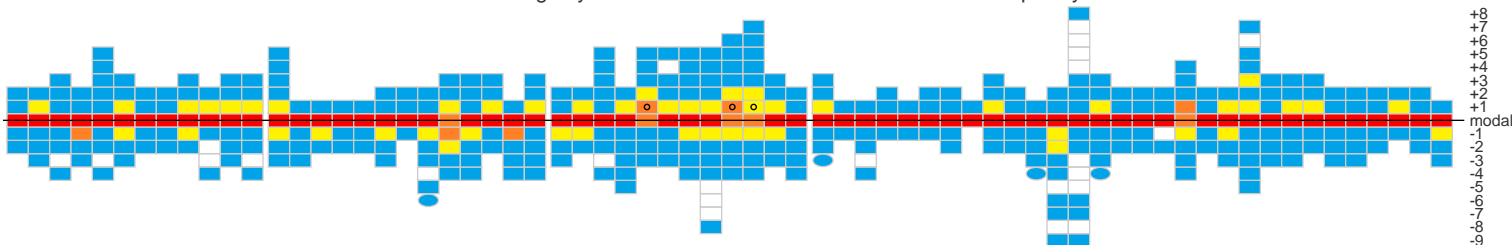


R-L21

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

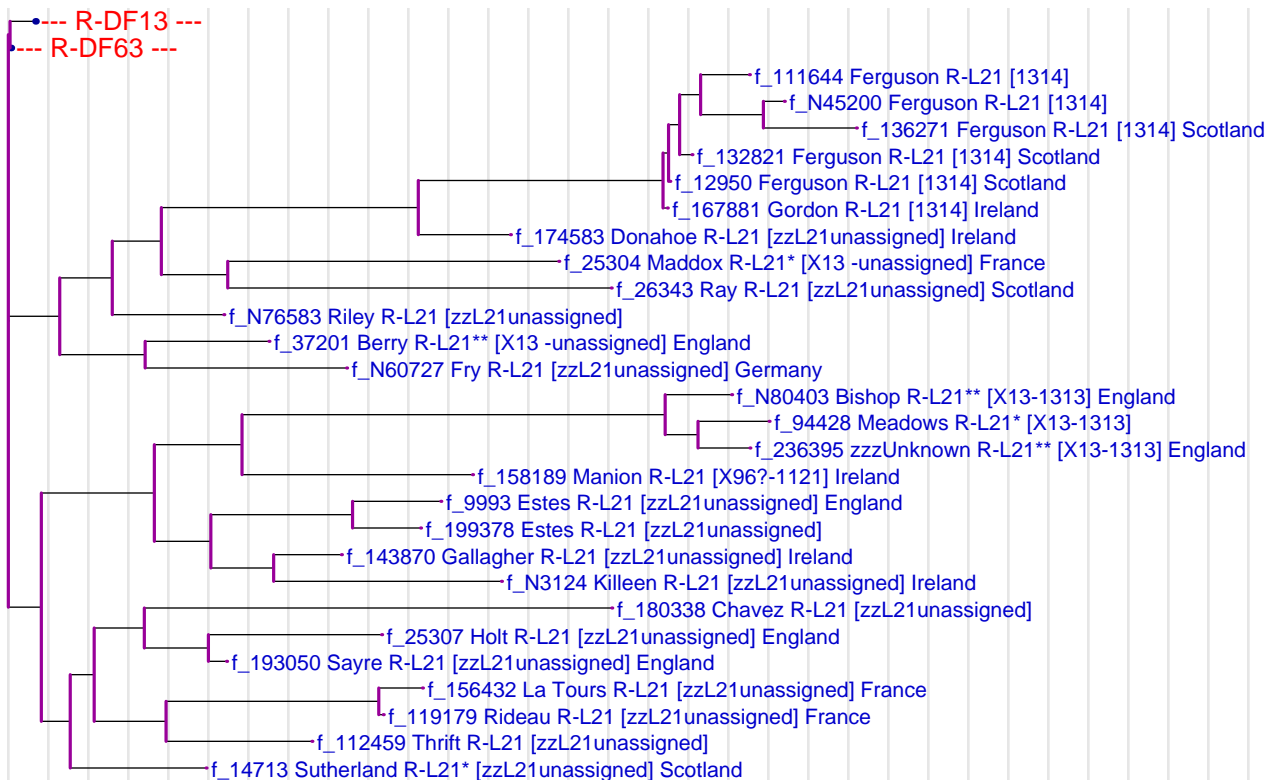
393	390	19	391	385a	385b	426	388	439	389i	392	389i-1	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	14	12	12	12	13	13	16	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	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 the whole tree including any subtrees. The color indicates the relative frequency of the alleles.



Age Analysis

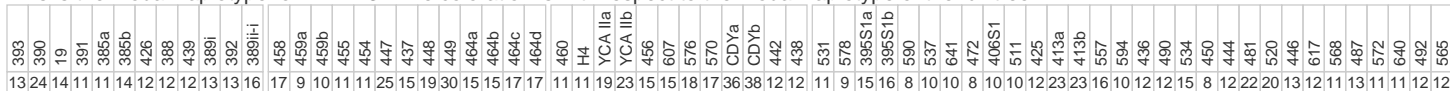
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5248	351616	85741	24.38%	138.76±13.88	3468.97±490.631



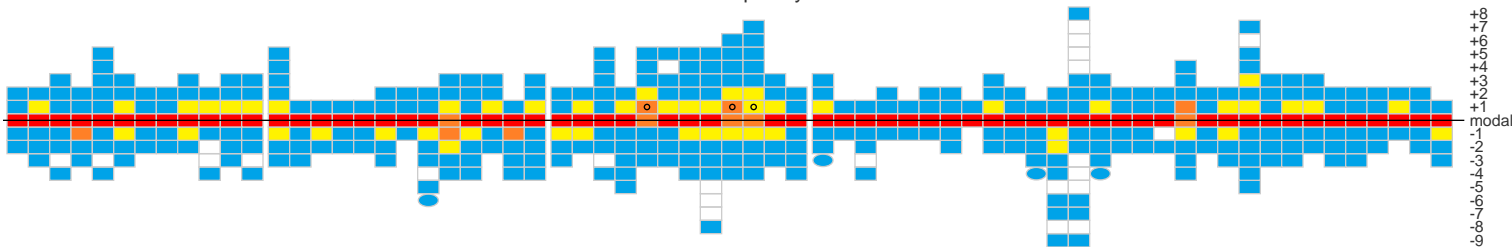
The vertical grey lines are separated 10 generations apart.

R-DF13

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

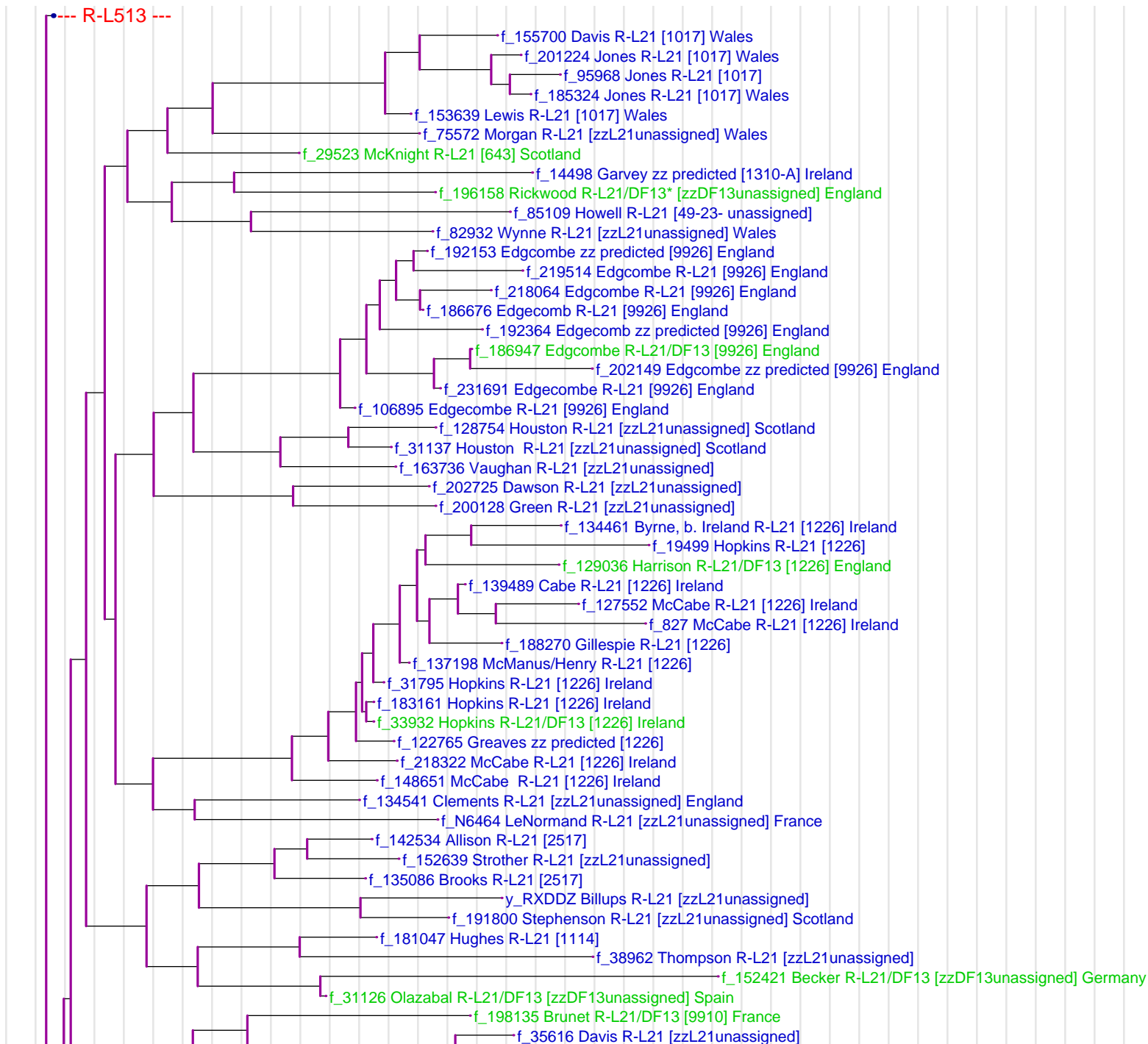


This is the marker distribution for R-DF13. The color indicates the relative frequency of the alleles.

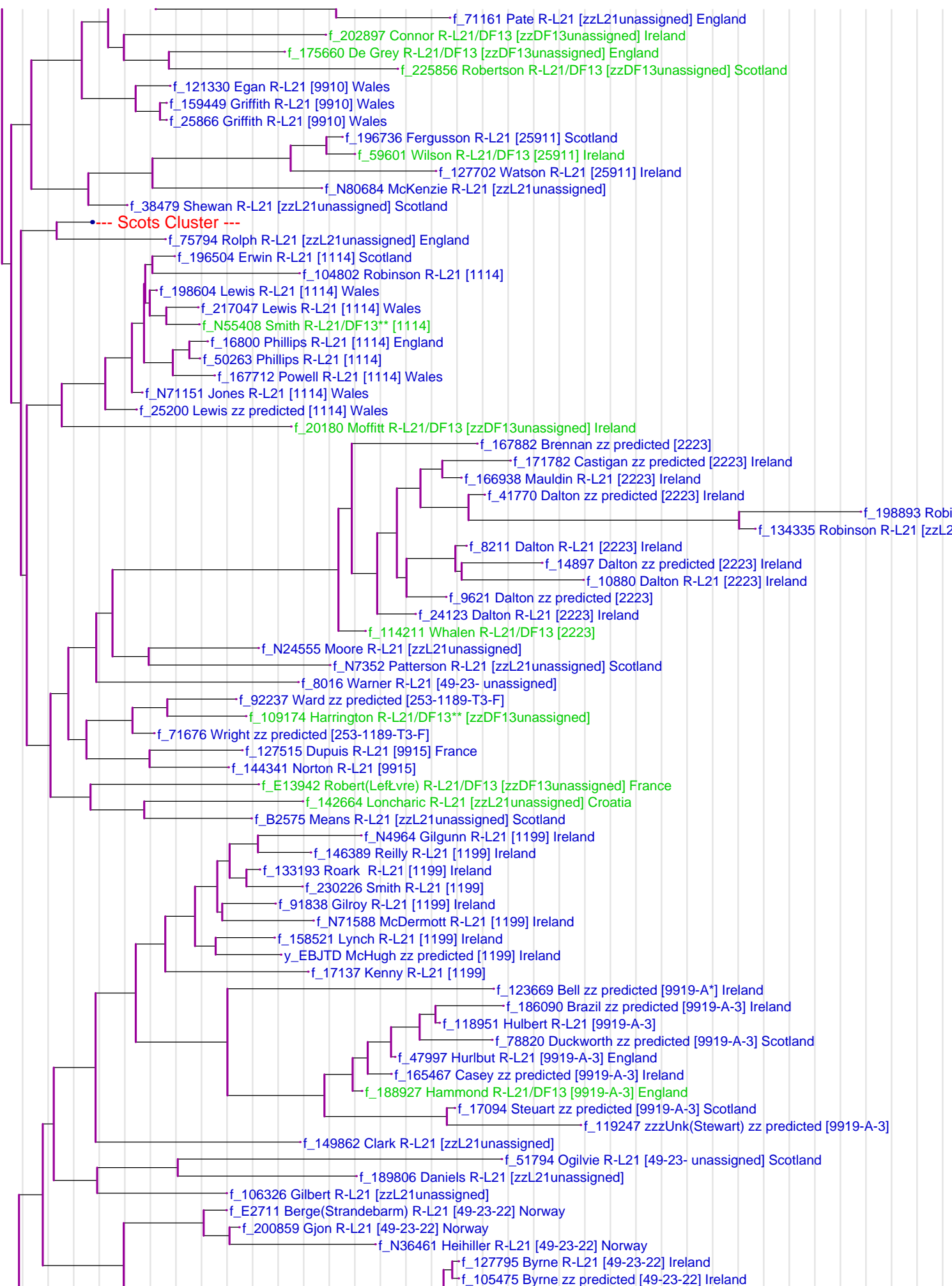


Age Analysis

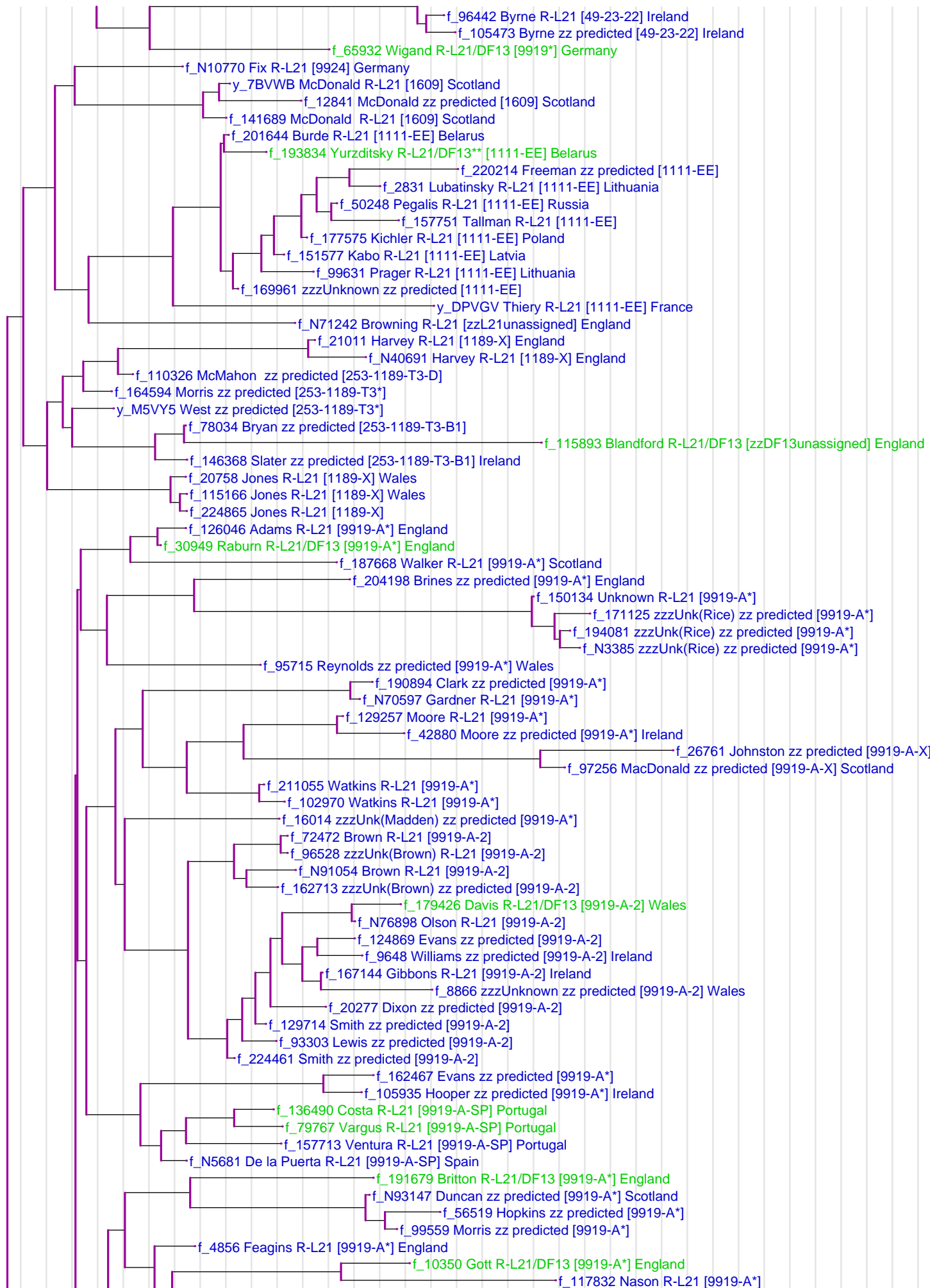
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5171	346457	84601	24.42%	138.98±13.90	3474.48±491.411



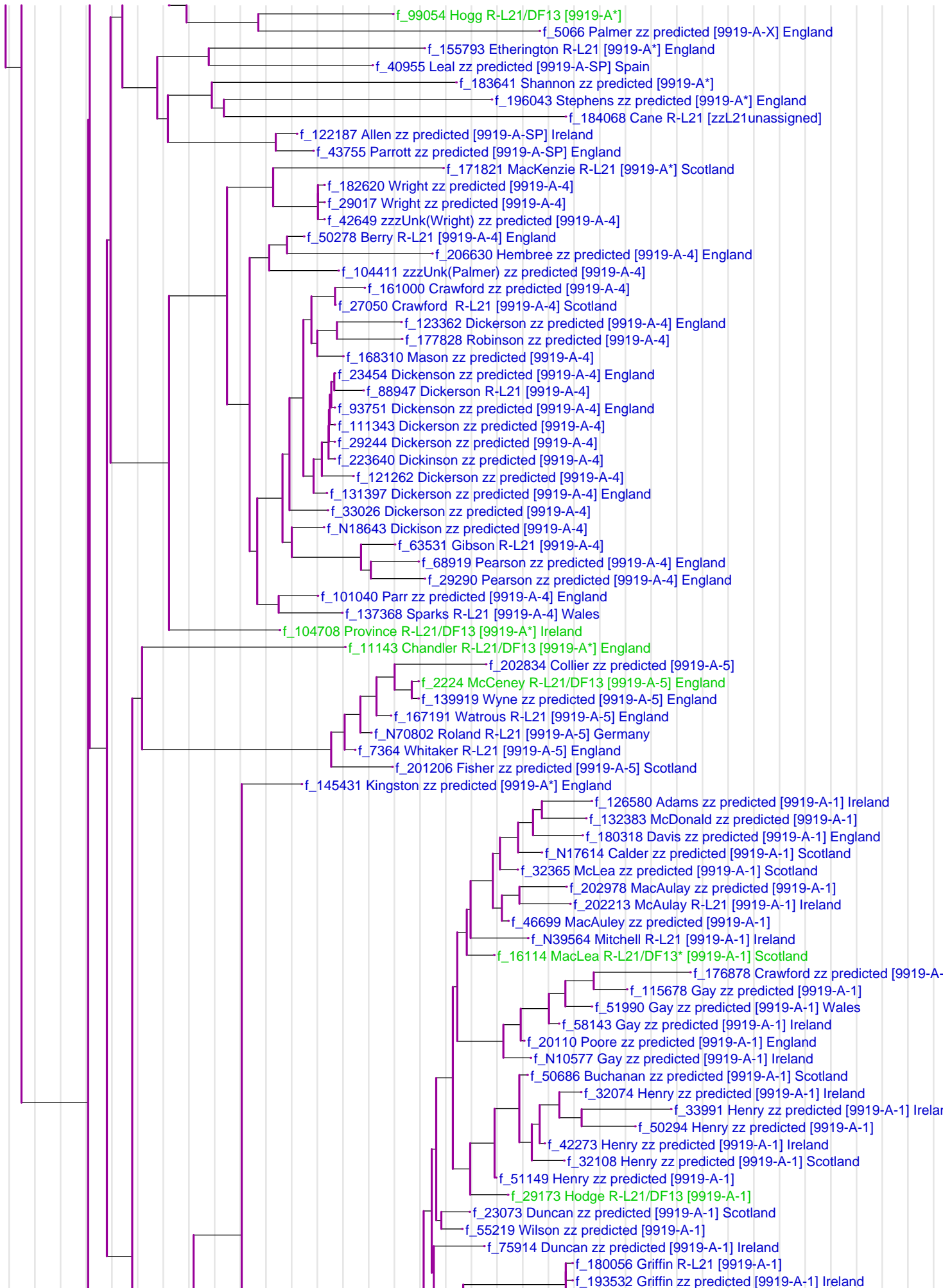
The vertical grey lines are separated 10 generations apart.



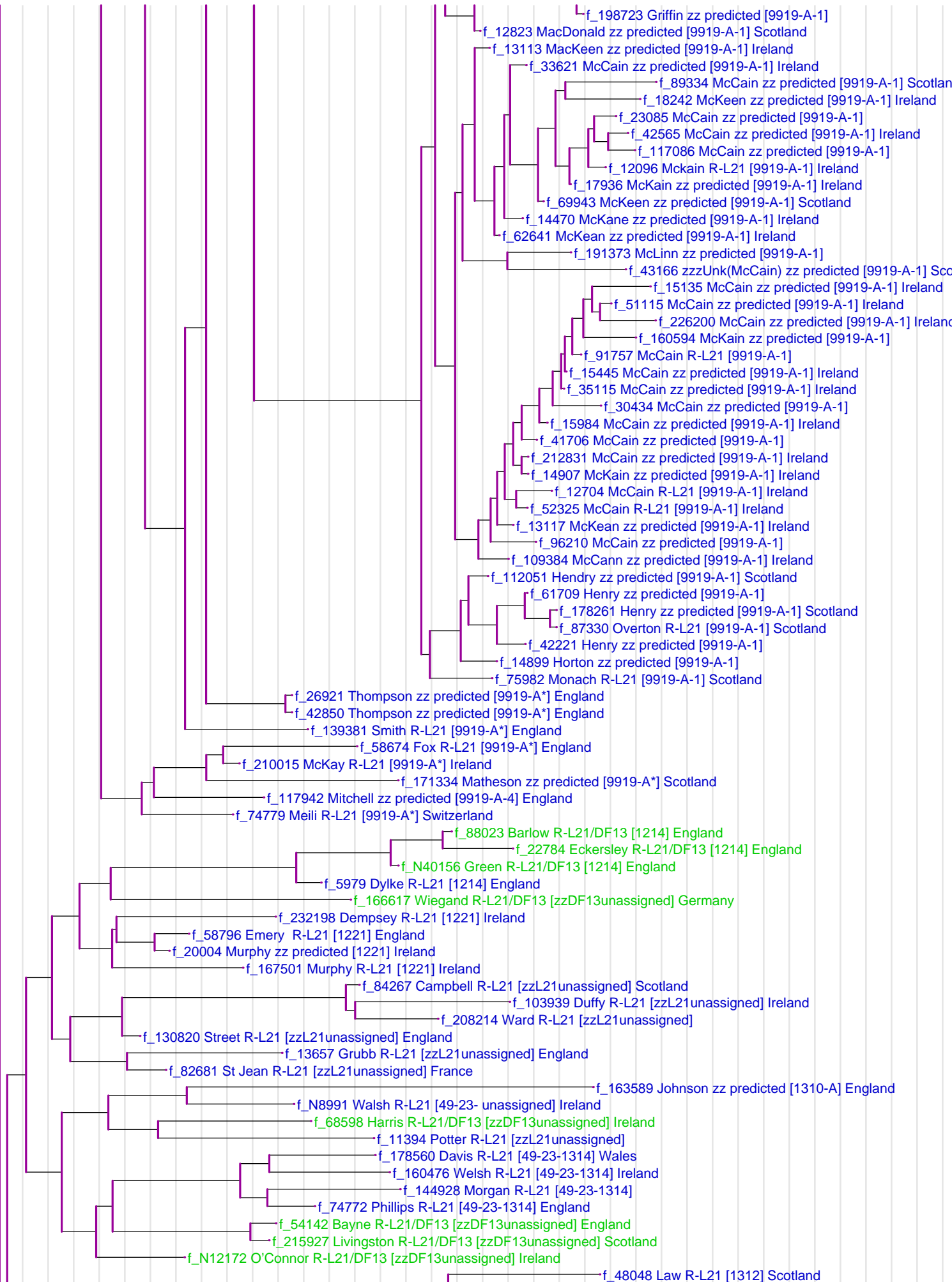
The vertical grey lines are separated 10 generations apart.



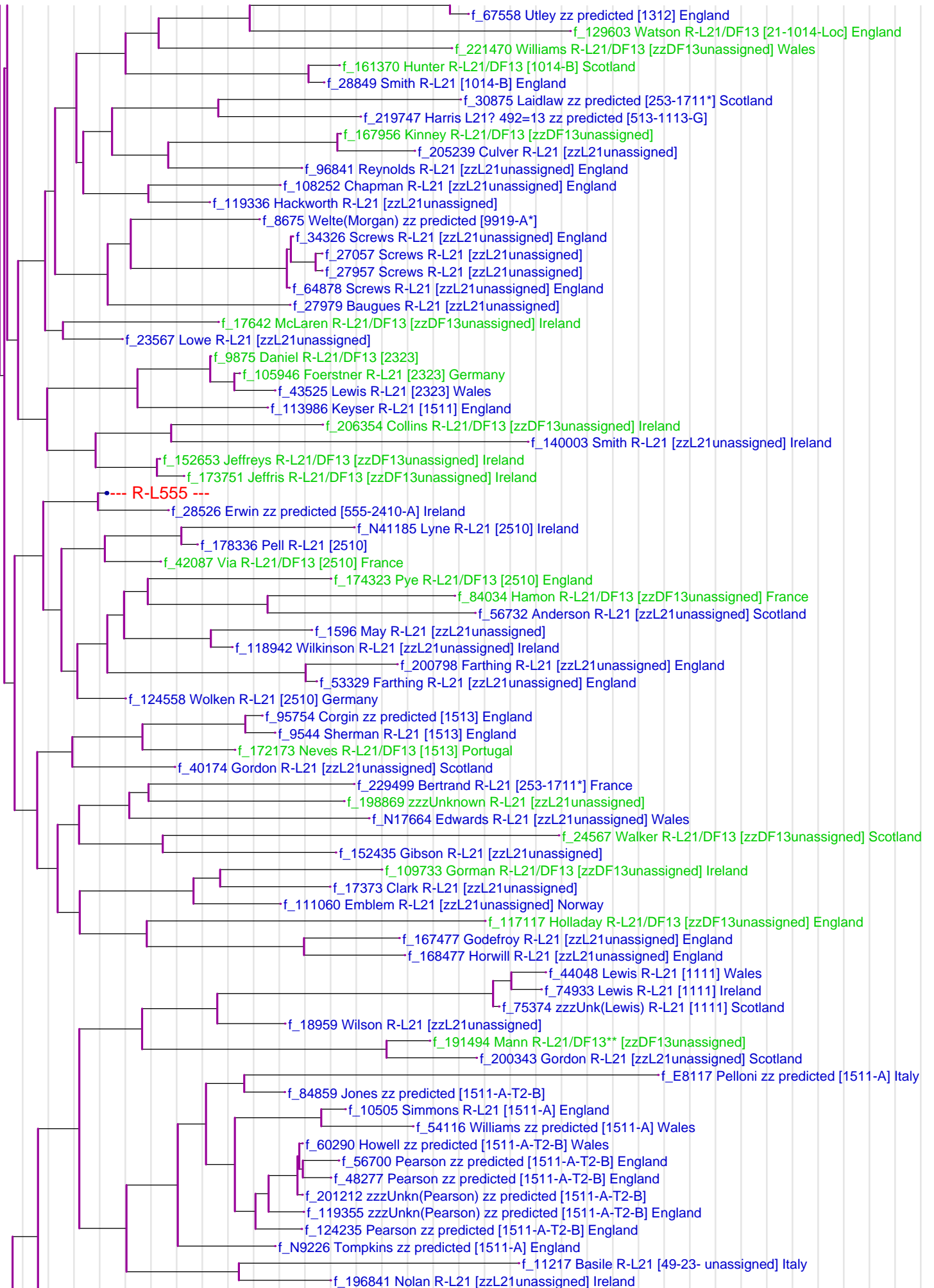
The vertical grey lines are separated 10 generations apart.



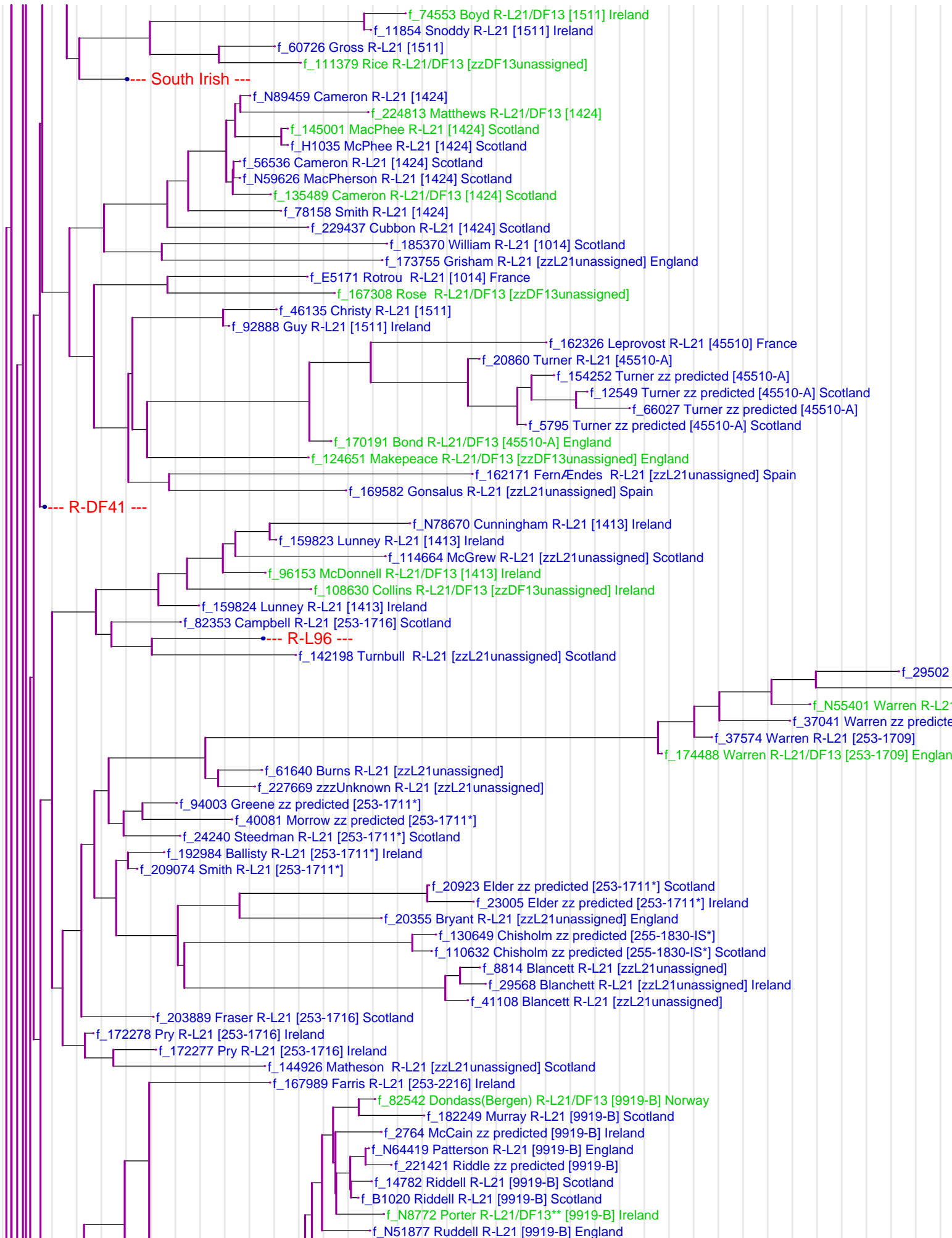
The vertical grey lines are separated 10 generations apart.



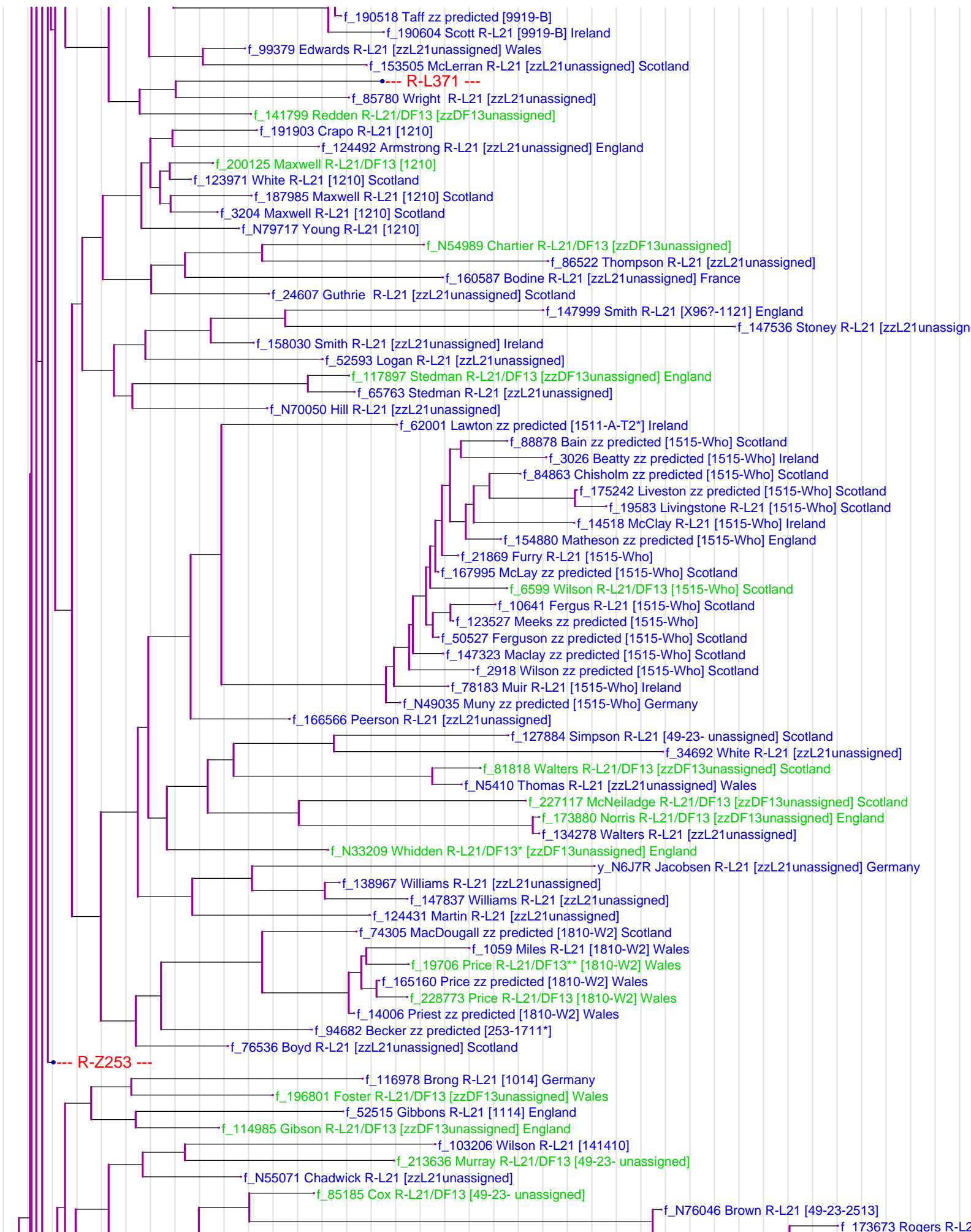
The vertical grey lines are separated 10 generations apart.



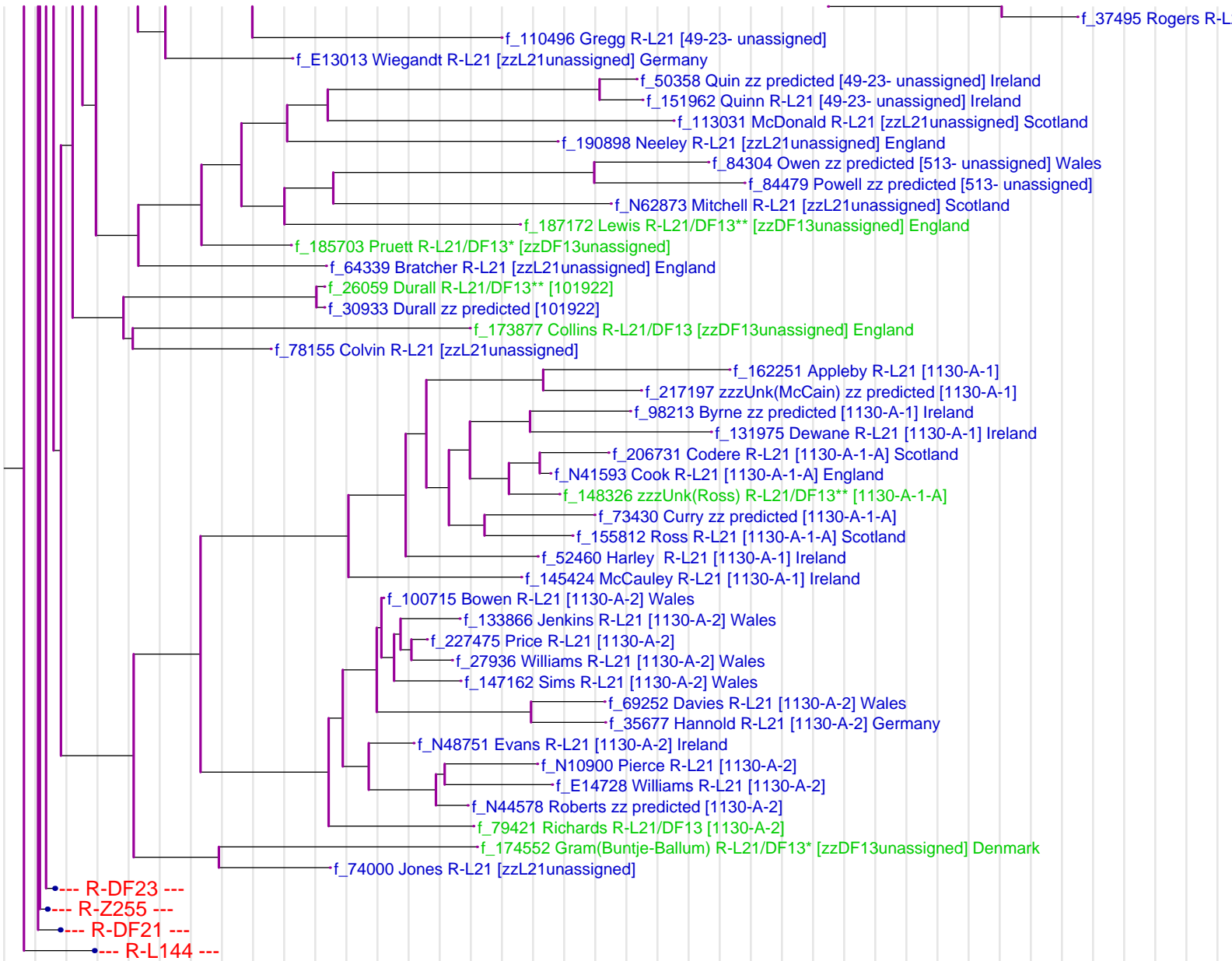
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



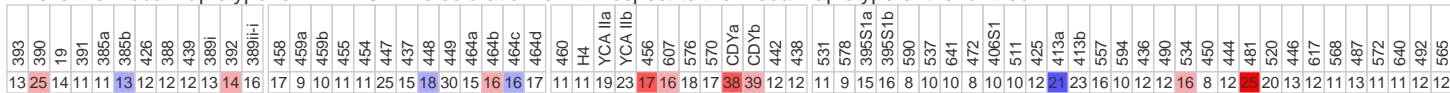
The vertical grey lines are separated 10 generations apart.



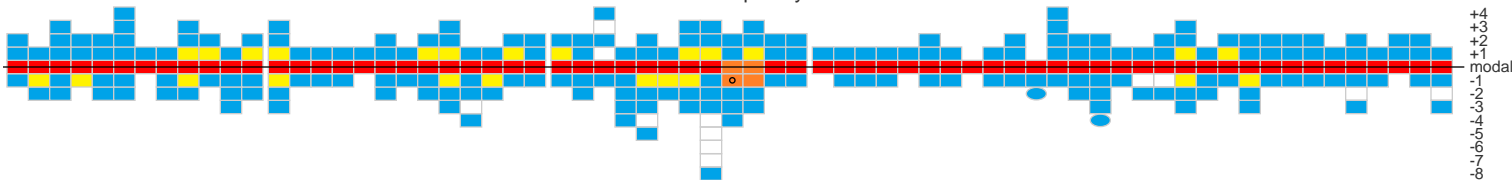
The vertical grey lines are separated 10 generations apart.

R-DF23

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

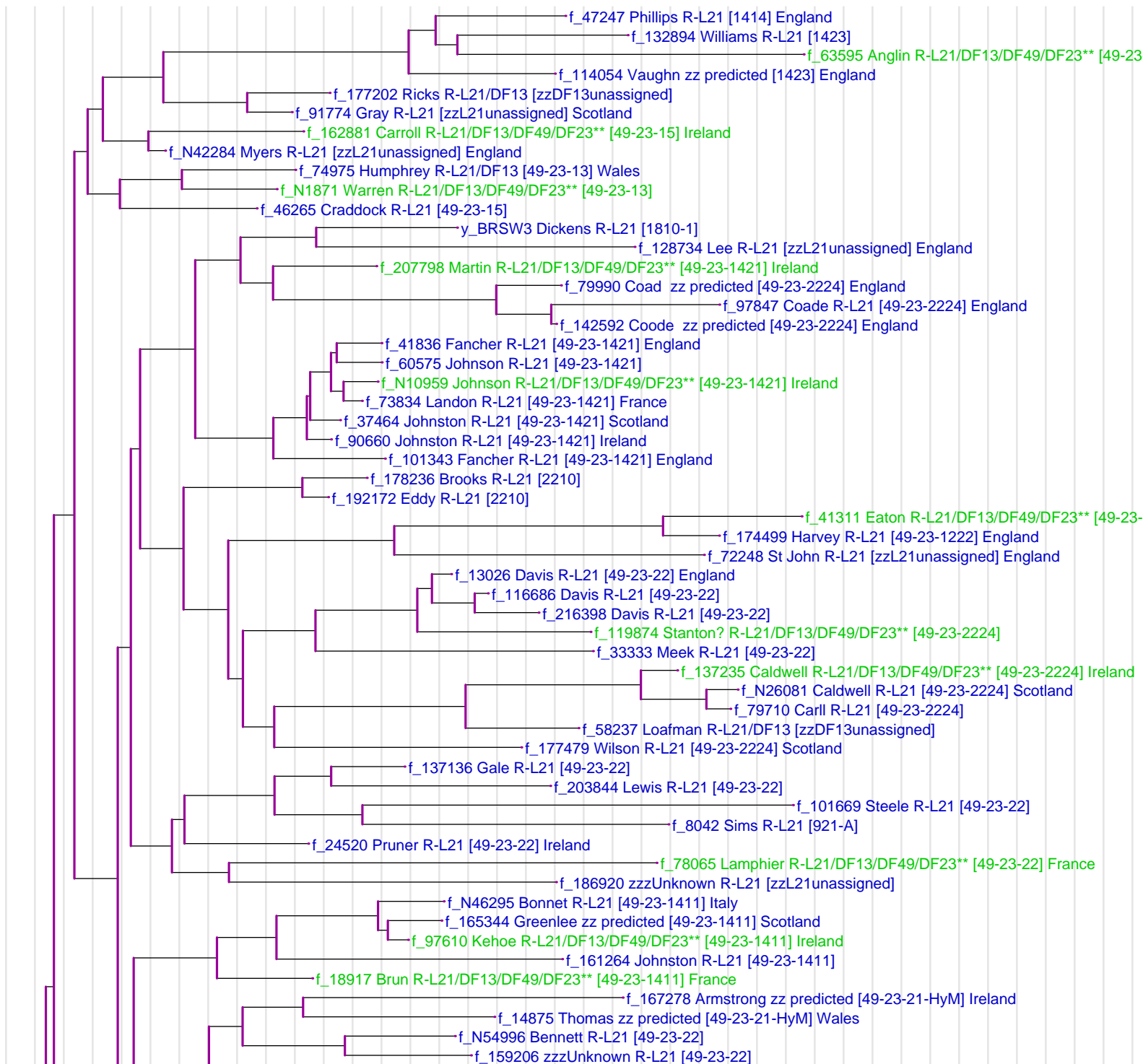


This is the marker distribution for R-DF23. The color indicates the relative frequency of the alleles.

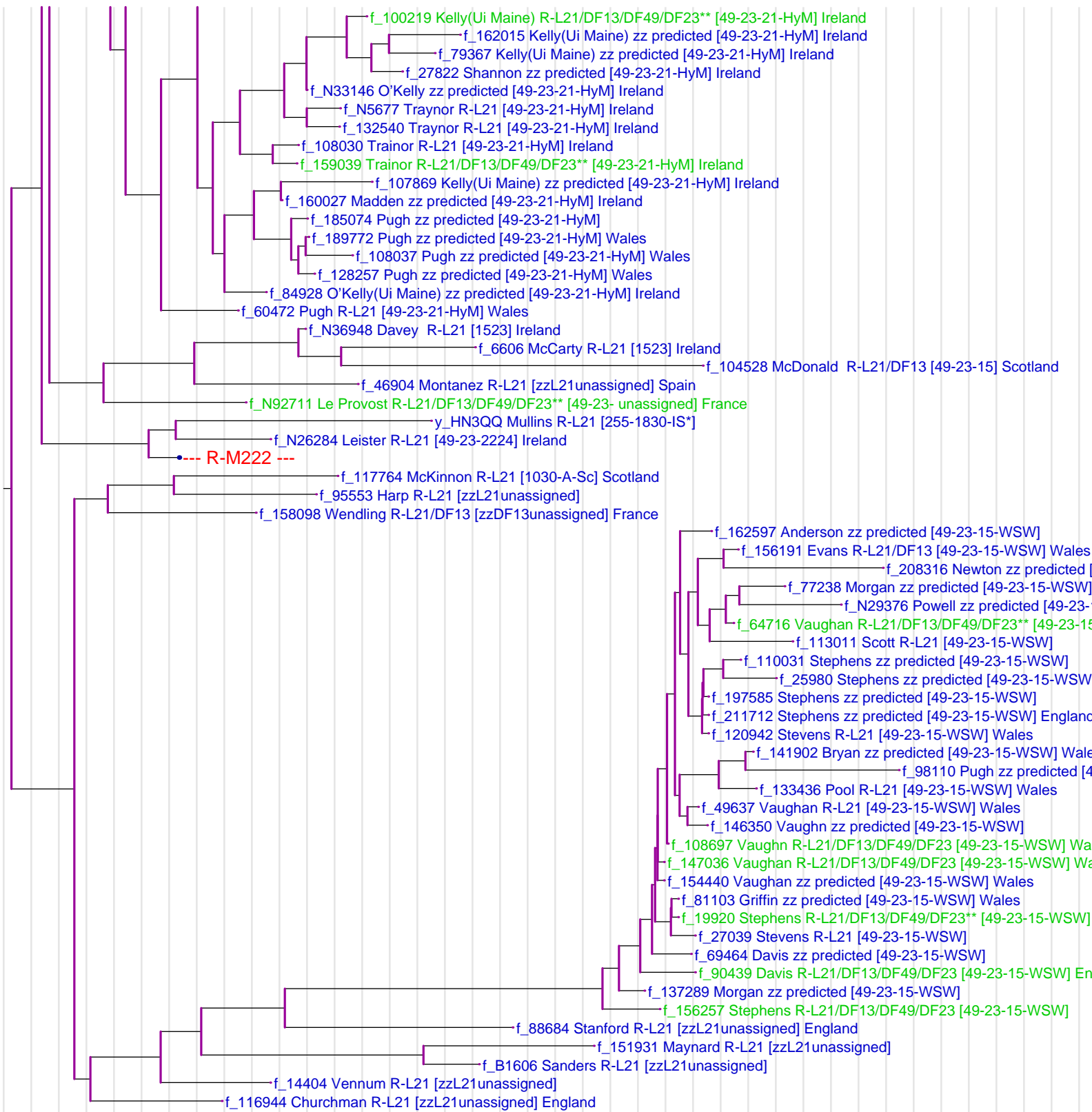


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
823	55141	8005	14.52%	78.26±7.83	1956.43±276.825



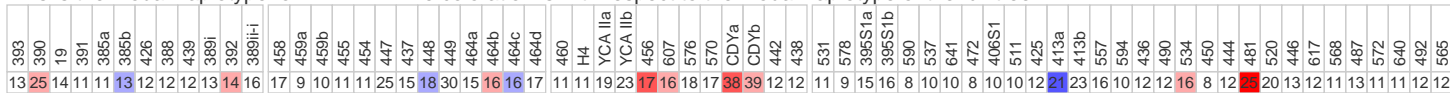
The vertical grey lines are separated 10 generations apart.



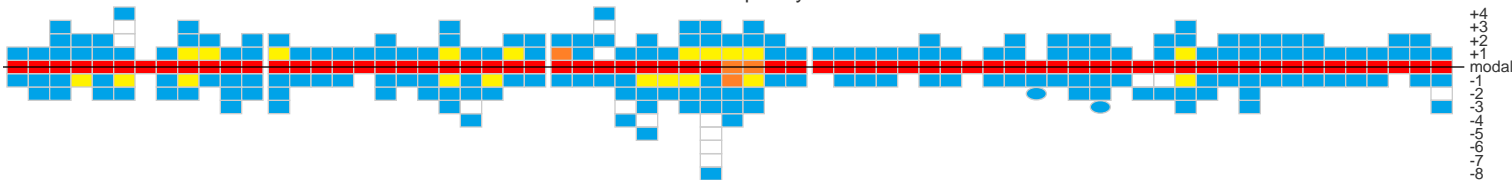
The vertical grey lines are separated 10 generations apart.

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)
709	47503	5422	11.41%	60.52±6.06	1513.01±214.097



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.



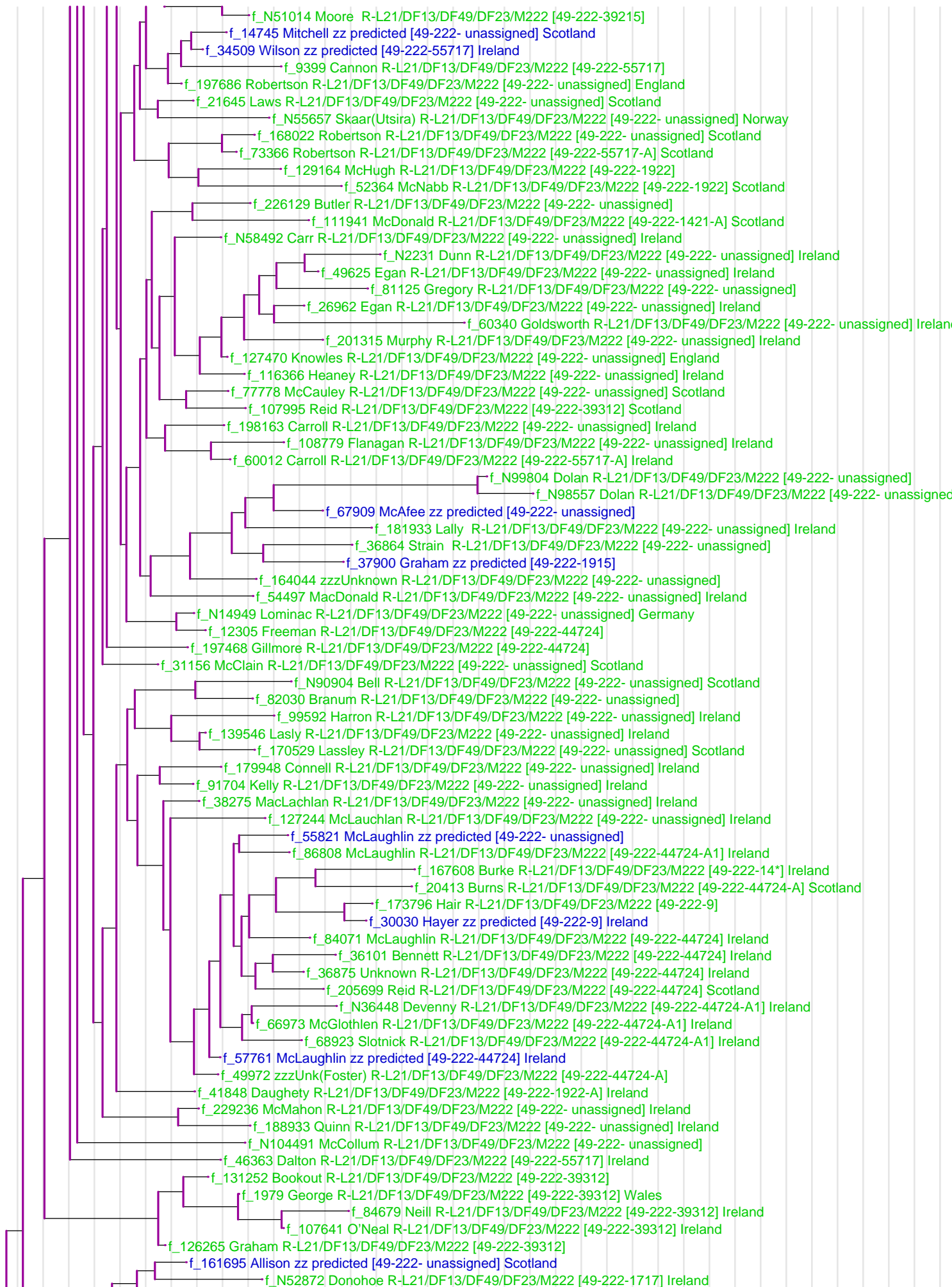
The vertical grey lines are separated 10 generations apart.



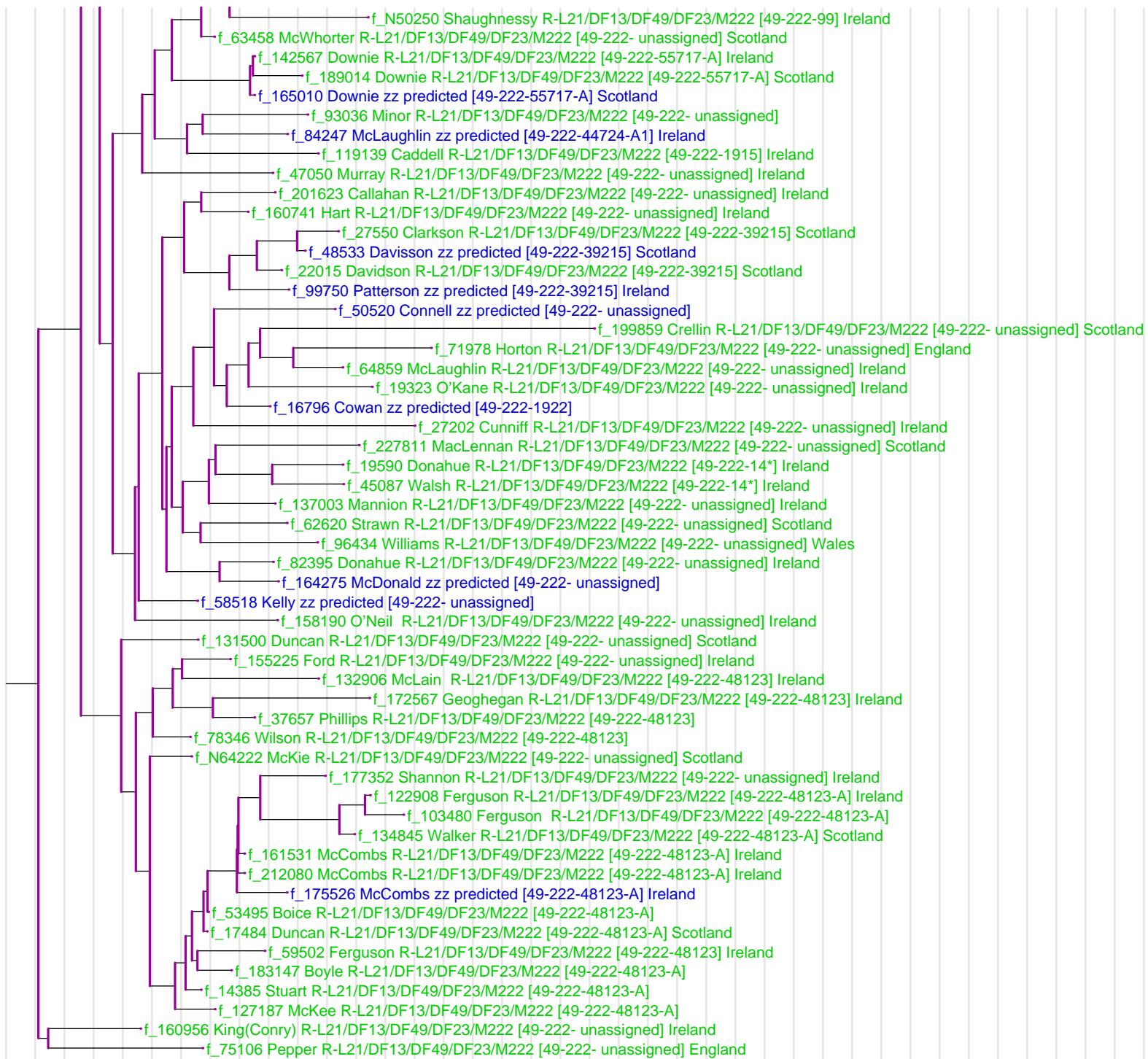
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



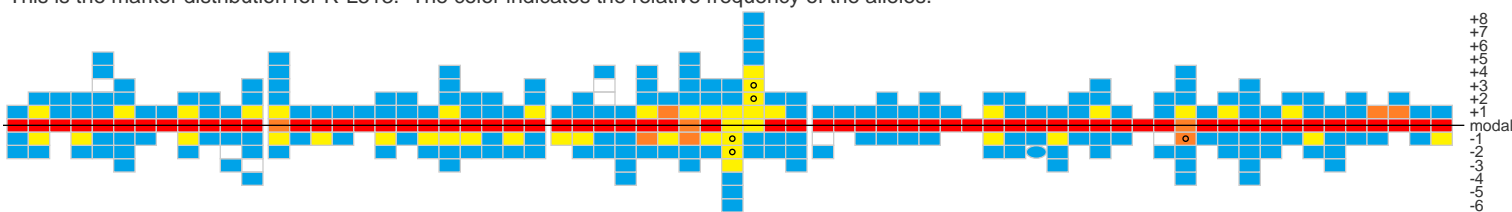
The vertical grey lines are separated 10 generations apart.

R-L513

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

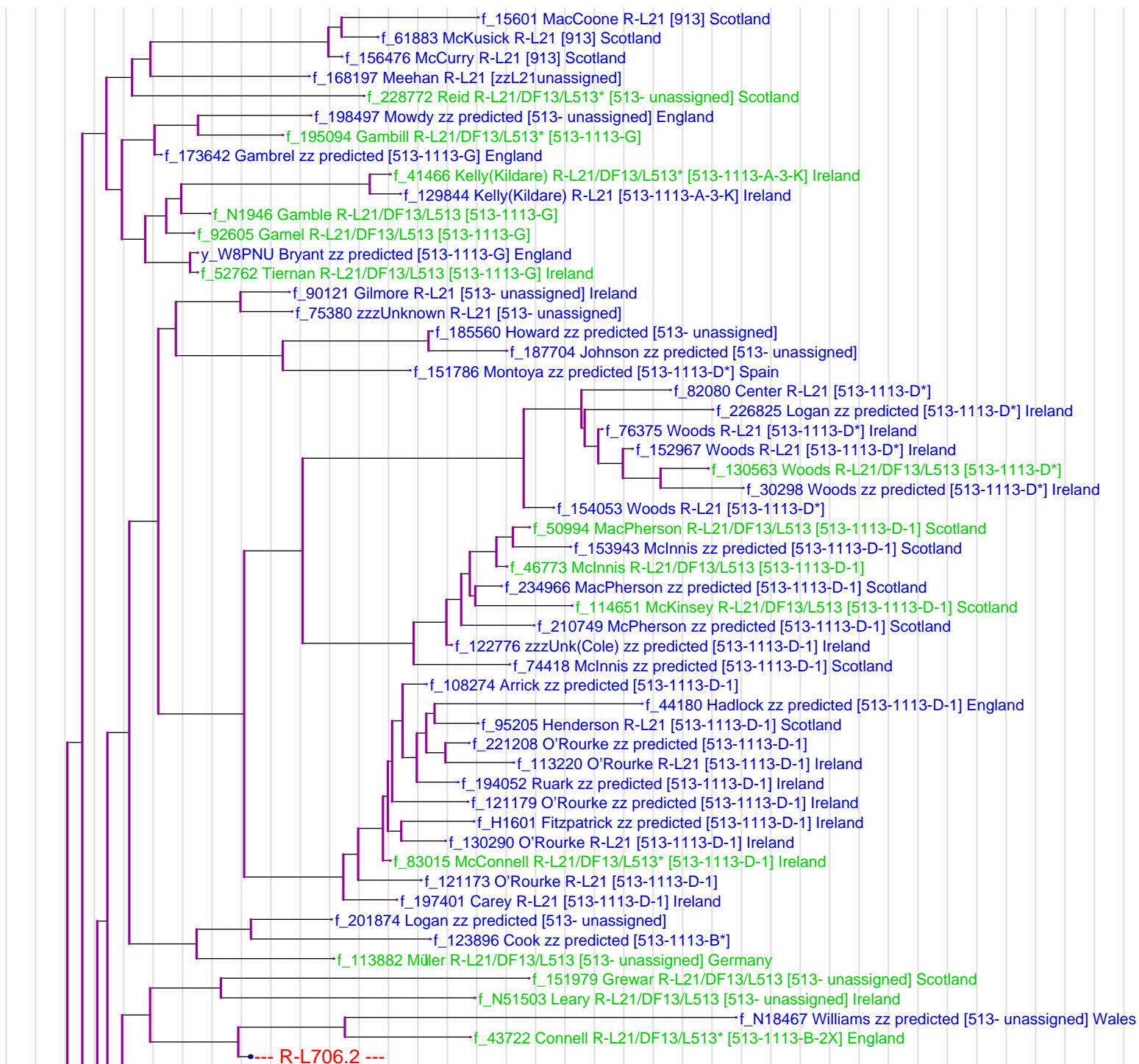
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	466	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565
13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

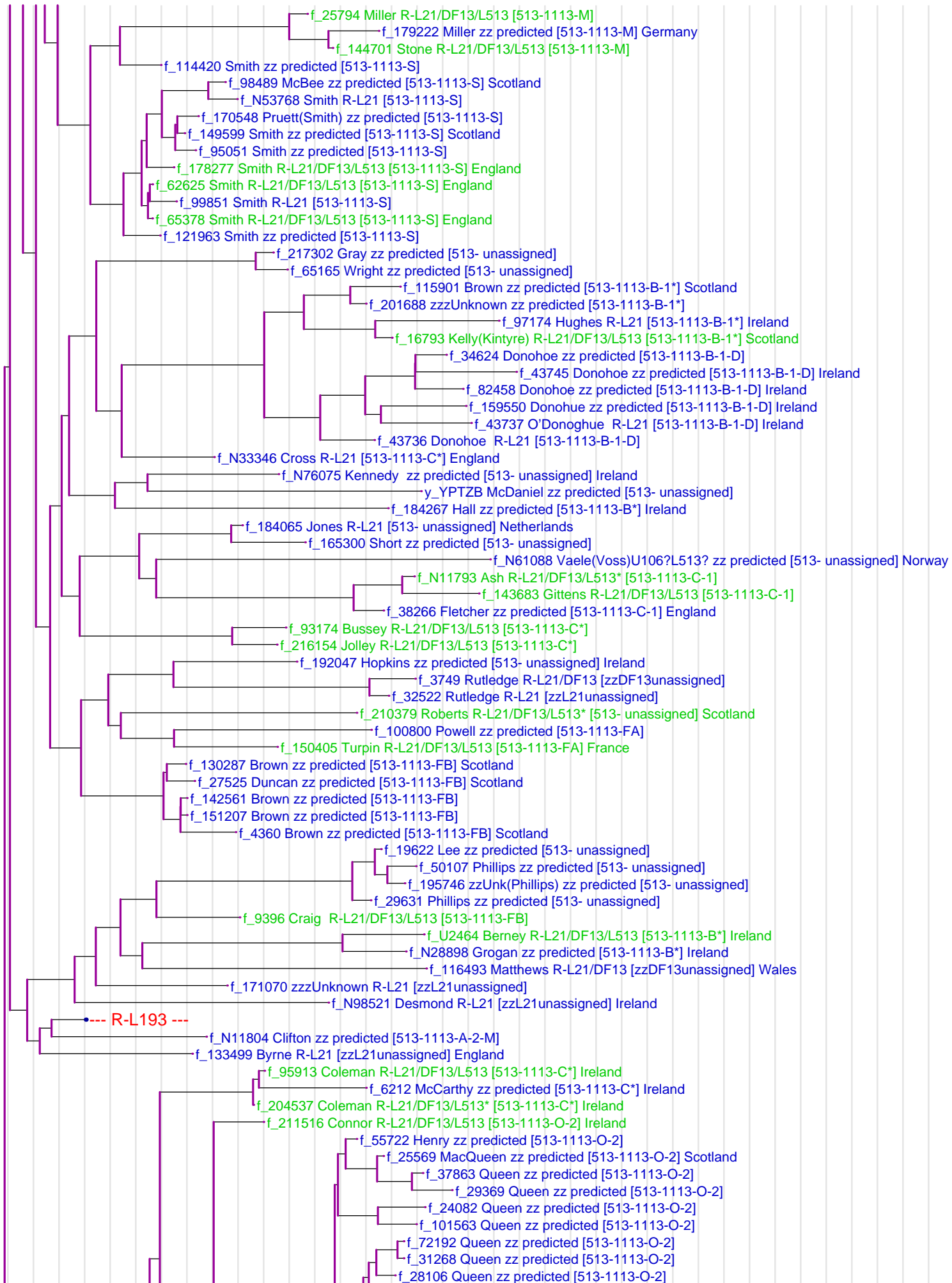


Age Analysis

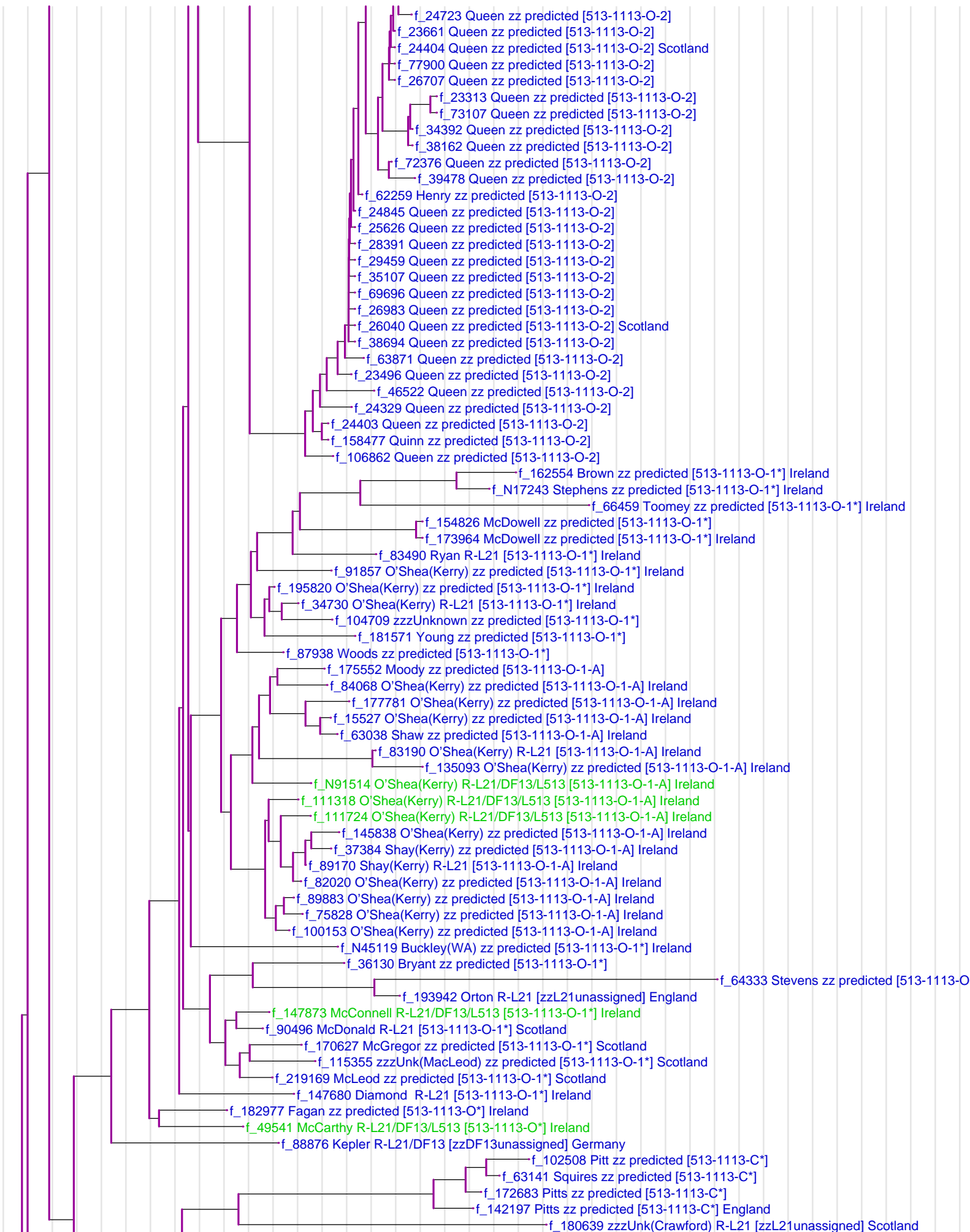
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
900	60300	13214	21.91%	122.99±12.31	3074.78±435.061



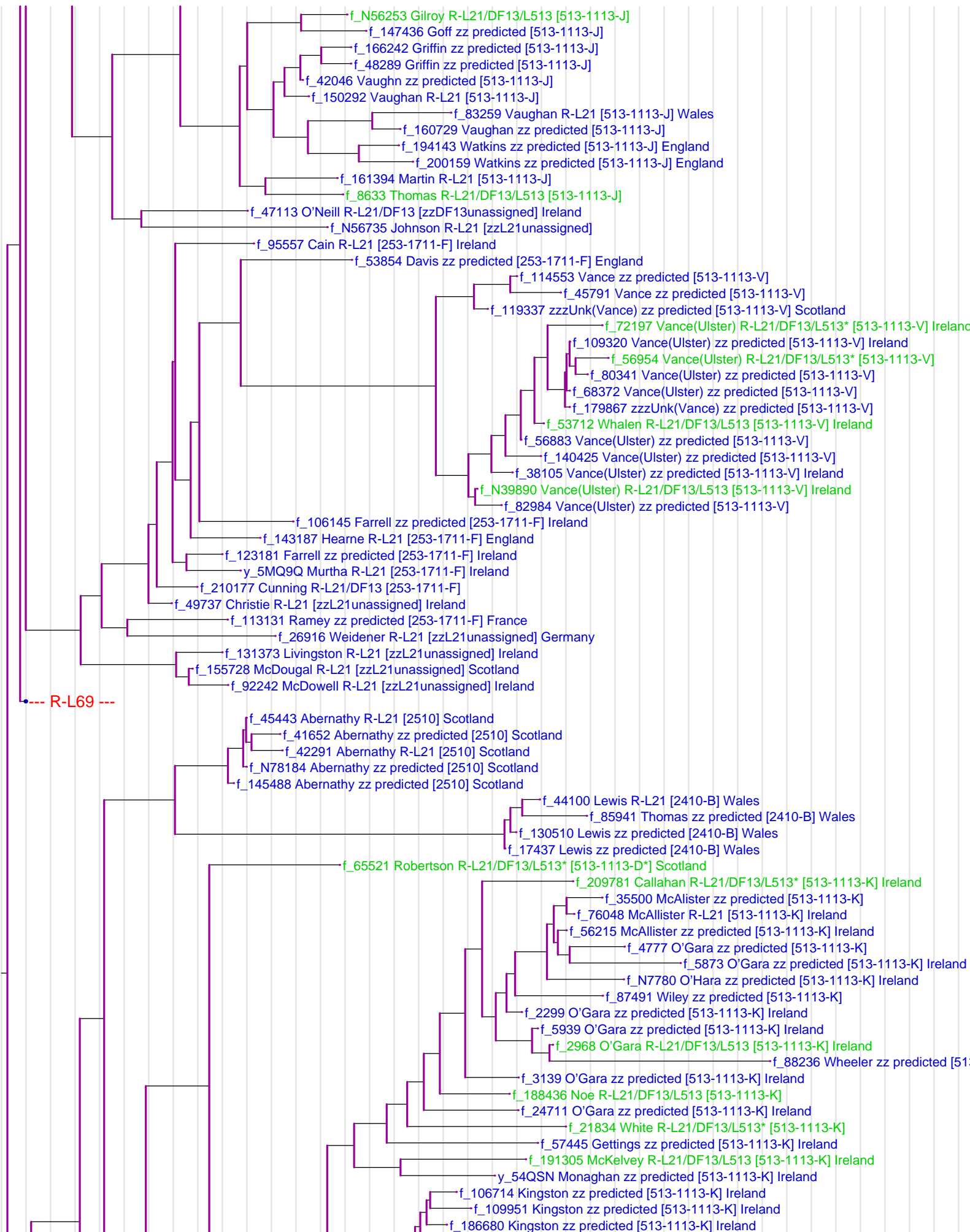
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



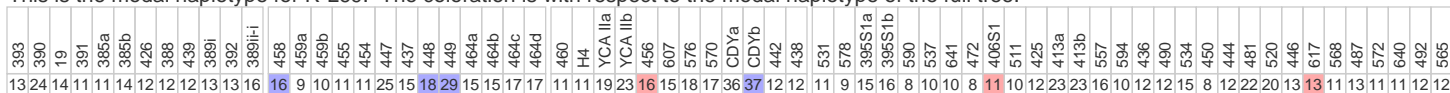
The vertical grey lines are separated 10 generations apart.



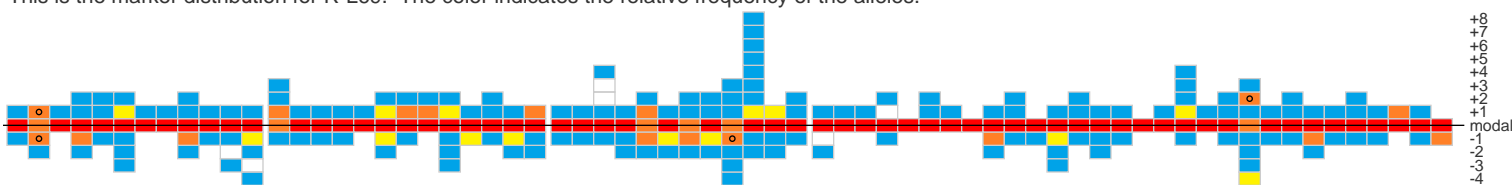
The vertical grey lines are separated 10 generations apart.

R-L69

This is the modal haplotype for R-L69. The coloration is with respect to the modal haplotype of the full tree.

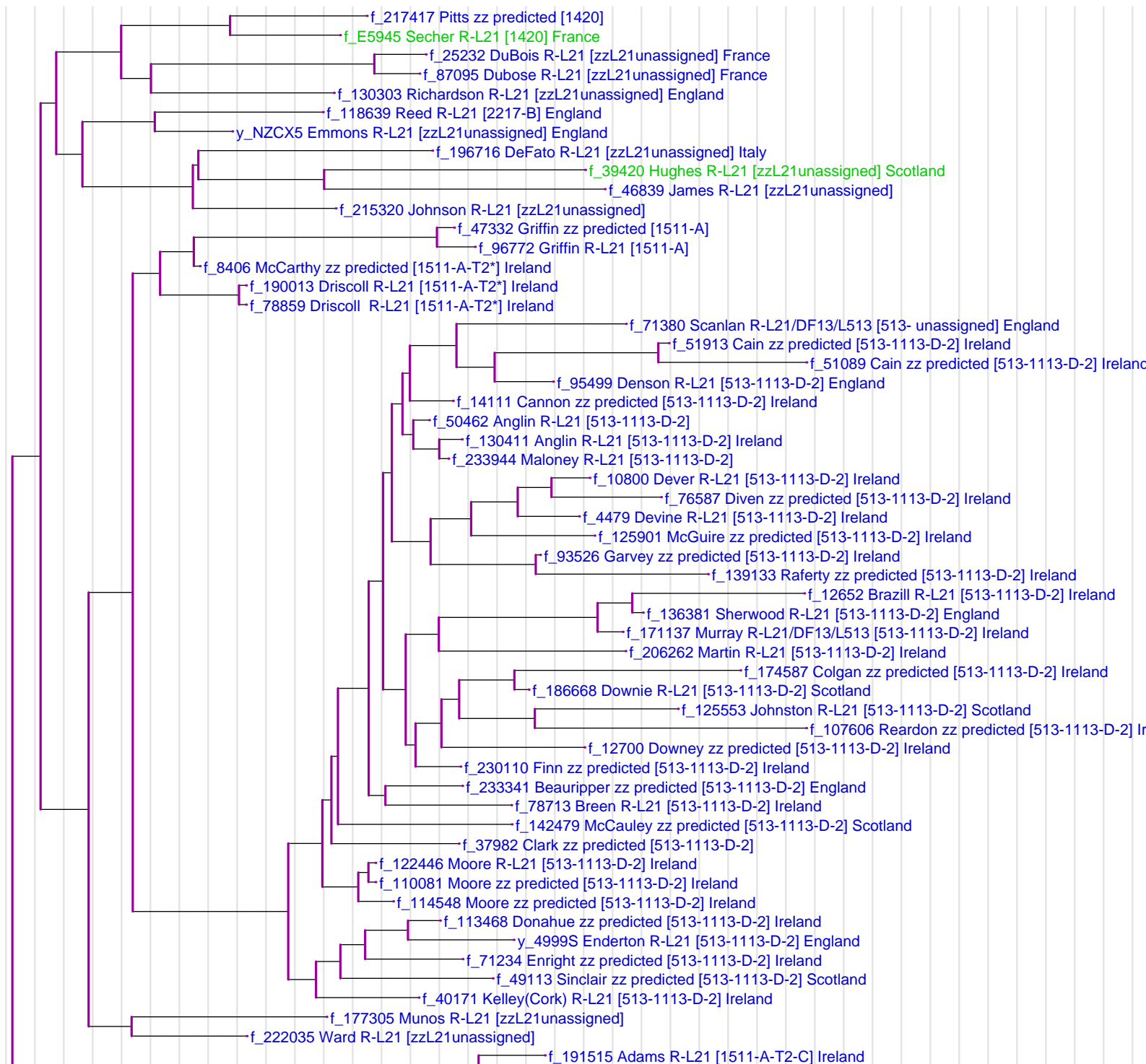


This is the marker distribution for R-L69. The color indicates the relative frequency of the alleles.

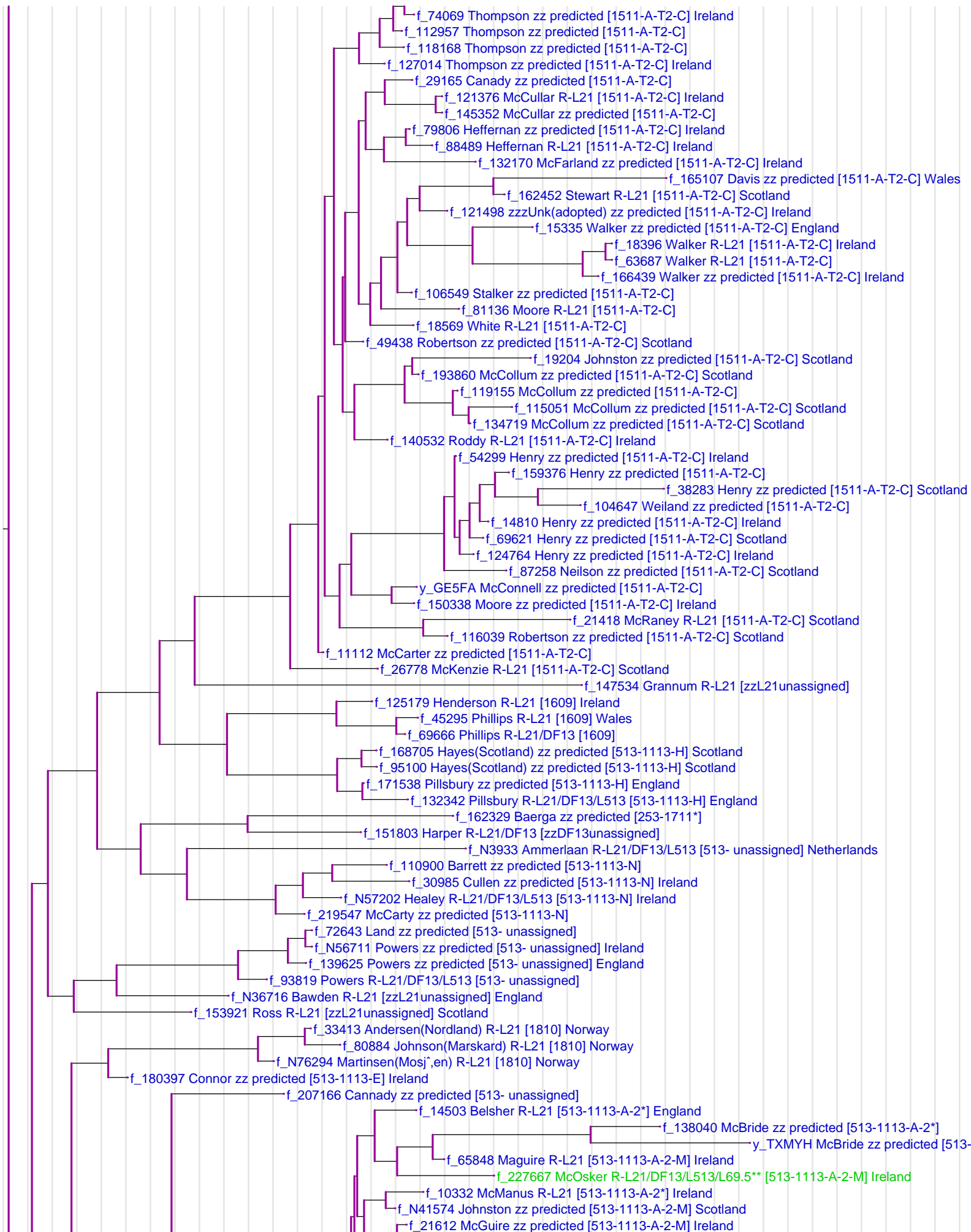


Age Analysis

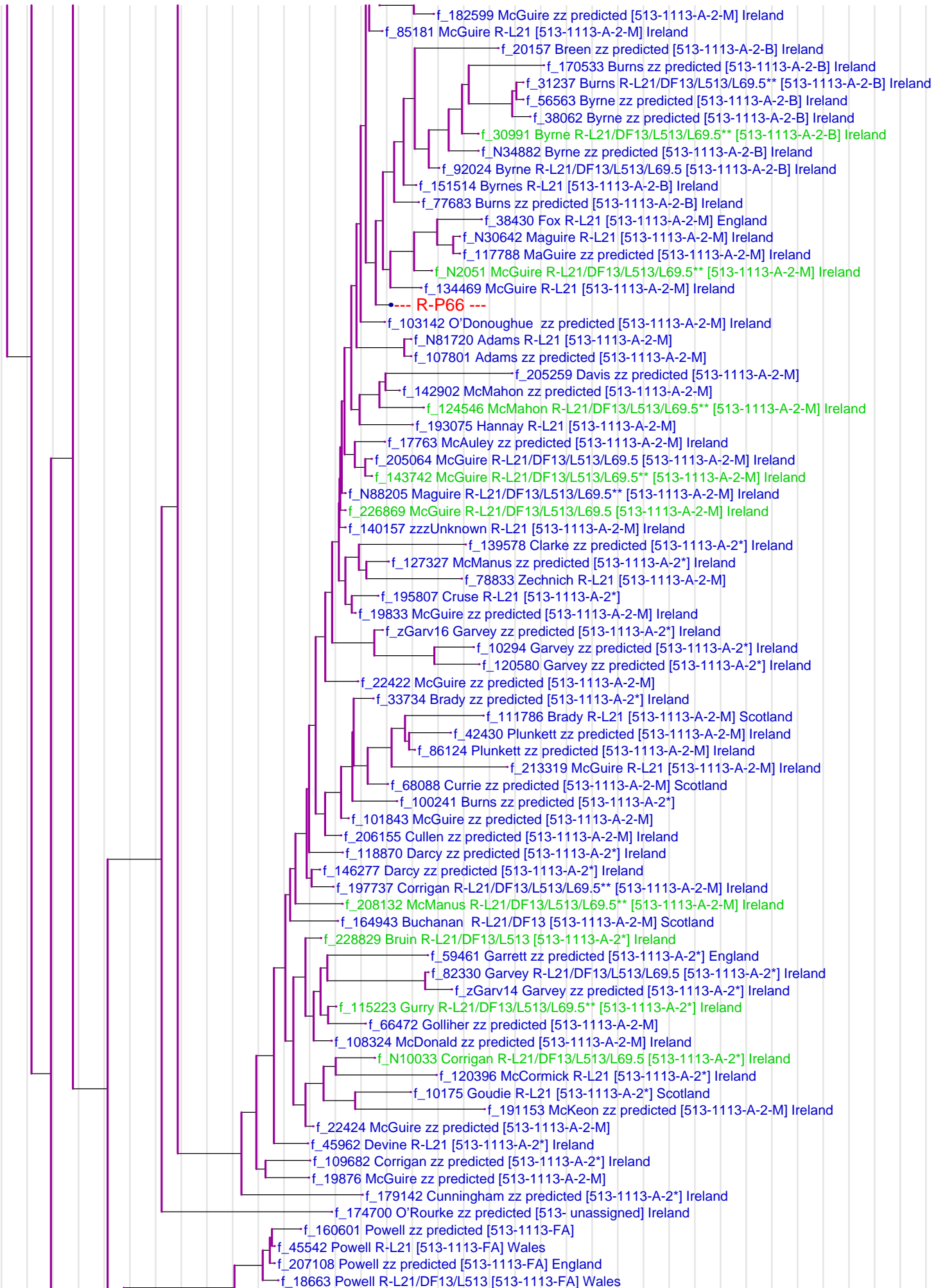
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
253	16951	3724	21.97%	123.34±12.38	3083.51±436.865



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.

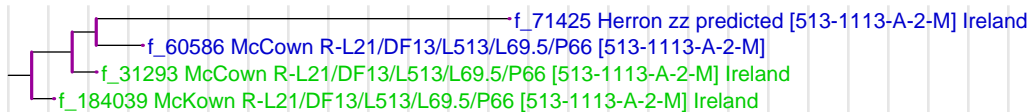
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565
13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

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



Age Analysis

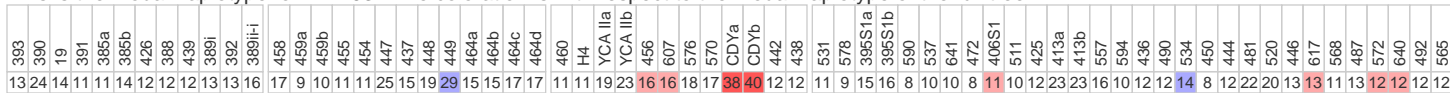
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	19	7.09%	36.75±4.35	918.748±142.334



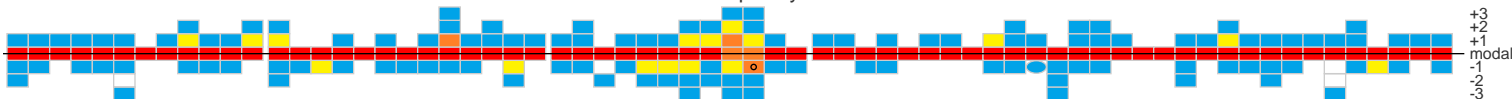
The vertical grey lines are separated 10 generations apart.

R-L193

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

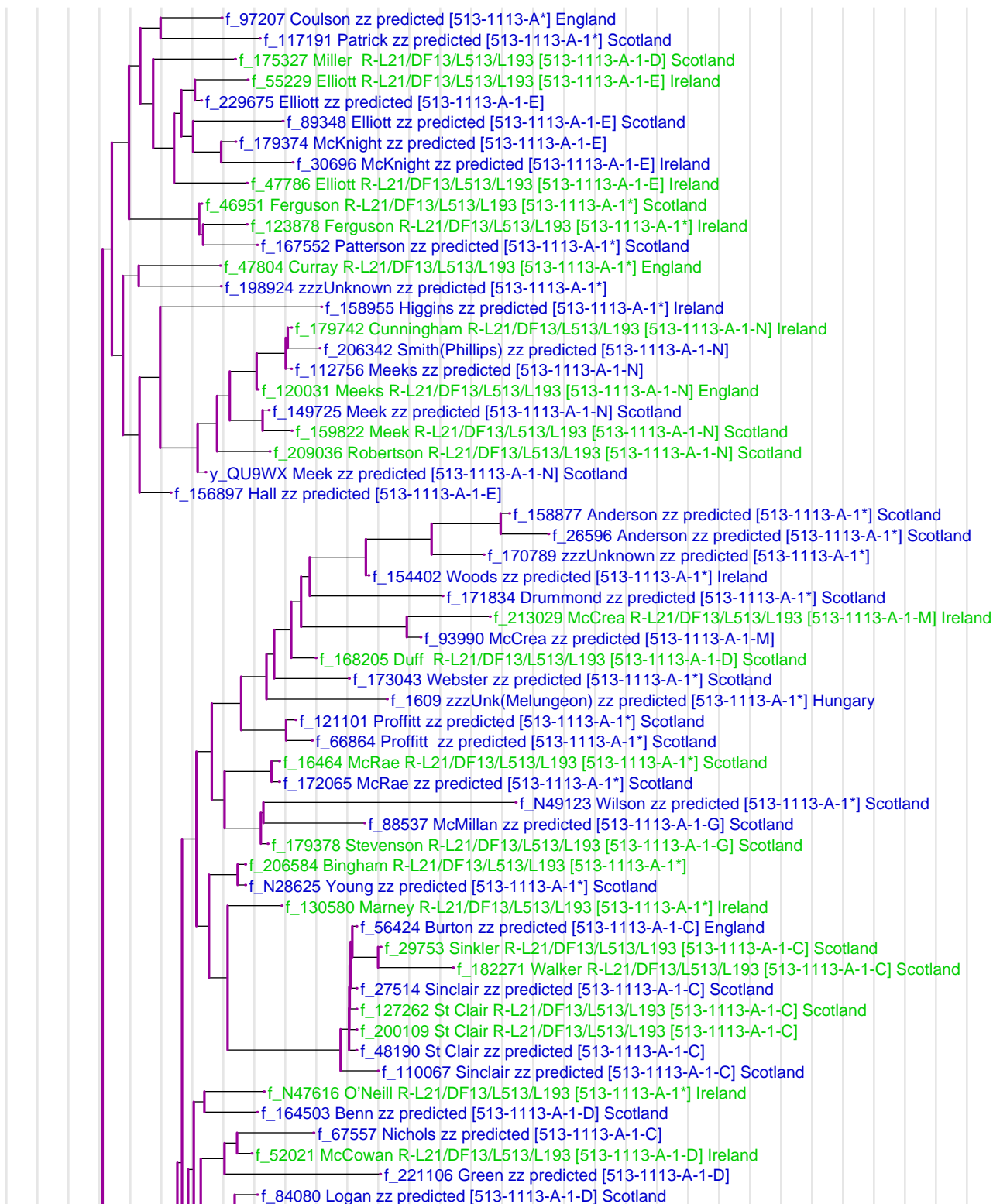


This is the marker distribution for R-L193. The color indicates the relative frequency of the alleles.

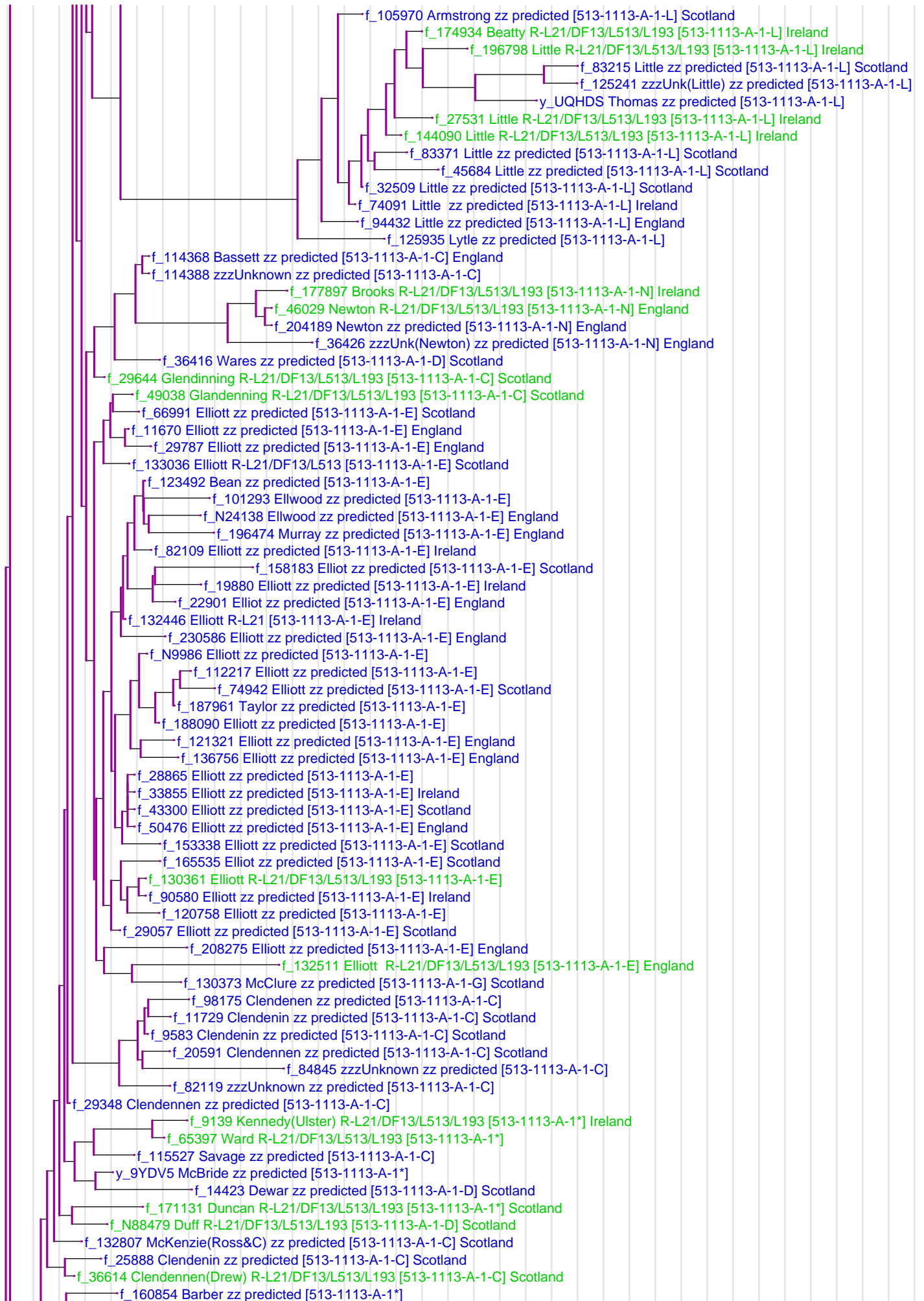


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
268	17956	1846	10.28%	54.19±5.44	1354.66±191.872



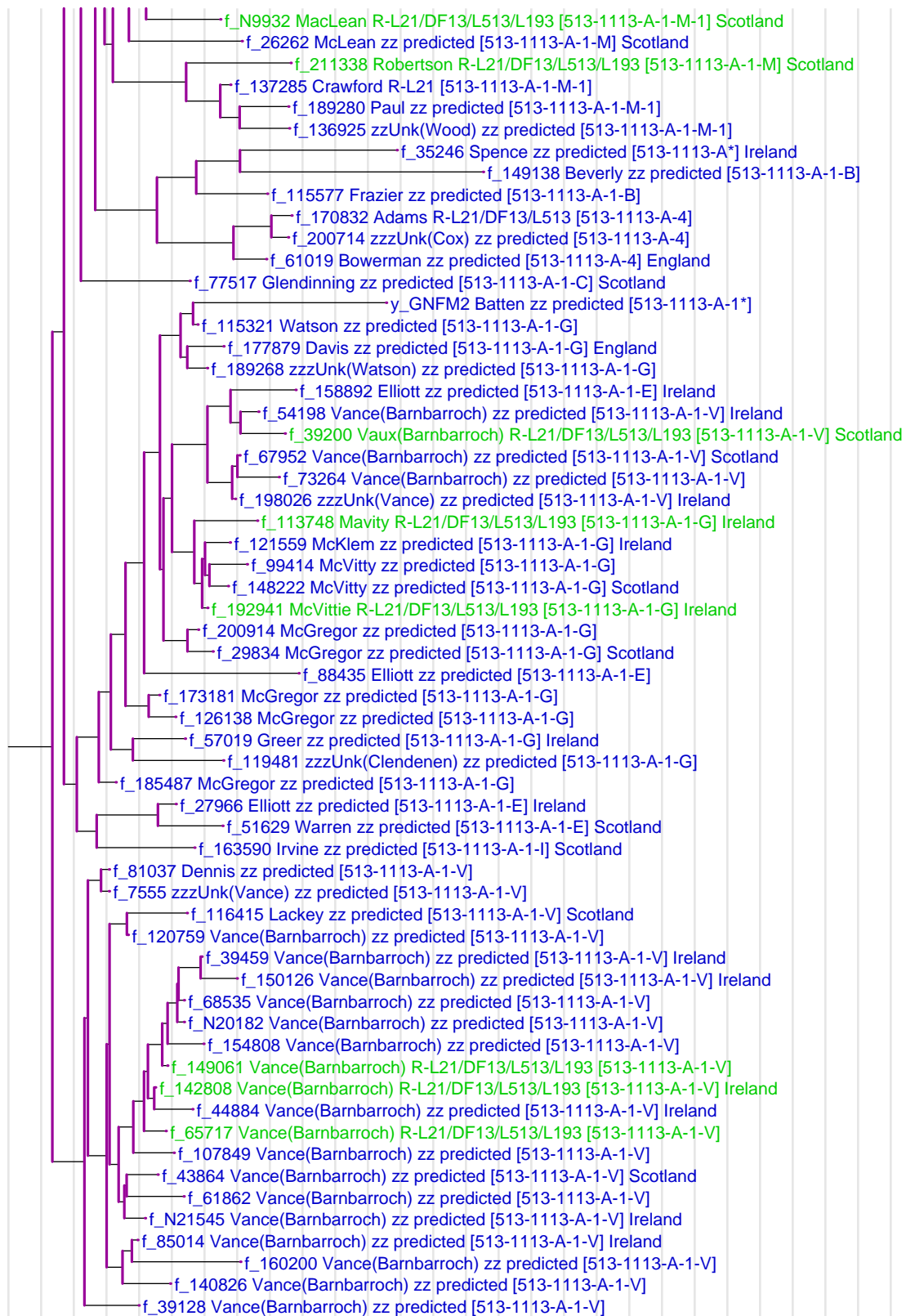
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



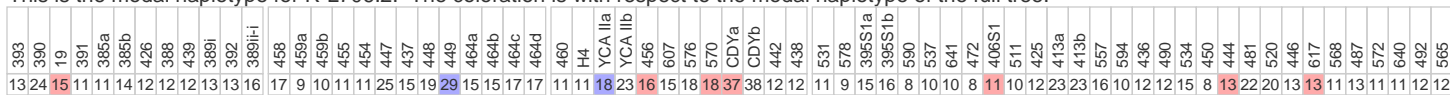
The vertical grey lines are separated 10 generations apart.



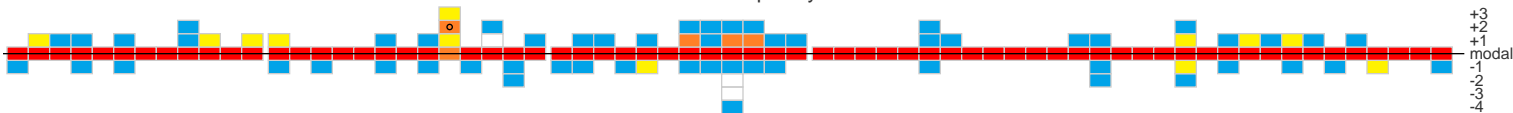
The vertical grey lines are separated 10 generations apart.

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.

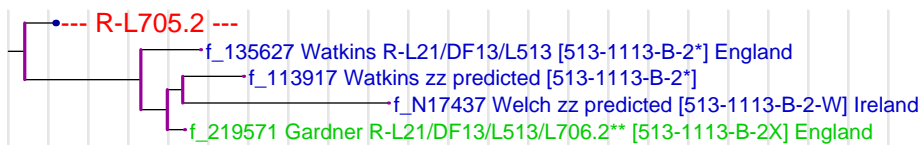


This is the marker distribution for R-L706.2. The color indicates the relative frequency of the alleles.



Age Analysis

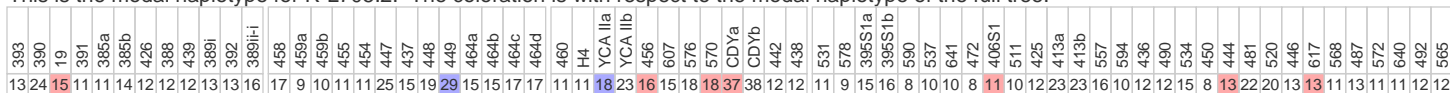
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
47	3149	289	9.18%	48.09±4.89	1202.32±171.504



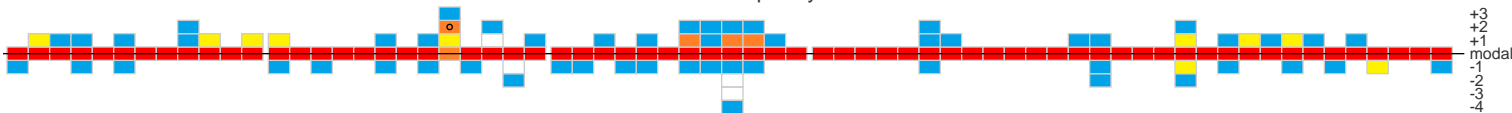
The vertical grey lines are separated 10 generations apart.

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.

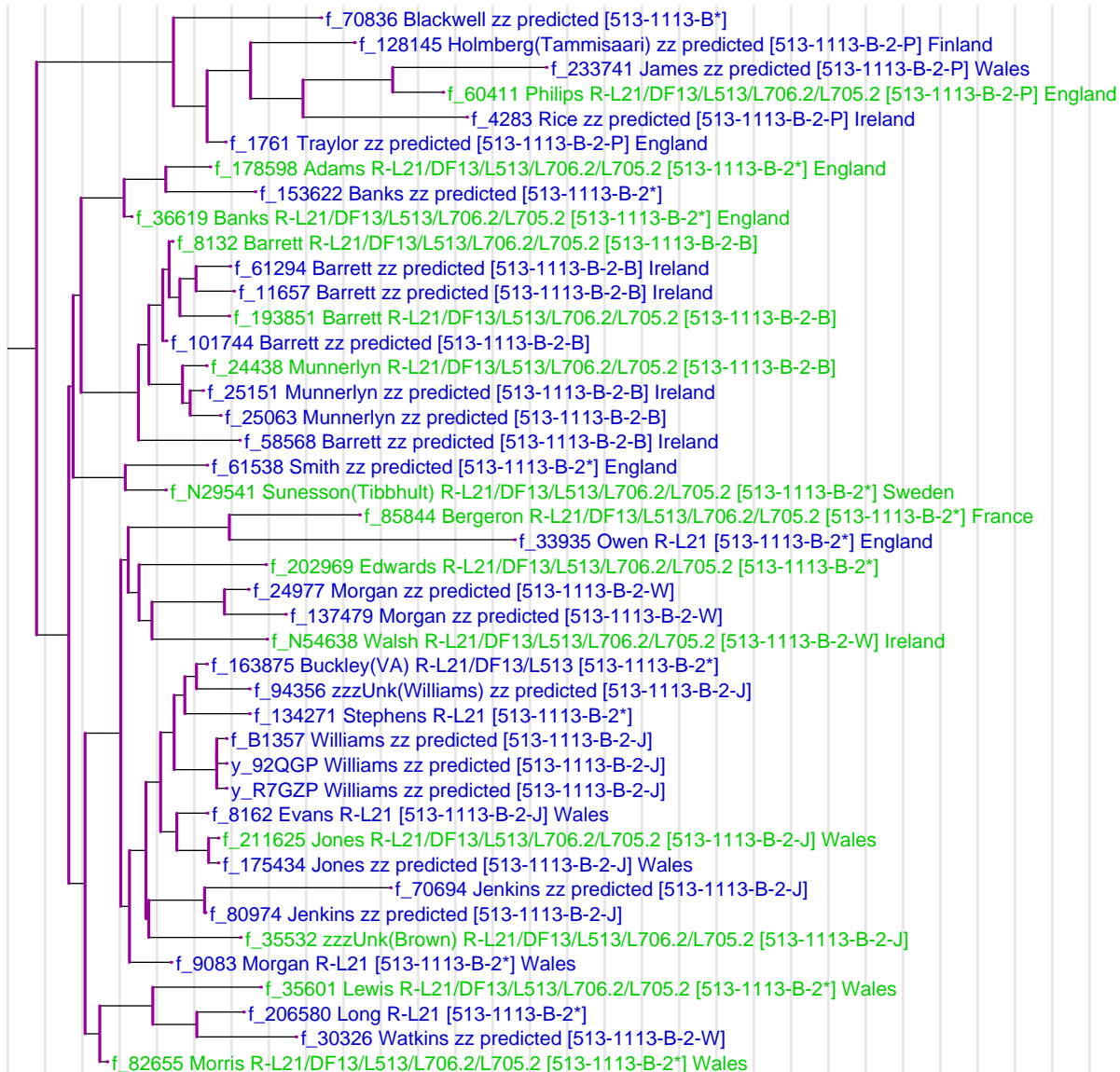


This is the marker distribution for R-L705.2. The color indicates the relative frequency of the alleles.



Age Analysis

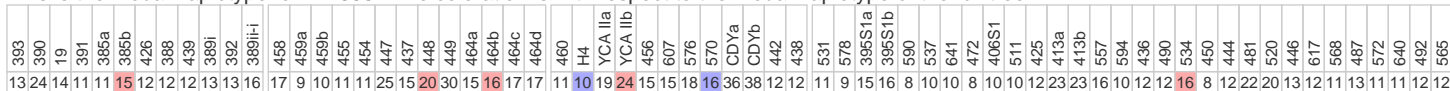
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
43	2881	263	9.13%	47.83±4.87	1195.63±170.685



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.

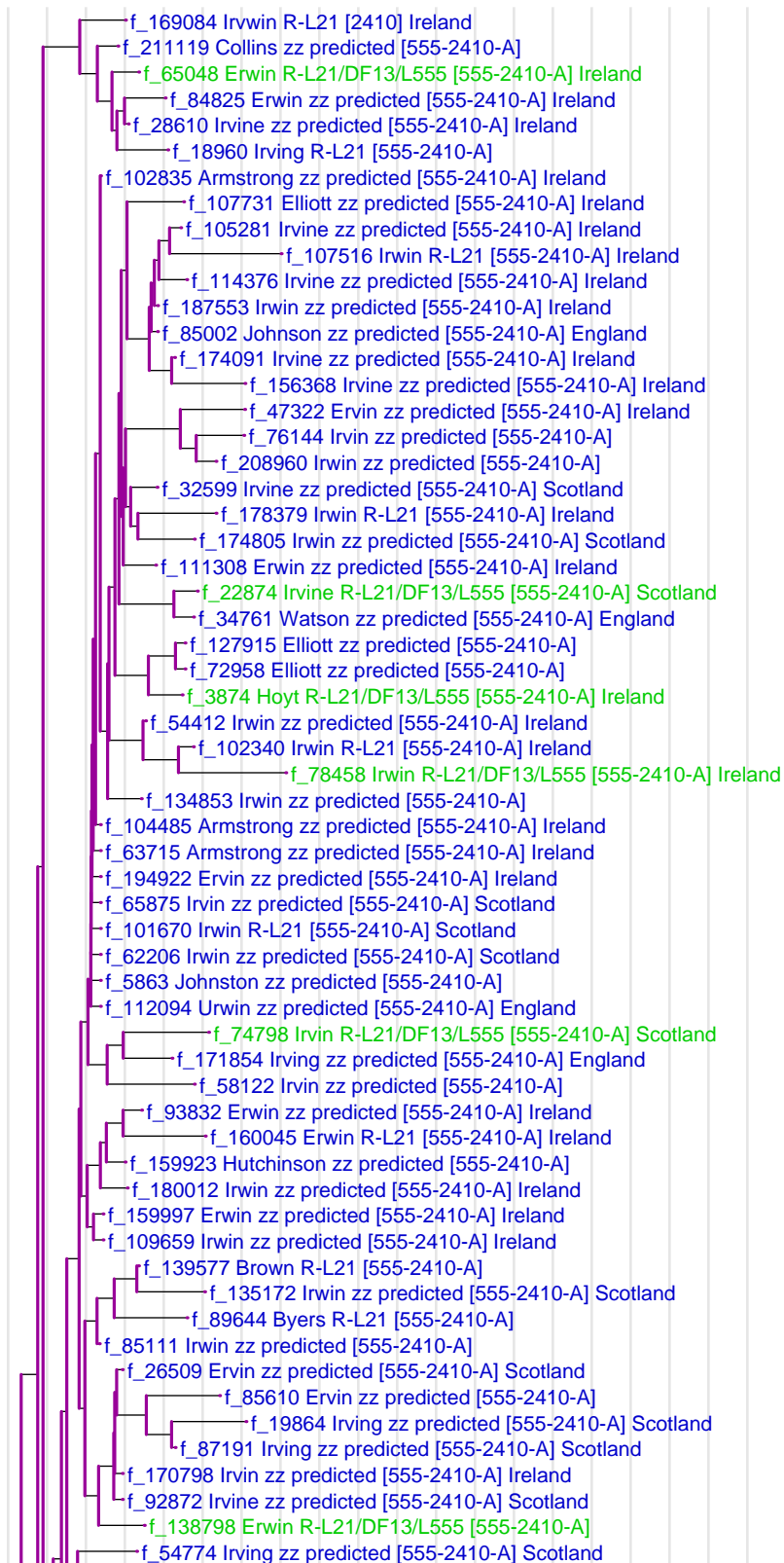


This is the marker distribution for R-L555. The color indicates the relative frequency of the alleles.

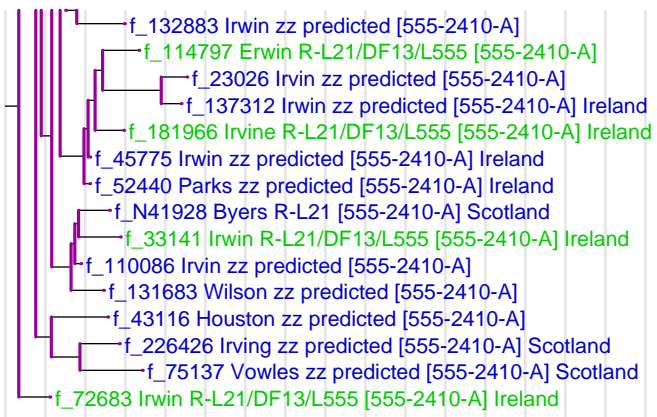


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
75	5025	173	3.44%	17.52±1.77	437.885±62.2443



The vertical grey lines are separated 10 generations apart.



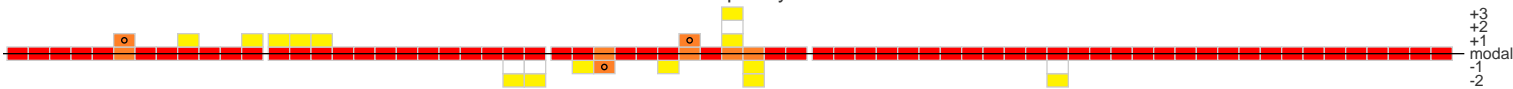
The vertical grey lines are separated 10 generations apart.

R-L96

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

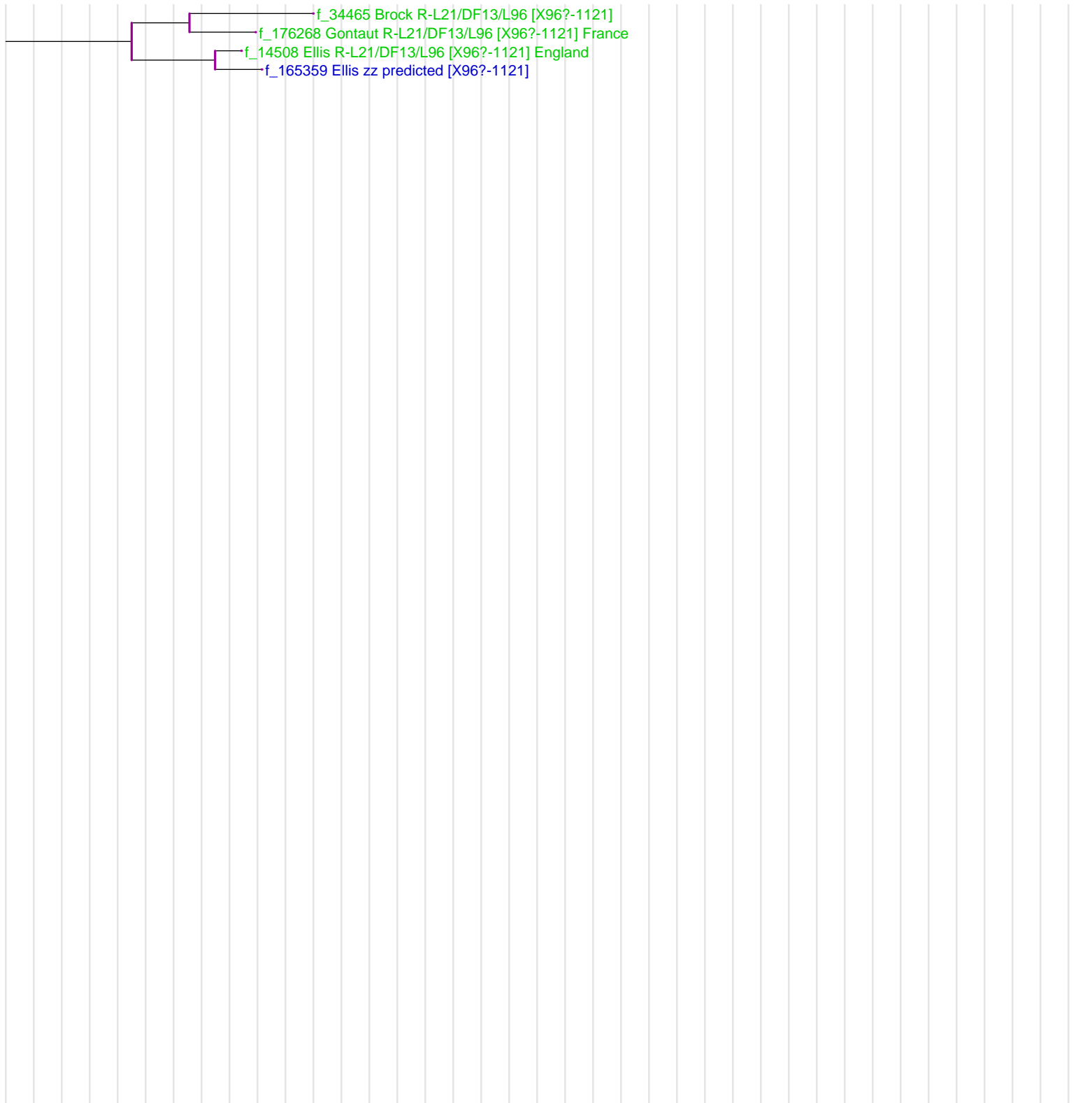
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	481	520	446	617	568	487	572	640	492	565	
13	24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

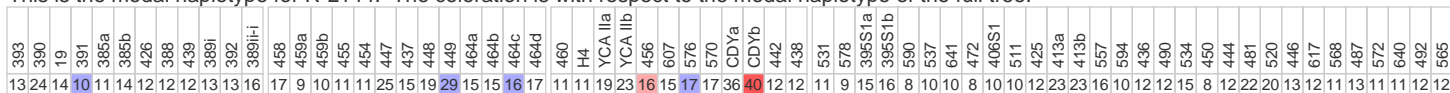
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
4	268	26	9.70%	50.98±6.05	1274.46±197.858



The vertical grey lines are separated 10 generations apart.

R-L144

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

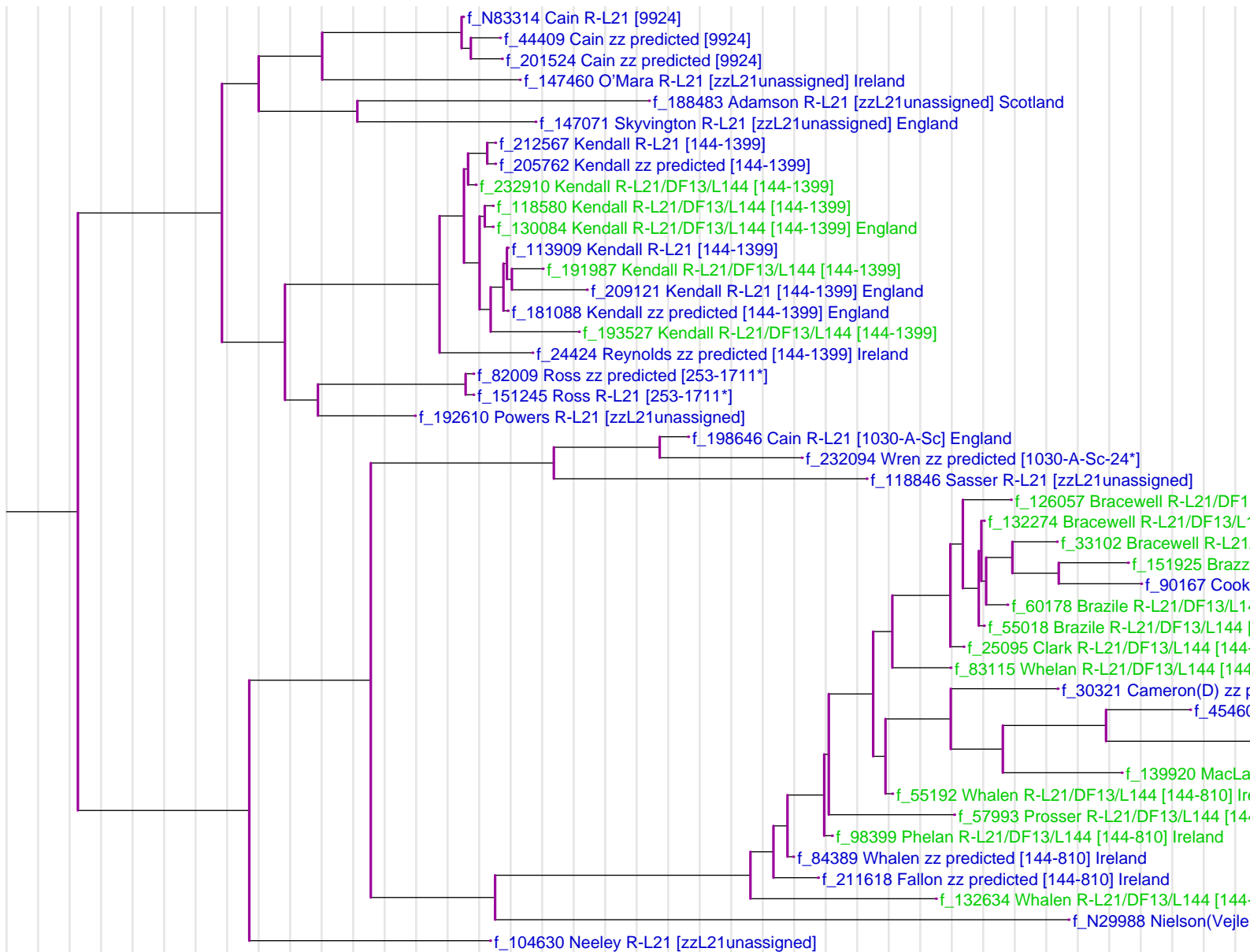


This is the marker distribution for R-L144. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
45	3015	796	26.40%	151.95±15.51	3798.73±542.9



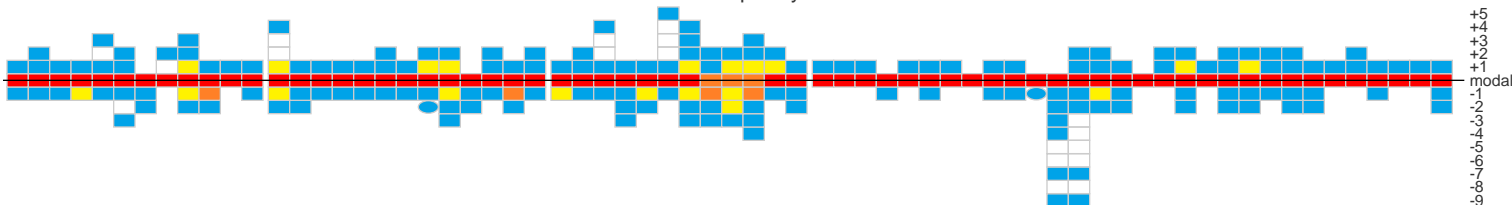
The vertical grey lines are separated 10 generations apart.

R-Z255

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

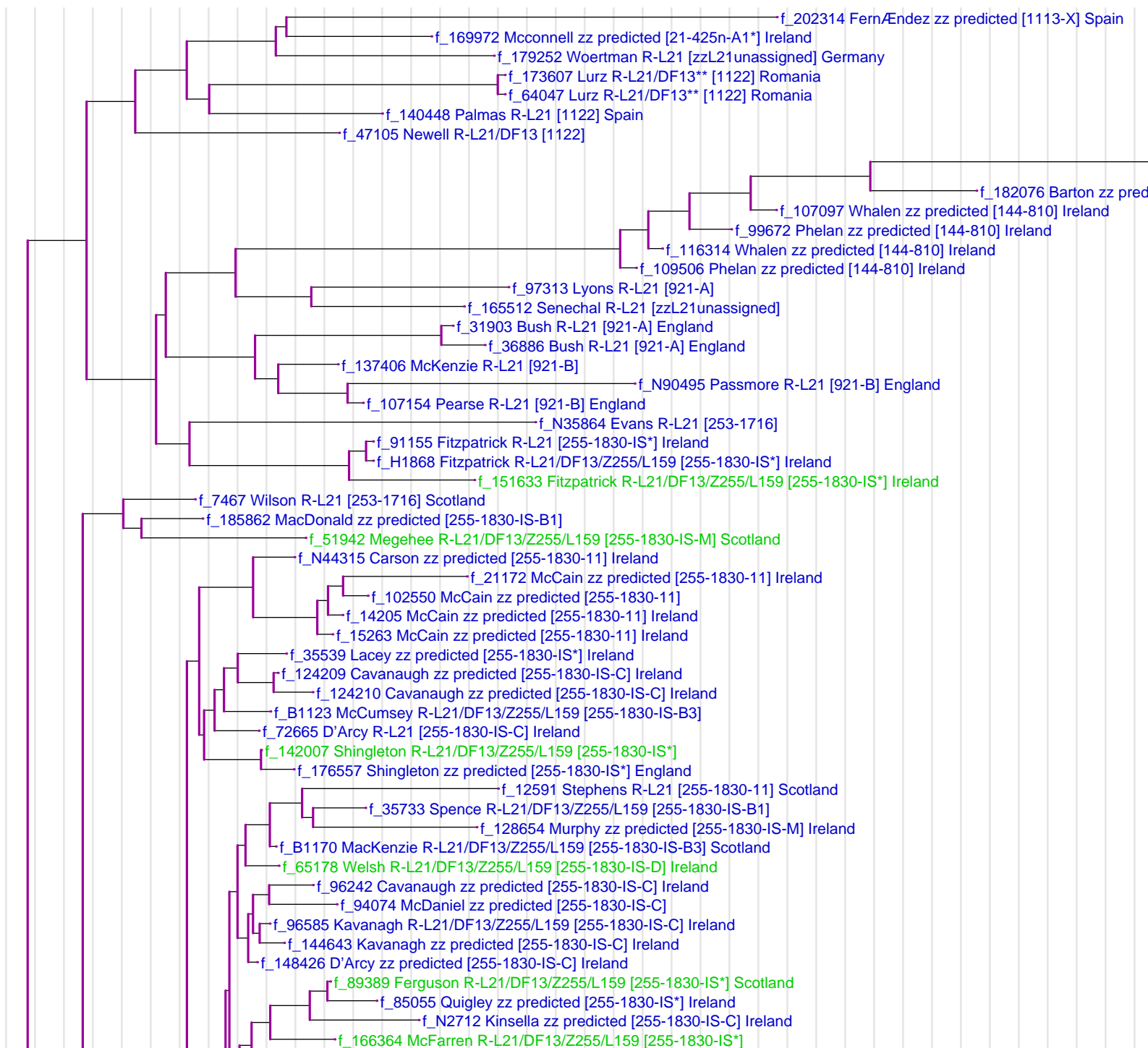
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	466	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	446	617	568	487	572	640	492	565	
13	24	14	11	14	12	12	12	14	13	16	17	9	10	11	11	25	15	18	30	15	15	17	17	11	11	11	19	23	16	15	18	18	24	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

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

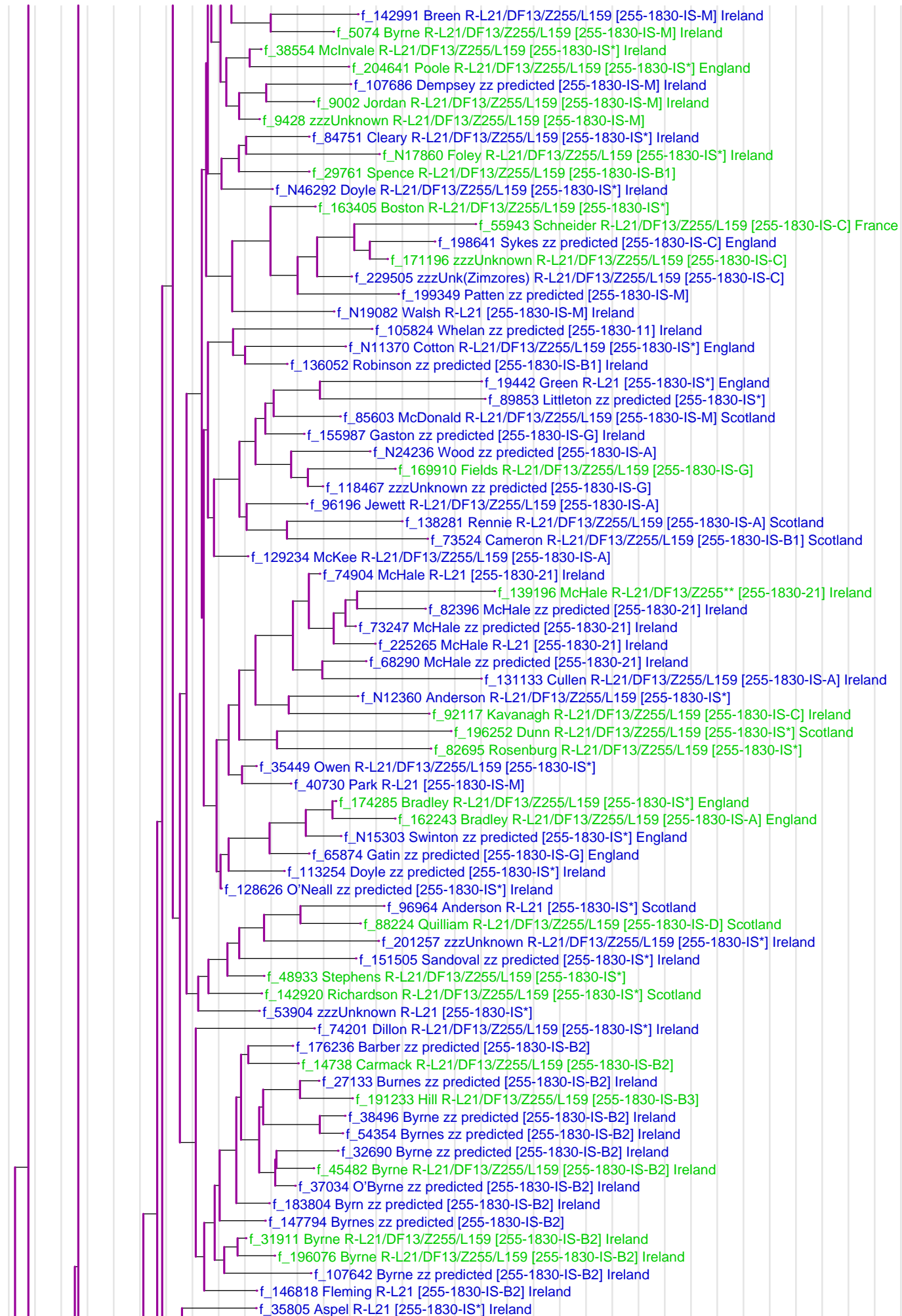


Age Analysis

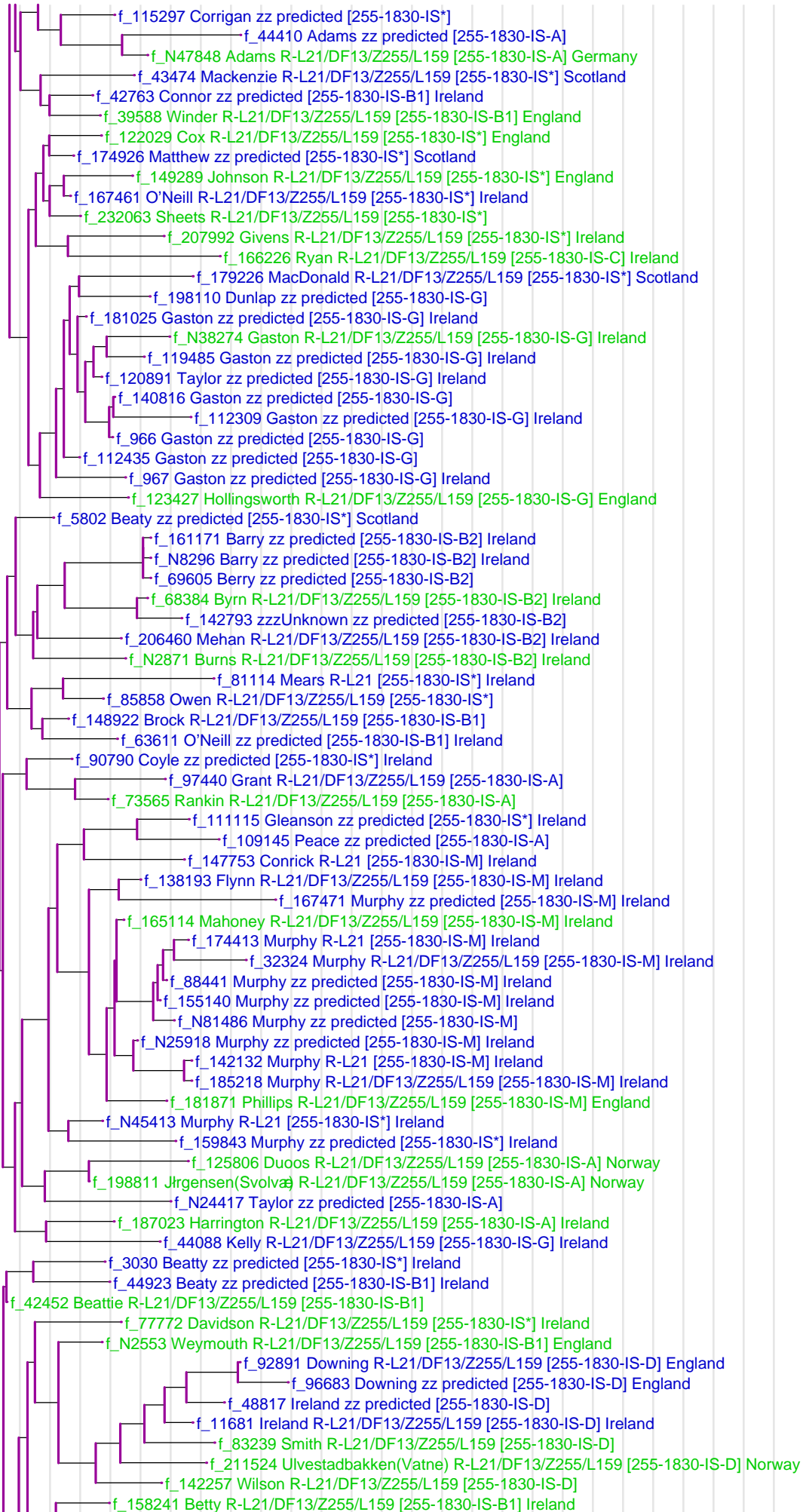
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
281	18827	2678	14.22%	76.56±7.68	1913.92±271.082



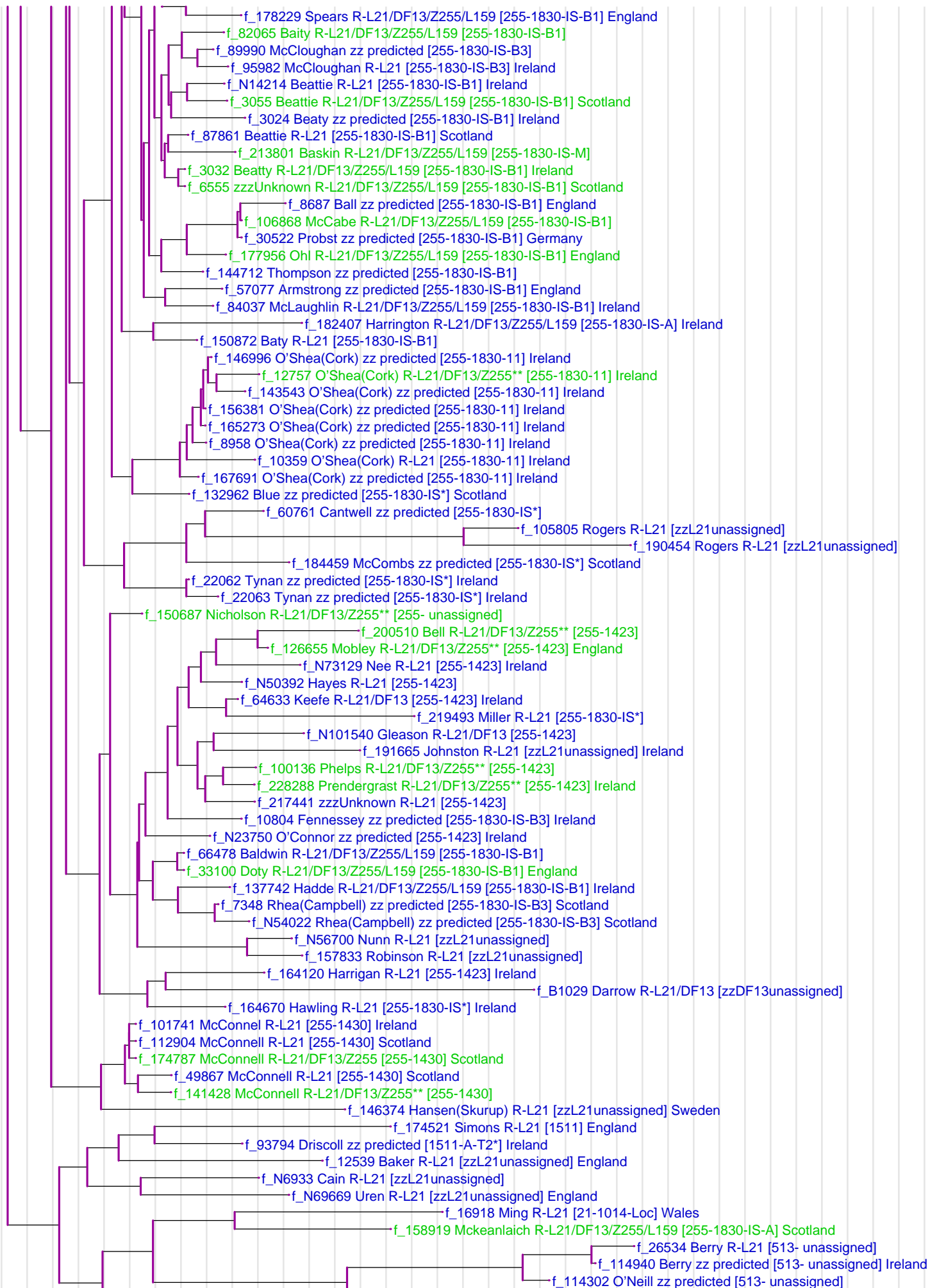
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

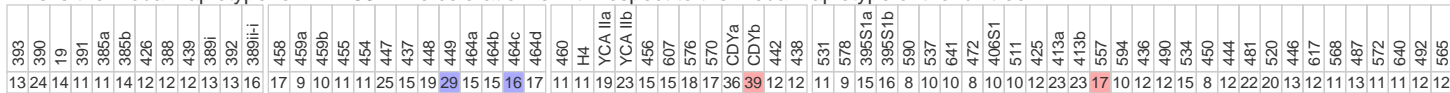


The vertical grey lines are separated 10 generations apart.

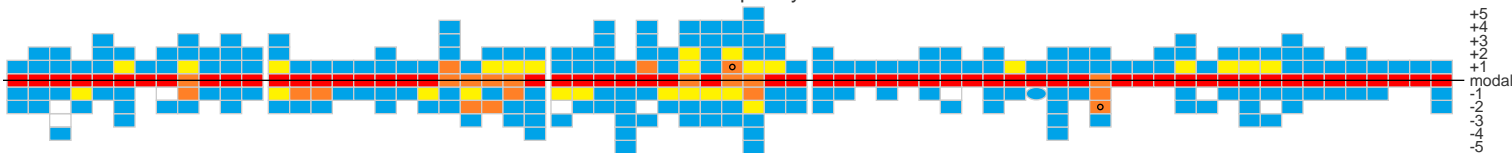
f_180800 McCroskey R-L21 [zzL21unassigned] Scotland
f_N25036 Coody R-L21 [zzL21unassigned]

R-Z253

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

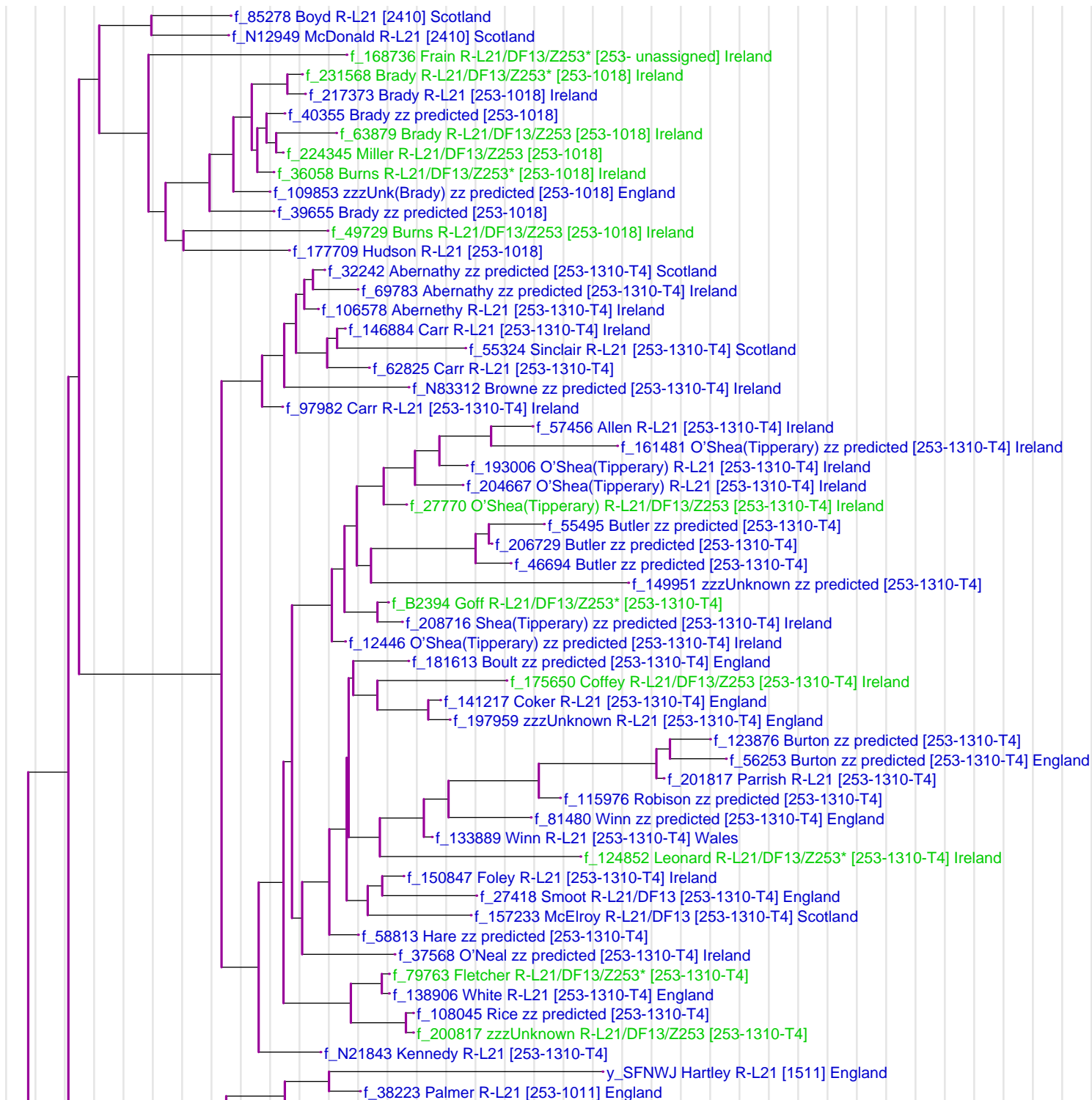


This is the marker distribution for R-Z253. The color indicates the relative frequency of the alleles.

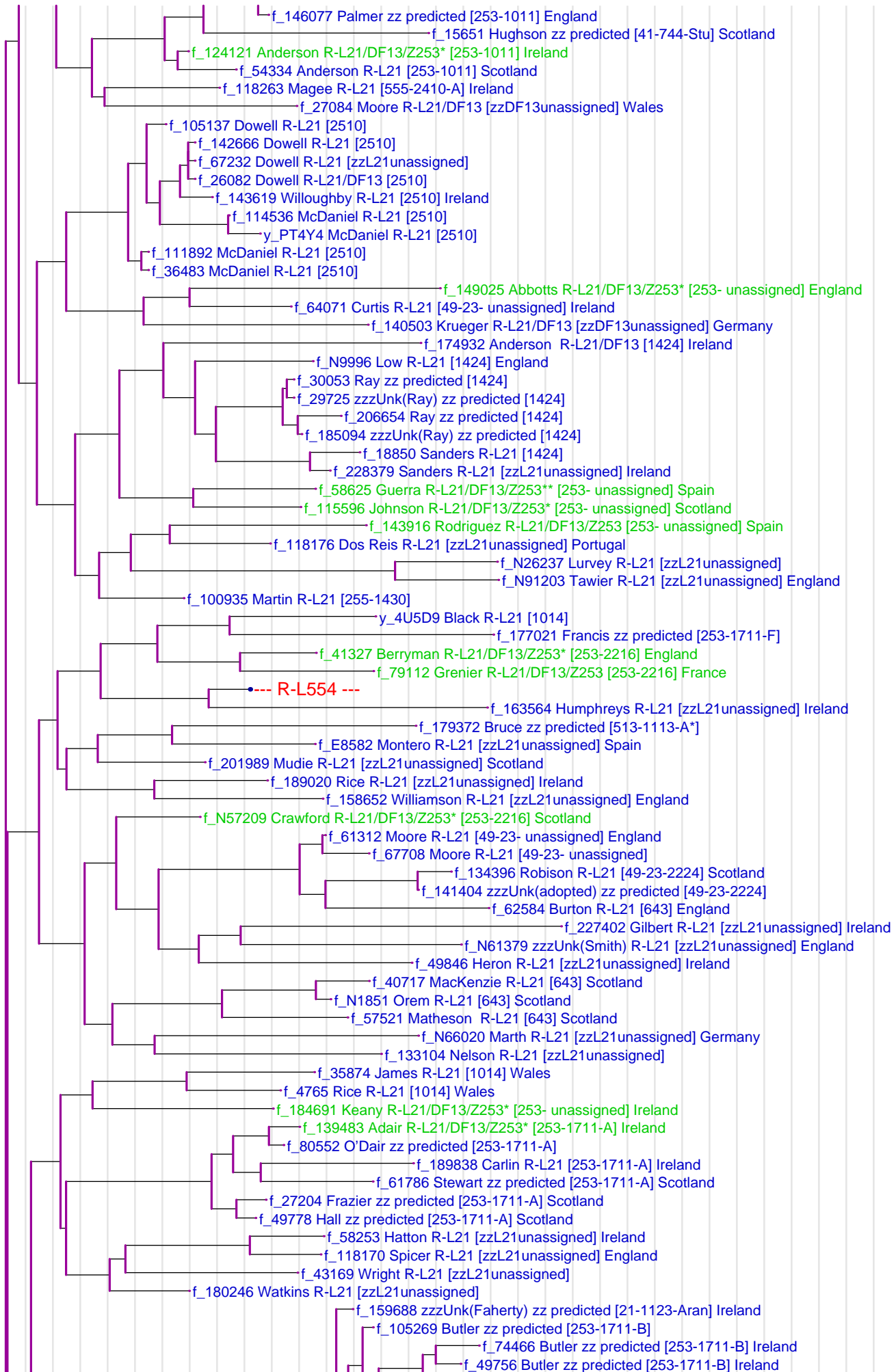


Age Analysis

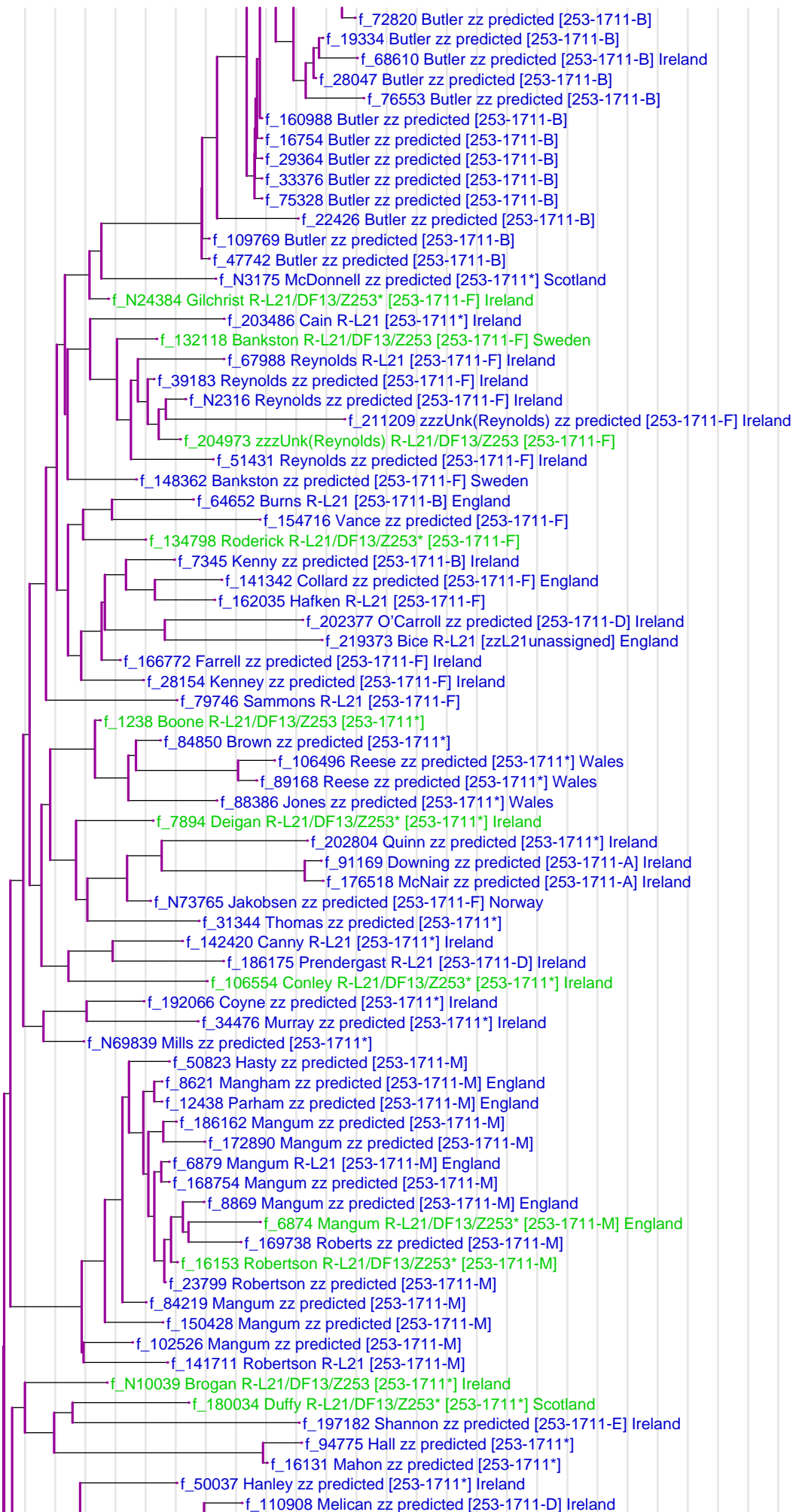
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
713	47771	10290	21.54%	120.64±12.08	3016.12±426.818



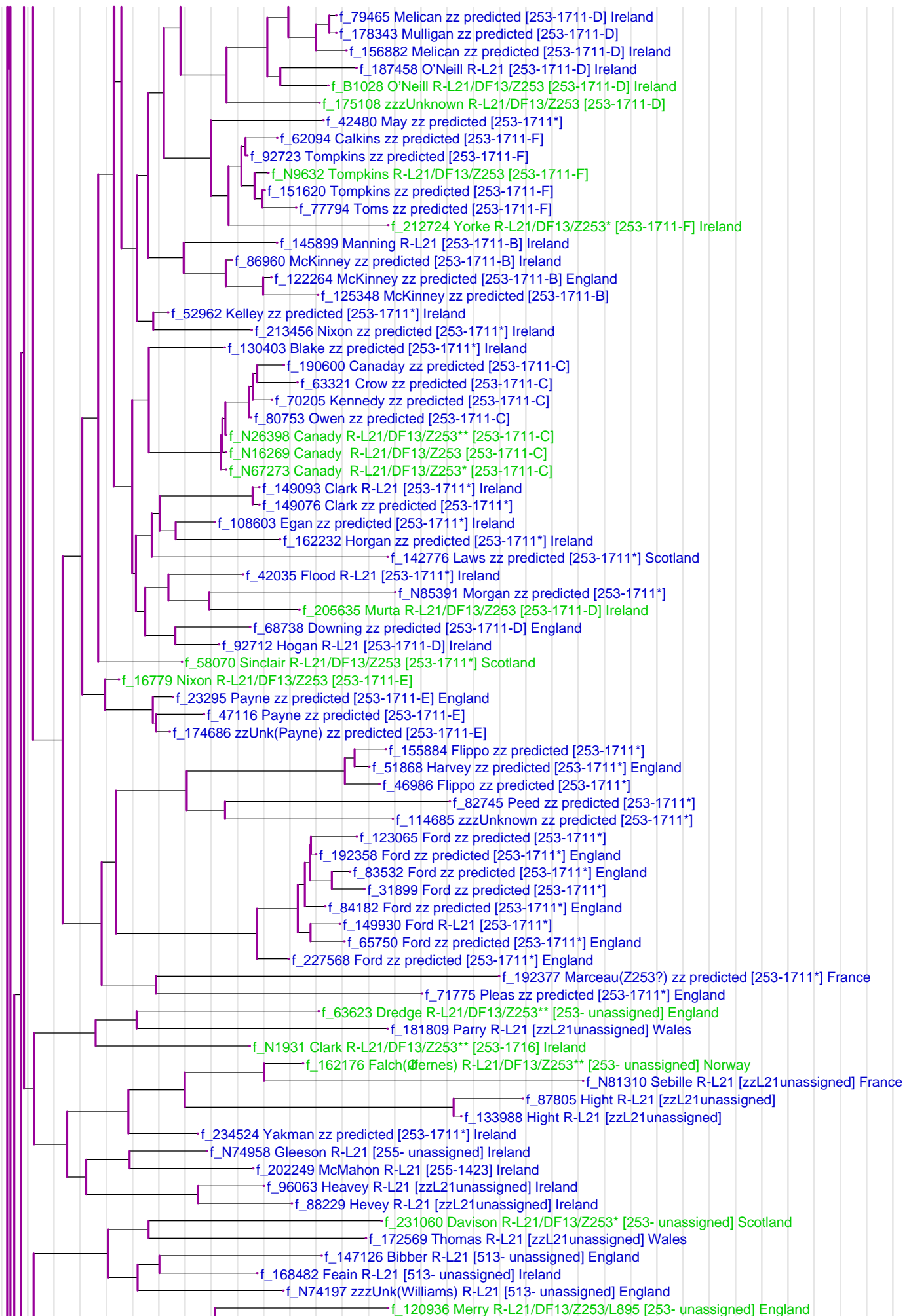
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



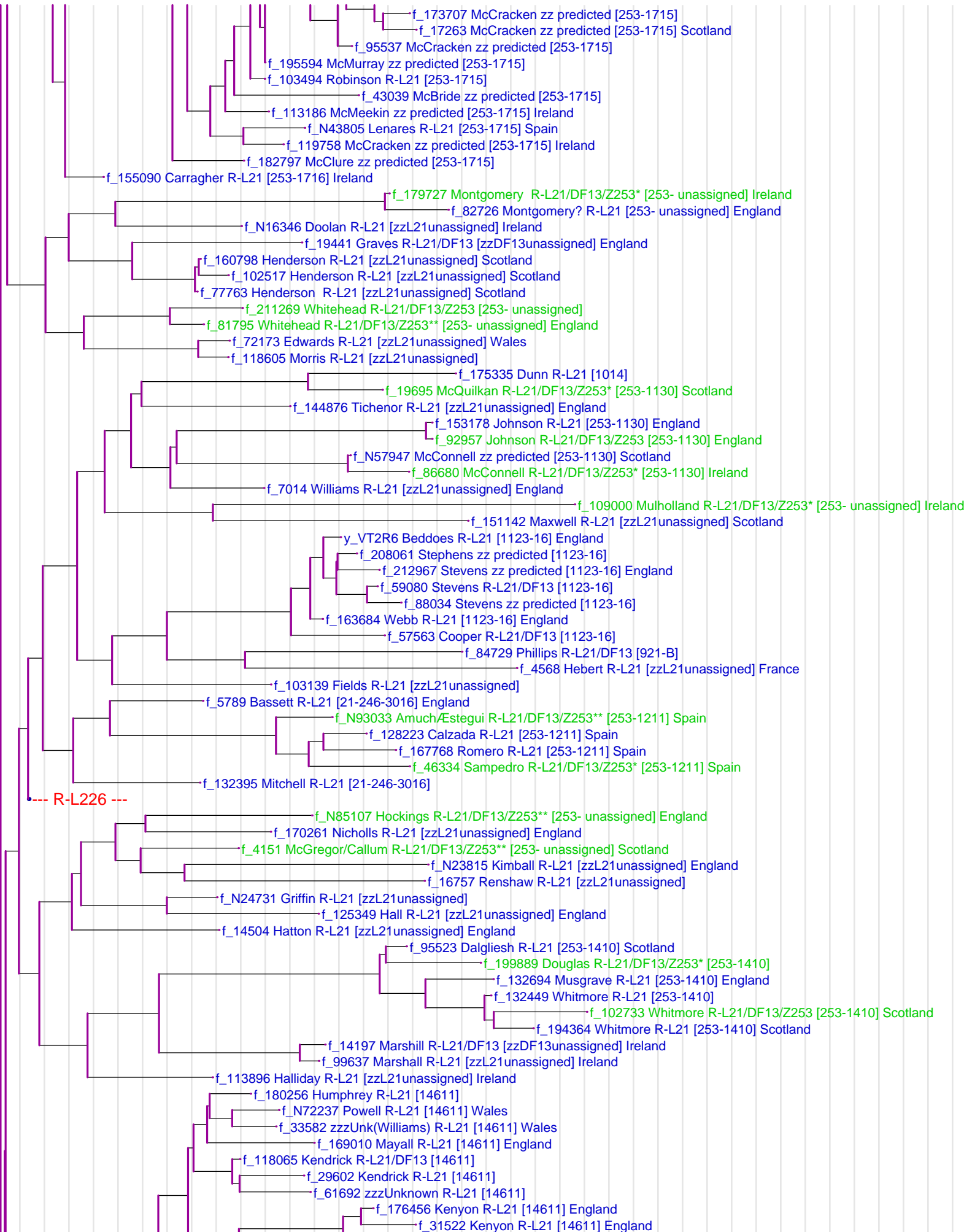
The vertical grey lines are separated 10 generations apart.



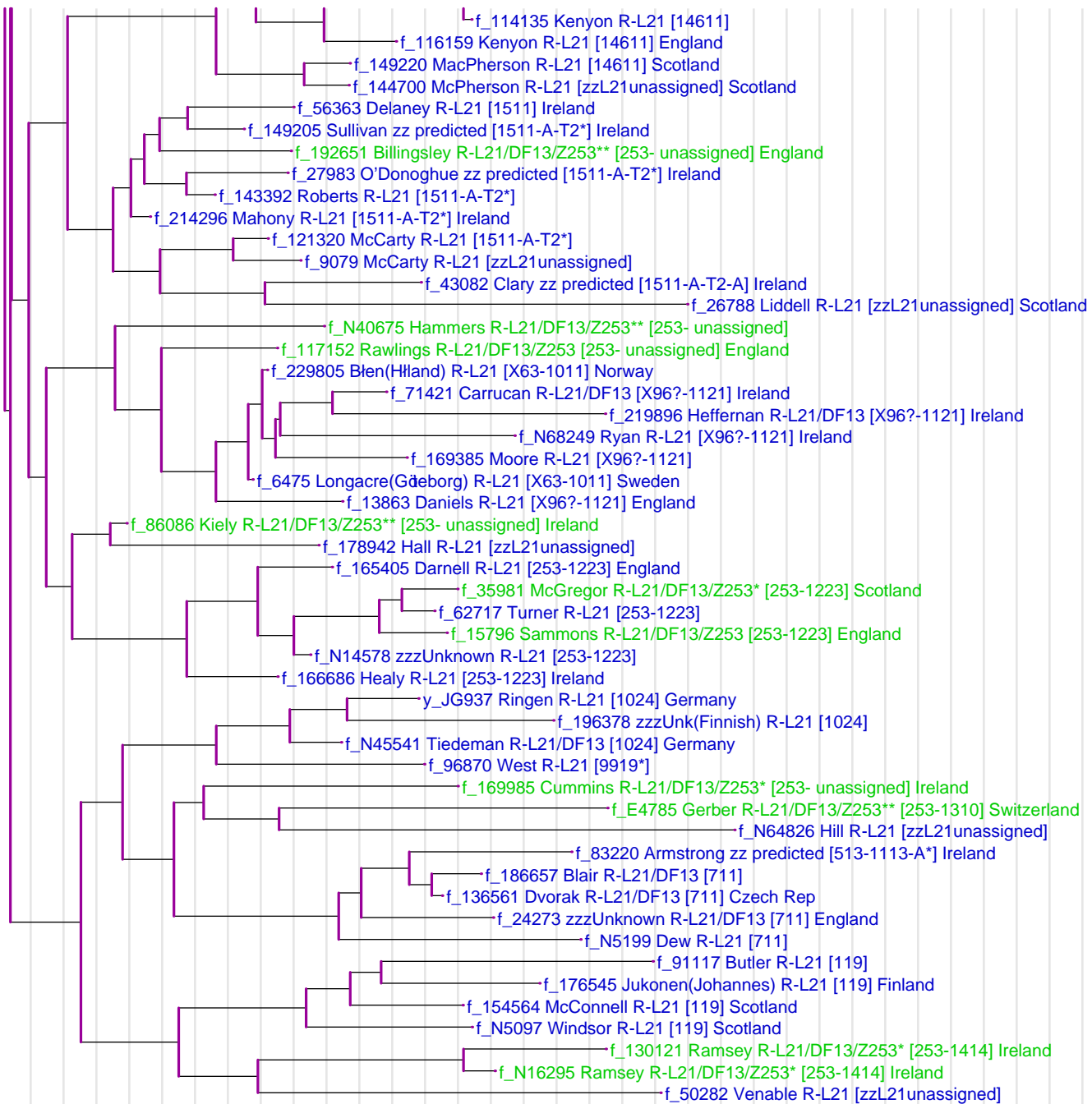
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



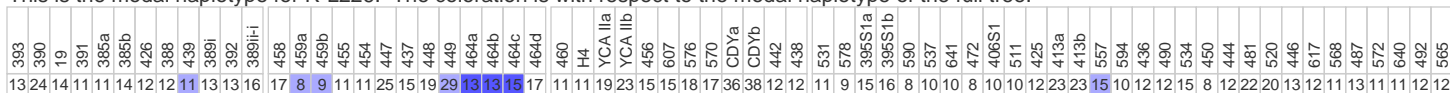
The vertical grey lines are separated 10 generations apart.



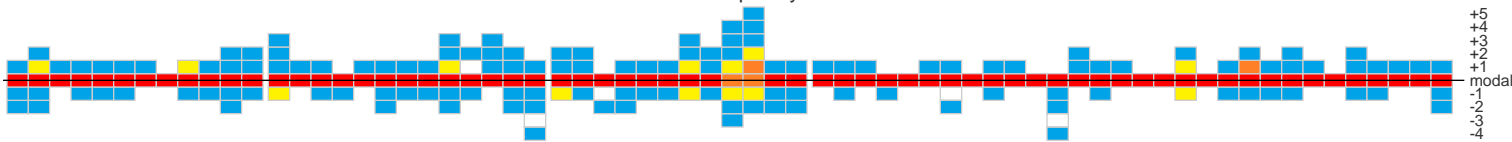
The vertical grey lines are separated 10 generations apart.

R-L226

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

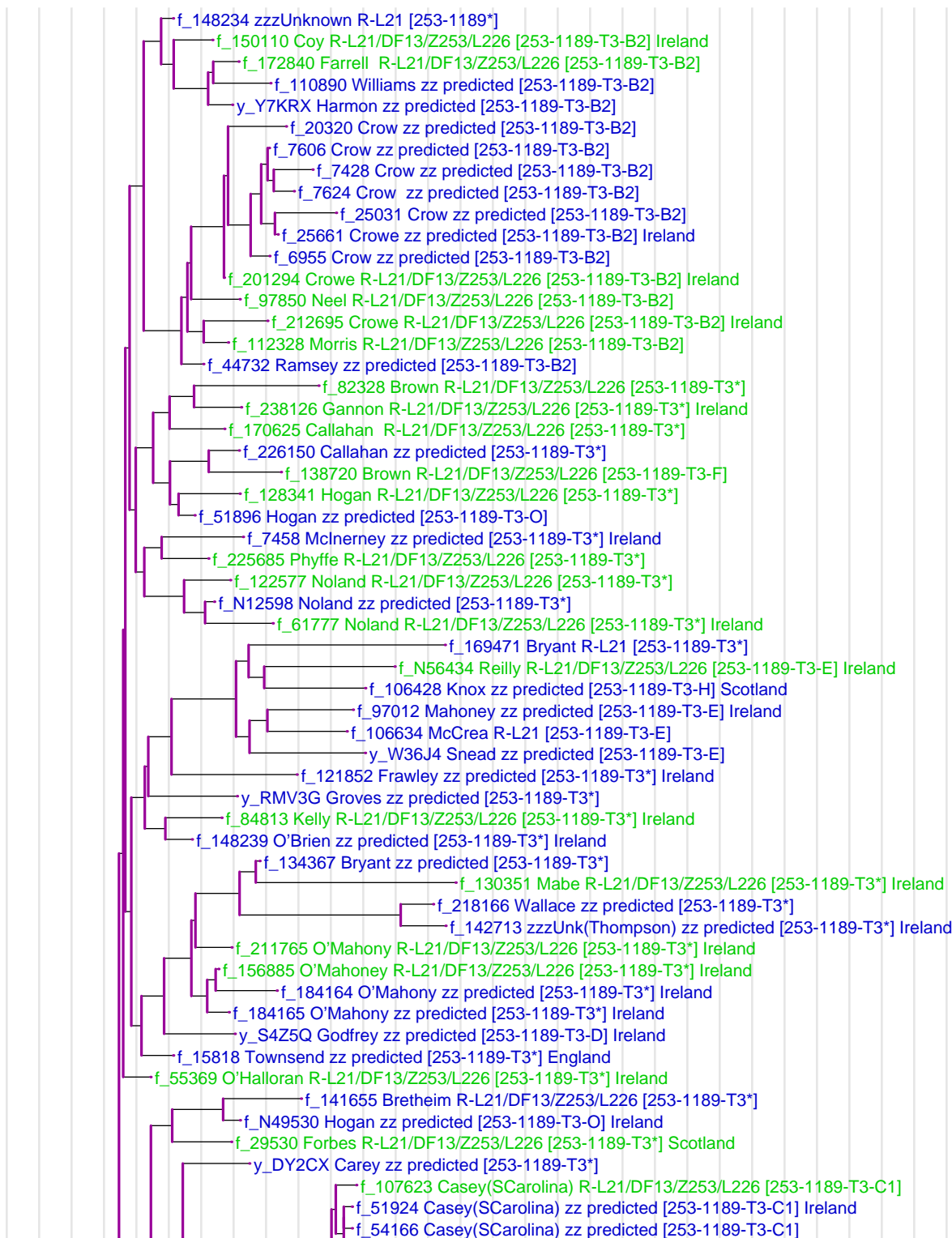


This is the marker distribution for R-L226. The color indicates the relative frequency of the alleles.

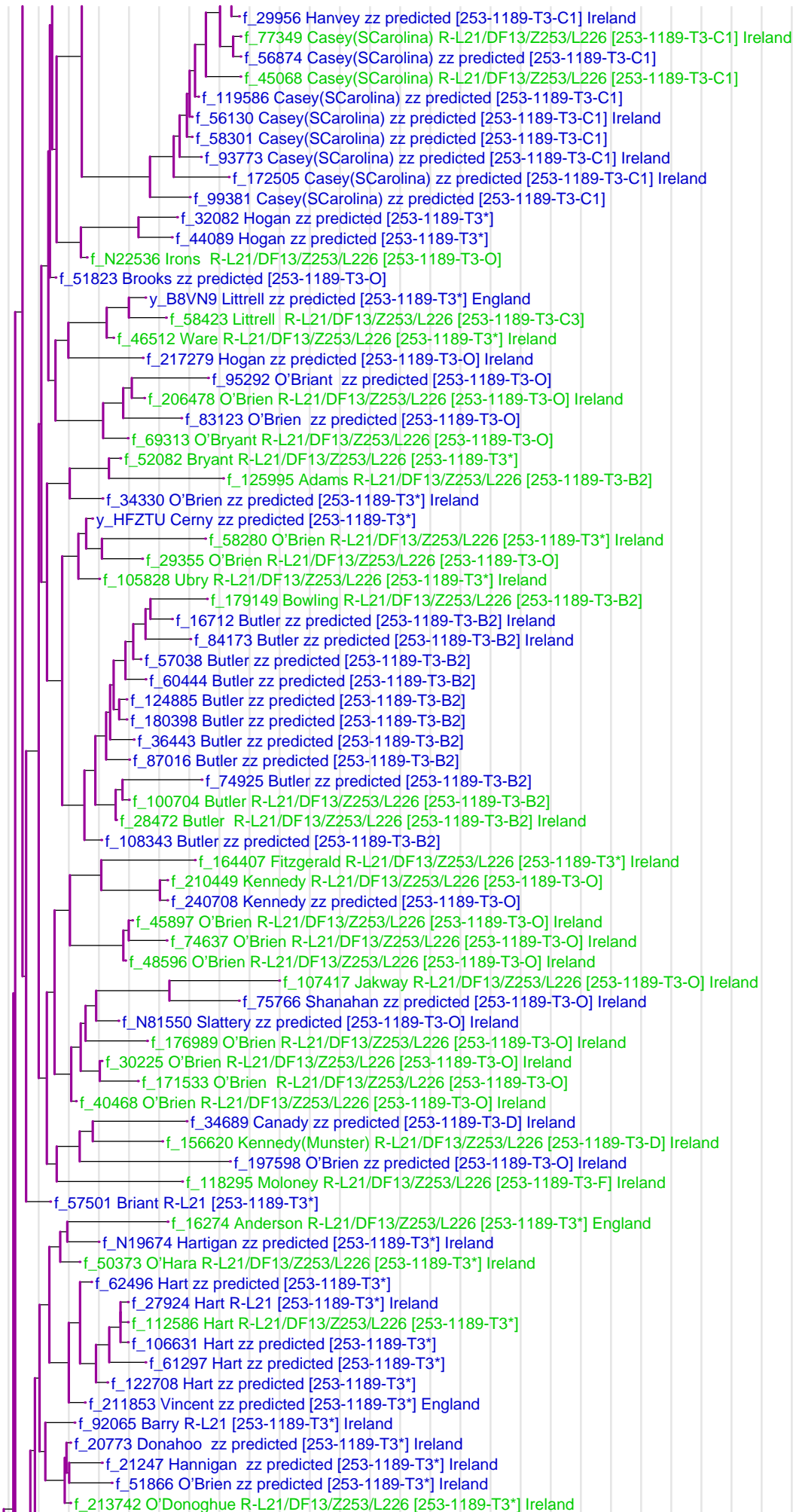


Age Analysis

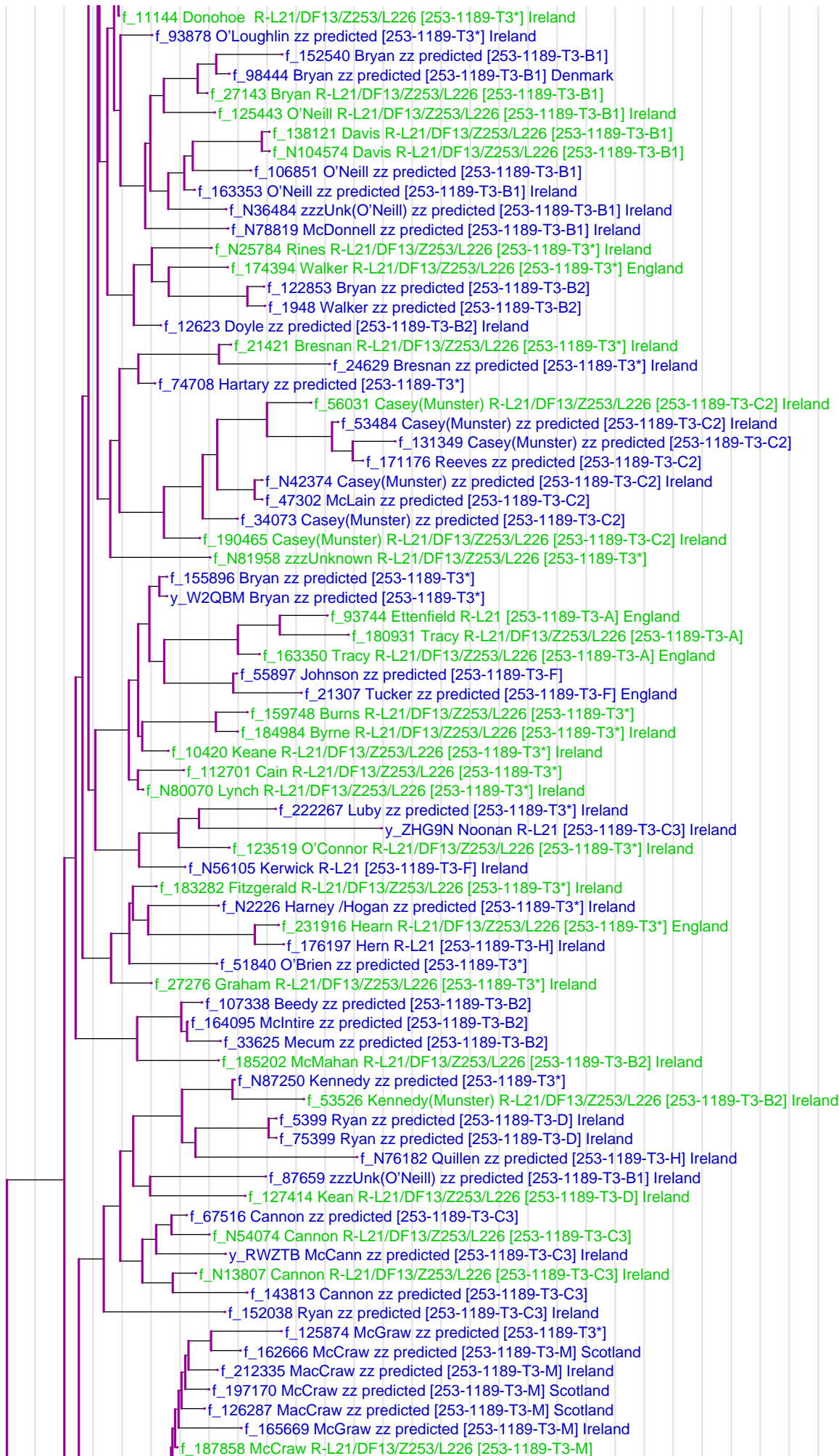
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
231	15477	1556	10.05%	52.93±5.31	1323.16±187.456



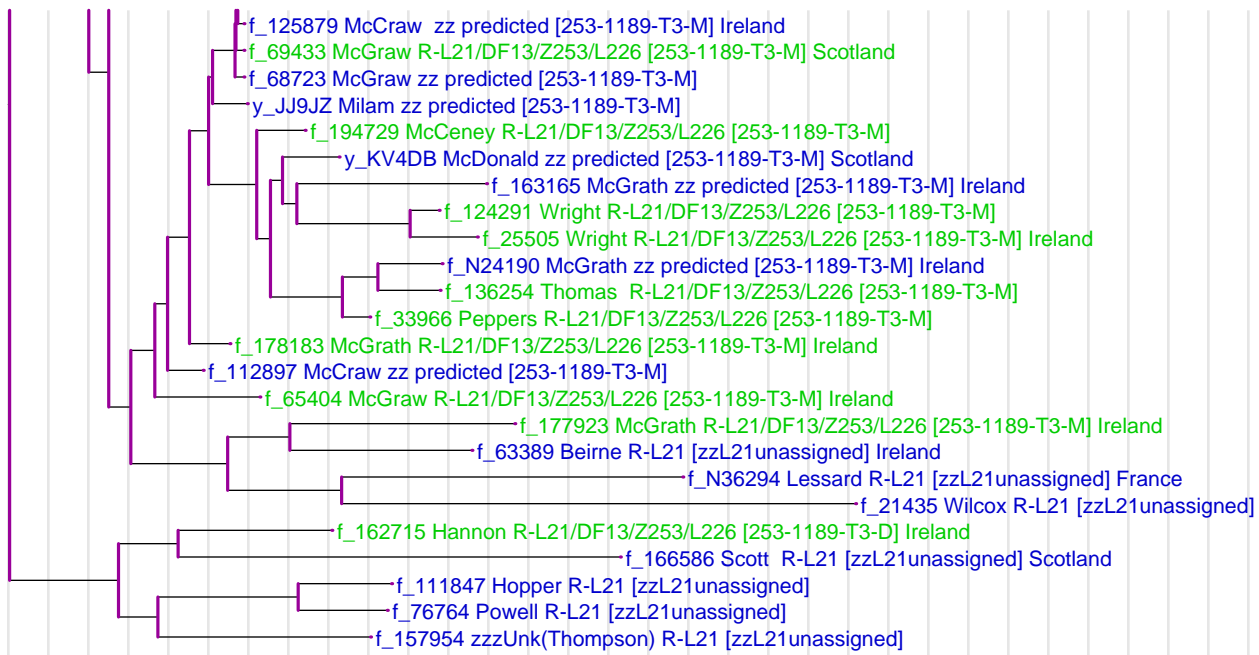
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



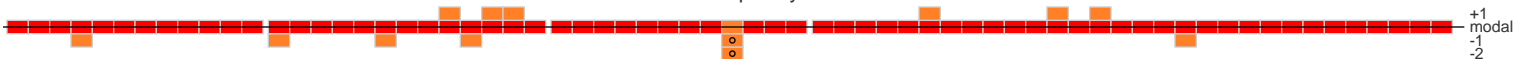
The vertical grey lines are separated 10 generations apart.

R-L554

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

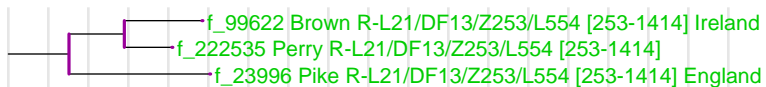
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13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

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



Age Analysis

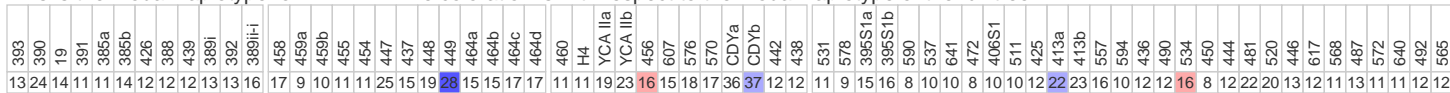
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	14	6.97%	36.08±4.47	902.049±143.558



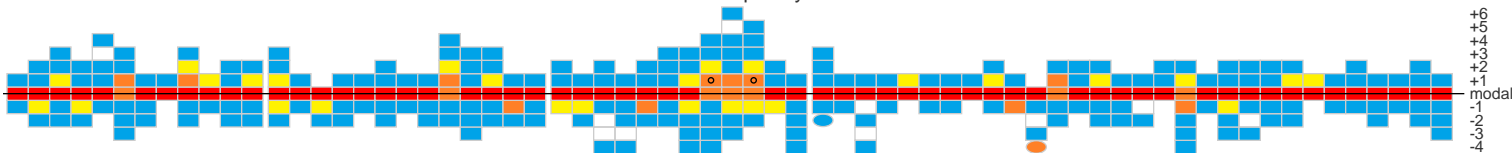
The vertical grey lines are separated 10 generations apart.

R-DF21

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

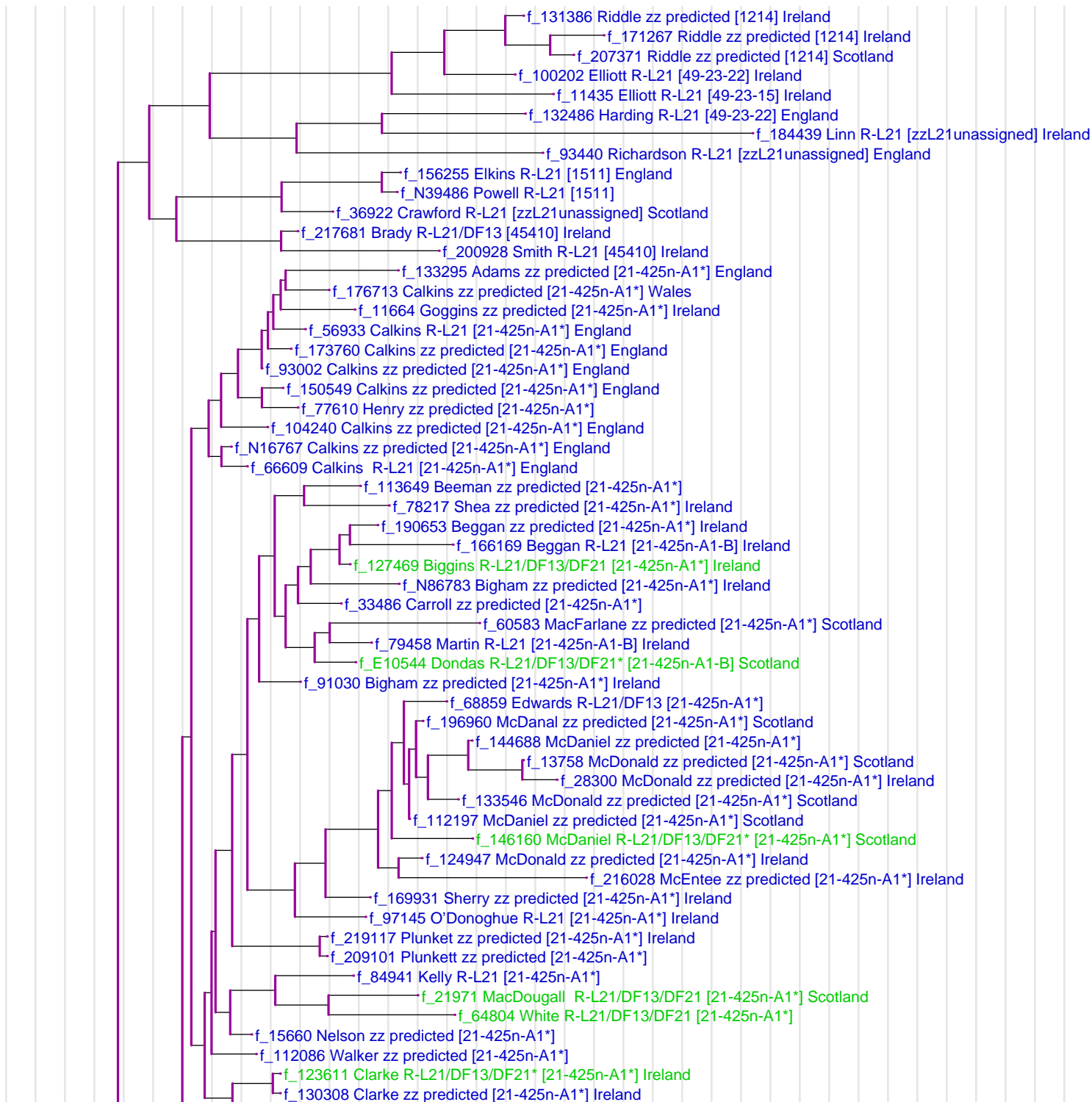


This is the marker distribution for R-DF21. The color indicates the relative frequency of the alleles.

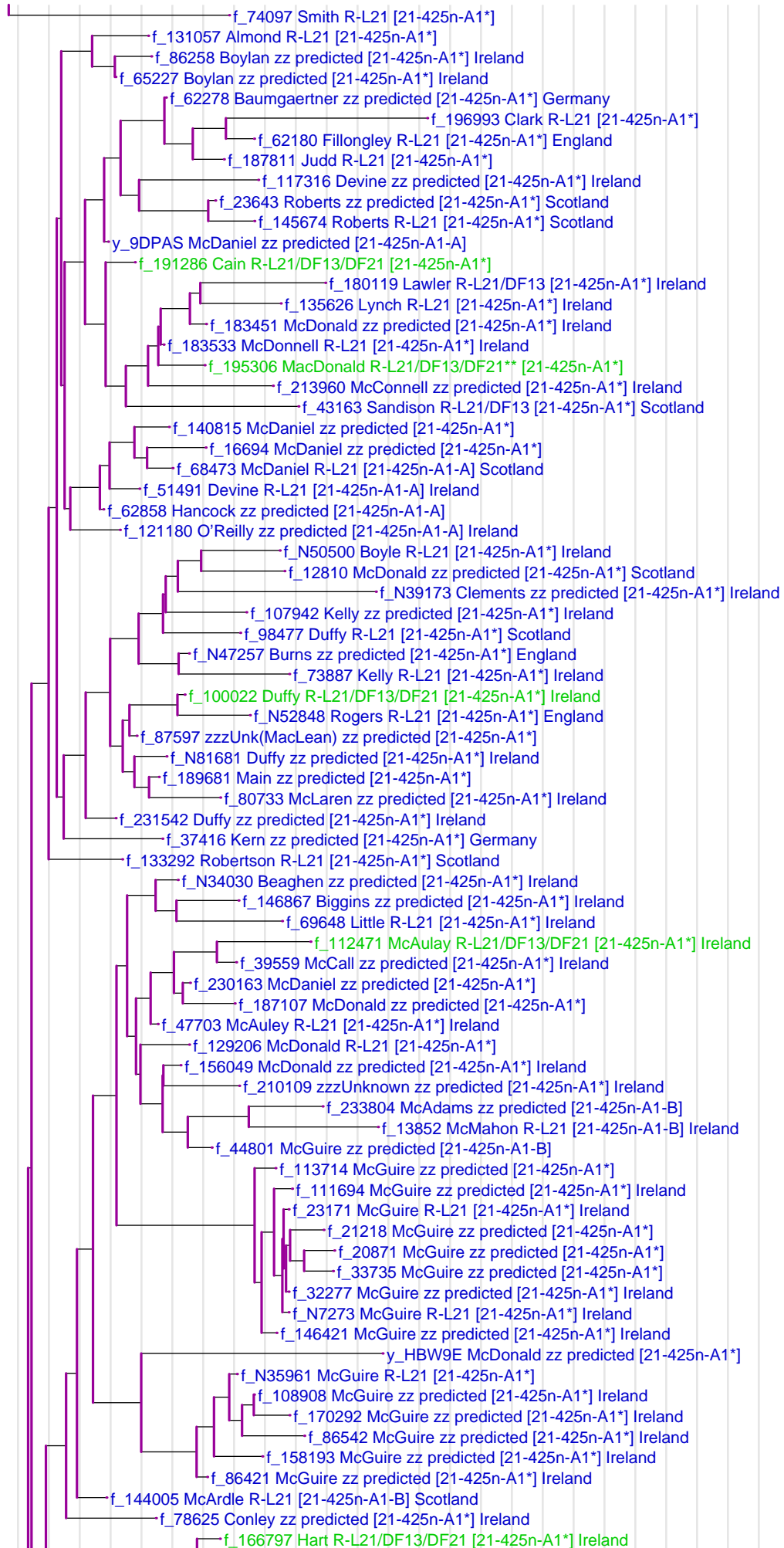


Age Analysis

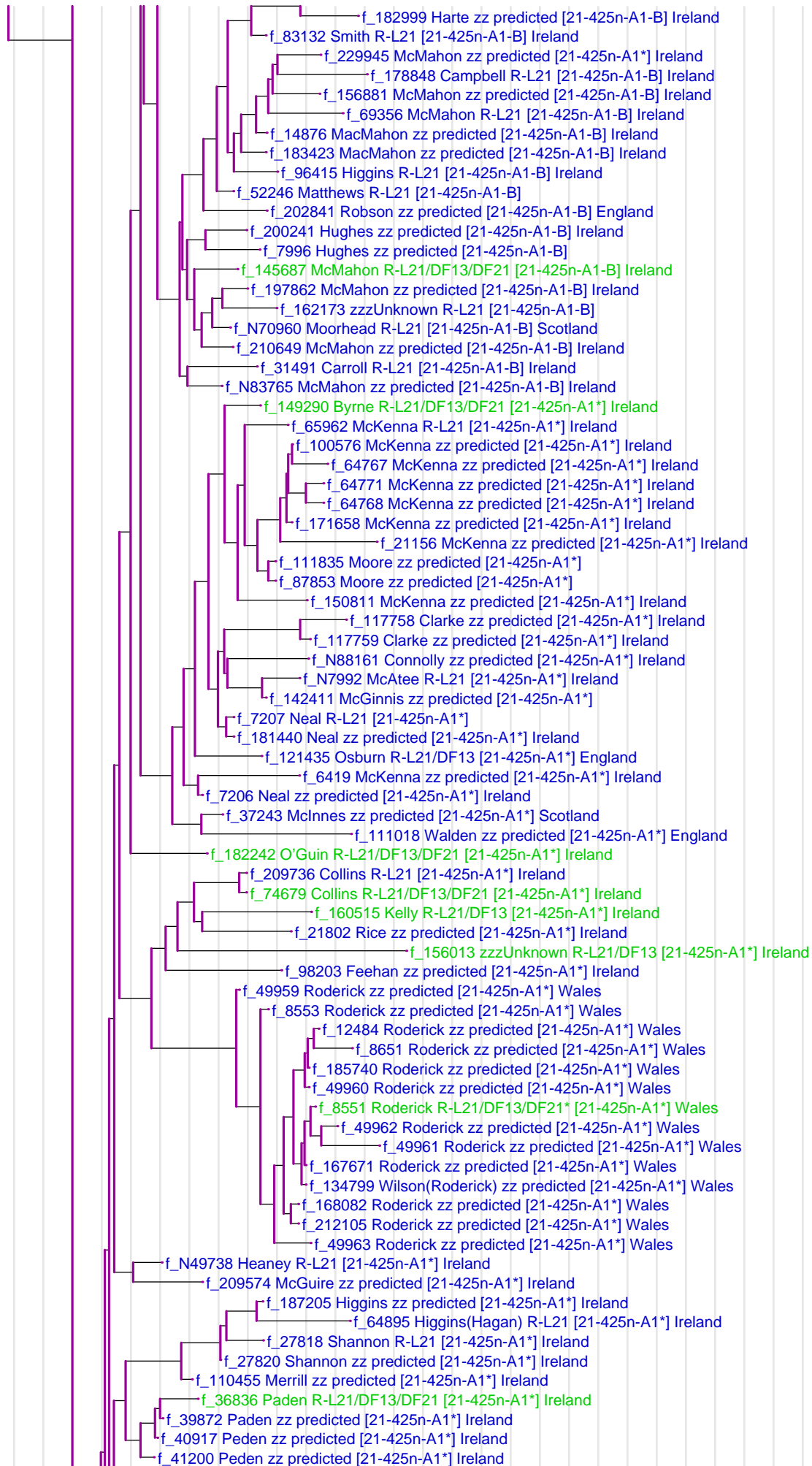
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
614	41138	8588	20.88%	116.50±11.67	2912.41±412.182



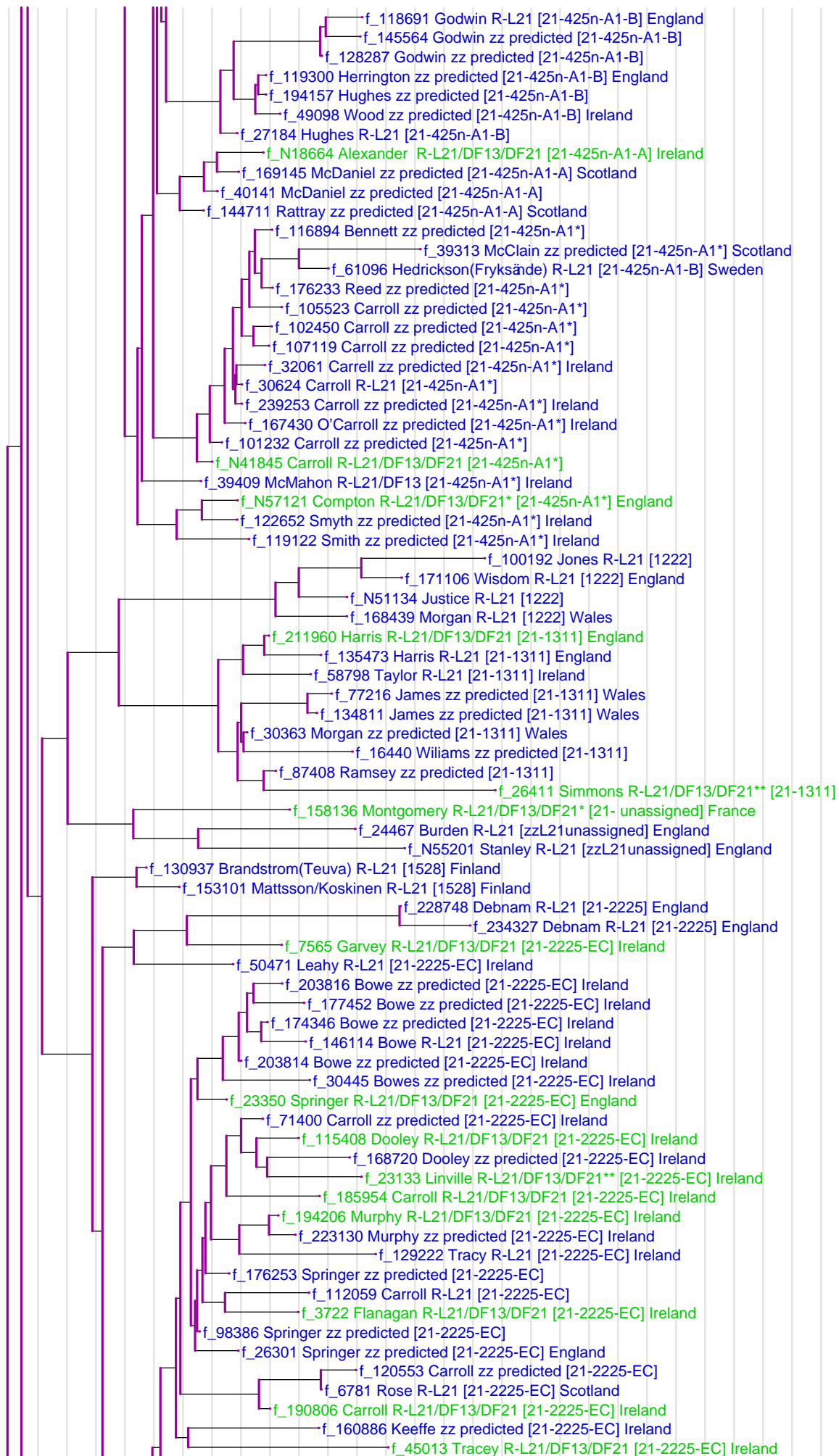
The vertical grey lines are separated 10 generations apart.



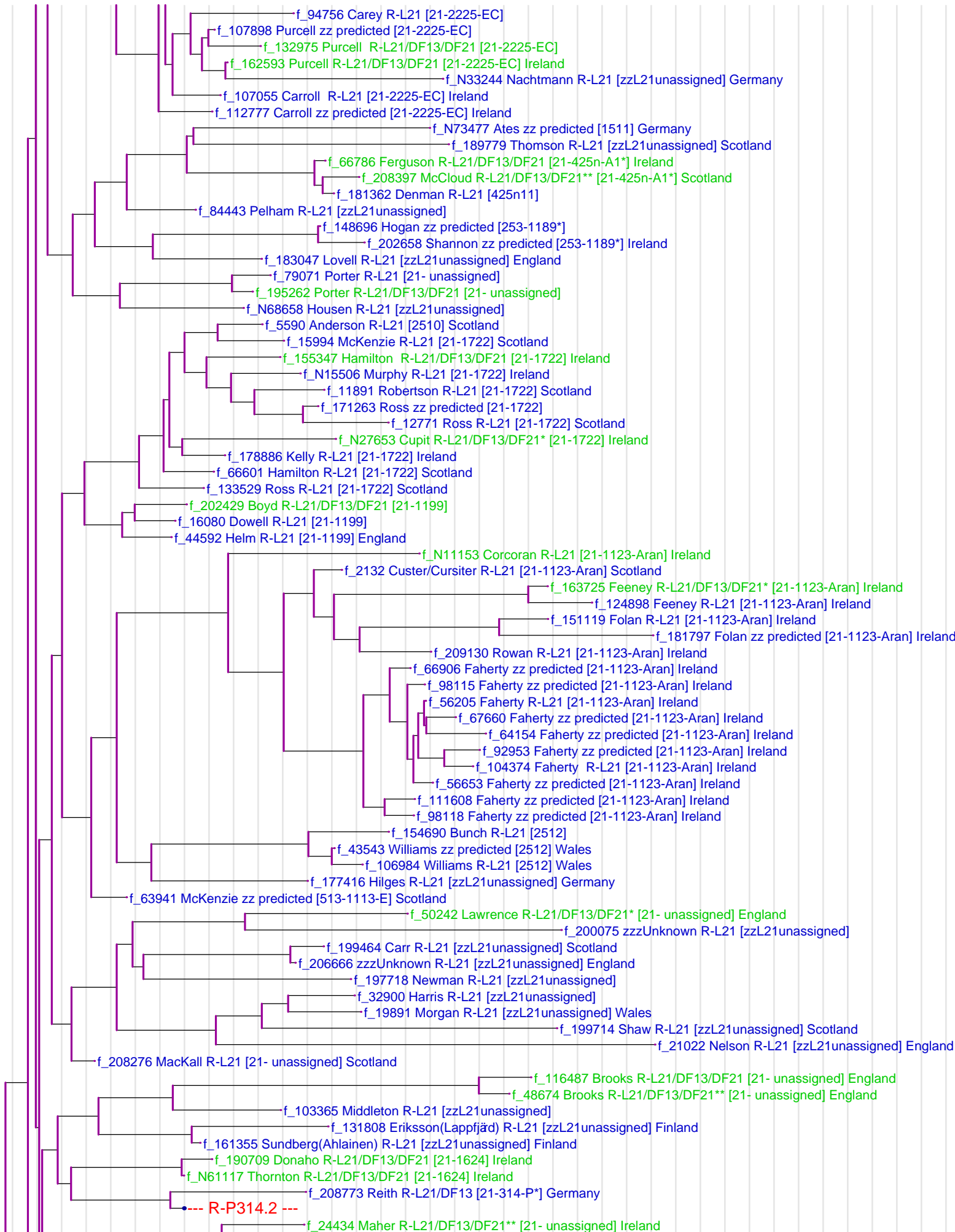
The vertical grey lines are separated 10 generations apart.



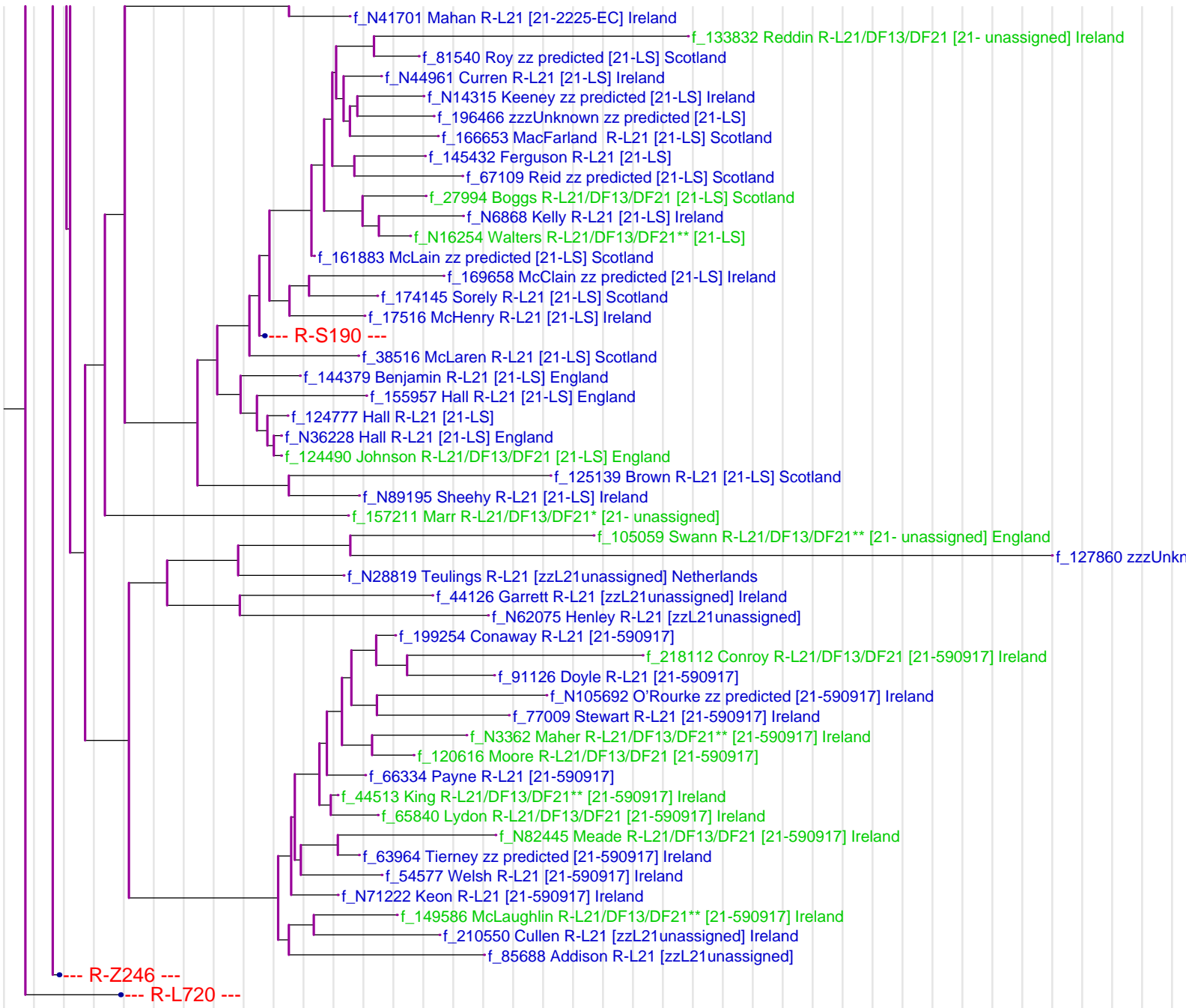
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



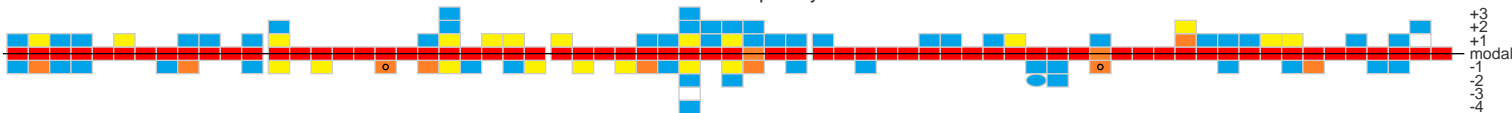
The vertical grey lines are separated 10 generations apart.

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.

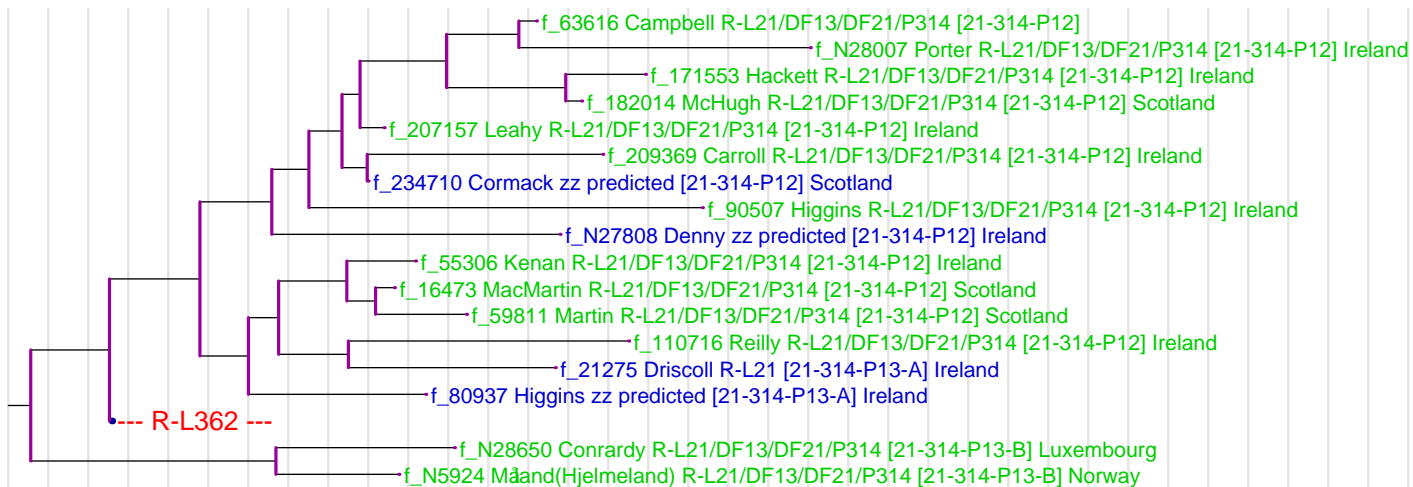
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	23	14	11	11	14	12	13	13	13	13	15	17	9	10	11	11	26	15	19	29	15	15	16	17	10	11	19	23	16	15	18	18	37	38	12	12	11	9	16	16	8	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

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



Age Analysis

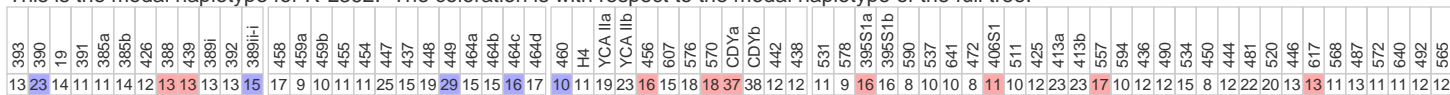
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
40	2680	346	12.91%	69.00±7.04	1725±246.518



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.

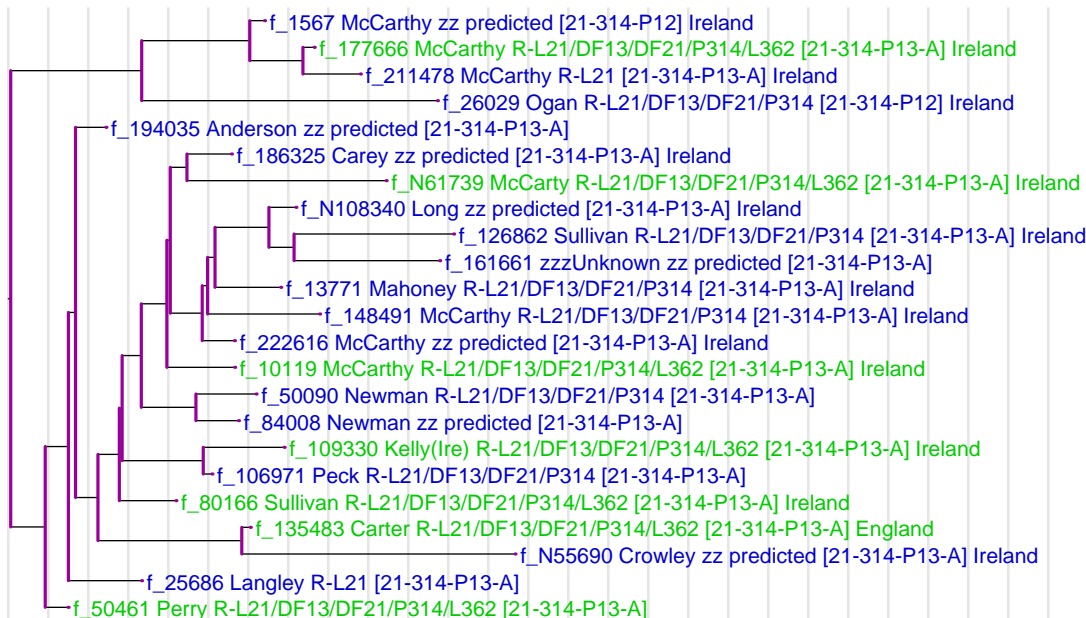


This is the marker distribution for R-L362. The color indicates the relative frequency of the alleles.



Age Analysis

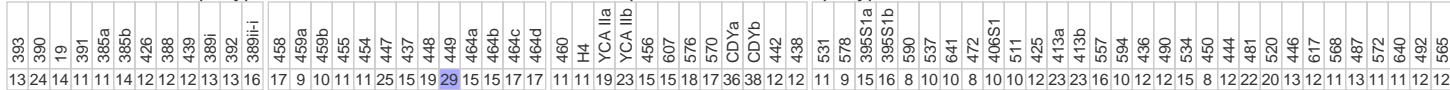
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
23	1541	131	8.50%	44.39±4.59	1109.76±159.687



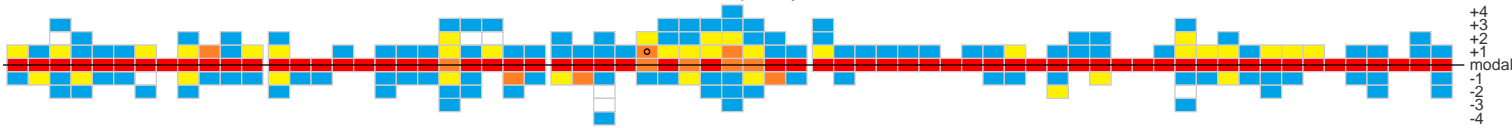
The vertical grey lines are separated 10 generations apart.

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

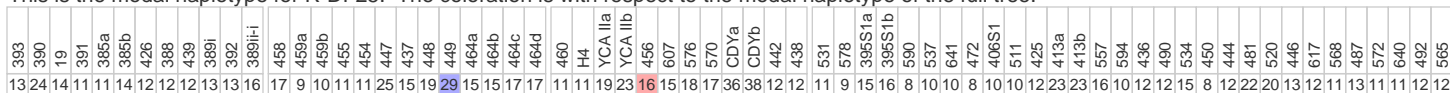
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
145	9715	1927	19.84%	110.06±11.07	2751.4±390.314



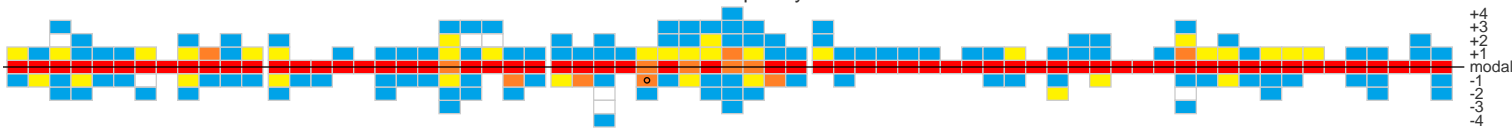
The vertical grey lines are separated 10 generations apart.

R-DF25

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

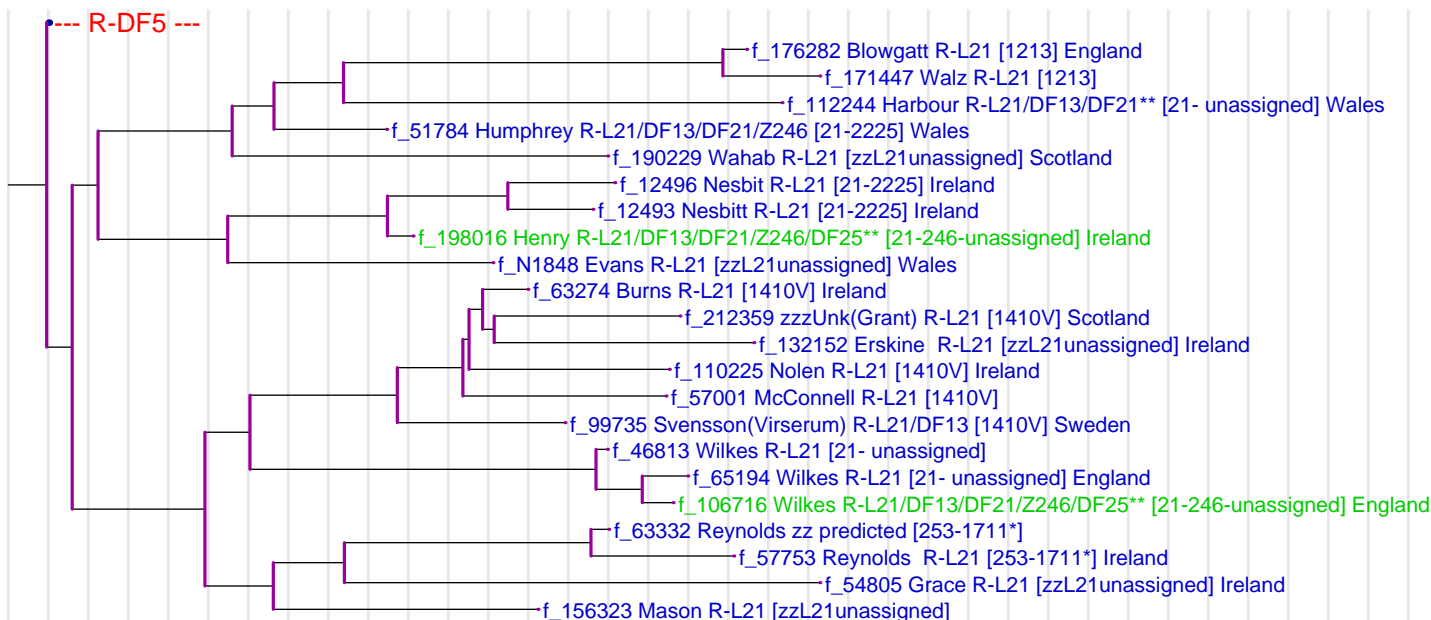


This is the marker distribution for R-DF25. The color indicates the relative frequency of the alleles.



Age Analysis

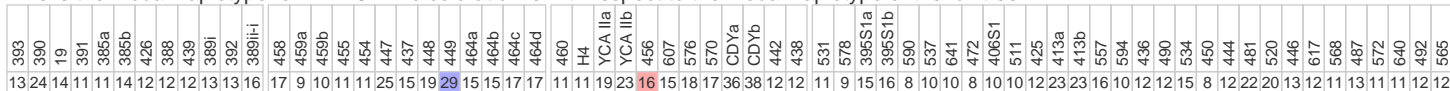
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
142	9514	1882	19.78%	109.72±11.04	2743.1±389.162



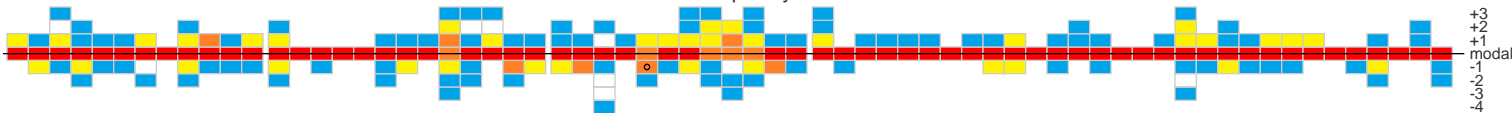
The vertical grey lines are separated 10 generations apart.

R-DF5

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

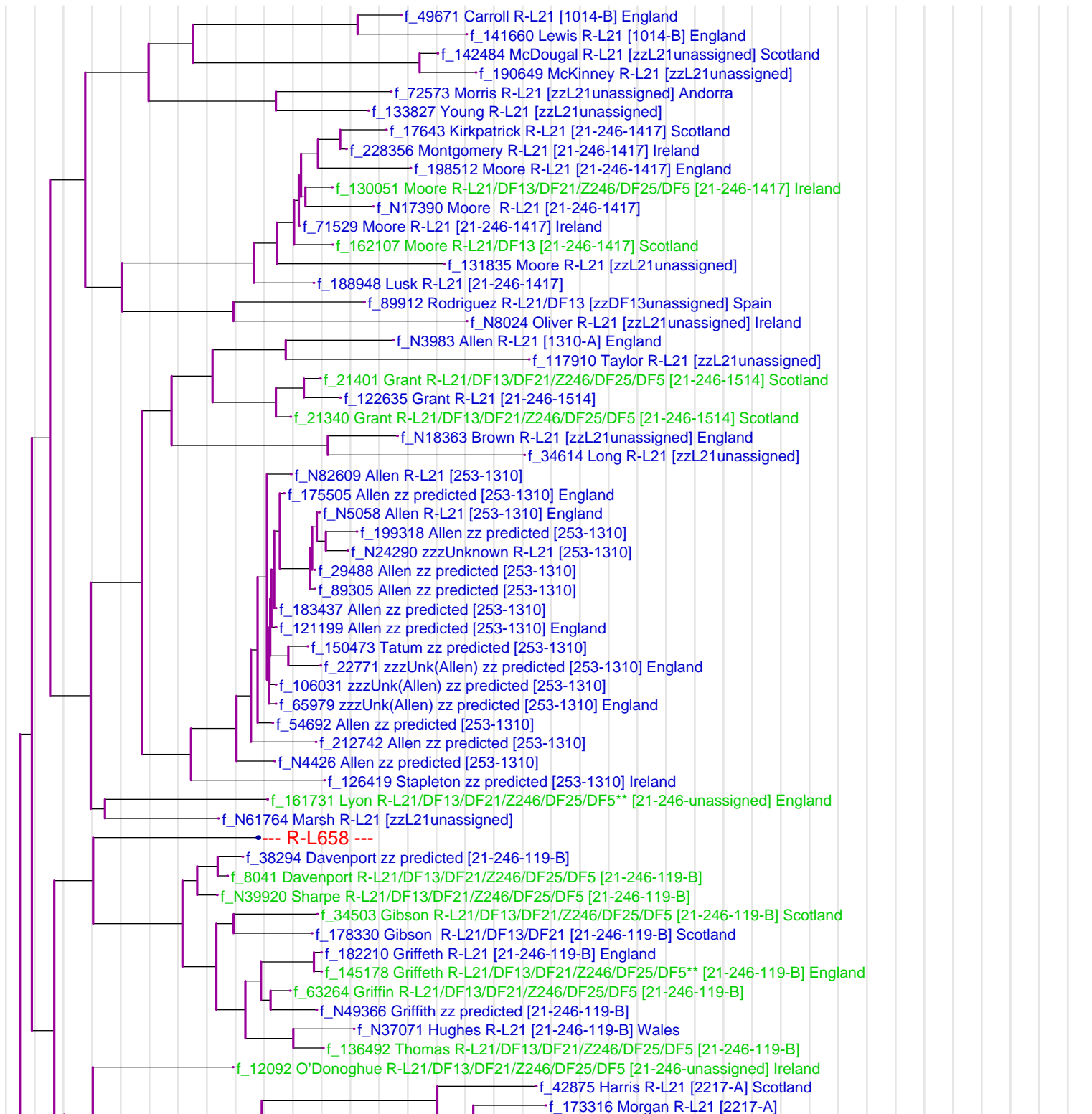


This is the marker distribution for R-DF5. The color indicates the relative frequency of the alleles.

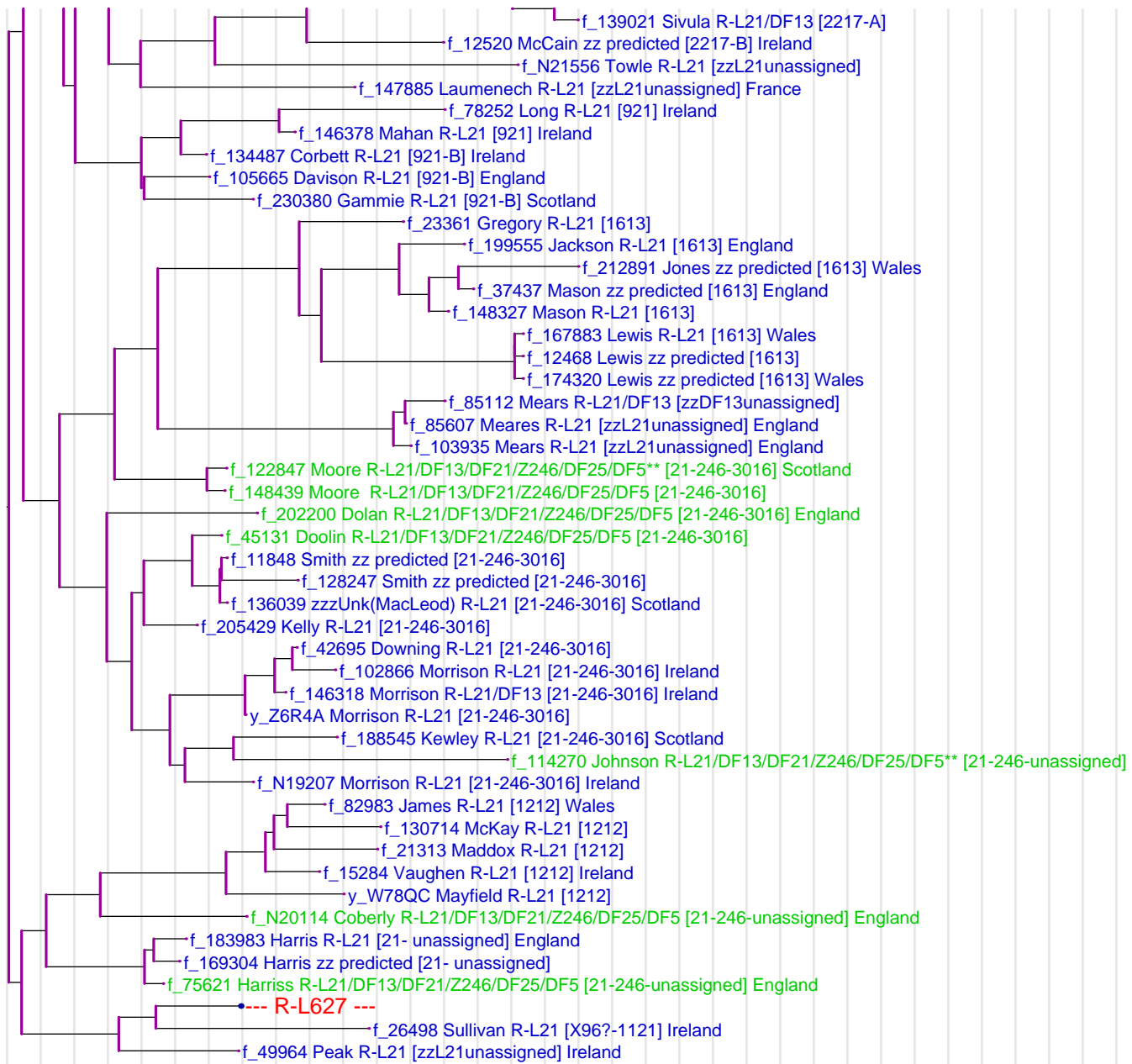


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
120	8040	1528	19.00%	104.97±10.57	2624.24±372.505



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.

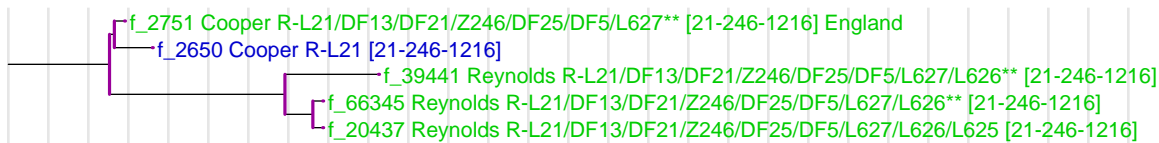
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565	
13	24	15	10	11	15	12	12	12	14	13	16	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	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-L627. The color indicates the relative frequency of the alleles.



Age Analysis

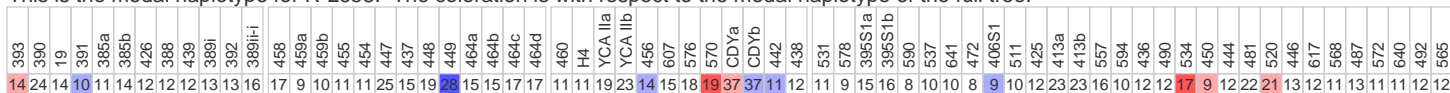
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	21	6.27%	32.36±3.71	808.928±123.146



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.

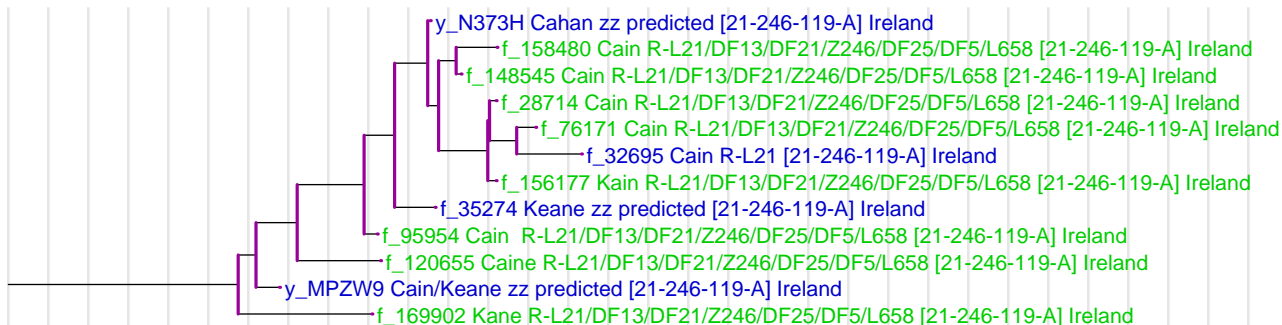


This is the marker distribution for R-L658. The color indicates the relative frequency of the alleles.



Age Analysis

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



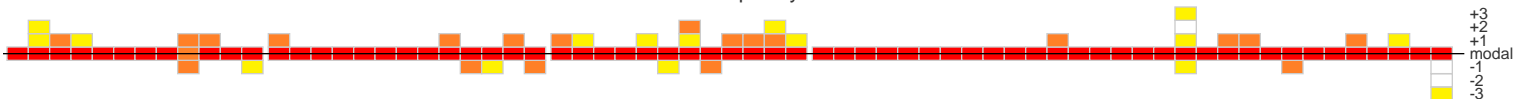
The vertical grey lines are separated 10 generations apart.

R-L720

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

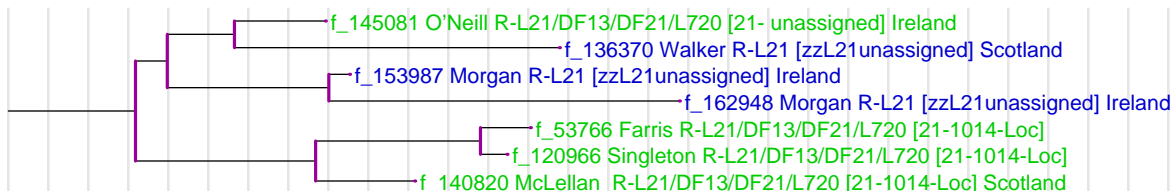
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	10	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	30	15	15	16	18	10	11	19	23	17	15	17	17	36	37	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

This is the marker distribution for R-L720. The color indicates the relative frequency of the alleles.



Age Analysis

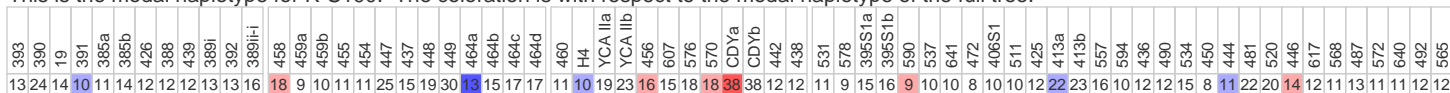
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
7	469	74	15.78%	85.63±9.57	2140.82±320.994



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.

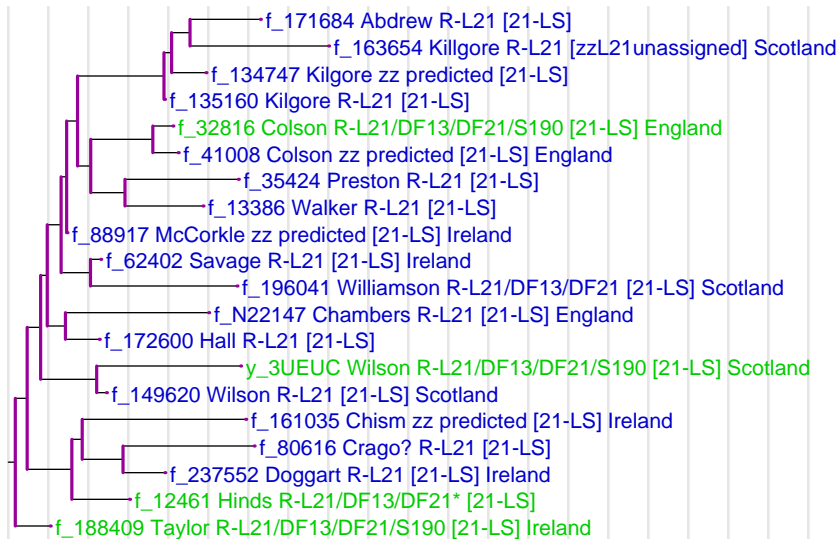


This is the marker distribution for R-S190. The color indicates the relative frequency of the alleles.



Age Analysis

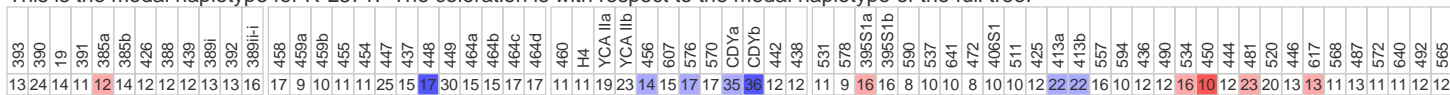
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
20	1340	94	7.01%	36.35±3.78	908.726±131.057



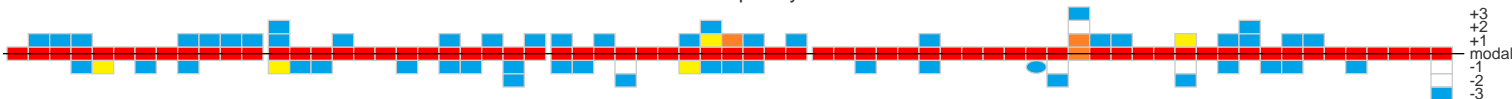
The vertical grey lines are separated 10 generations apart.

R-L371

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

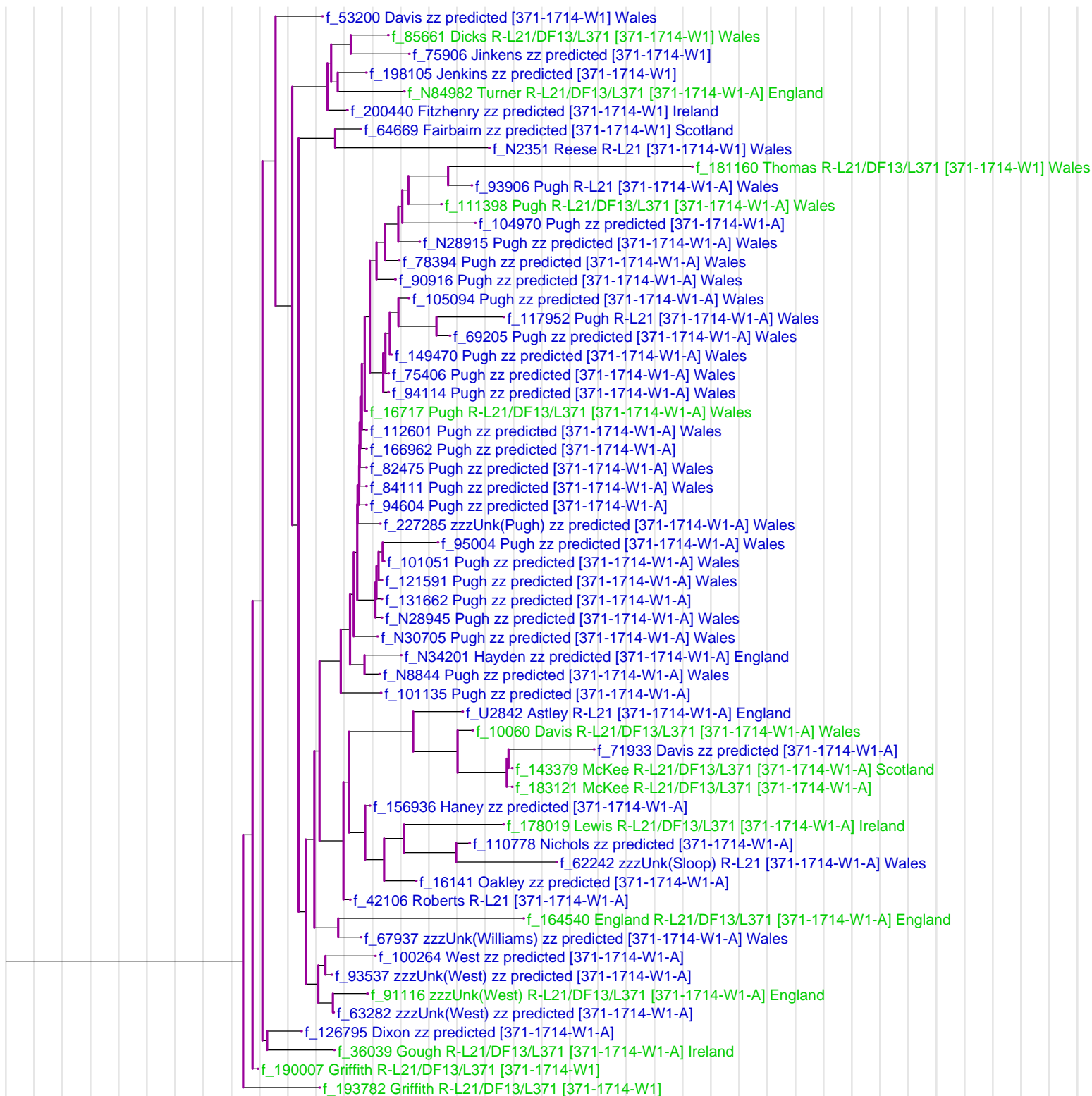


This is the marker distribution for R-L371. The color indicates the relative frequency of the alleles.



Age Analysis

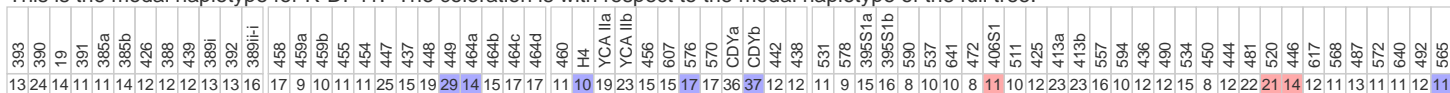
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
58	3886	213	5.48%	28.18±2.86	704.453±100.299



The vertical grey lines are separated 10 generations apart.

R-DF41

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

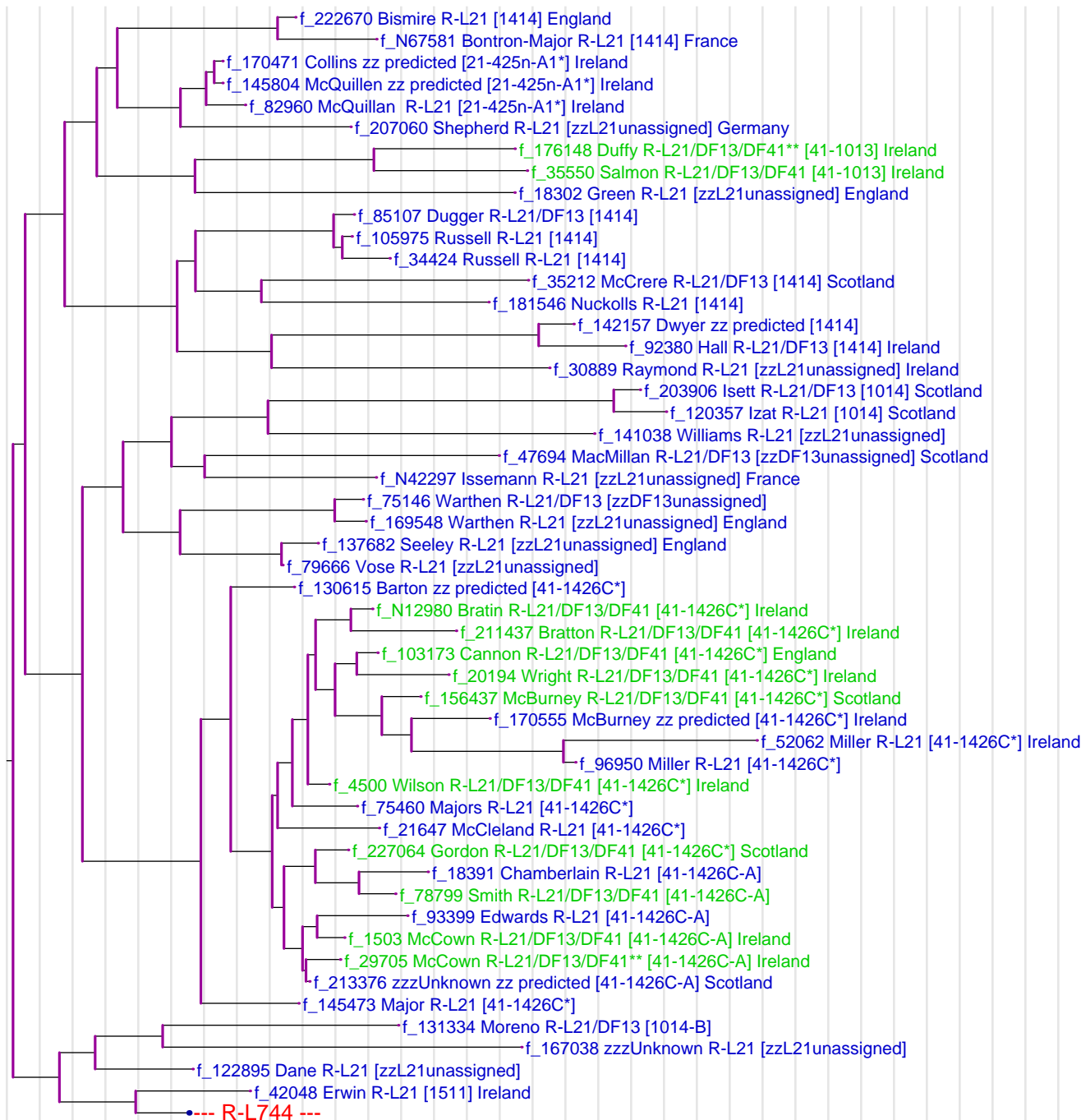


This is the marker distribution for R-DF41. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
110	7370	1137	15.43%	83.57±8.42	2089.27±296.628



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.

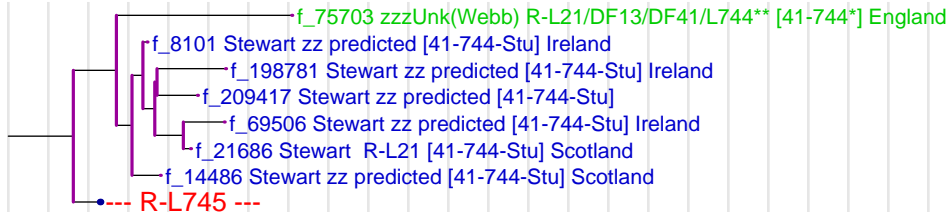
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	444	444	481	520	446	617	568	487	572	640	492	565			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

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



Age Analysis

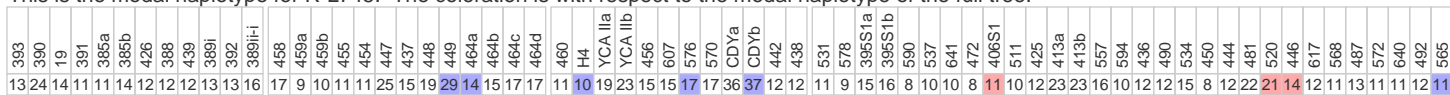
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
60	4020	191	4.75%	24.33±2.46	608.355±86.5933



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.

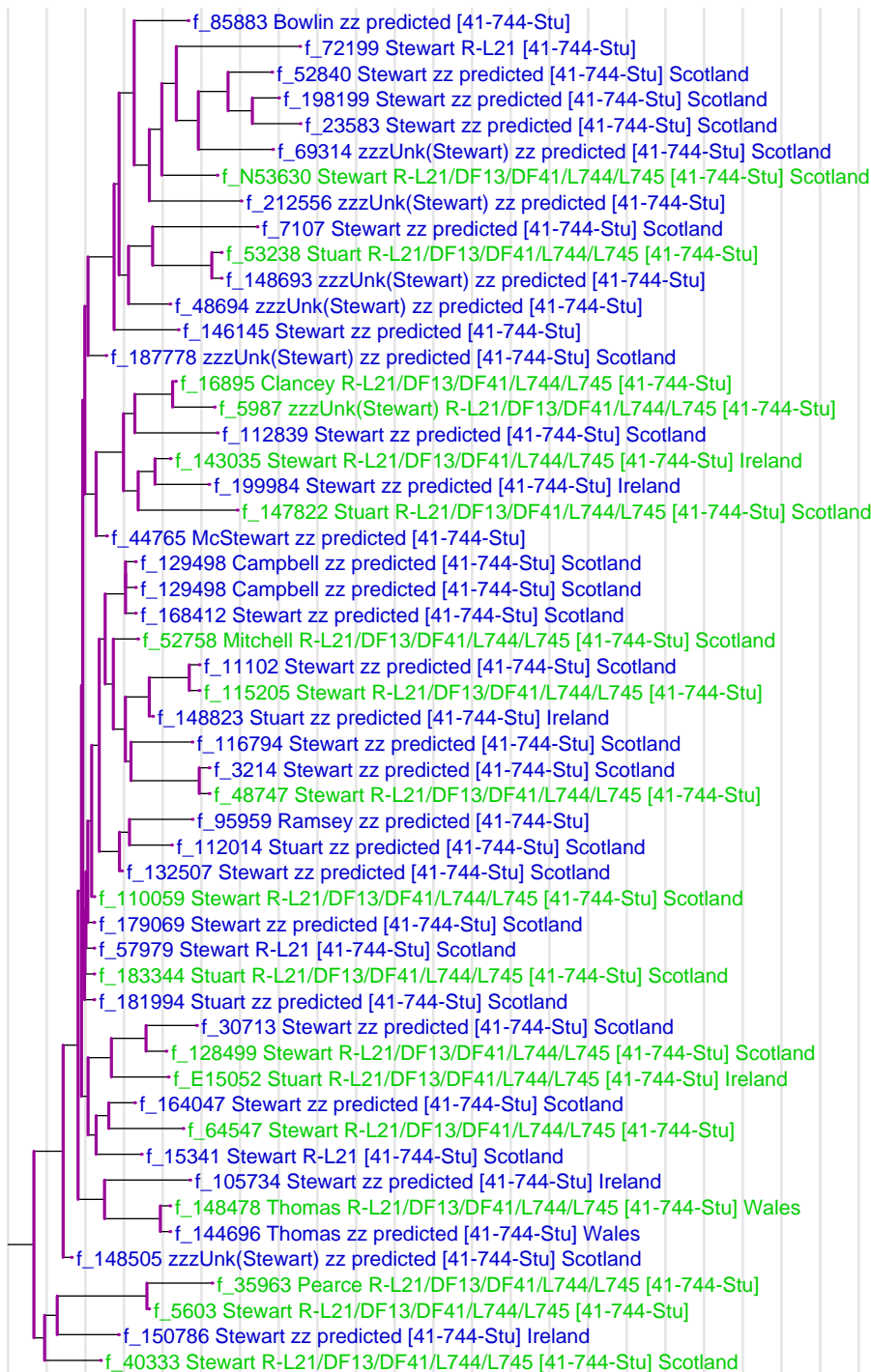


This is the marker distribution for R-L745. The color indicates the relative frequency of the alleles.



Age Analysis

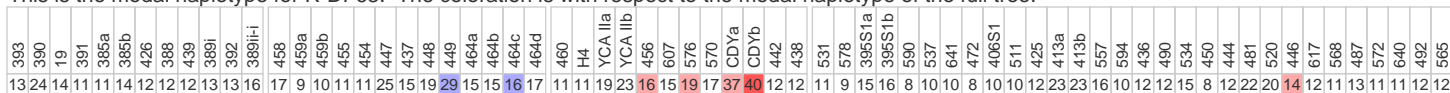
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
53	3551	171	4.82%	24.67±2.50	616.791±87.8691



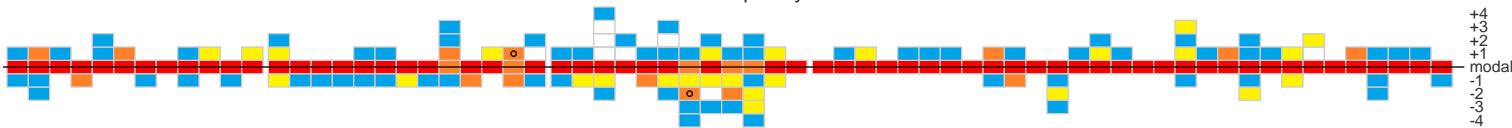
The vertical grey lines are separated 10 generations apart.

R-DF63

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

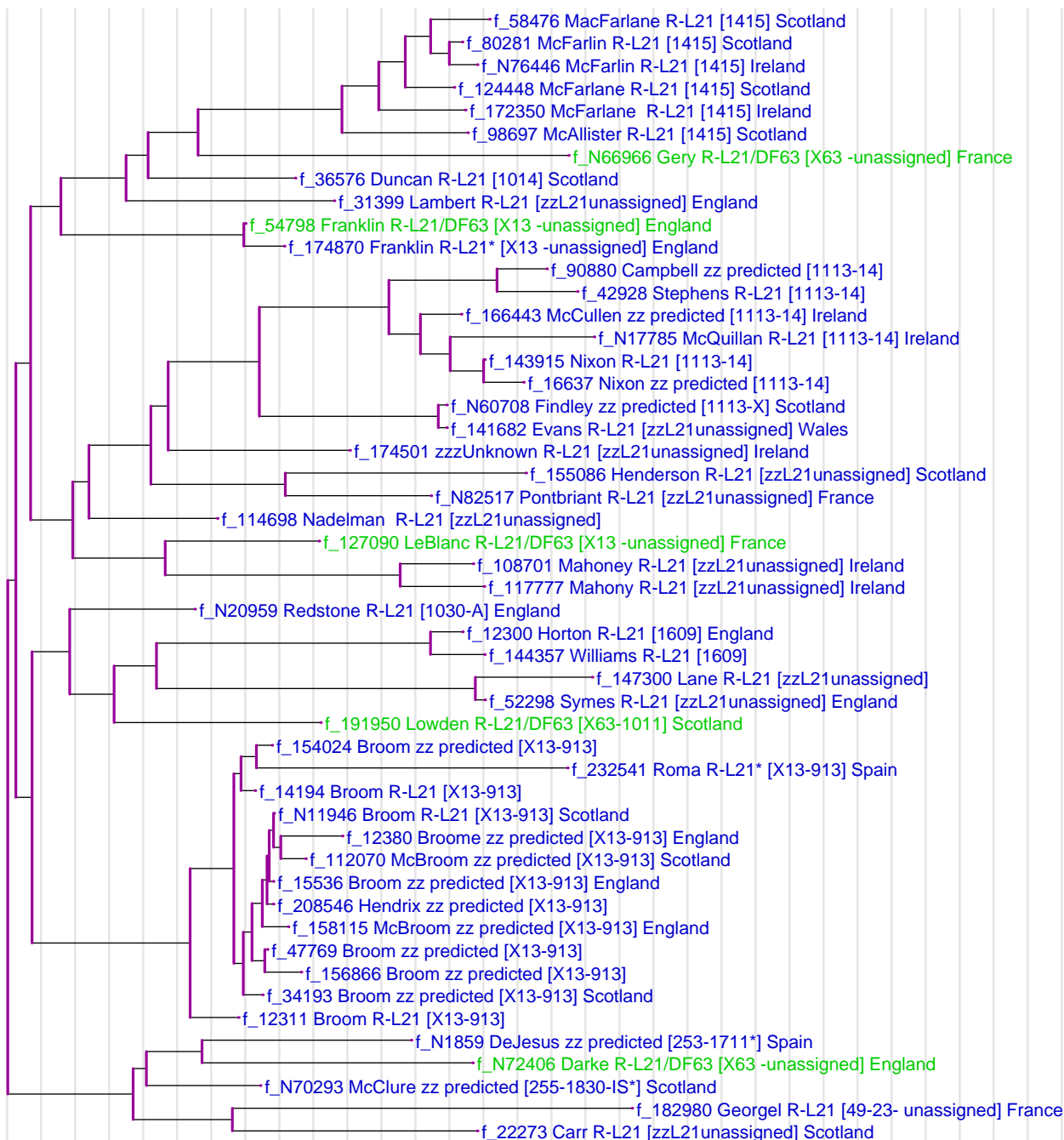


This is the marker distribution for R-DF63. The color indicates the relative frequency of the alleles.



Age Analysis

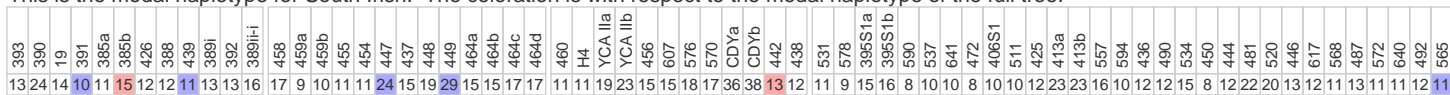
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
50	3350	689	20.57%	114.58±11.66	2864.43±408.751



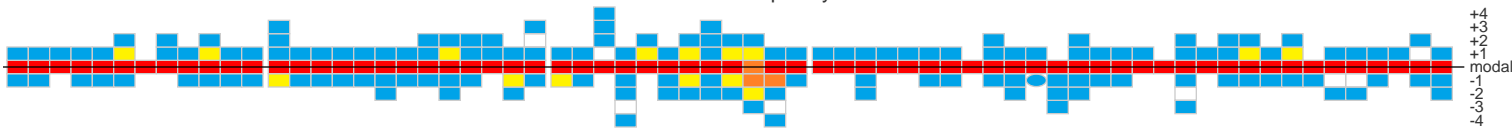
The vertical grey lines are separated 10 generations apart.

South Irish

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

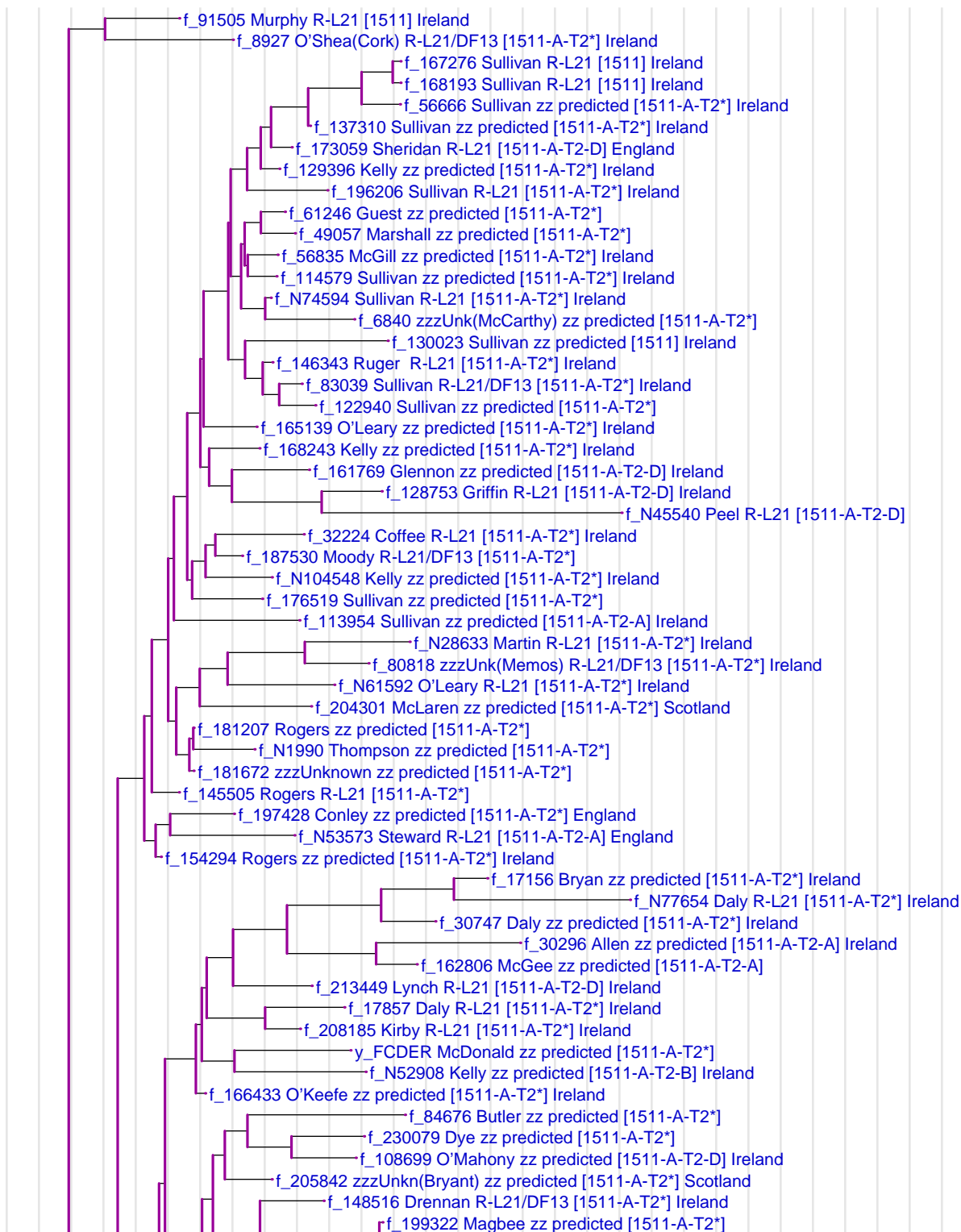


This is the marker distribution for South Irish. The color indicates the relative frequency of the alleles.

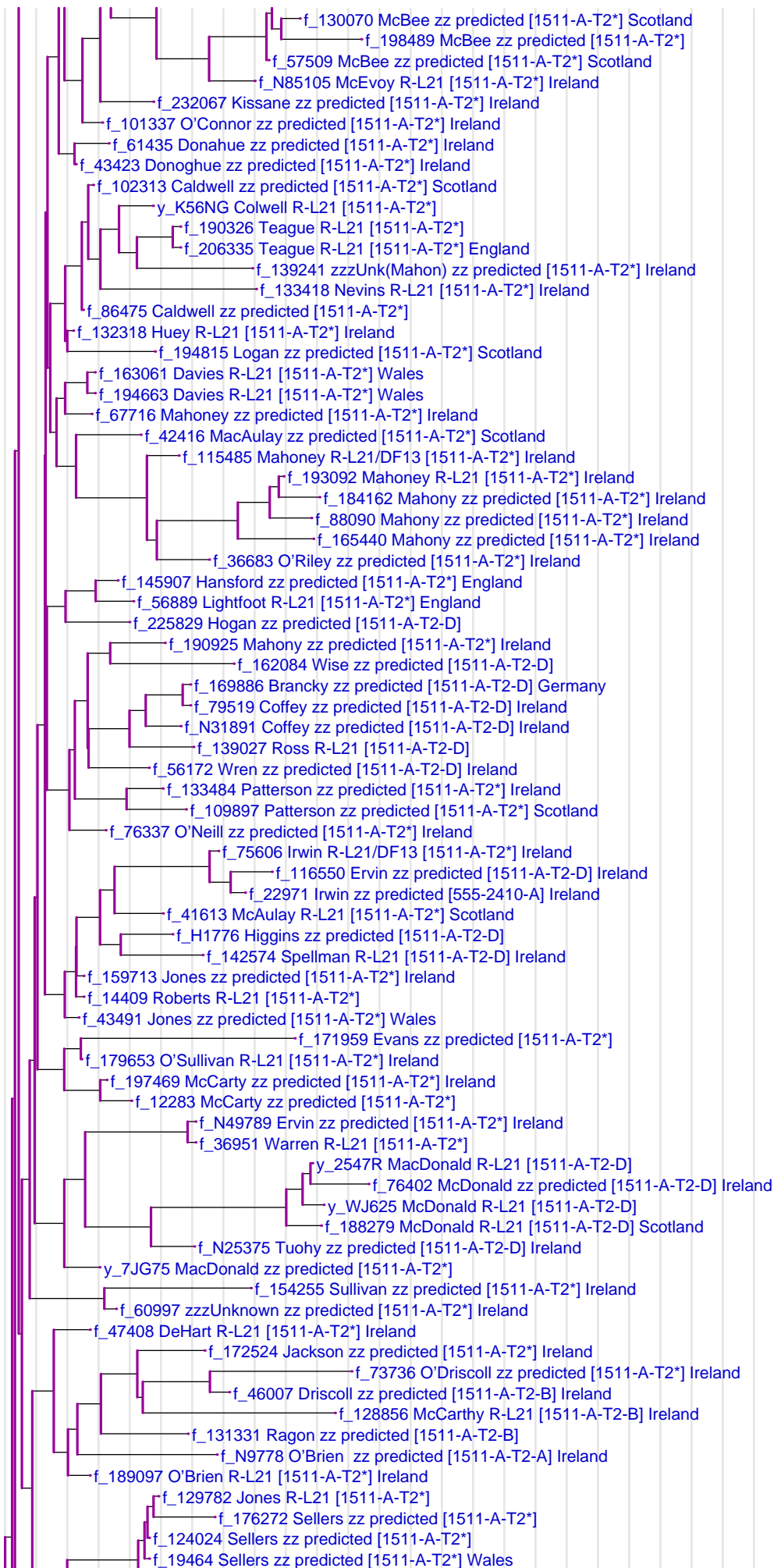


Age Analysis

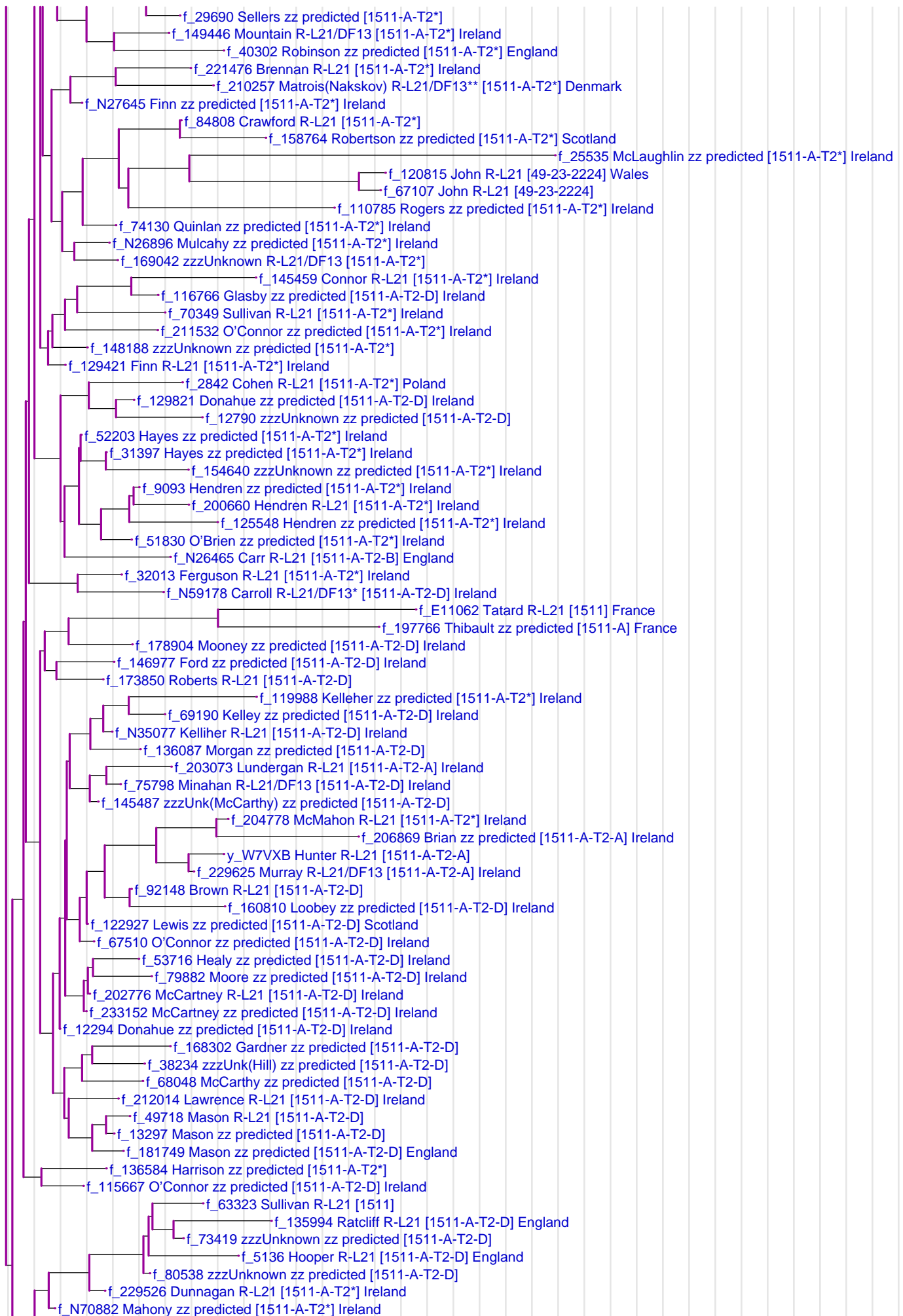
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
235	15745	1544	9.81%	51.56±5.17	1288.93±182.601



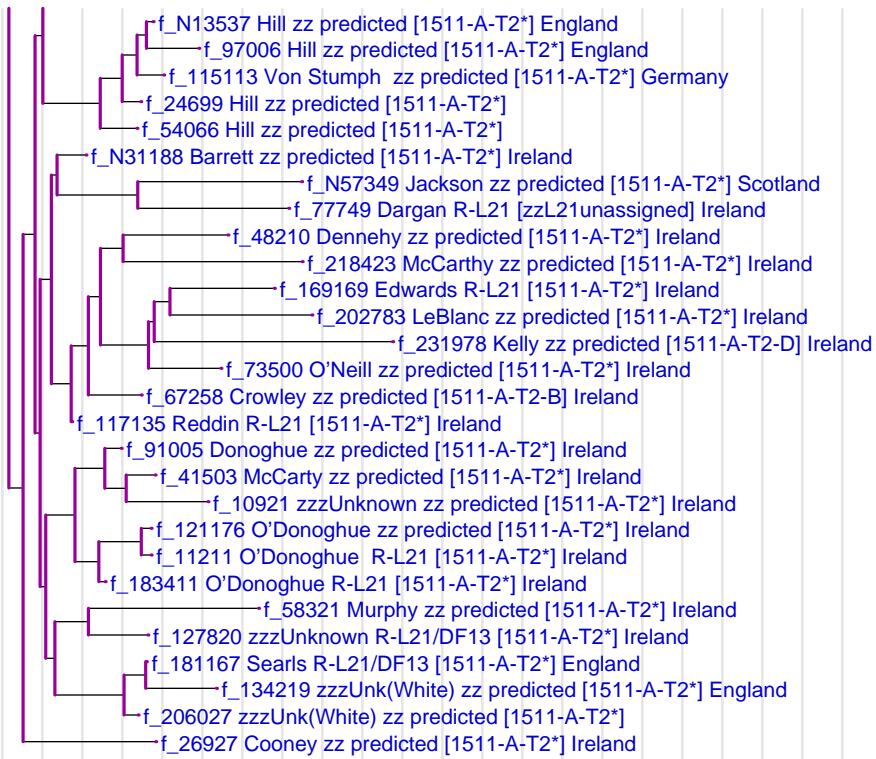
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.



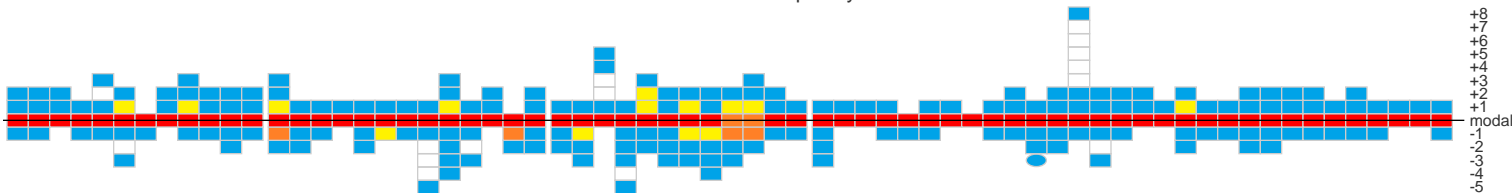
The vertical grey lines are separated 10 generations apart.

Scots Cluster

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

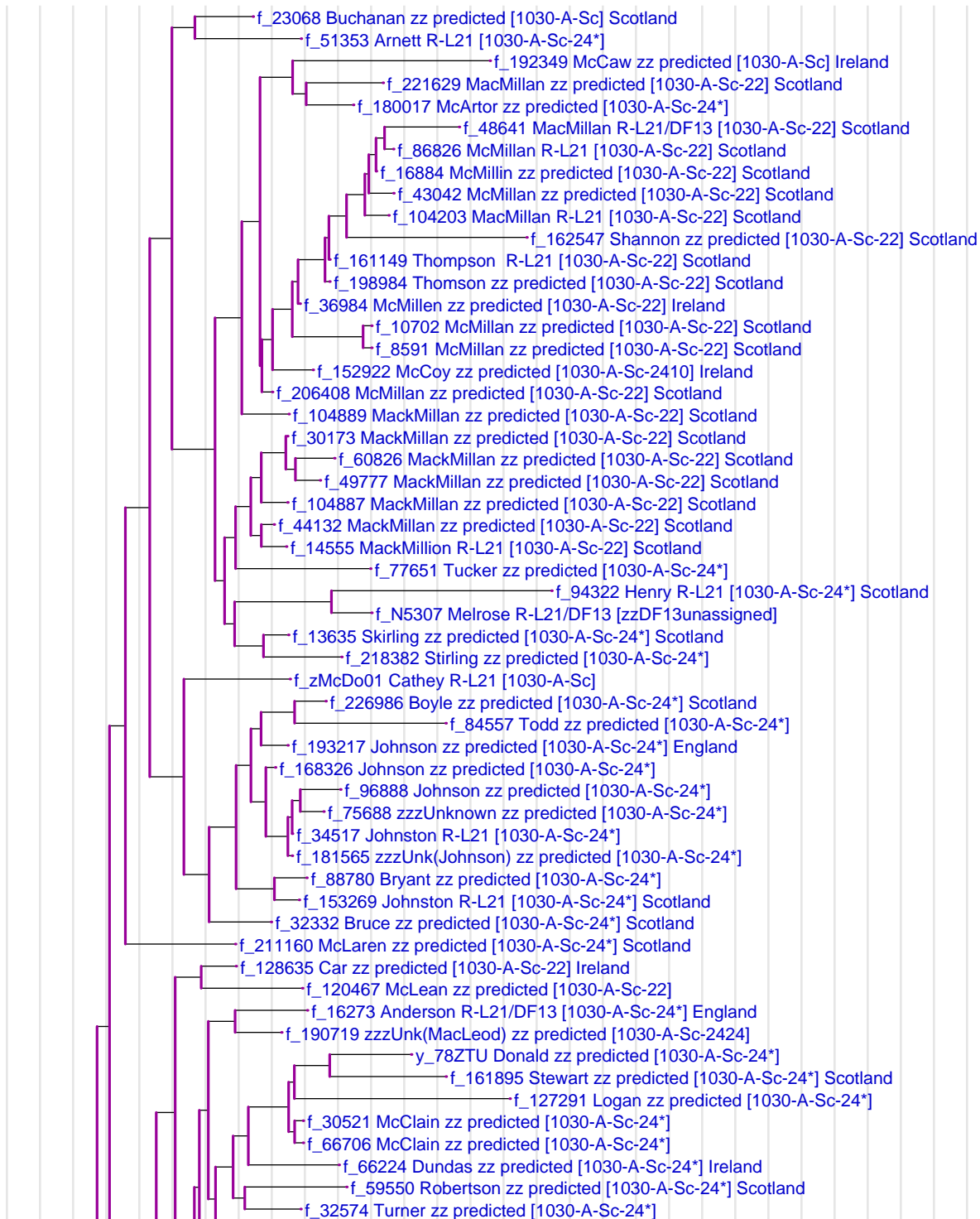
393	390	19	391	385a	385b	426	388	439	389i	392	389i-1	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	466	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	446	617	568	487	572	640	492	565
13	24	14	10	11	14	12	12	13	13	13	17	18	9	10	11	11	25	15	19	30	15	15	17	17	11	12	19	24	15	15	18	17	37	38	12	12	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	15	8	11	22	20	13	12	11	13	11	12	12	

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

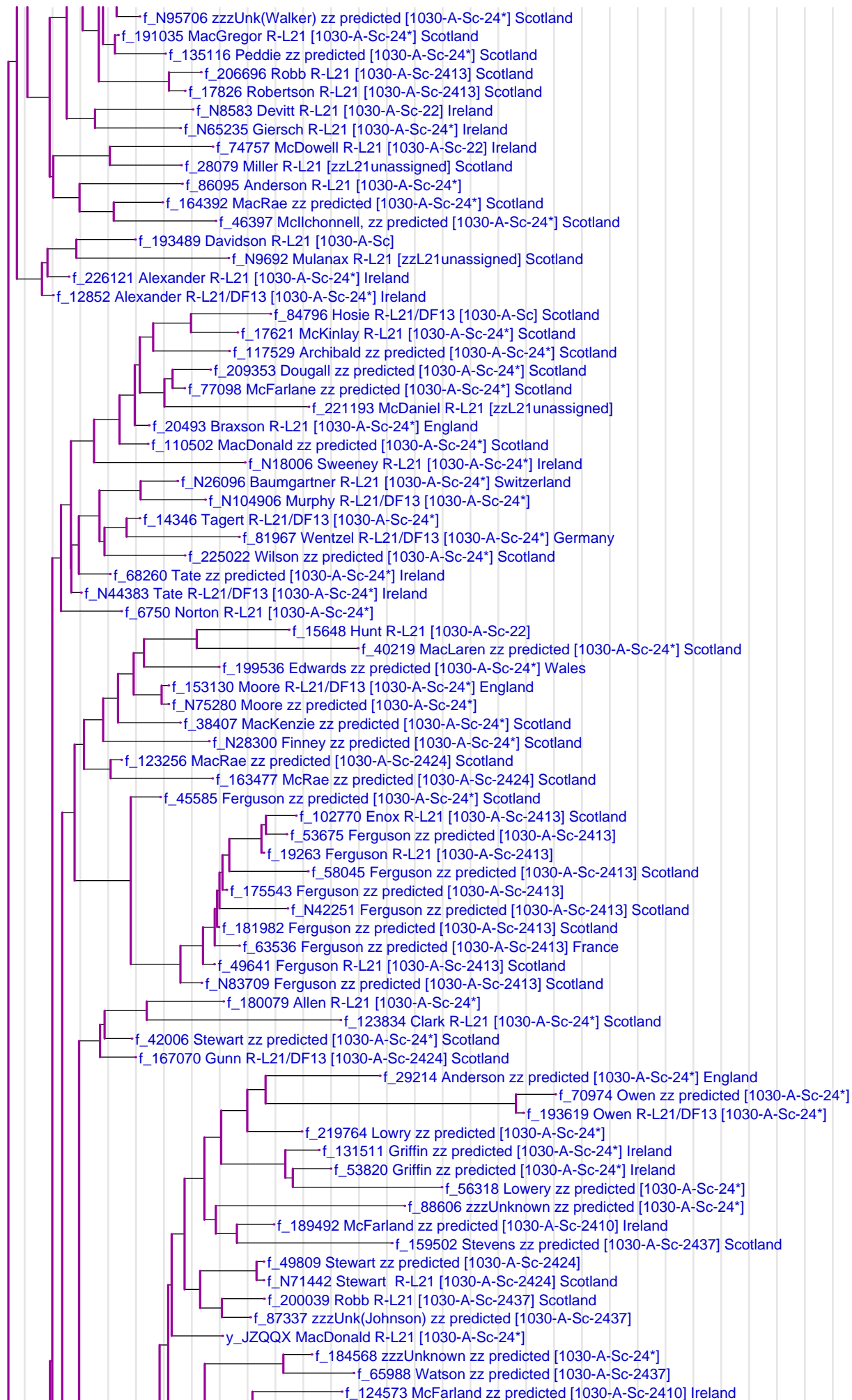


Age Analysis

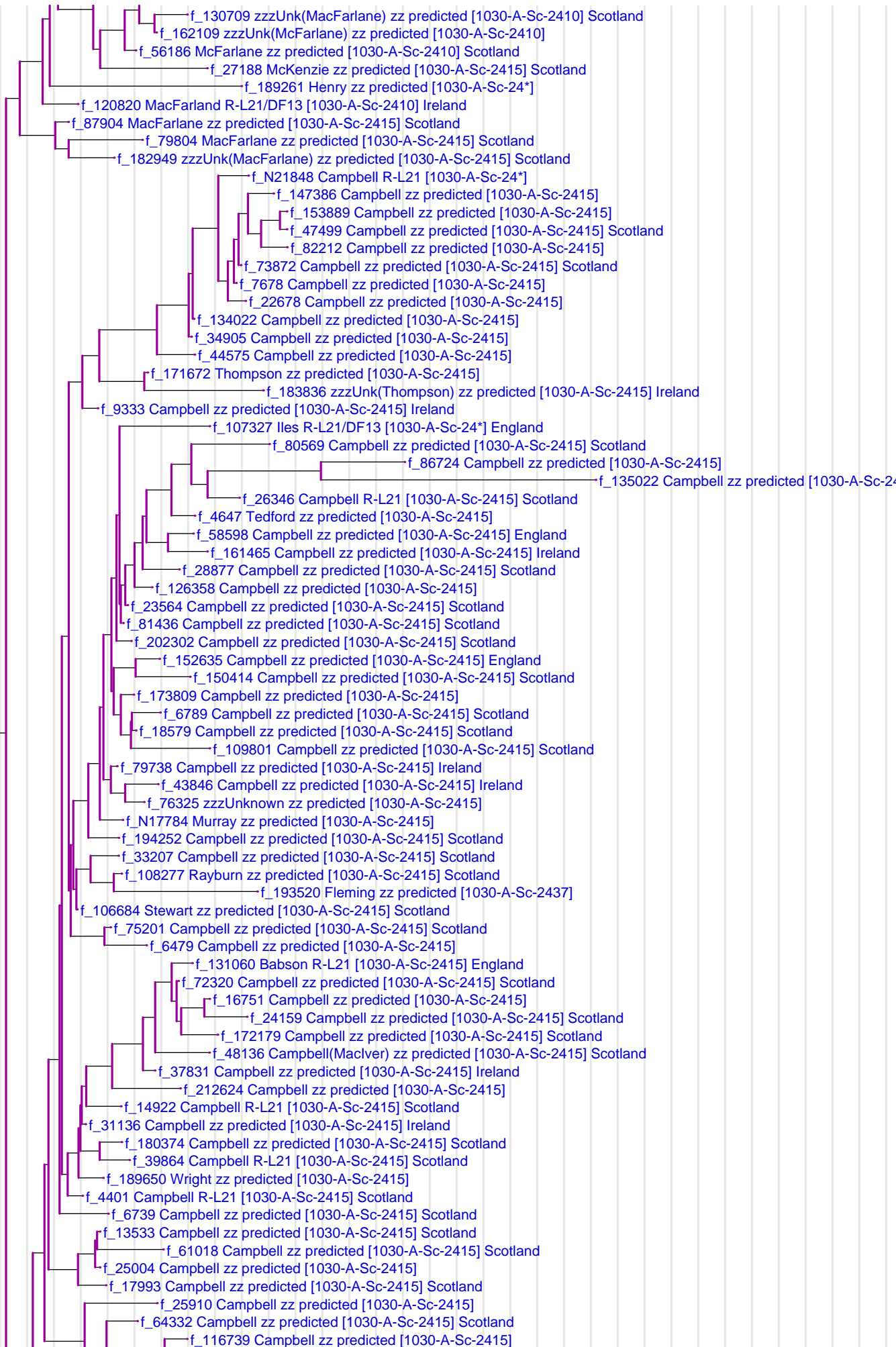
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
701	46967	5225	11.12%	58.90±5.90	1472.42±208.355



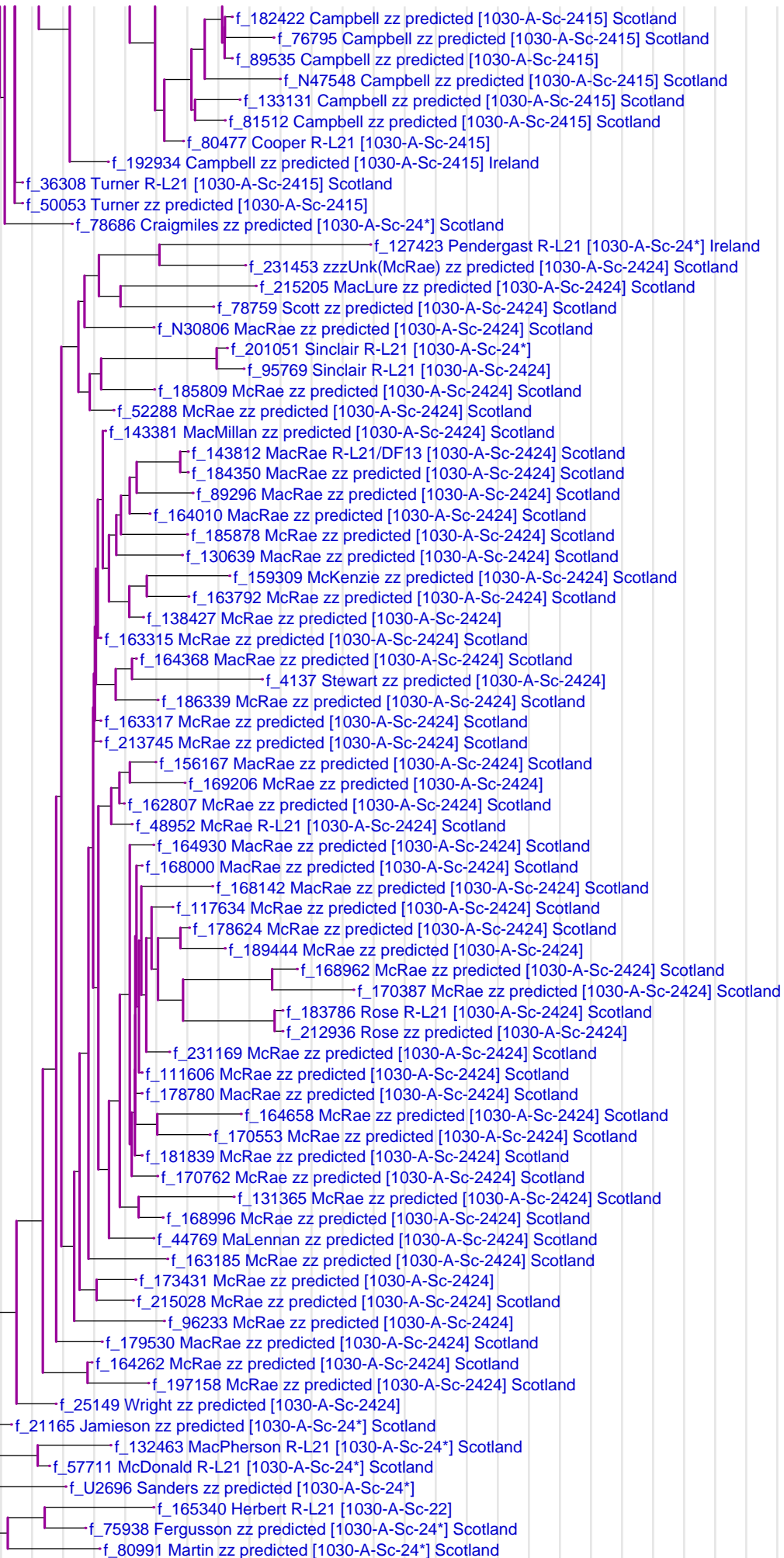
The vertical grey lines are separated 10 generations apart.



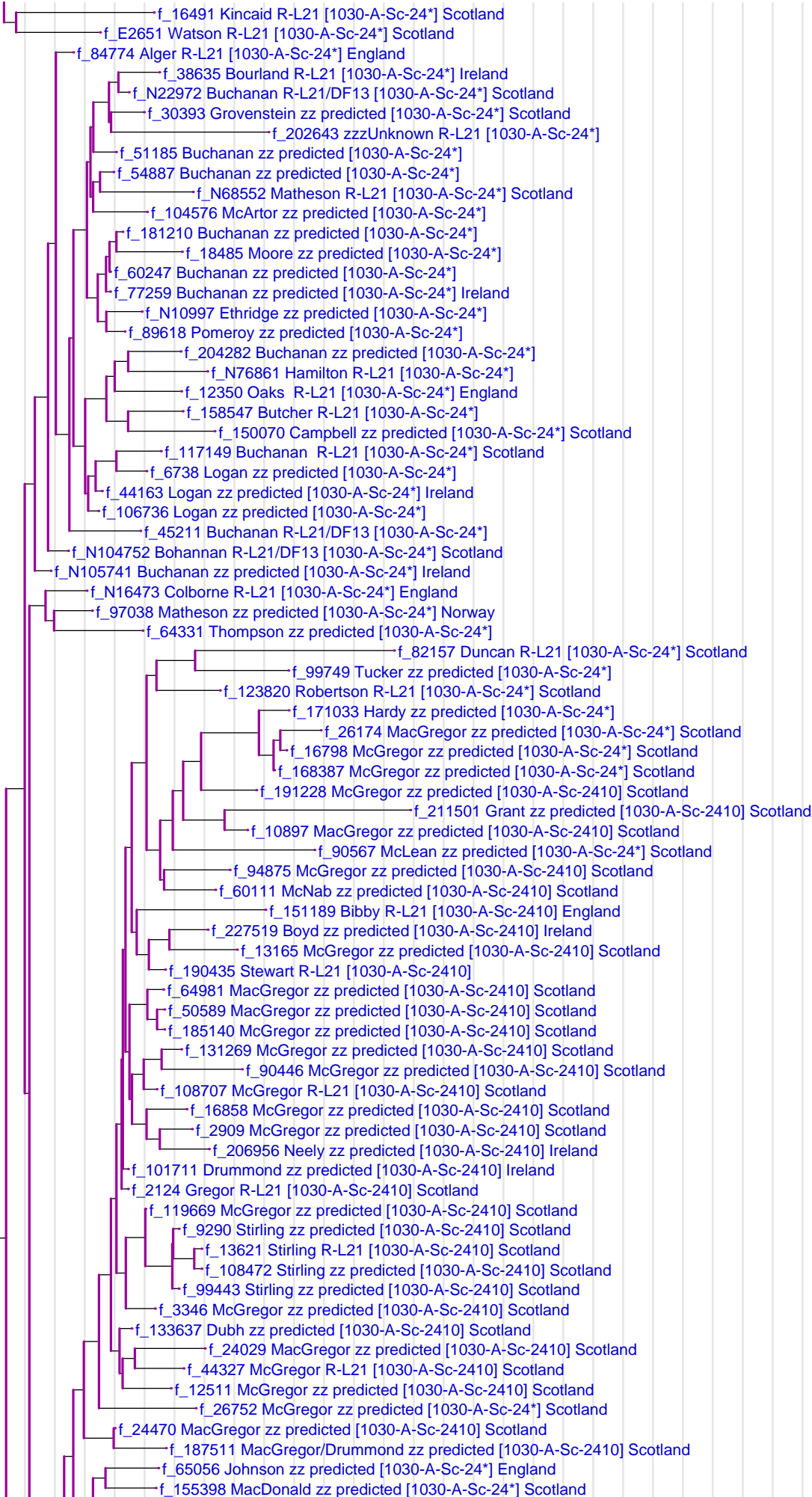
The vertical grey lines are separated 10 generations apart.



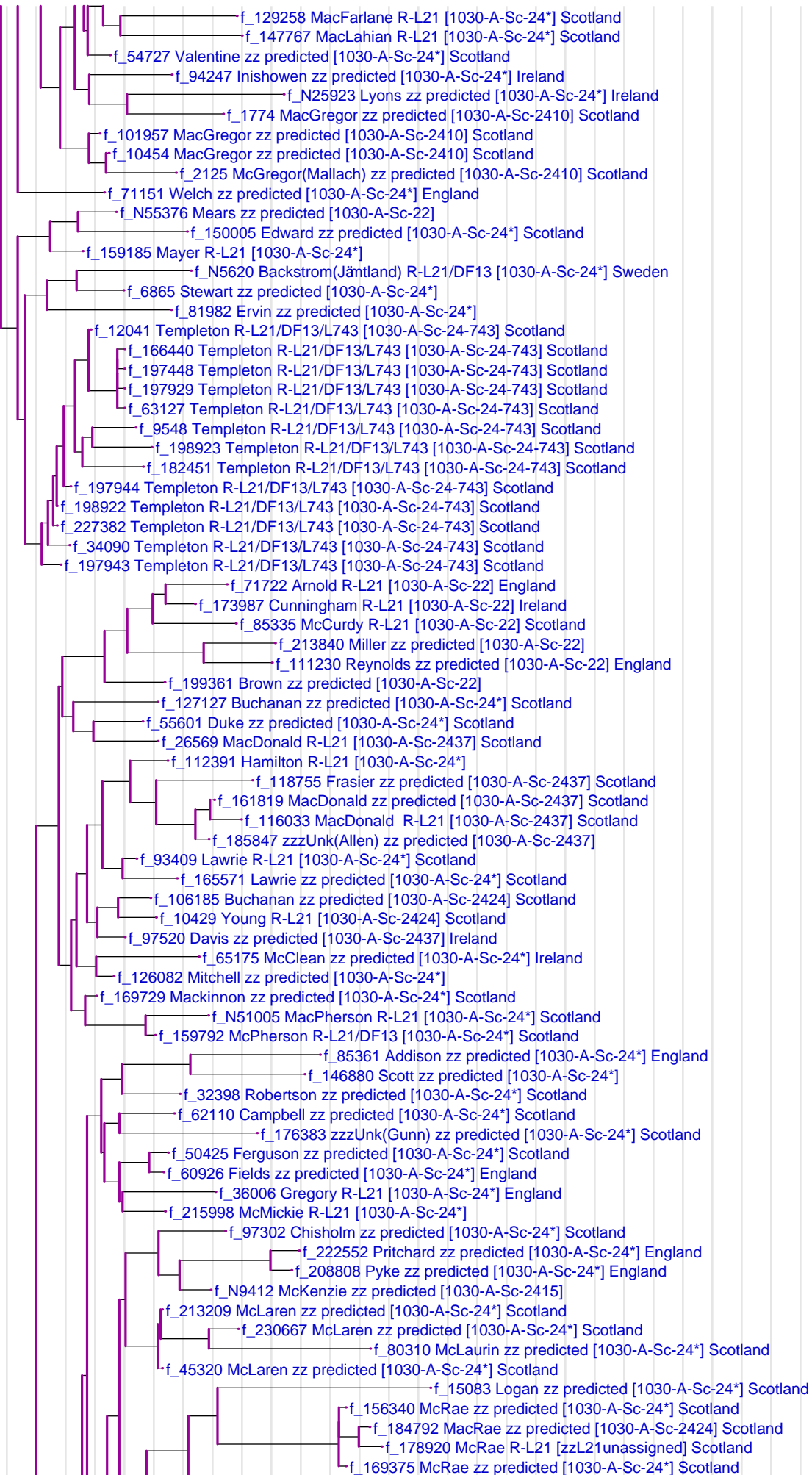
The vertical grey lines are separated 10 generations apart.



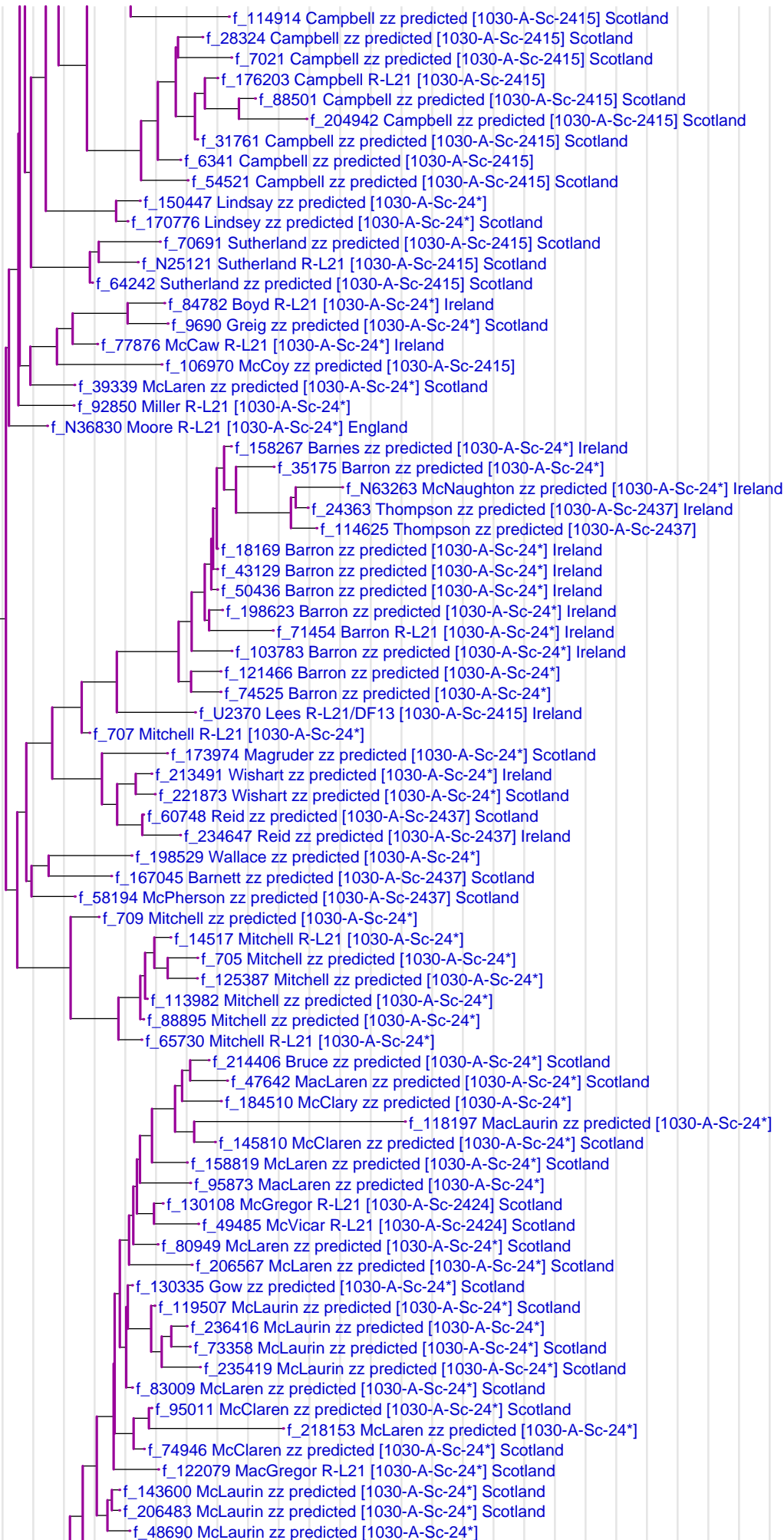
The vertical grey lines are separated 10 generations apart.



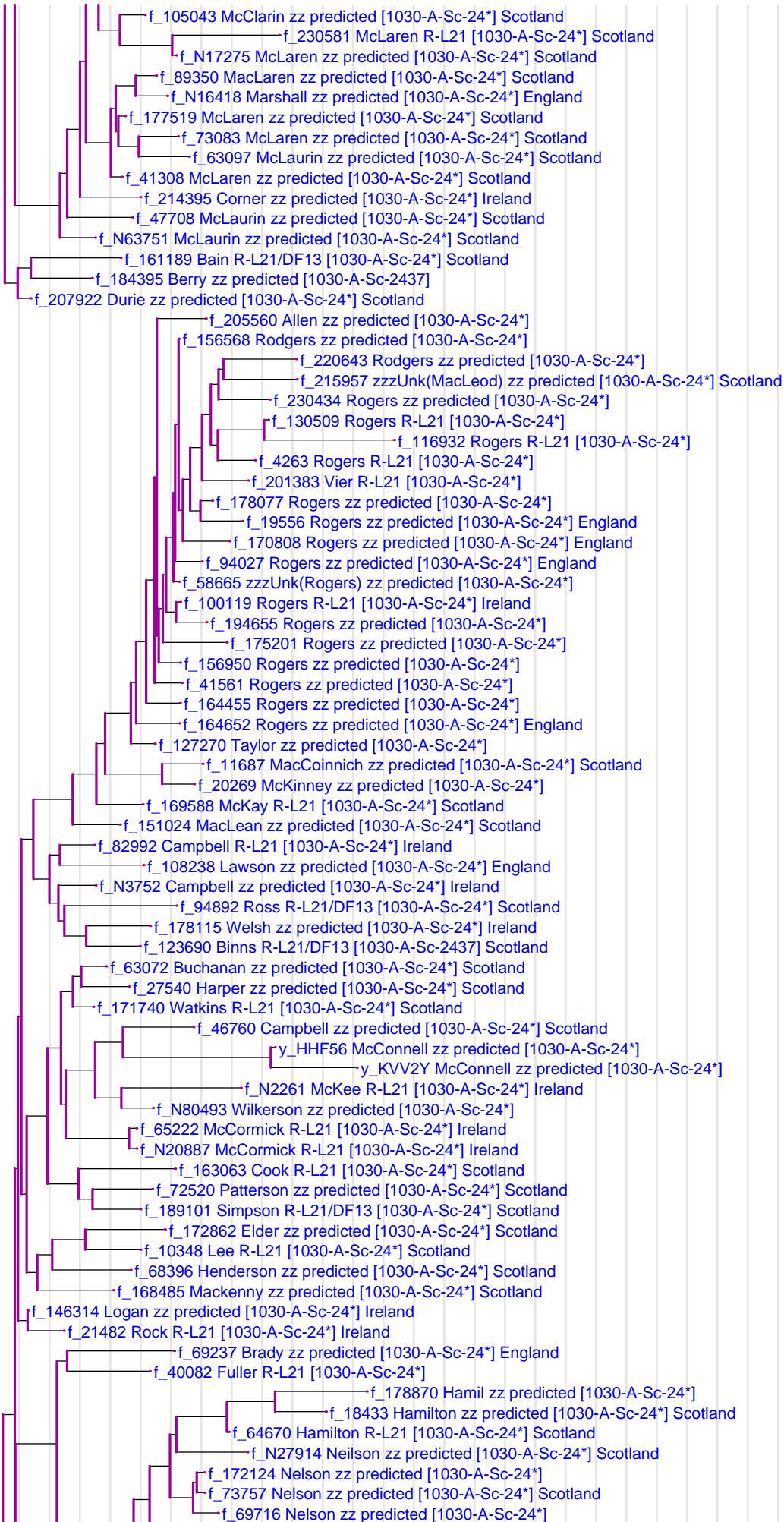
The vertical grey lines are separated 10 generations apart.



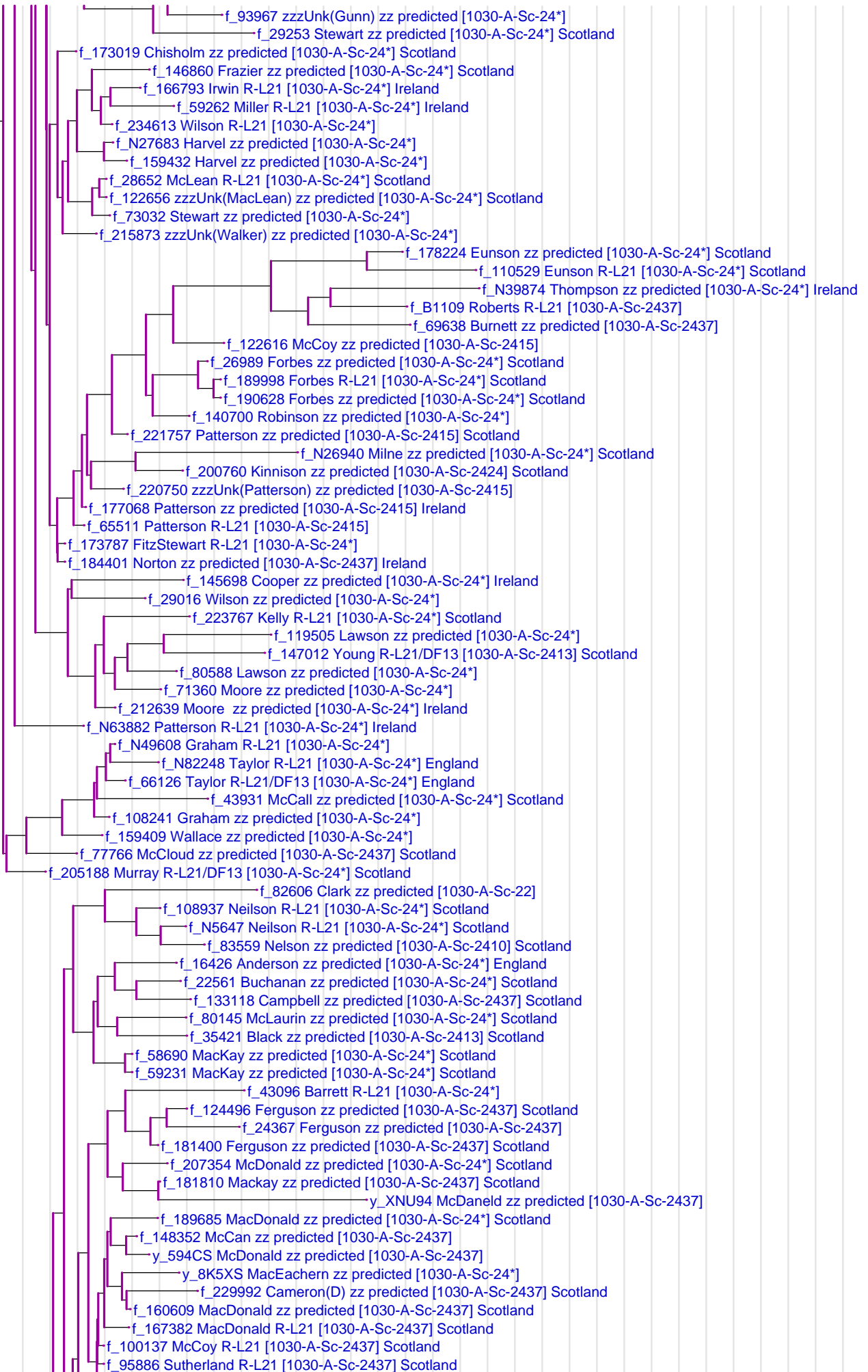
The vertical grey lines are separated 10 generations apart.



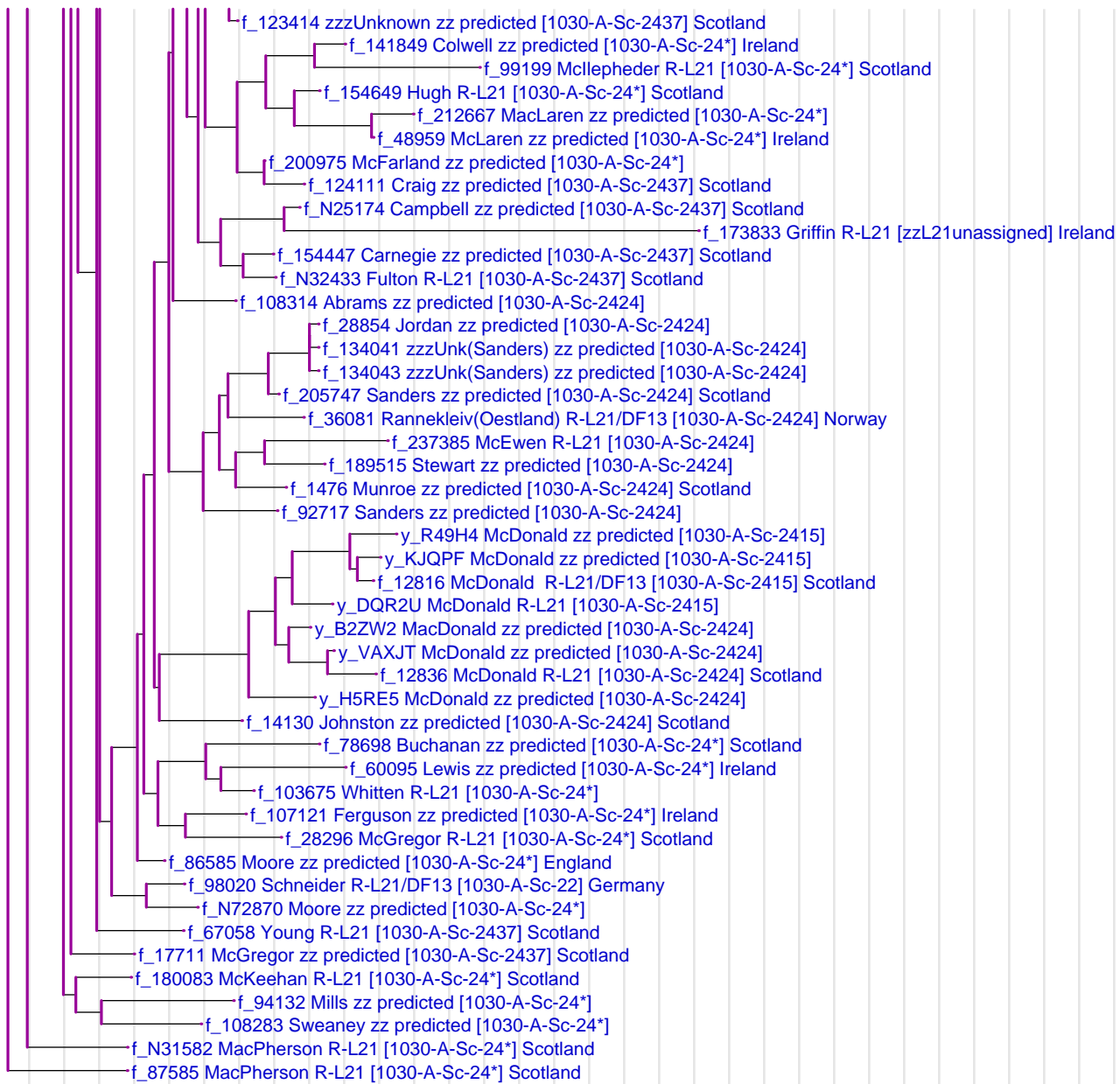
The vertical grey lines are separated 10 generations apart.



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: 3468.97±490.631 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	11	11	14	12	12	13	13	16	17	9	10	11	11	25	15	19	30	15	15	17	17	11	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: 3474.48±491.411 years																																								
R-DF23																										Age: 1956.43±276.825 years																																								
R-M222																										Age: 1513.01±214.097 years																																								
R-L513																										Age: 3074.78±435.061 years																																								
R-L69																										Age: 3083.51±436.865 years																																								
R-P66																										Age: 918.748±142.334 years																																								
R-L193																										Age: 1354.66±191.872 years																																								
R-L706.2																										Age: 1202.32±171.504 years																																								
R-L705.2																										Age: 1195.63±170.685 years																																								
R-L555																										Age: 437.885±62.2443 years																																								
R-L96																										Age: 1274.46±197.858 years																																								
R-L144																										Age: 3798.73±542.9 years																																								
R-Z255																										Age: 1913.92±271.082 years																																								
R-Z253																										Age: 3016.12±426.818 years																																								
R-L226																										Age: 1323.16±187.456 years																																								
R-L554																										Age: 902.049±143.558 years																																								
R-DF21																										Age: 2912.41±412.182 years																																								
R-P314.2																										Age: 1725±246.518 years																																								
R-L362																										Age: 1109.76±159.687 years																																								
R-Z246																										Age: 2751.4±390.314 years																																								
R-DF25																										Age: 2743.1±389.162 years																																								
R-DF5																										Age: 2624.24±372.505 years																																								
R-L627																										Age: 808.928±123.146 years																																								
R-L658																										Age: 523.808±76.4389 years																																								
R-L720																										Age: 2140.82±320.994 years																																								
R-S190																										Age: 908.726±131.057 years																																								
R-L371																										Age: 704.453±100.299 years																																								
R-DF41																										Age: 2089.27±296.628 years																																								
R-L744																										Age: 608.355±86.5933 years																																								
R-L745																										Age: 616.791±87.8691 years																																								
R-DF63																										Age: 2864.43±408.751 years																																								
South Irish																										Age: 1288.93±182.601 years																																								
Scots Cluster																										Age: 1472.42±208.355 years																																								

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 2012-07-27 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 or more 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%	

