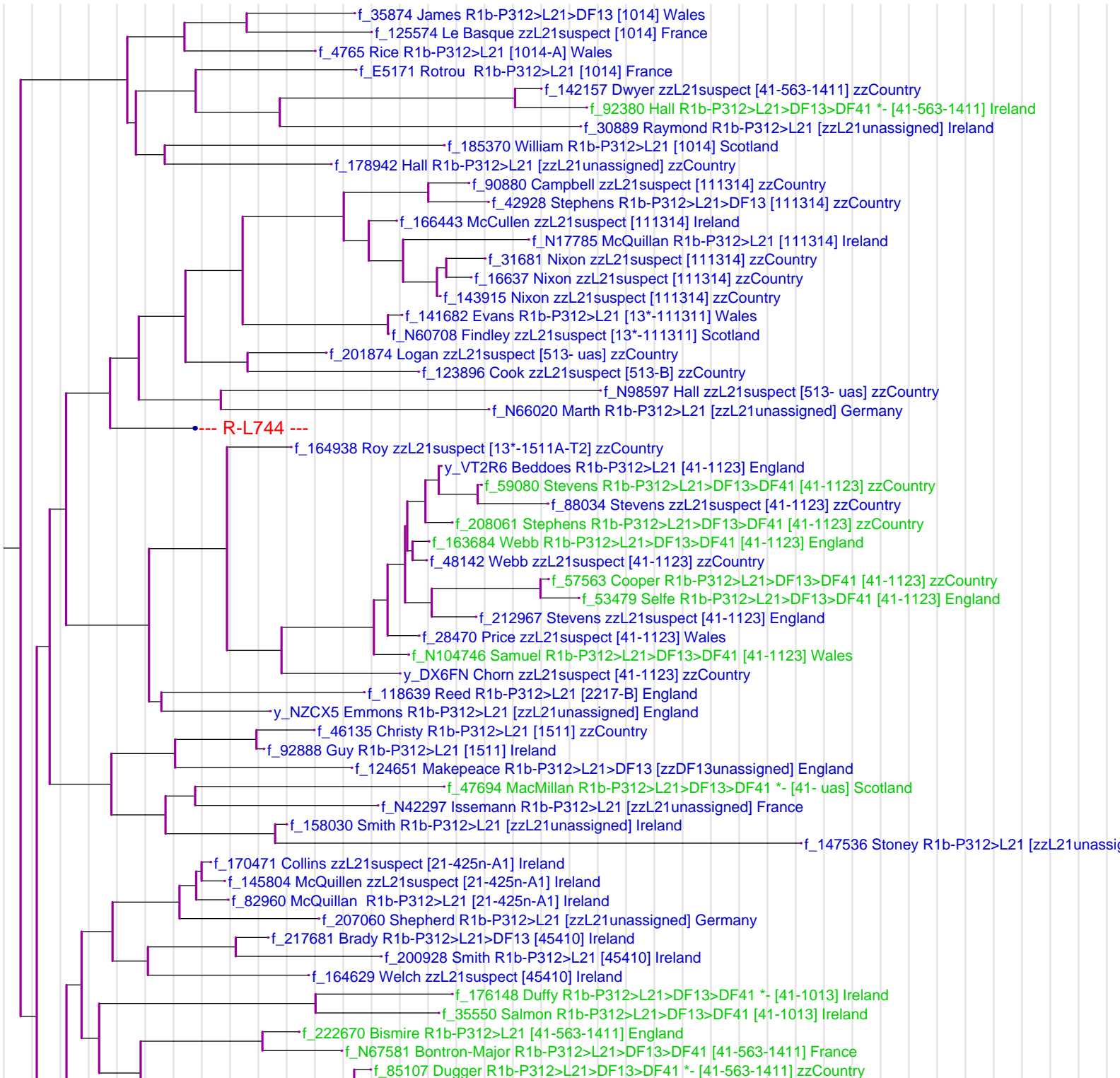


This is the marker distribution for R-DF41. The color indicates the relative frequency of the alleles.

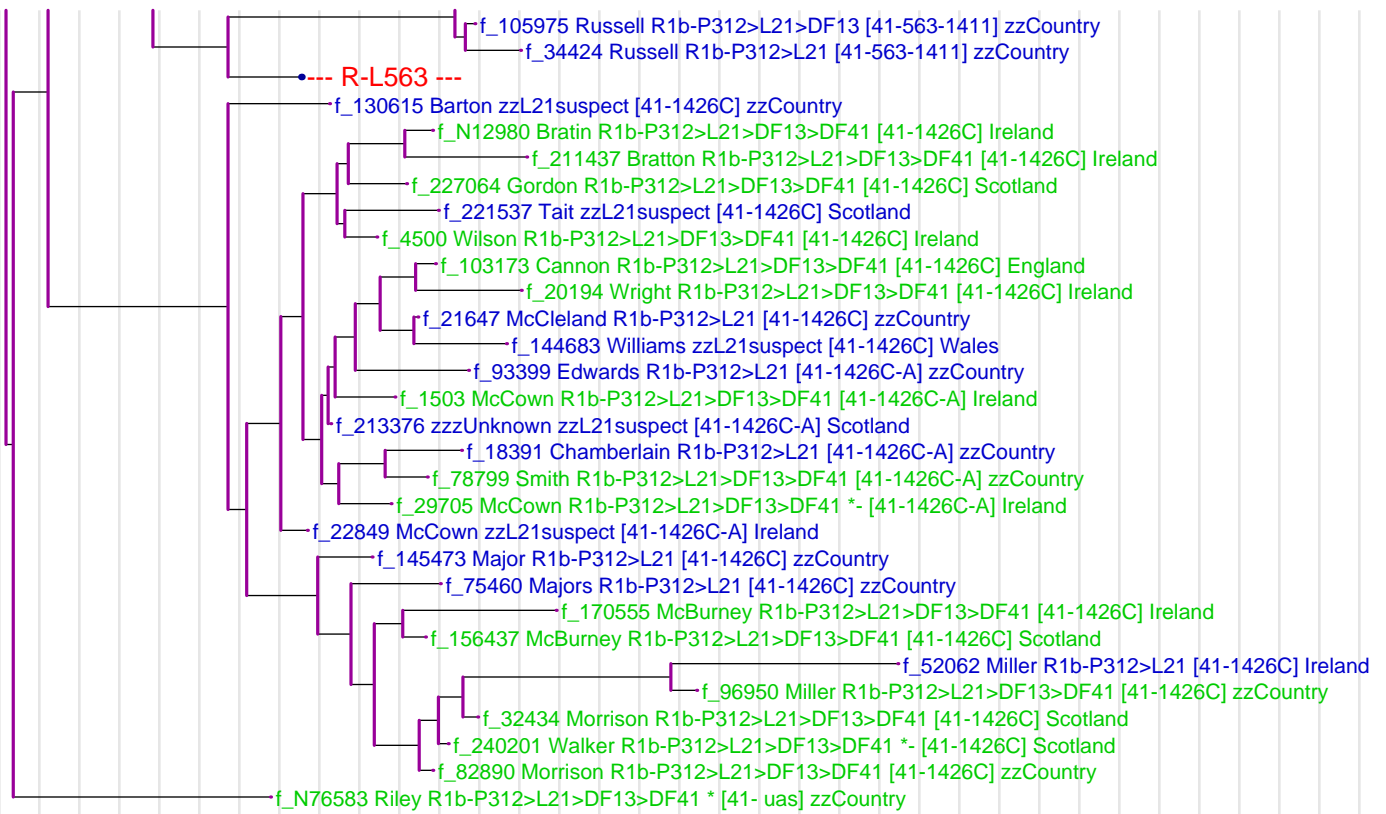


## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
157	10519	1970	18.73%	103.28±10.39	2582.08±366.198



The vertical grey lines are separated 10 generations apart.



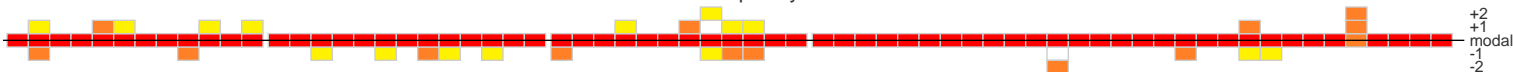
The vertical grey lines are separated 10 generations apart.

# R-L563

This is the modal haplotype for R-L563. 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	13	13	13	29	17	9	10	11	11	25	14	19	29	15	16	16	16	17	12	10	19	23	15	15	17	17	35	36	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	11	12	12	15	8	12	21	20	12	12	11	13	11	11	12	12

This is the marker distribution for R-L563. The color indicates the relative frequency of the alleles.



## Age Analysis

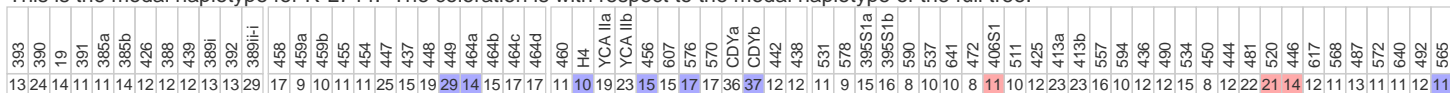
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
7	469	49	10.45%	55.12±6.13	1377.88±206.042



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.

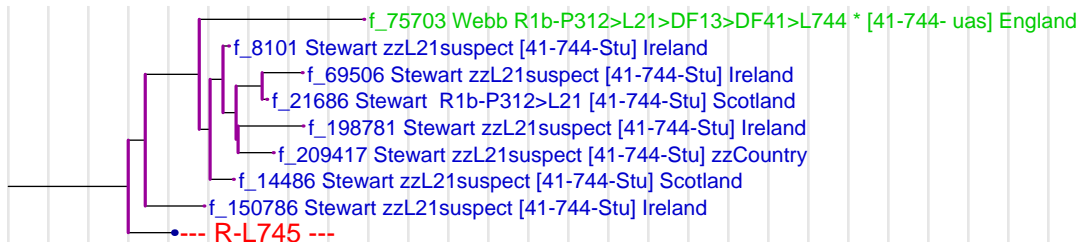


This is the marker distribution for R-L744. The color indicates the relative frequency of the alleles.



## Age Analysis

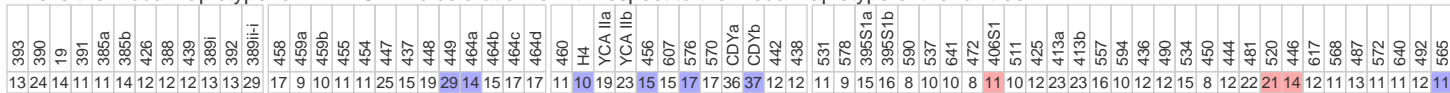
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
65	4355	208	4.78%	24.46±2.48	611.618±87.0148



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.

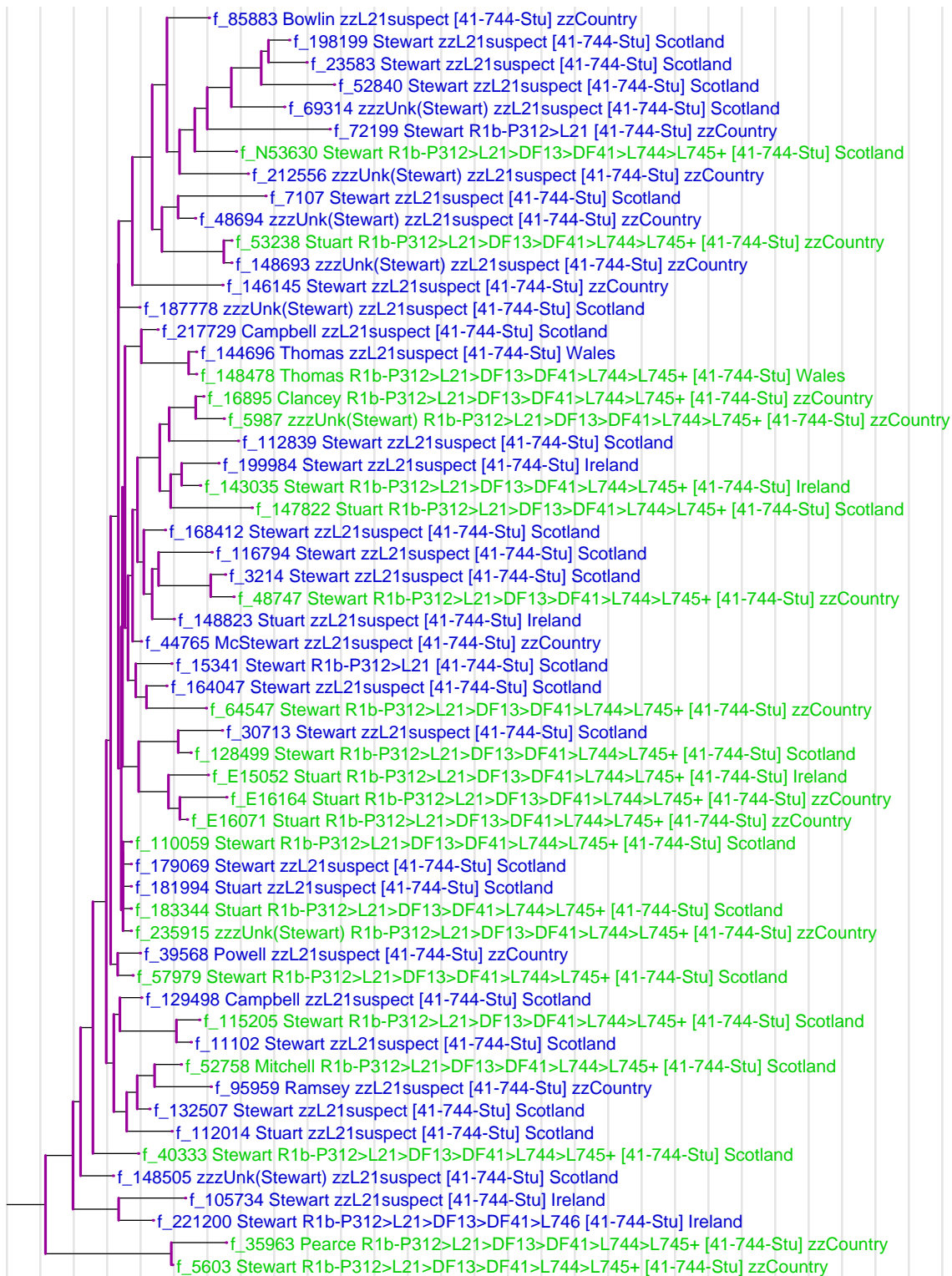


This is the marker distribution for R-L745. The color indicates the relative frequency of the alleles.



## Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
57	3819	184	4.82%	24.68±2.50	617.115±87.8704

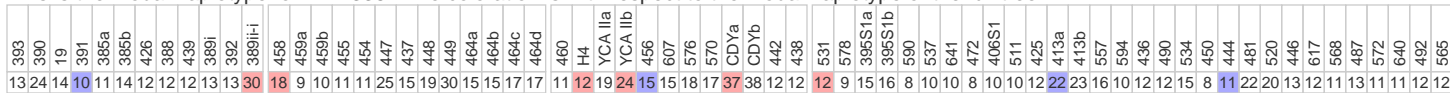


The vertical grey lines are separated 10 generations apart.

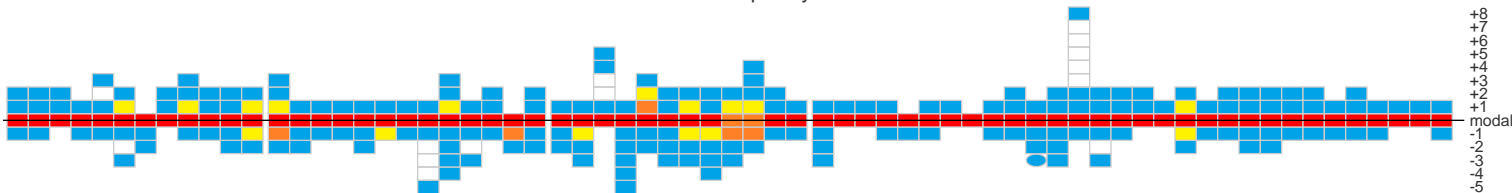


# R-L1335

This is the modal haplotype for R-L1335. The coloration is with respect to the modal haplotype of the full tree.

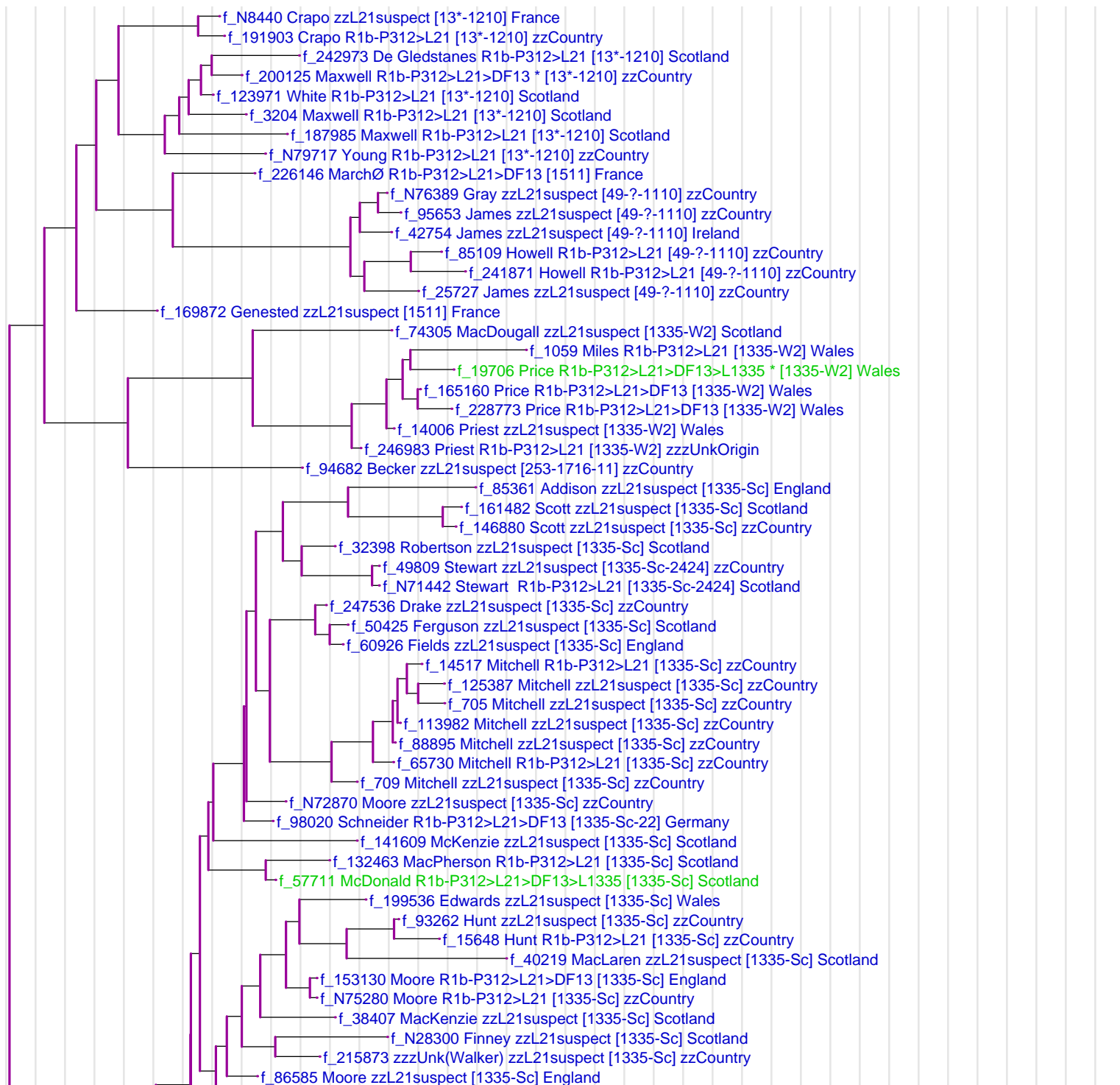


This is the marker distribution for R-L1335. The color indicates the relative frequency of the alleles.

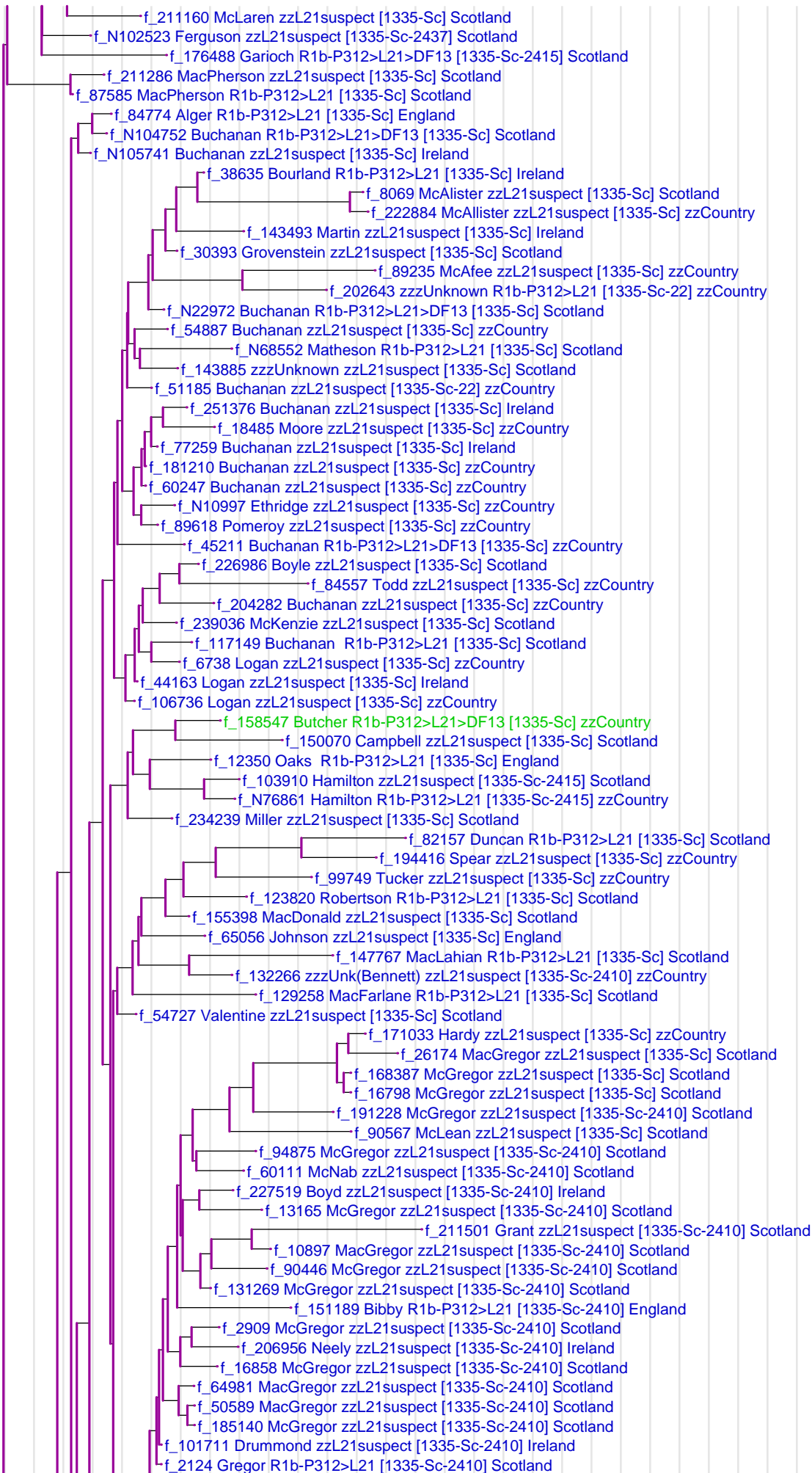


## Age Analysis

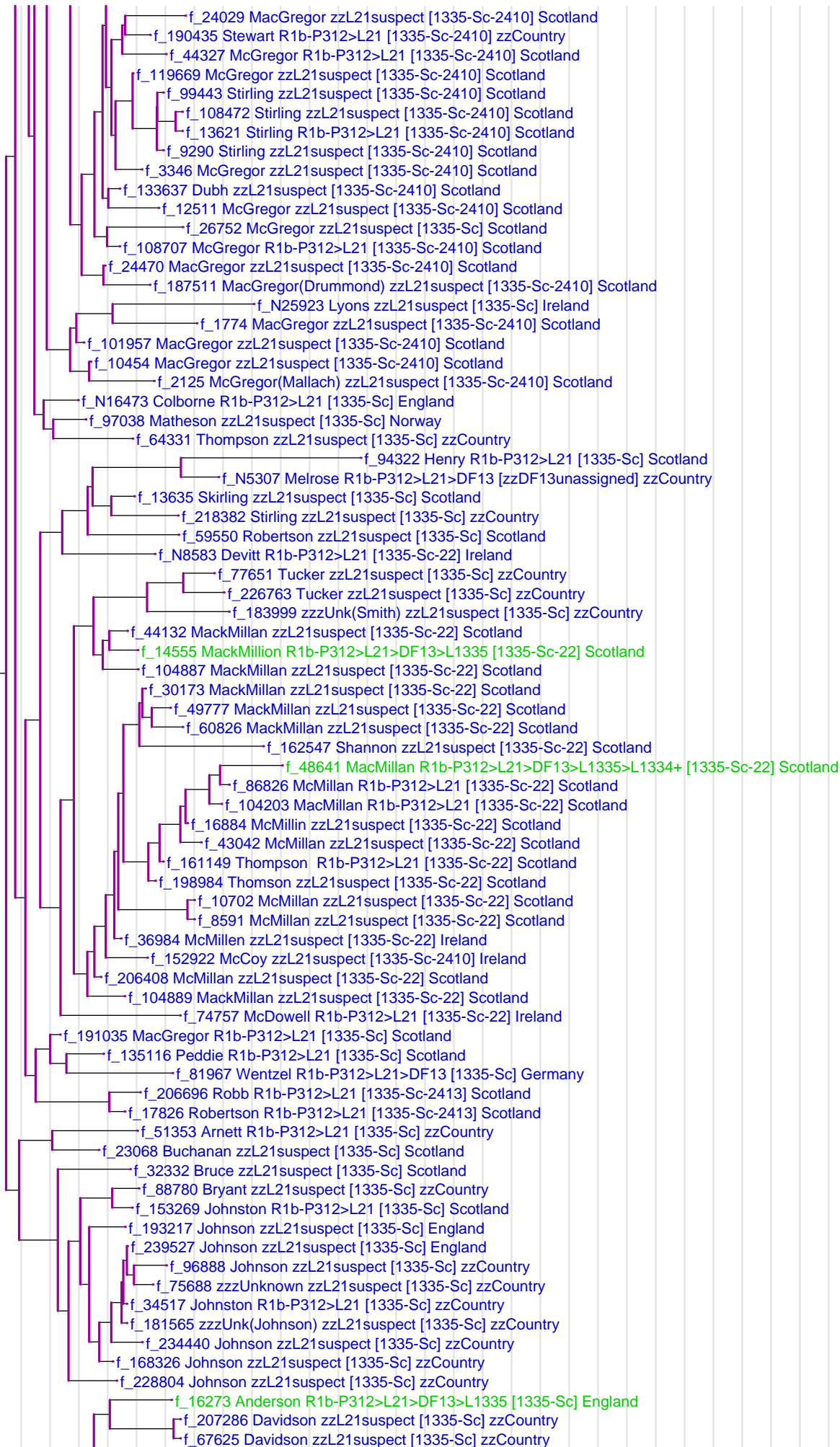
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
835	55945	6706	11.99%	63.75±6.38	1593.75±225.504



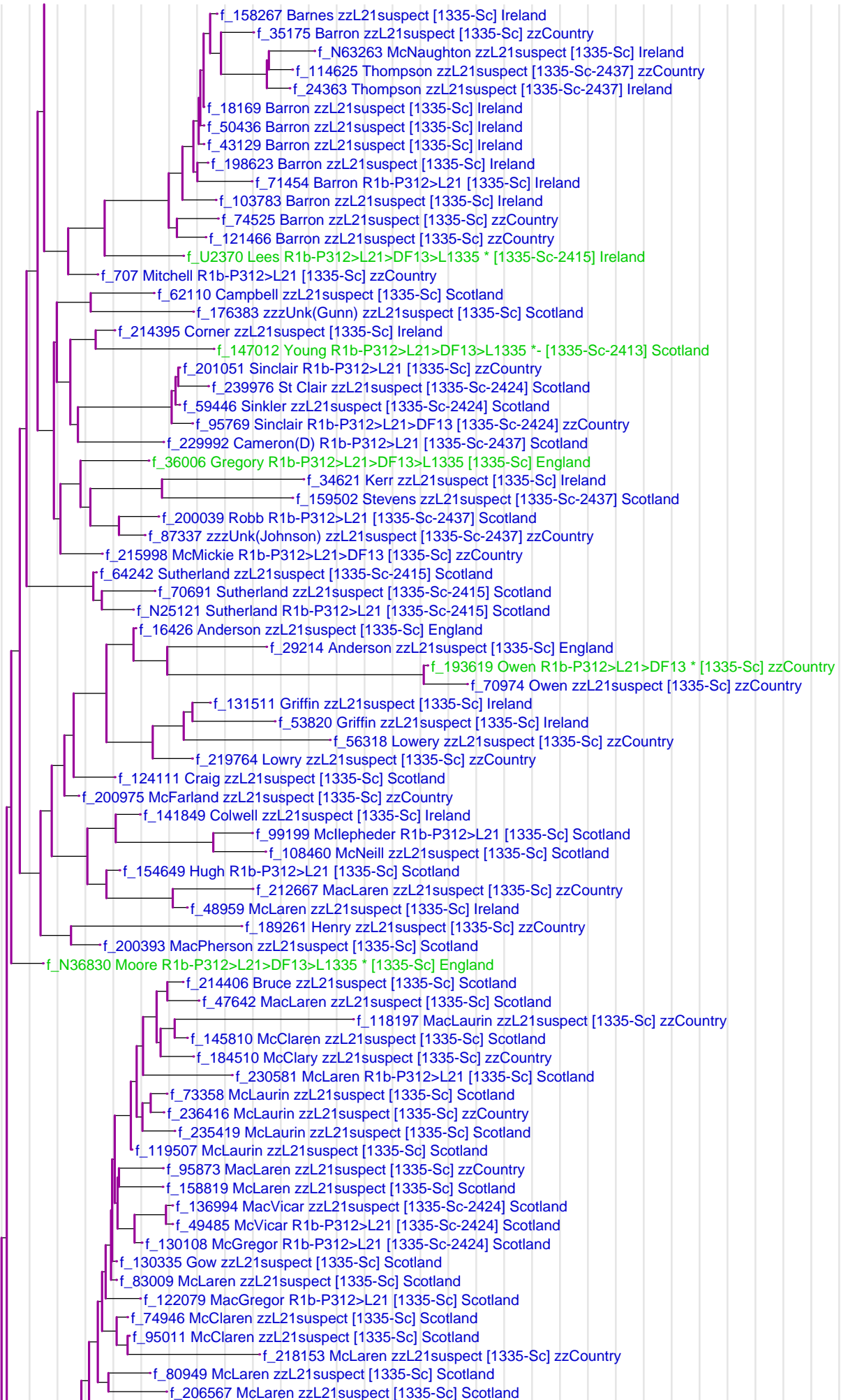
The vertical grey lines are separated 10 generations apart.



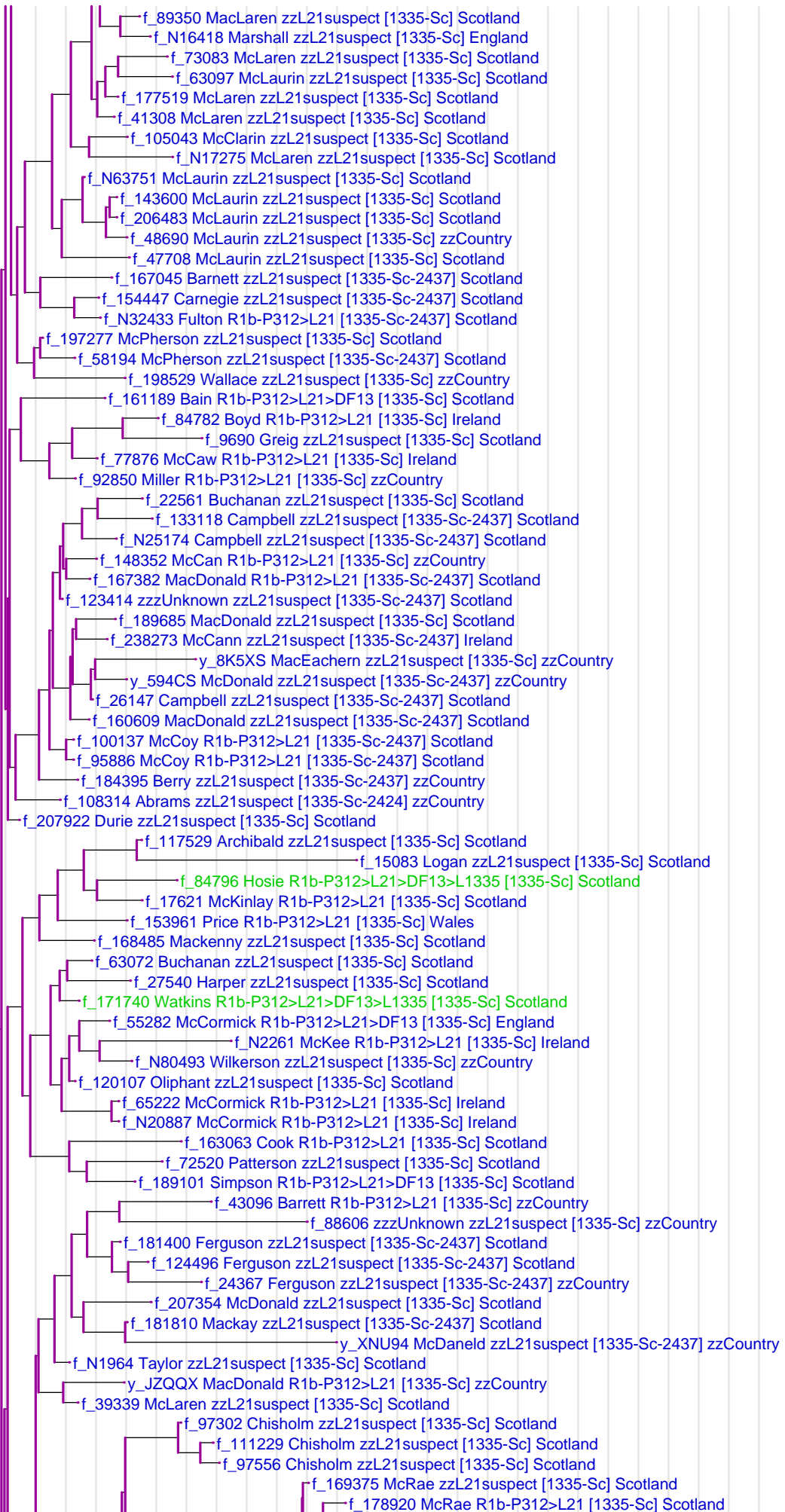
The vertical grey lines are separated 10 generations apart.



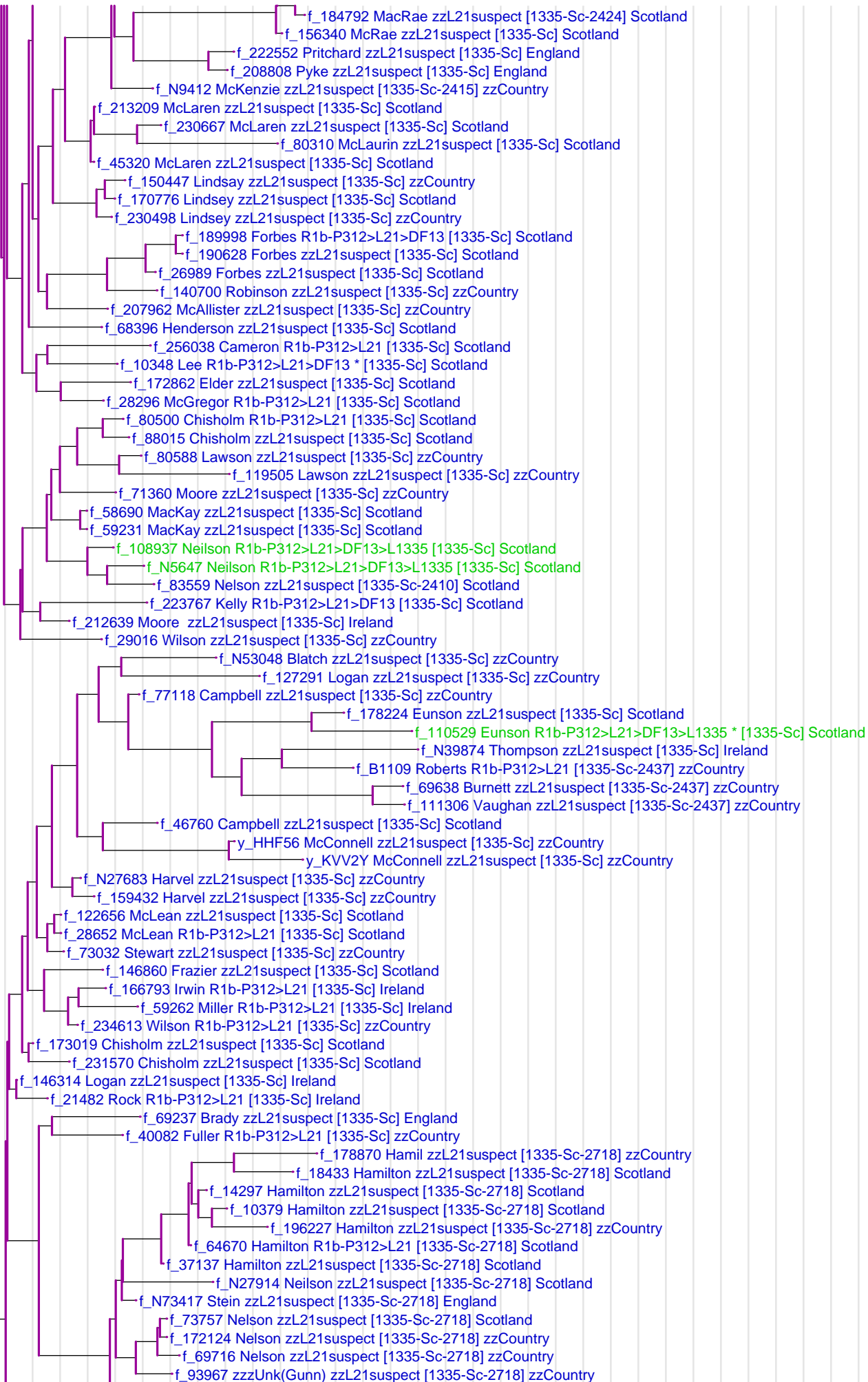
The vertical grey lines are separated 10 generations apart.



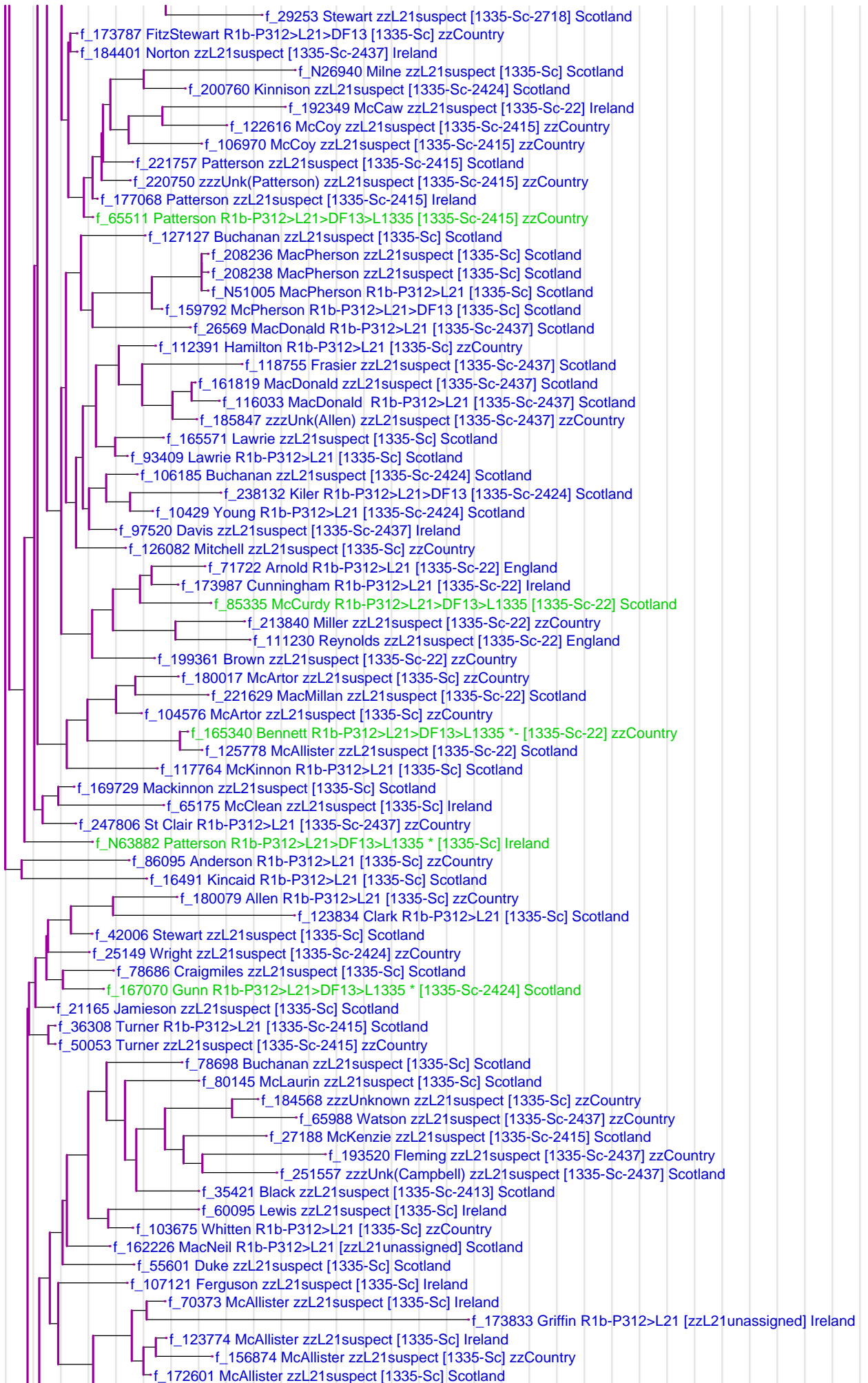
The vertical grey lines are separated 10 generations apart.



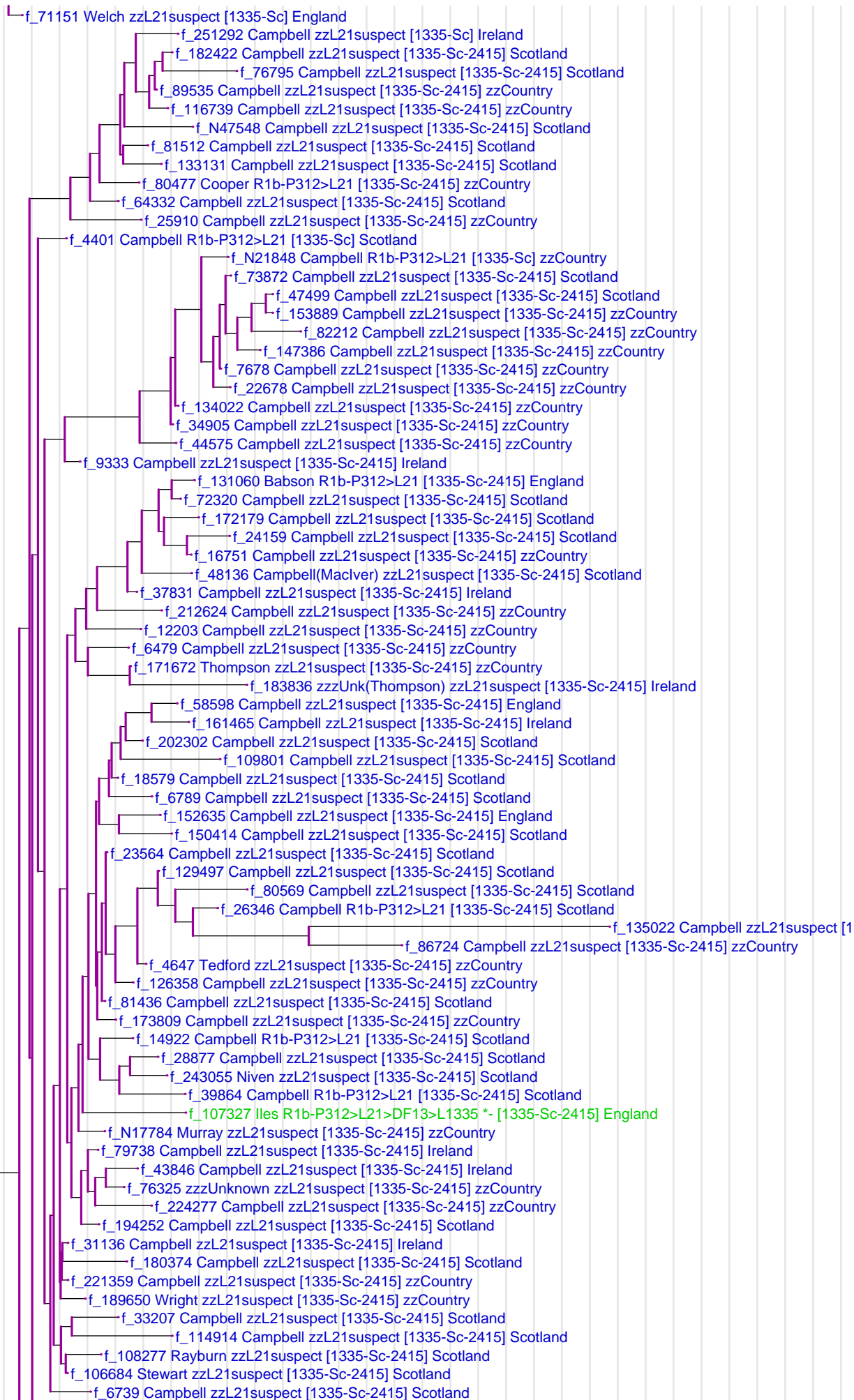
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

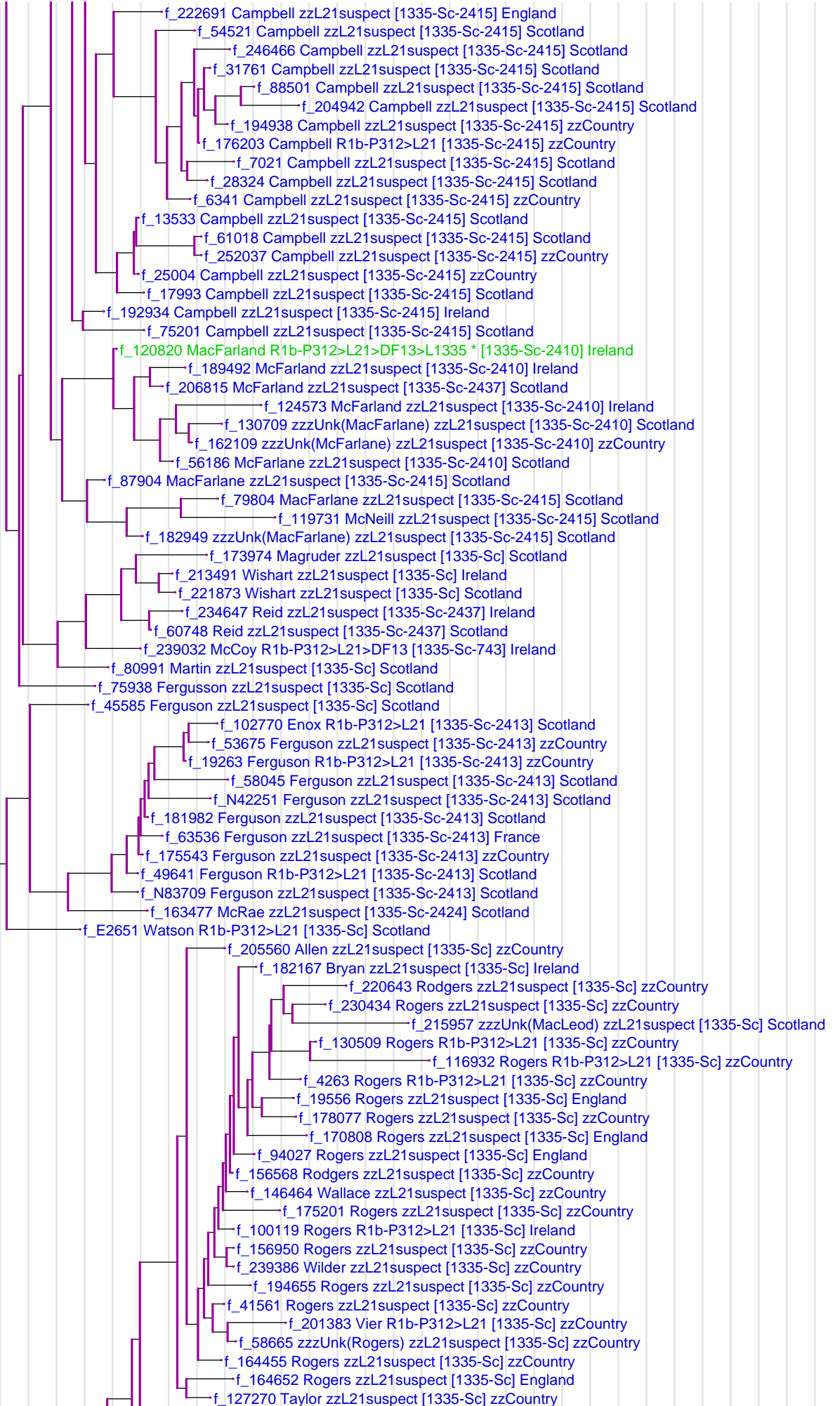


The vertical grey lines are separated 10 generations apart.

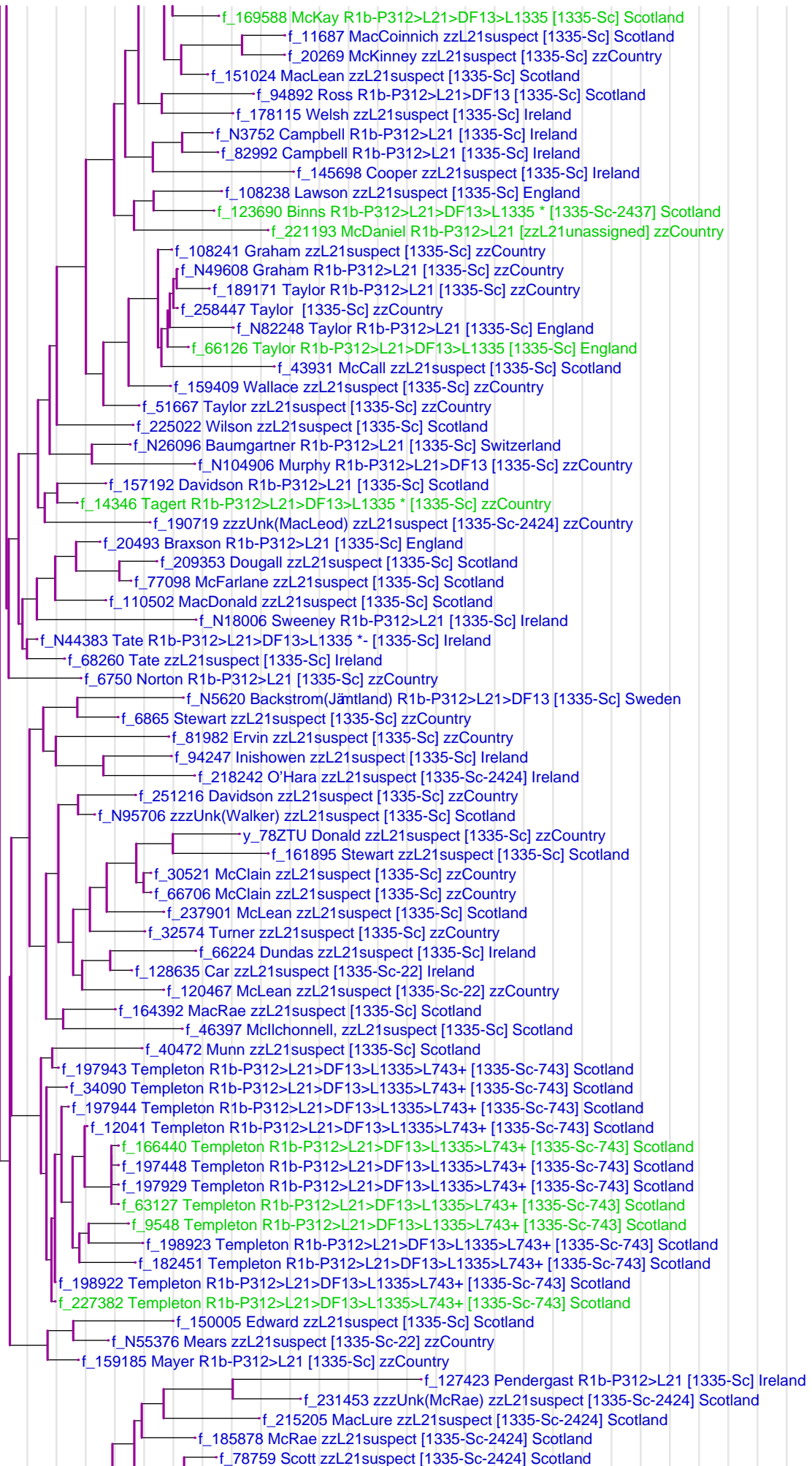


The vertical grey lines are separated 10 generations apart.

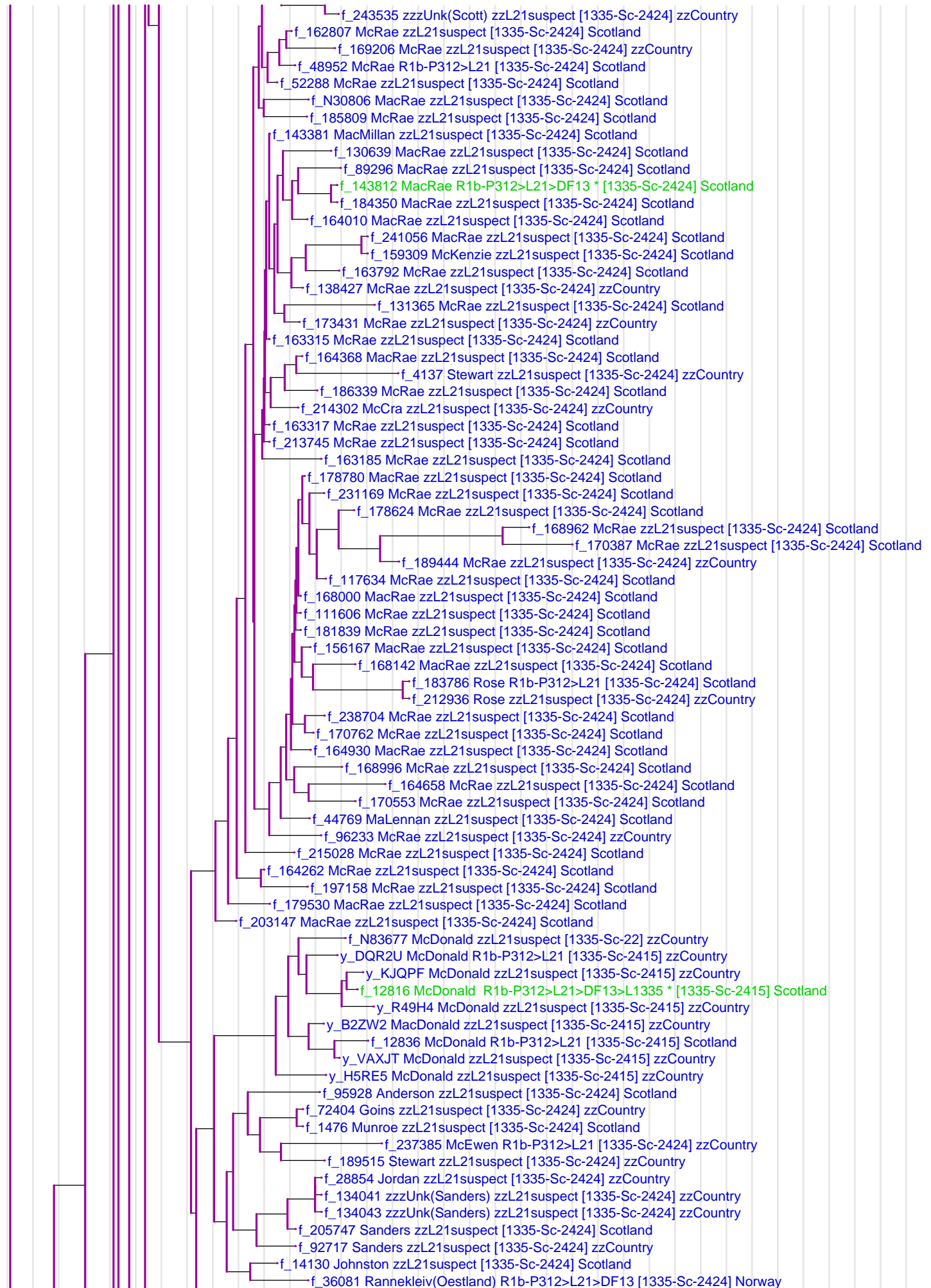




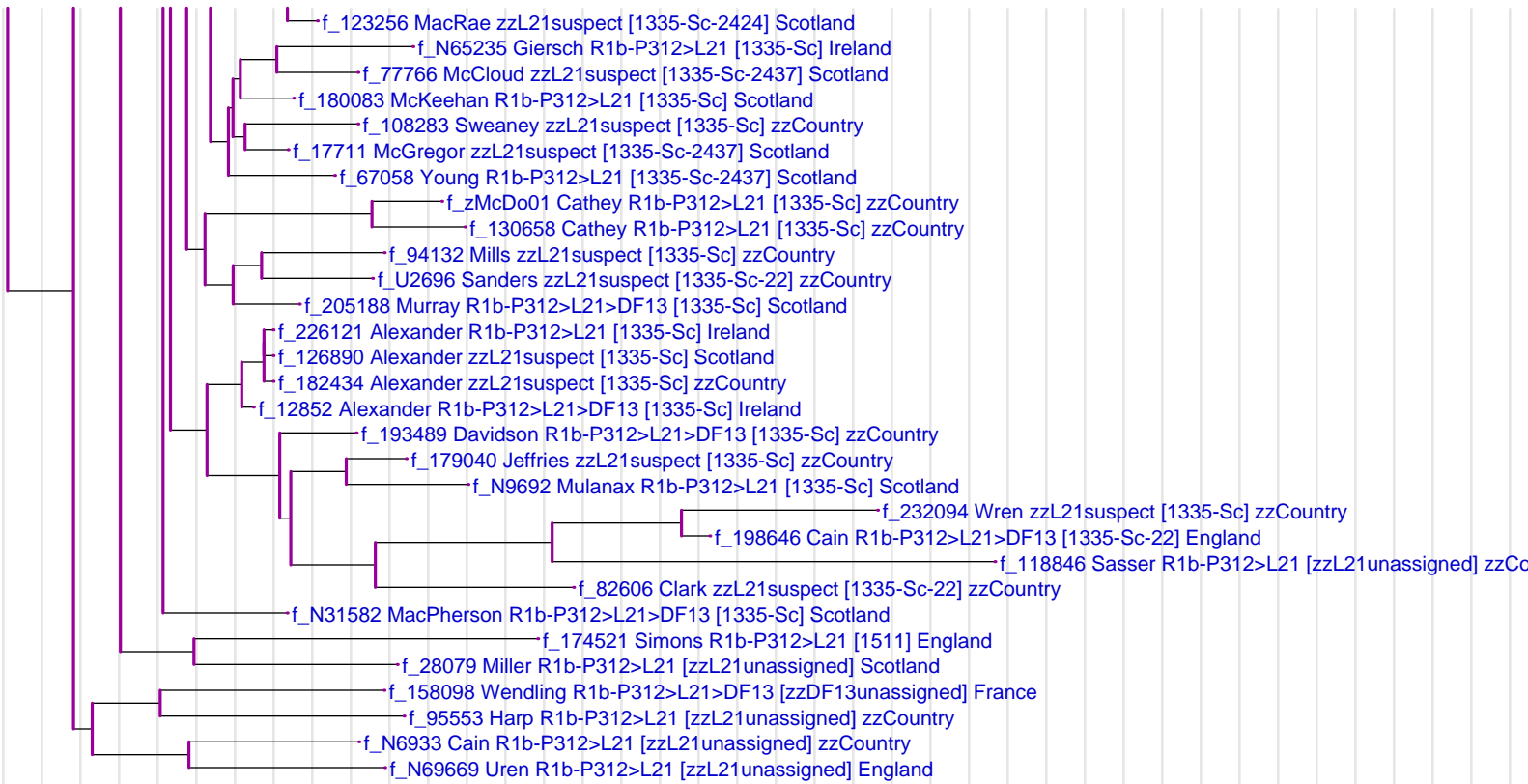
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



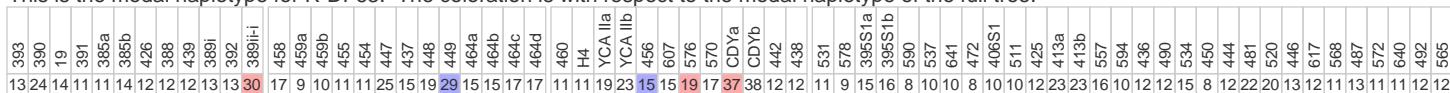
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

# R-DF63

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

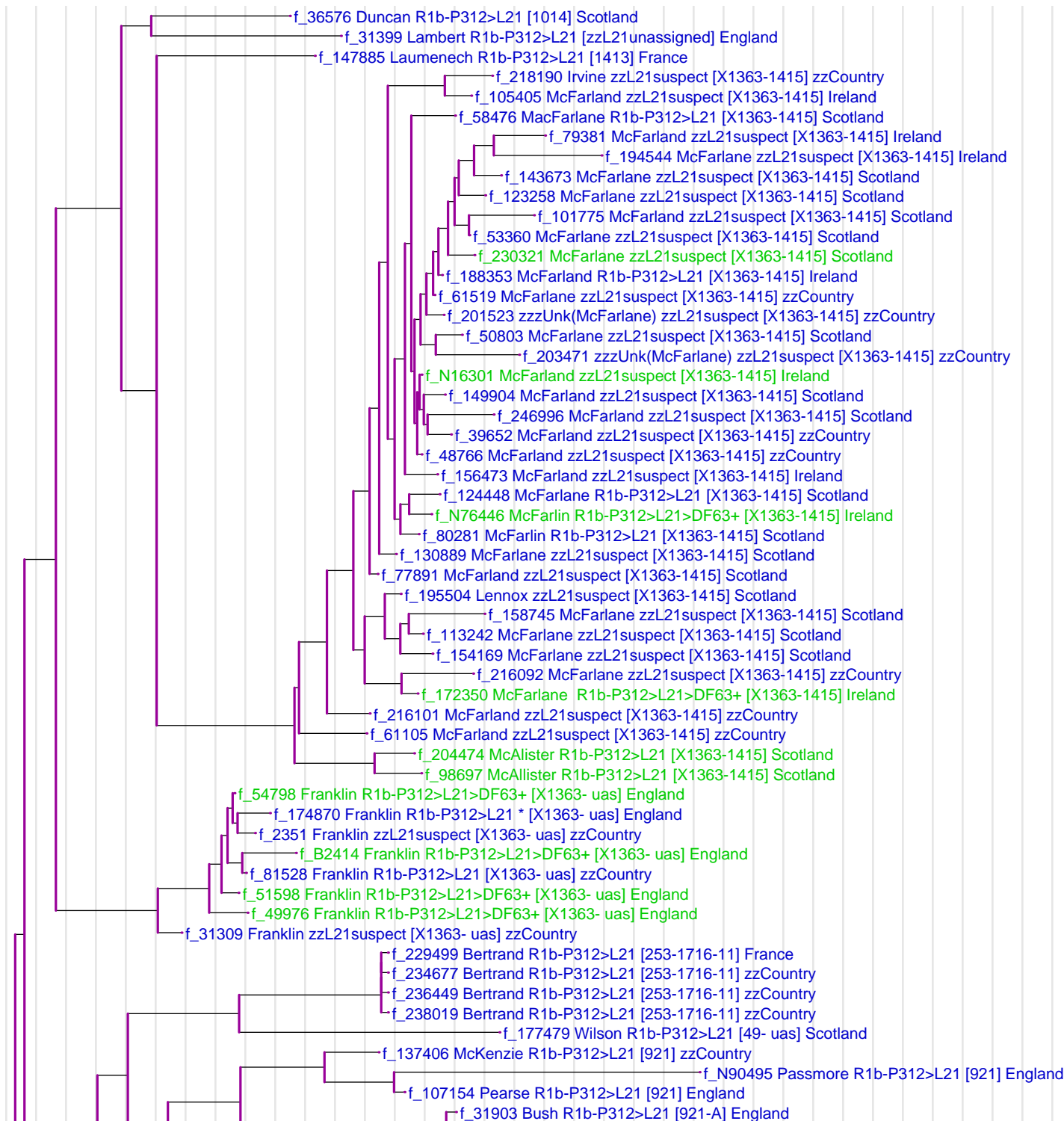


This is the marker distribution for R-DF63. The color indicates the relative frequency of the alleles.

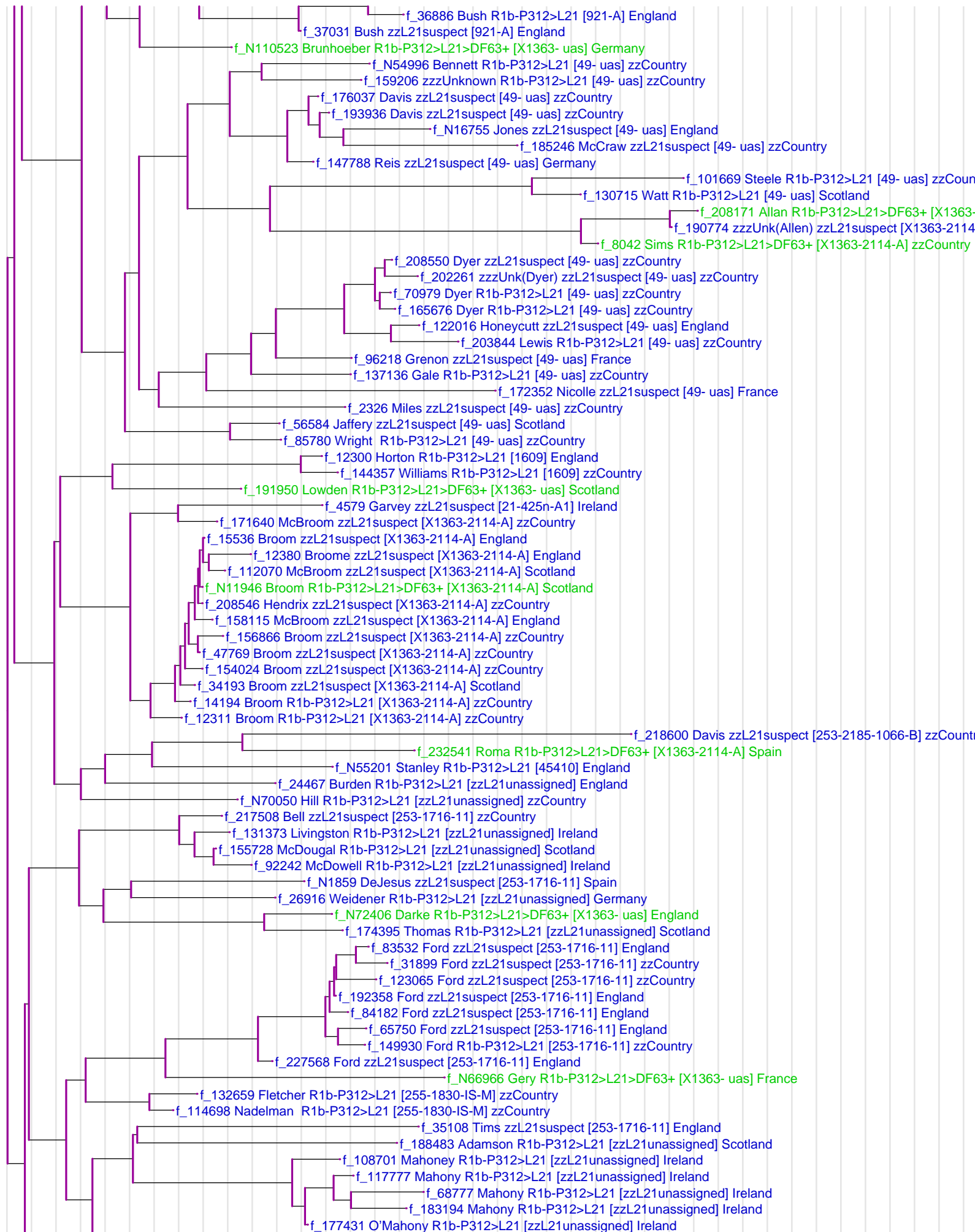


## Age Analysis

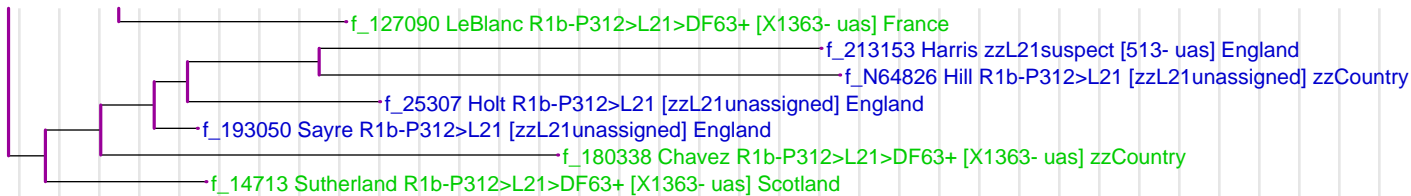
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
138	9246	2174	23.51%	133.15±13.40	3328.65±472.329



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: 3528.61±499.055 years

393	390	19	391	385a	385b	426	388	439	389i	392	389iH	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA Ila	YCA Iib	456	607	576	570	CDYa	CDYb	442	438	531	578	395St1a	395St1b	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	16	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	15	8	12	22	20	13	12	11	13	11	11	12	12		
R-DF13																											Age: 3533.24±499.711 years																																							
R-DF49																											Age: 2132.53±301.671 years																																							
R-DF23																											Age: 1981.61±280.324 years																																							
R-M222																											Age: 1520.21±215.062 years																																							
R-L513																											Age: 3038.17±429.876 years																																							
R-P66																											Age: 187.97±29.7502 years																																							
R-L193																											Age: 1388.31±196.607 years																																							
R-L706.2																											Age: 1187.88±169.33 years																																							
R-L705.2																											Age: 1214.5±173.212 years																																							
R-L555																											Age: 463.967±65.9437 years																																							
R-L96																											Age: 1212.79±184.996 years																																							
R-Z255																											Age: 1706.32±241.673 years																																							
R-Z253																											Age: 3079.77±435.786 years																																							
R-L226																											Age: 1249.24±176.96 years																																							
R-L554																											Age: 902.049±143.558 years																																							
R-Z2185																											Age: 3137.57±444.762 years																																							
R-L1066																											Age: 2895.45±410.71 years																																							
R-DF21																											Age: 3020.39±427.375 years																																							
R-P314.2																											Age: 1905.56±271.434 years																																							
R-L362																											Age: 1021.59±146.985 years																																							
R-Z246																											Age: 2892.79±410.235 years																																							
R-DF25																											Age: 2893.81±410.401 years																																							
R-DF5																											Age: 2736.61±388.582 years																																							
R-L627																											Age: 808.928±123.146 years																																							
R-L658																											Age: 602.584±87.7433 years																																							
R-L720																											Age: 1171.84±176.615 years																																							
R-S424																											Age: 1310.94±185.86 years																																							
R-S190																											Age: 1315.4±186.633 years																																							
R-L371																											Age: 741.379±105.492 years																																							
R-DF41																											Age: 2582.08±366.198 years																																							
R-L563																											Age: 1377.88±206.042 years																																							
R-L744																											Age: 611.618±87.0148 years																																							
R-L745																											Age: 617.115±87.8704 years																																							



# Cluster Modals (continued...)

R-L1335

Age: 1593.75±225.504 years

393	390	19	391	385a	385b	426	388	439	389i	392	389iH	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	567	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	30	18	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	15	15	19	17	37	38	12	12	12	9	15	16	8	10	10	8	10	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

R-DF63

Age: 3328.65±472.329 years

13	24	14	11	11	14	12	12	13	13	30	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	15	15	19	17	37	38	12	12	12	9	15	16	8	10	10	8	10	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
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# 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 Mike Walsh's Excel spreadsheet on 2012-12-24, while the SNP data came primarily from the L21+, Scottish, and Irish FTDNA projects on 2012-12-27. 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%	

