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	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

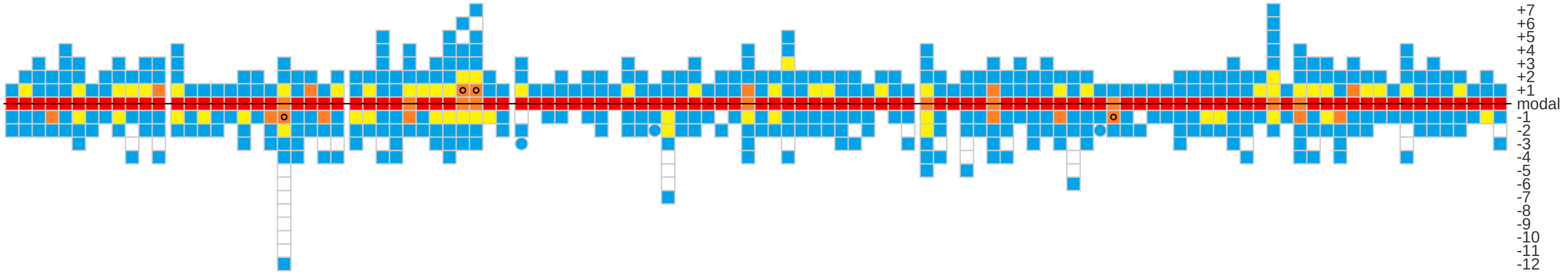
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	30	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	36	38	12	12

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
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

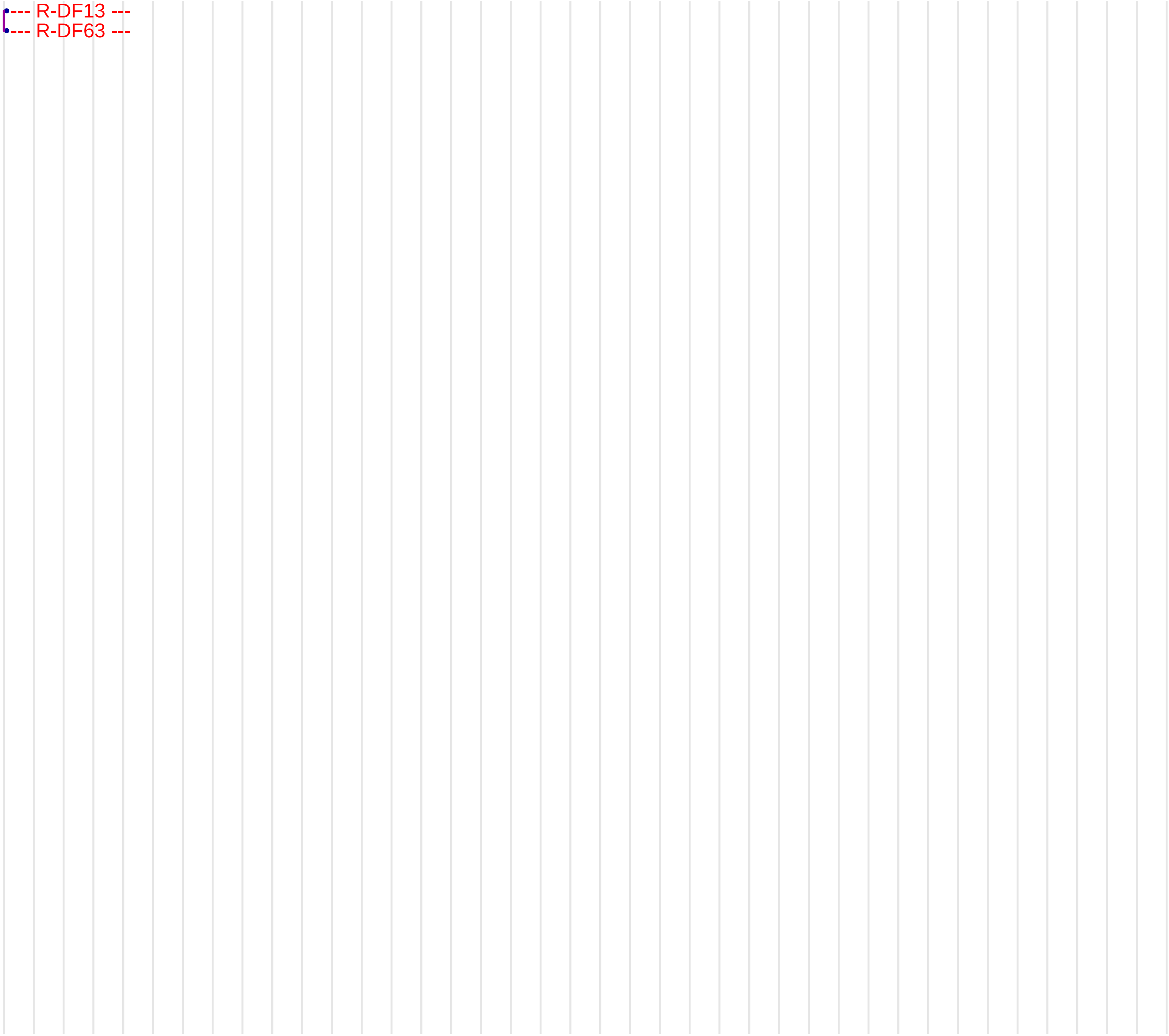
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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)
1247	83549	20068	24.02%	136.40±13.65	3410±482.428



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

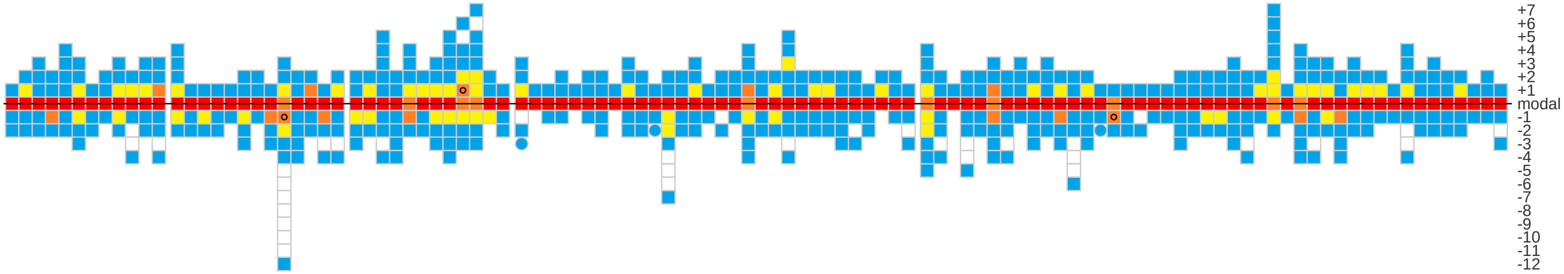
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	30	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	36	38	12	12

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
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

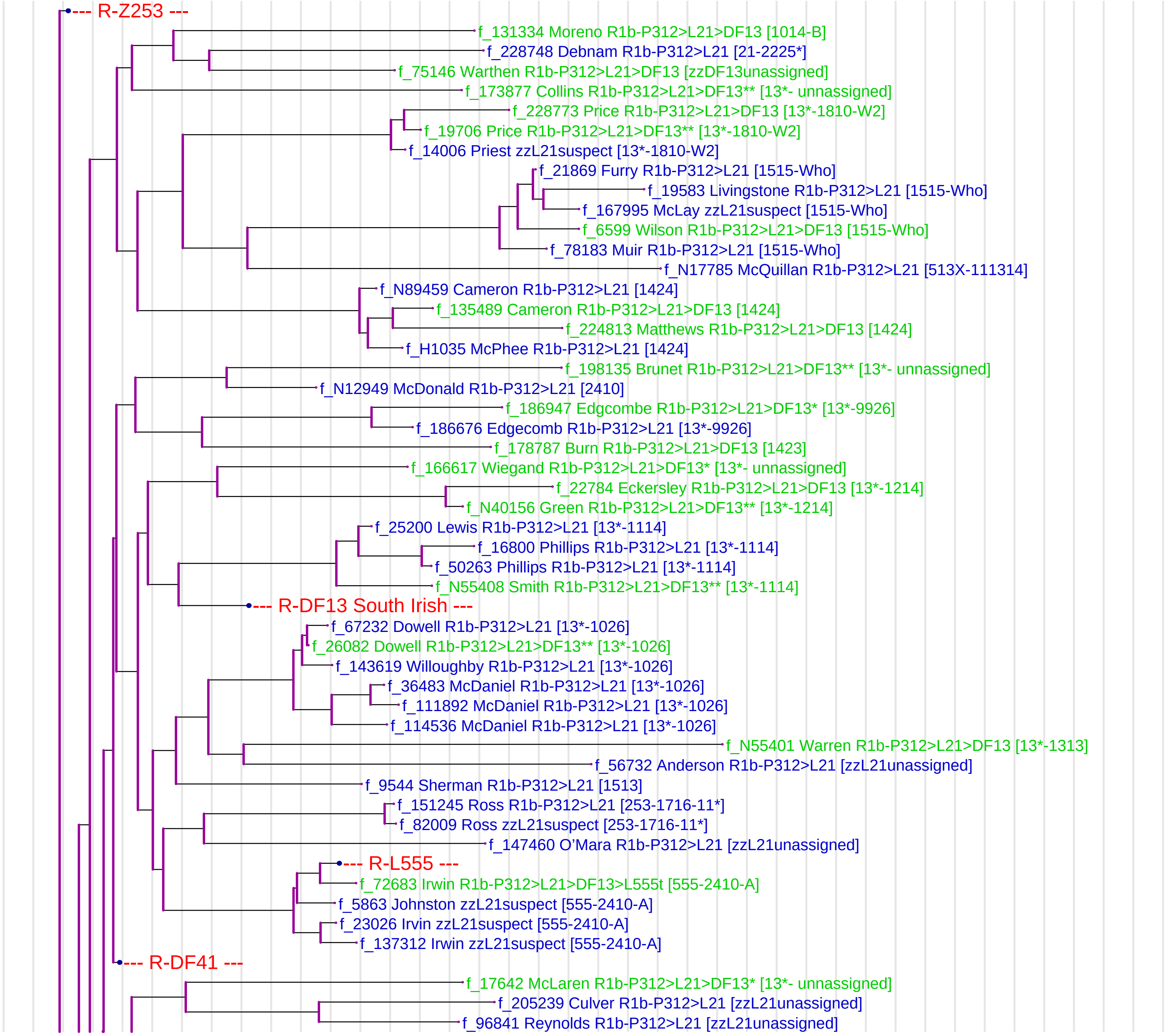
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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

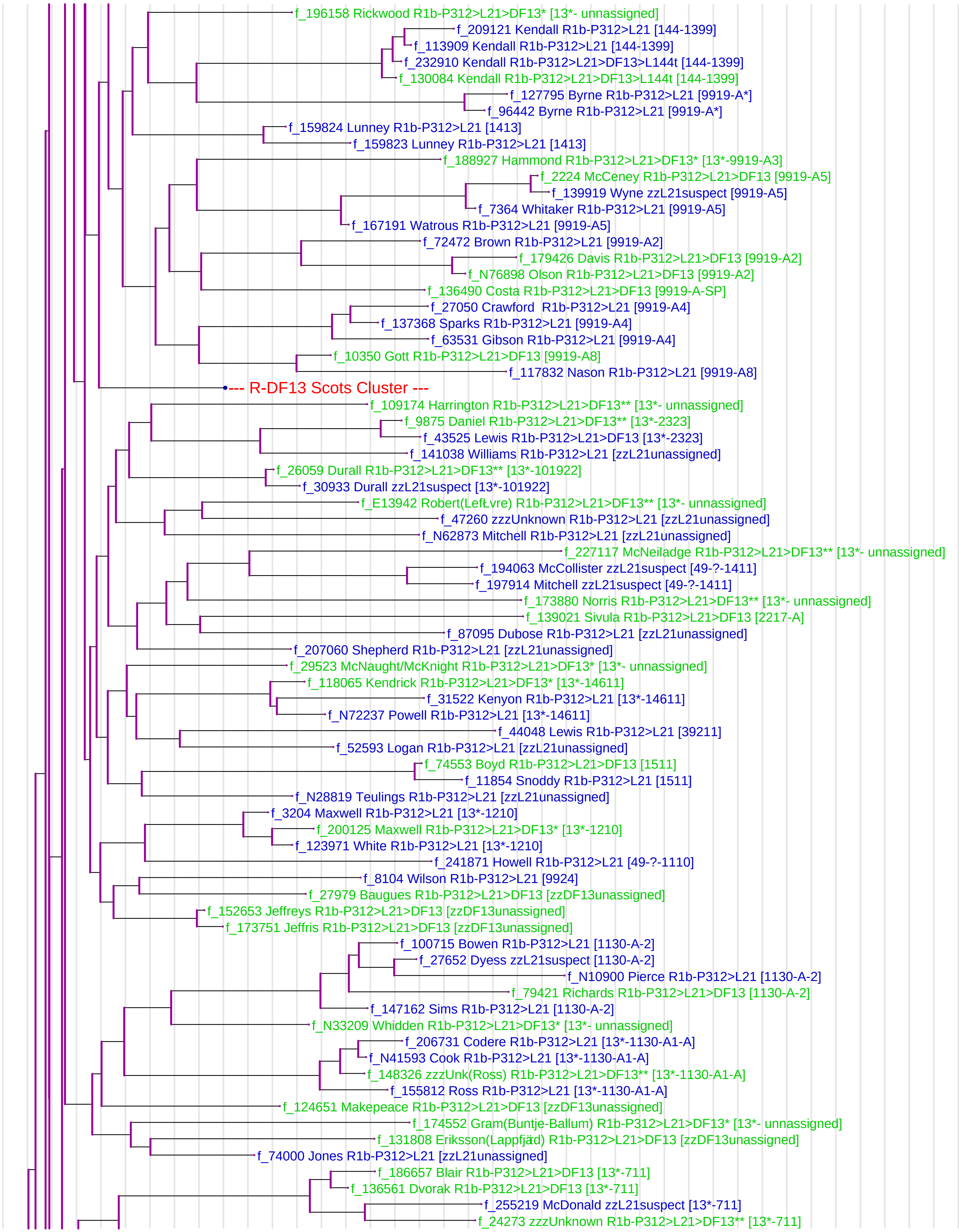


Age Analysis

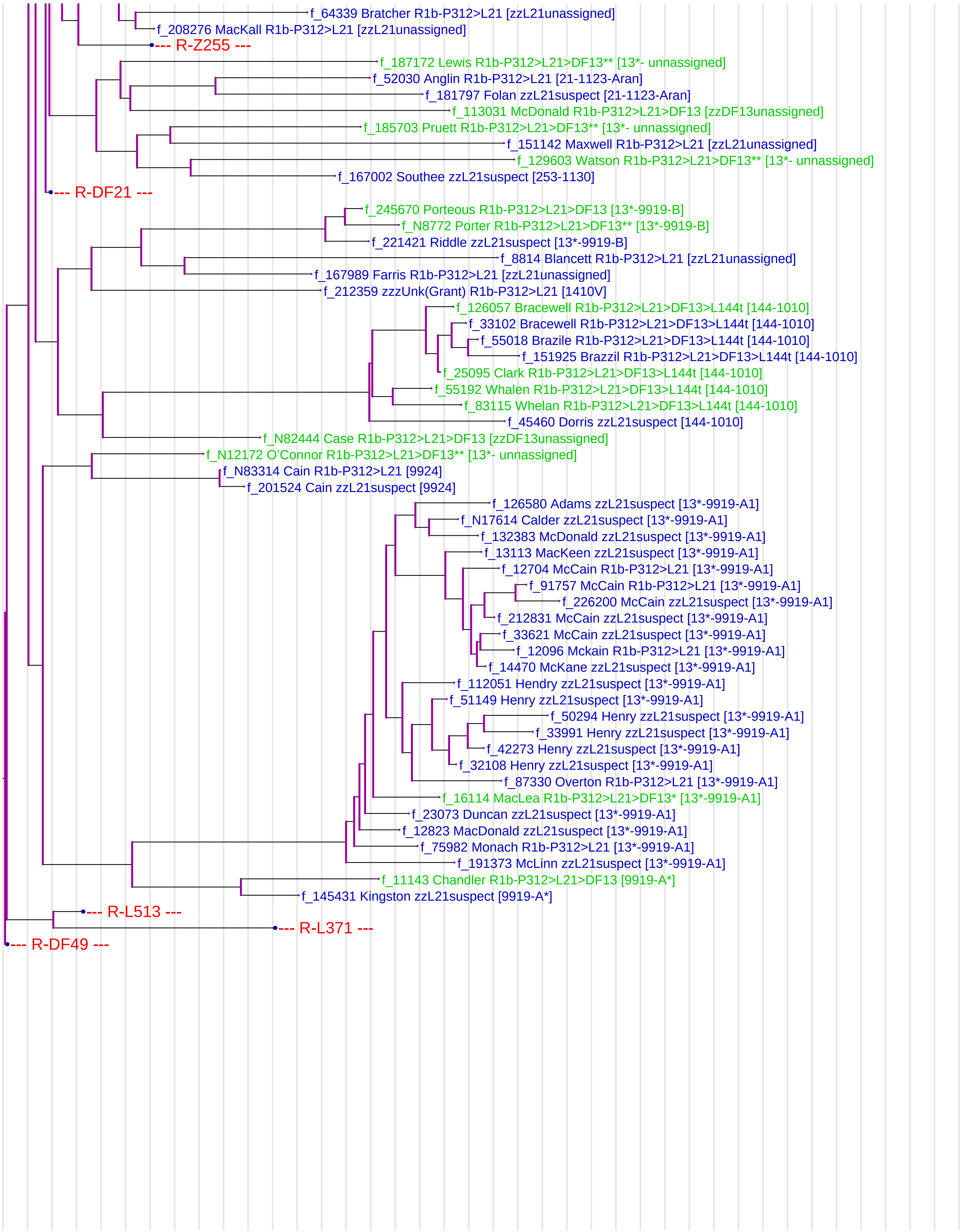
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
1222	81874	19676	24.03%	136.48±13.66	3412.03±482.719



The vertical grey lines are separated 10 generations apart.



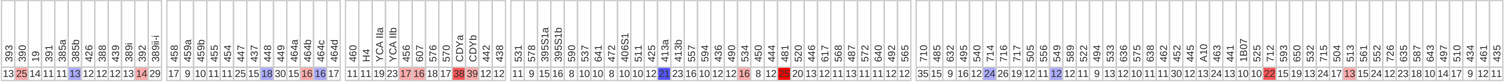
The vertical grey lines are separated 10 generations apart.



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	25	14	11	11	13	12	12	12	13	14	29

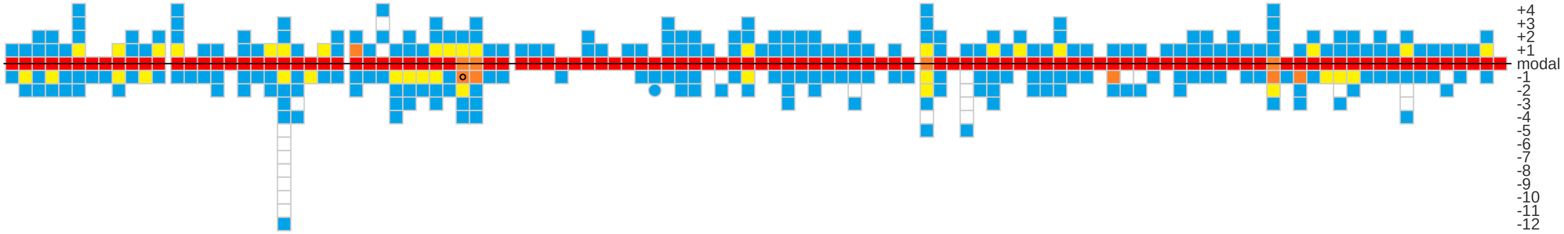
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	18	30	15	16	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	17	16	18	17	38	39	12	12

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
11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12

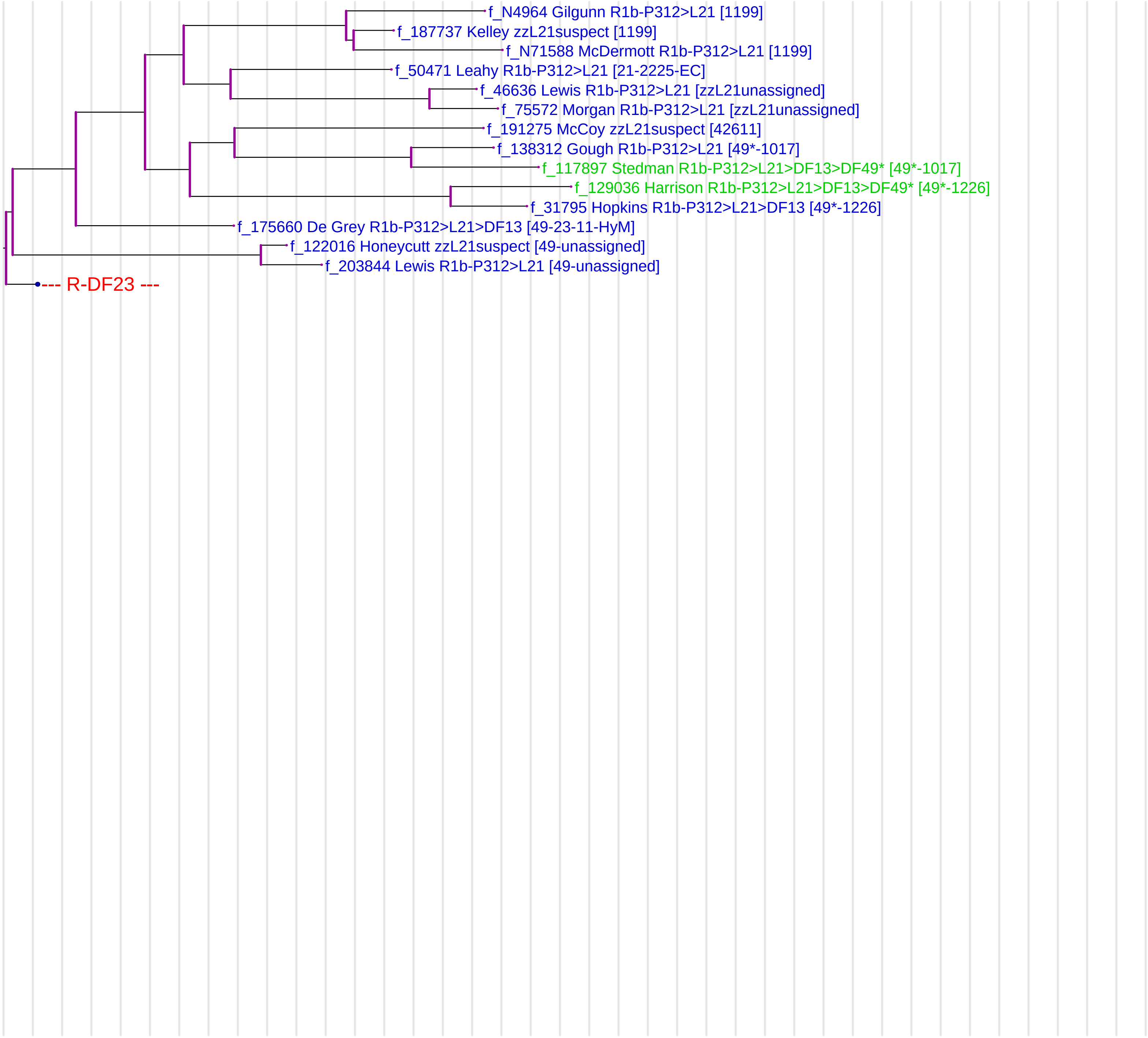
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	24	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	22	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

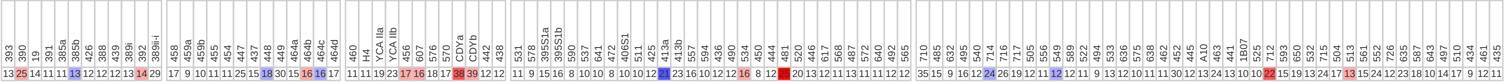
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
233	15611	2249	14.41%	77.61±7.79	1940.34±274.91



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	25	14	11	11	13	12	12	12	13	14	29

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	18	30	15	16	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	17	16	18	17	38	39	12	12

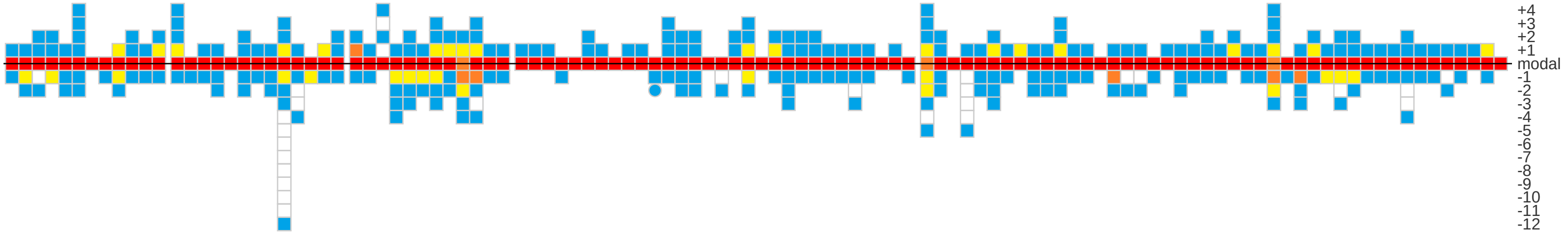
531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594
11	9	15	16	8	10	10	8	10	10	12	21	23	16	10

436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
12	12	16	8	12	25	20	13	12	11	13	11	11	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10
35	15	9	16	12	24	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	13

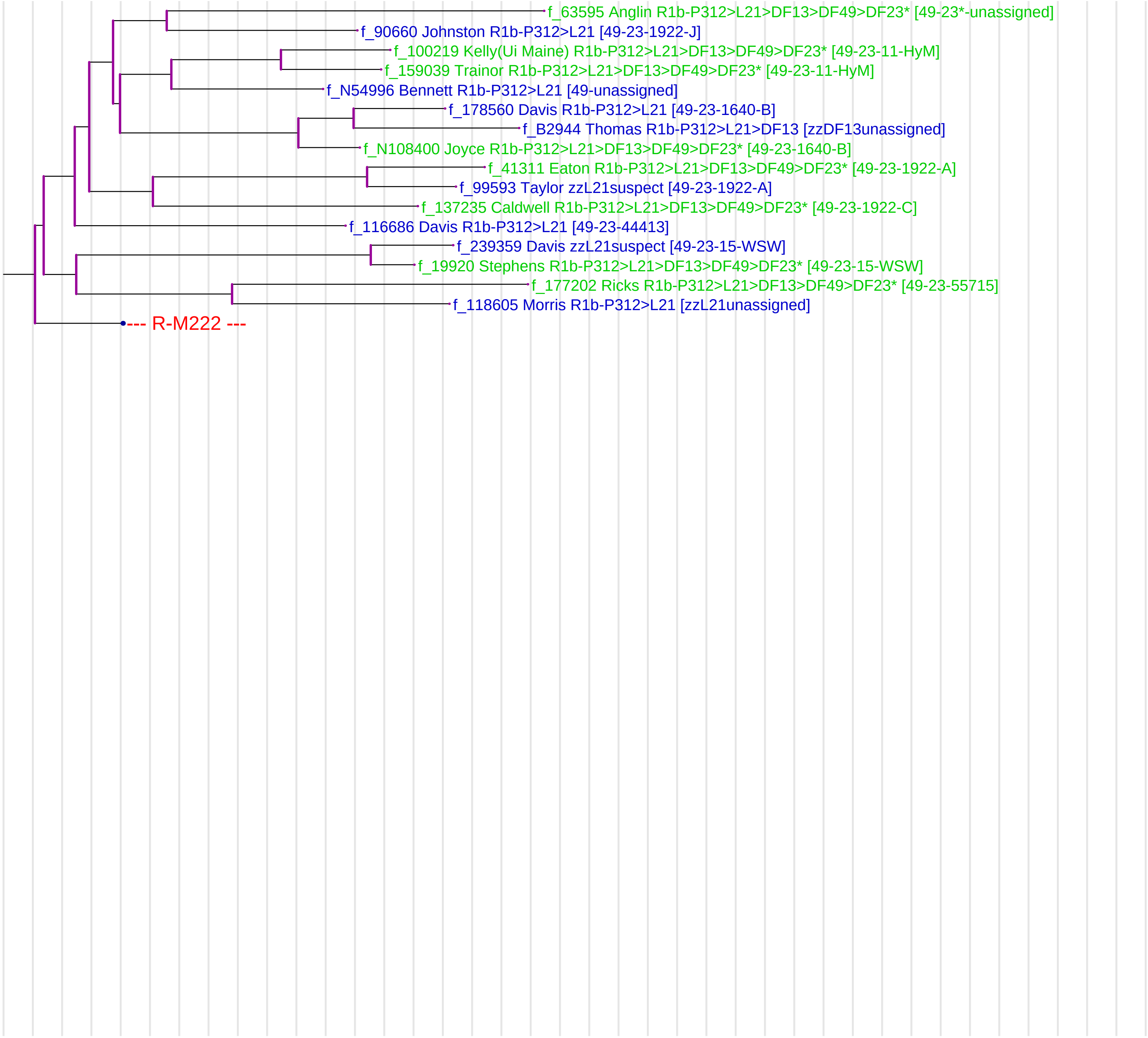
463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
24	13	10	10	22	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11

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)
219	14673	1878	12.80%	68.36±6.86	1709.1±242.169



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	25	14	11	11	13	12	12	12	13	14	29

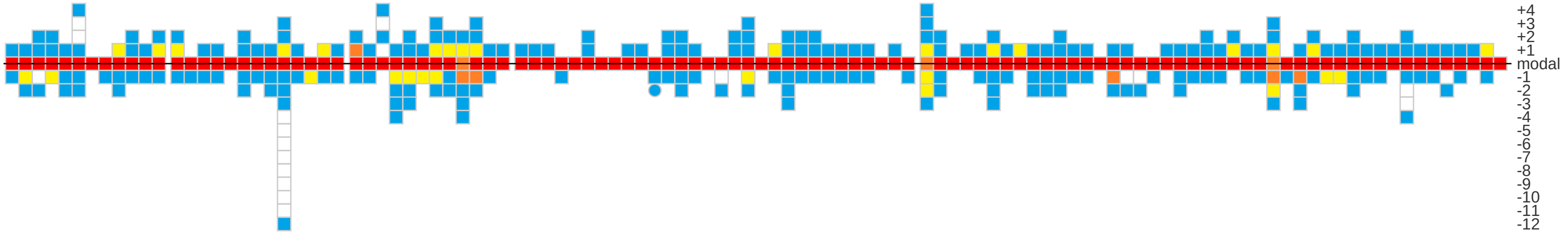
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	18	30	15	16	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	17	16	18	17	38	39	12	12

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
11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12

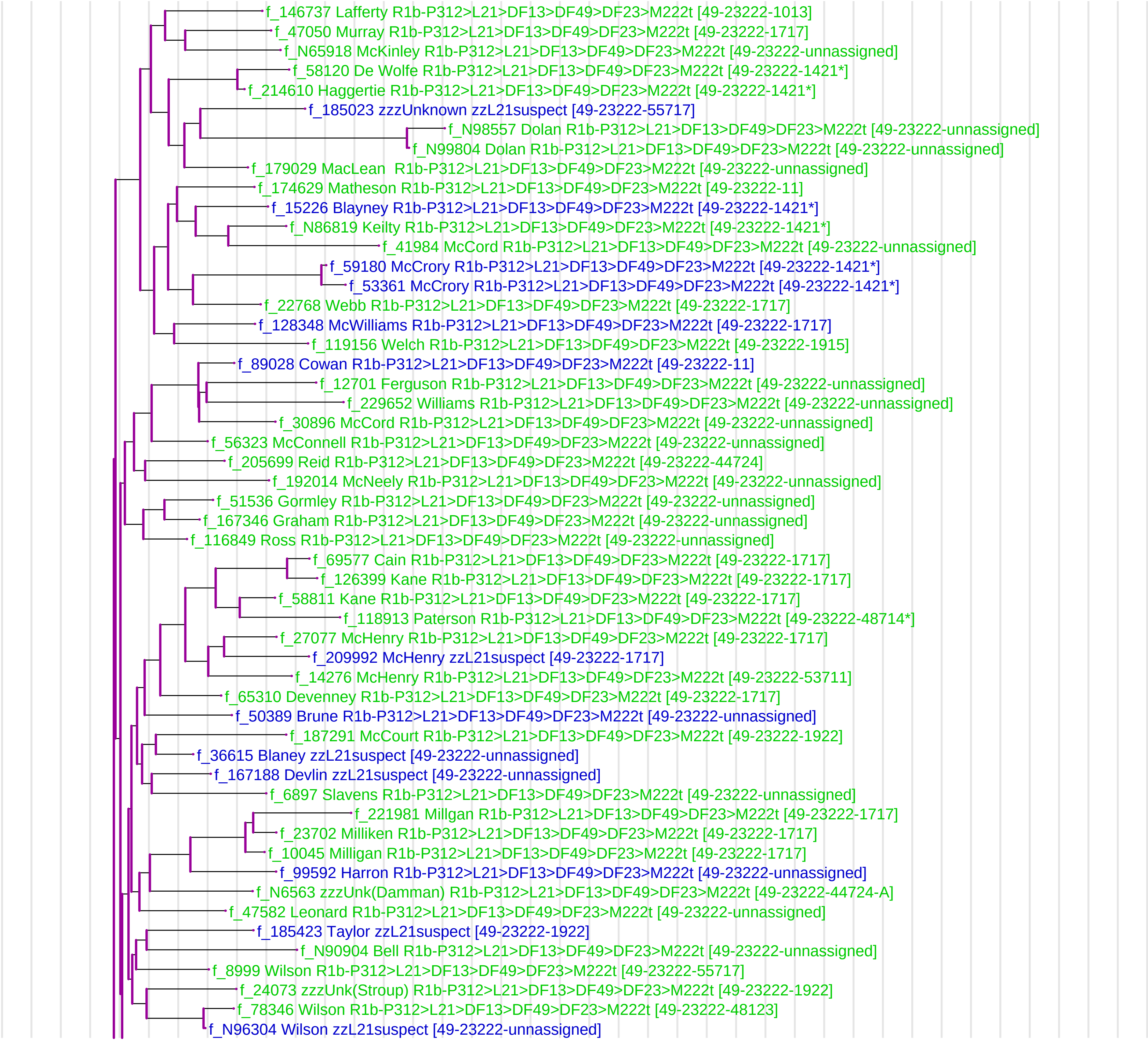
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	24	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	22	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11

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)
203	13601	1512	11.12%	58.85±5.91	1471.3±208.499



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	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

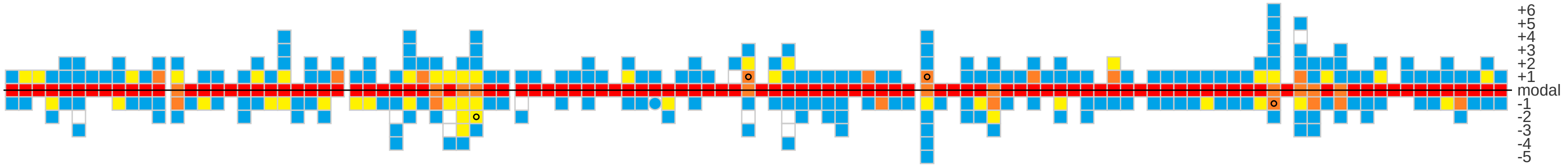
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	38	39	12	12

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
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	11	12	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	26	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	14	24	16	12	15	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

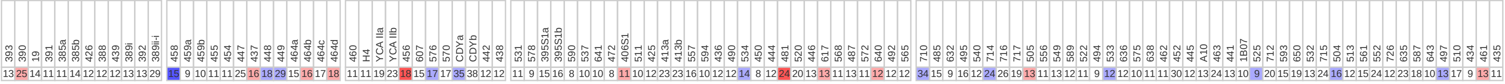
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
181	12127	2459	20.28%	112.78±11.33	2819.52±399.736

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	389ii-i
13	25	14	11	11	14	12	12	12	13	13	29

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
15	9	10	11	11	25	16	18	29	15	16	17	18

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	18	15	17	17	35	38	12	12

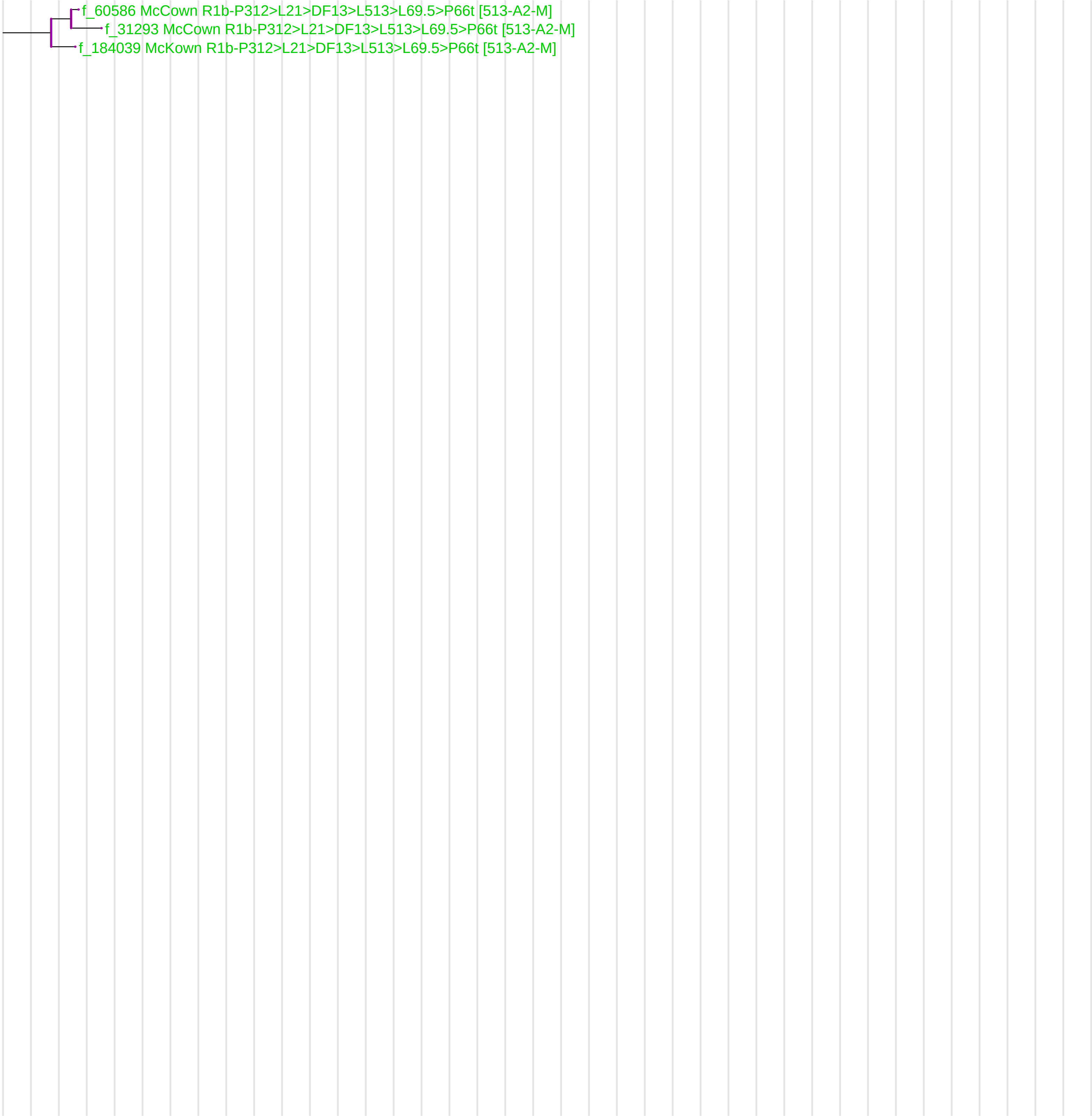
531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	24	20	13	13	11	13	11	12	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
34	15	9	16	12	24	26	19	13	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	9	20	15	19	13	24	16	12	15	24	12	23	18	10	13	17	9	13	11

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

Age Analysis

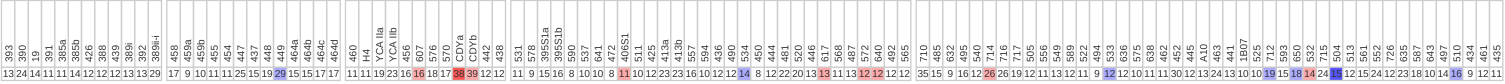
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	3	1.49%	7.52±0.92	187.97±29.7502



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

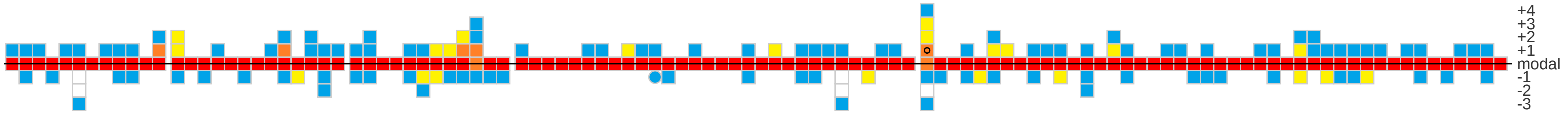
460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	16	18	17	38	39	12	12

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
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	12	12	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463
35	15	9	16	12	26	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24

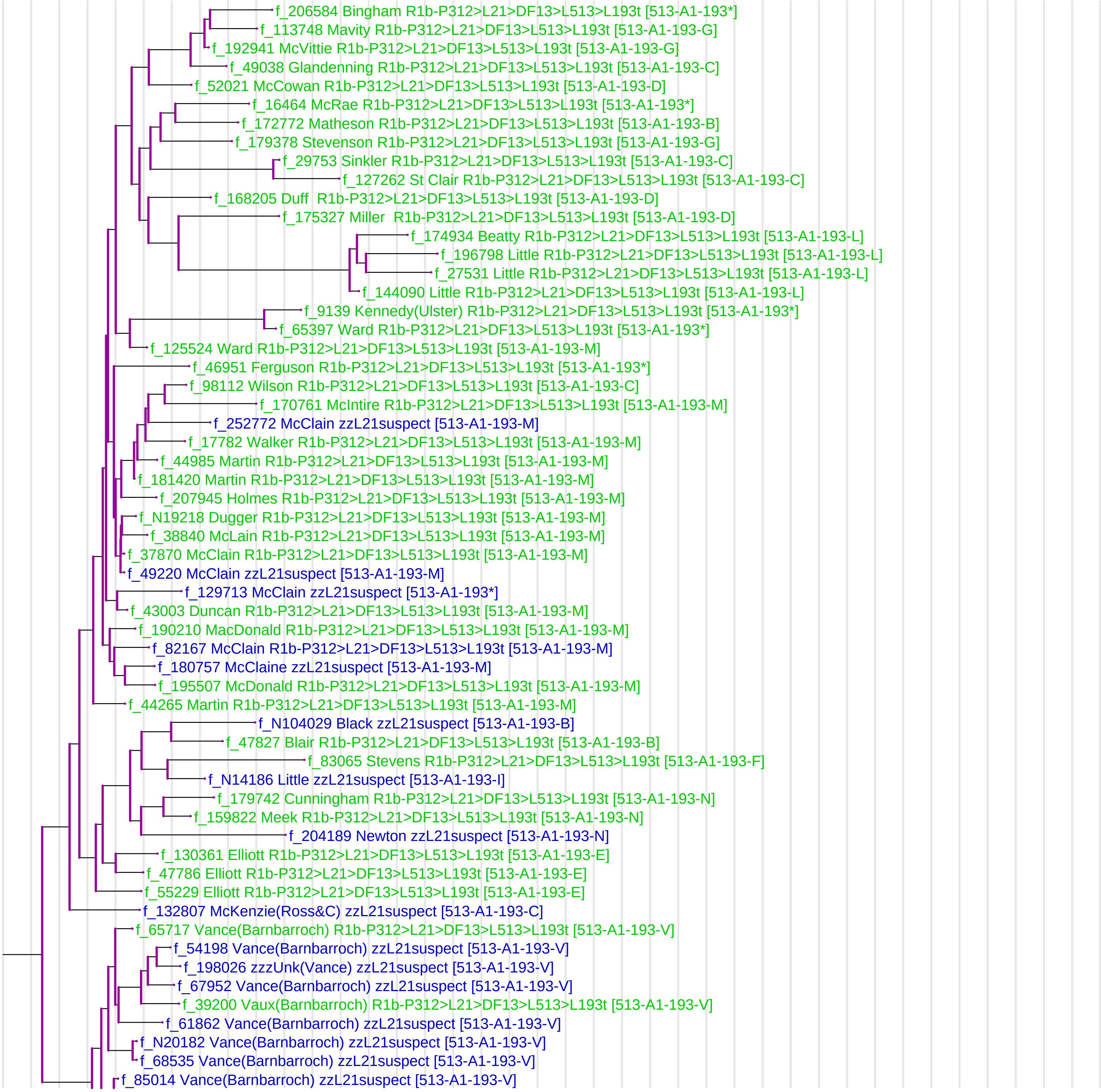
441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
13	10	10	19	15	18	14	24	15	12	15	24	12	23	18	10	14	16	9	12	11

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

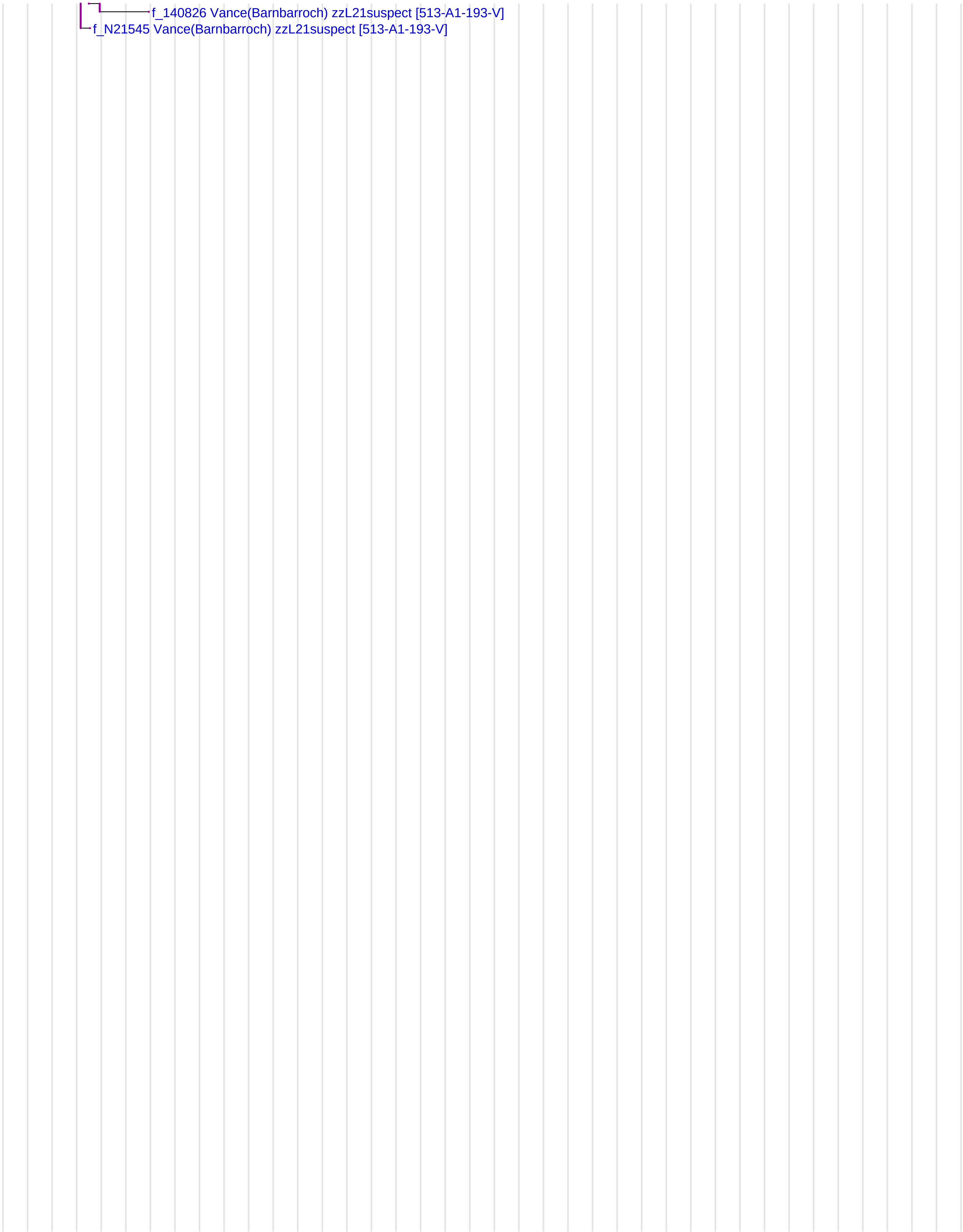


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
60	4020	345	8.58%	44.83±4.54	1120.83±159.577



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	15	11	11	14	12	12	12	13	13	29

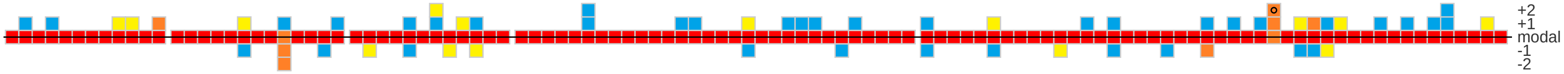
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	31	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	18	23	16	15	18	18	37	38	12	12

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
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12

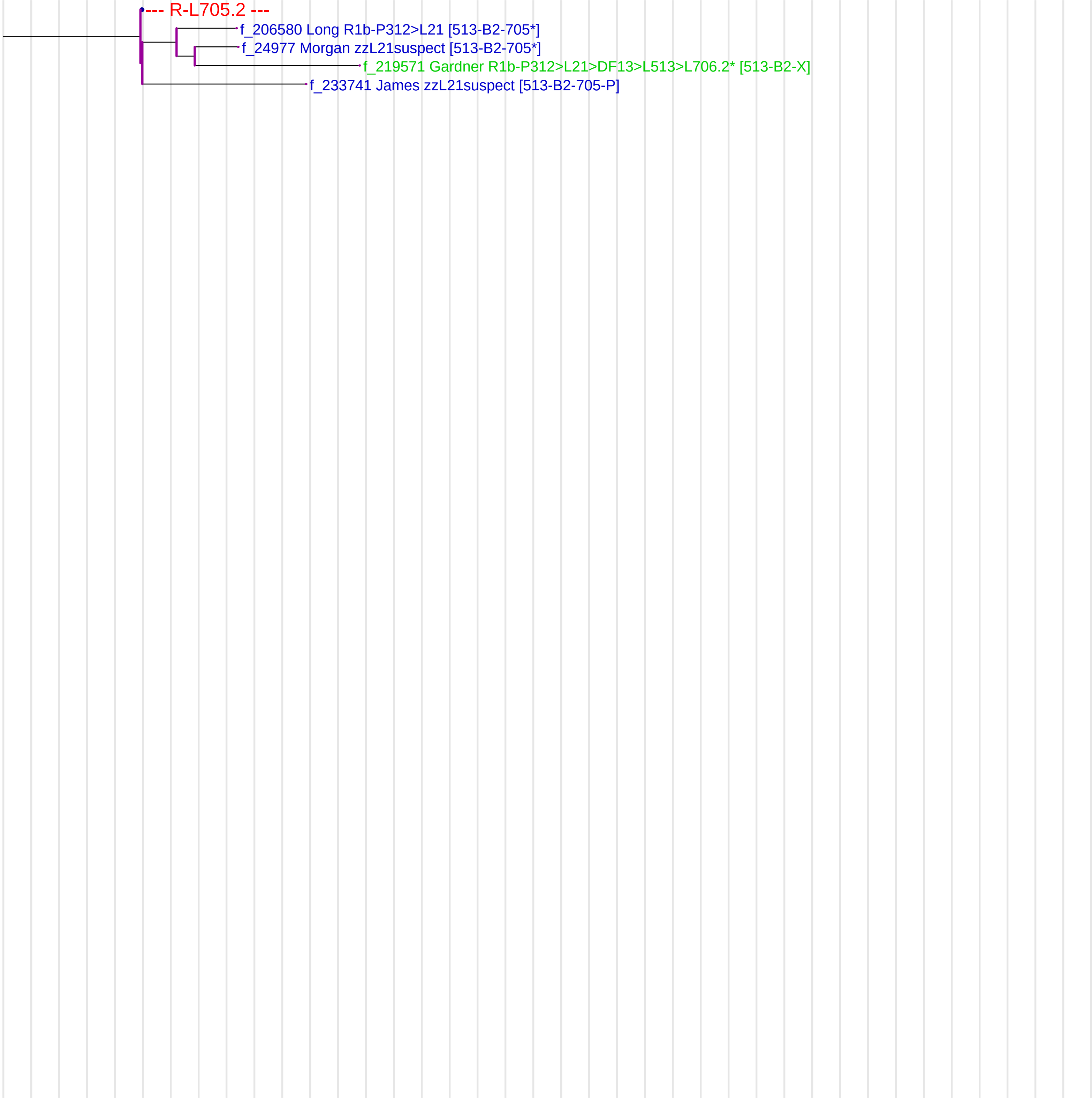
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
34	15	9	16	12	26	26	19	12	12	13	12	11	9	12	12	10	11	11	30	12	13	23	13	10	10	20	15	17	13	25	15	12	15	24	12	23	18	10	14	16	9	12	11

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



Age Analysis

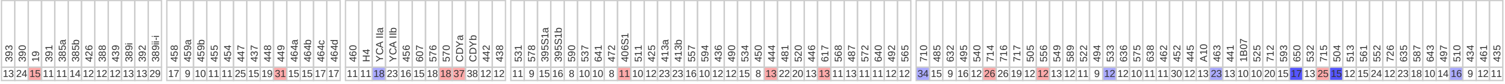
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
11	737	55	7.46%	38.76±4.15	968.975±141.947



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	15	11	11	14	12	12	12	13	13	29

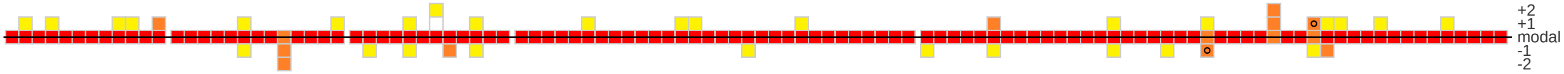
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	31	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	18	23	16	15	18	18	37	38	12	12

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
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12

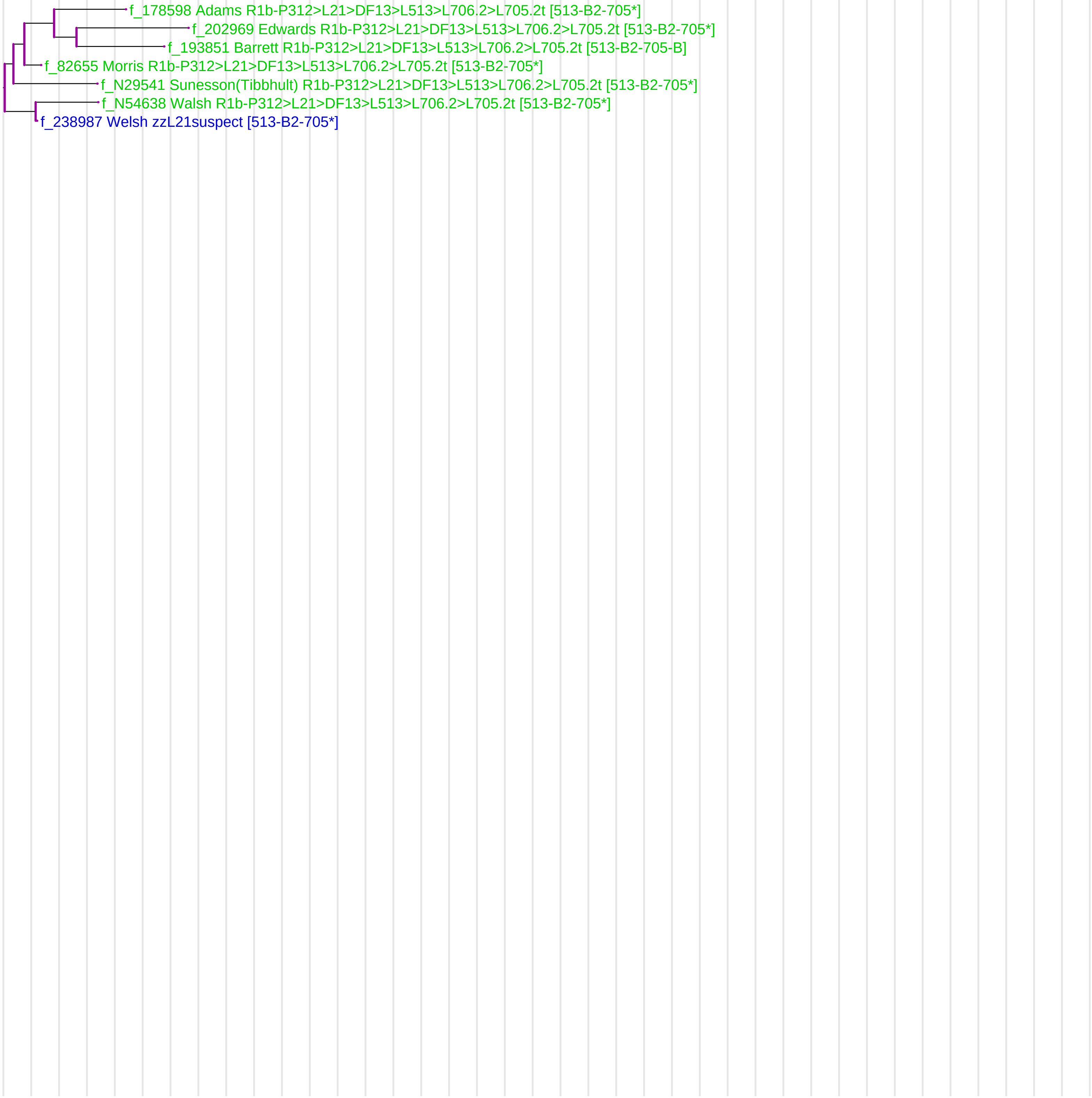
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
34	15	9	16	12	26	26	19	12	12	13	12	11	9	12	12	10	11	11	30	12	13	23	13	10	10	20	15	17	13	25	15	12	15	24	12	23	18	10	14	16	9	12	11

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)
7	469	29	6.18%	31.90±3.53	797.572±119.012



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	15	12	12	12	13	13	29

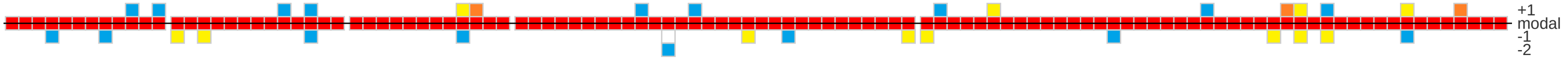
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	20	30	15	16	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	24	15	15	18	16	36	38	12	12

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
11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12

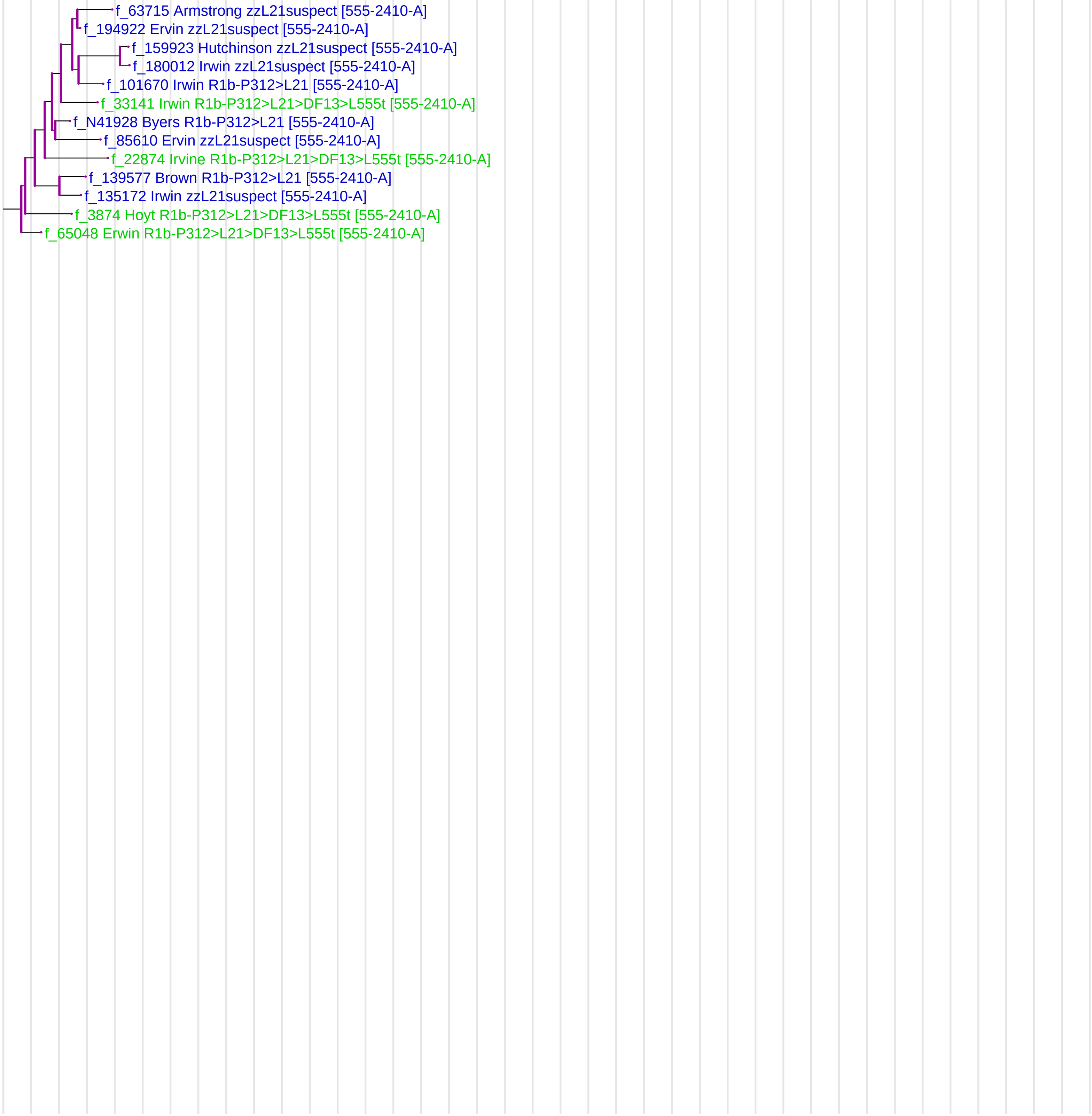
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
34	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	21	13	24	16	12	14	24	12	26	18	10	14	17	9	12	11

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



Age Analysis

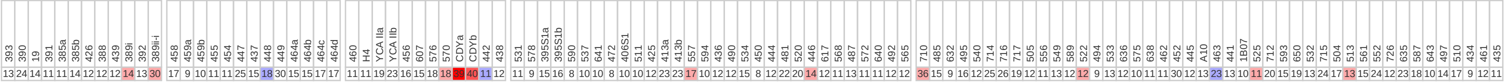
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
13	871	28	3.21%	16.34±1.73	408.401±59.4434



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	389ii-i
13	24	14	11	11	14	12	12	12	14	13	30

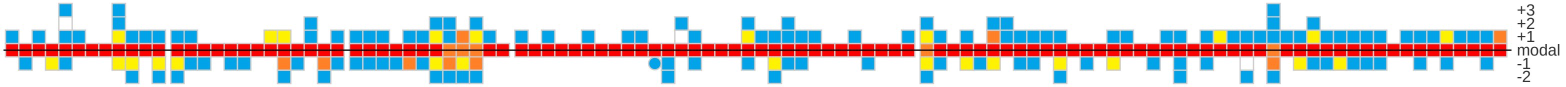
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	18	30	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	18	39	40	11	12

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
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

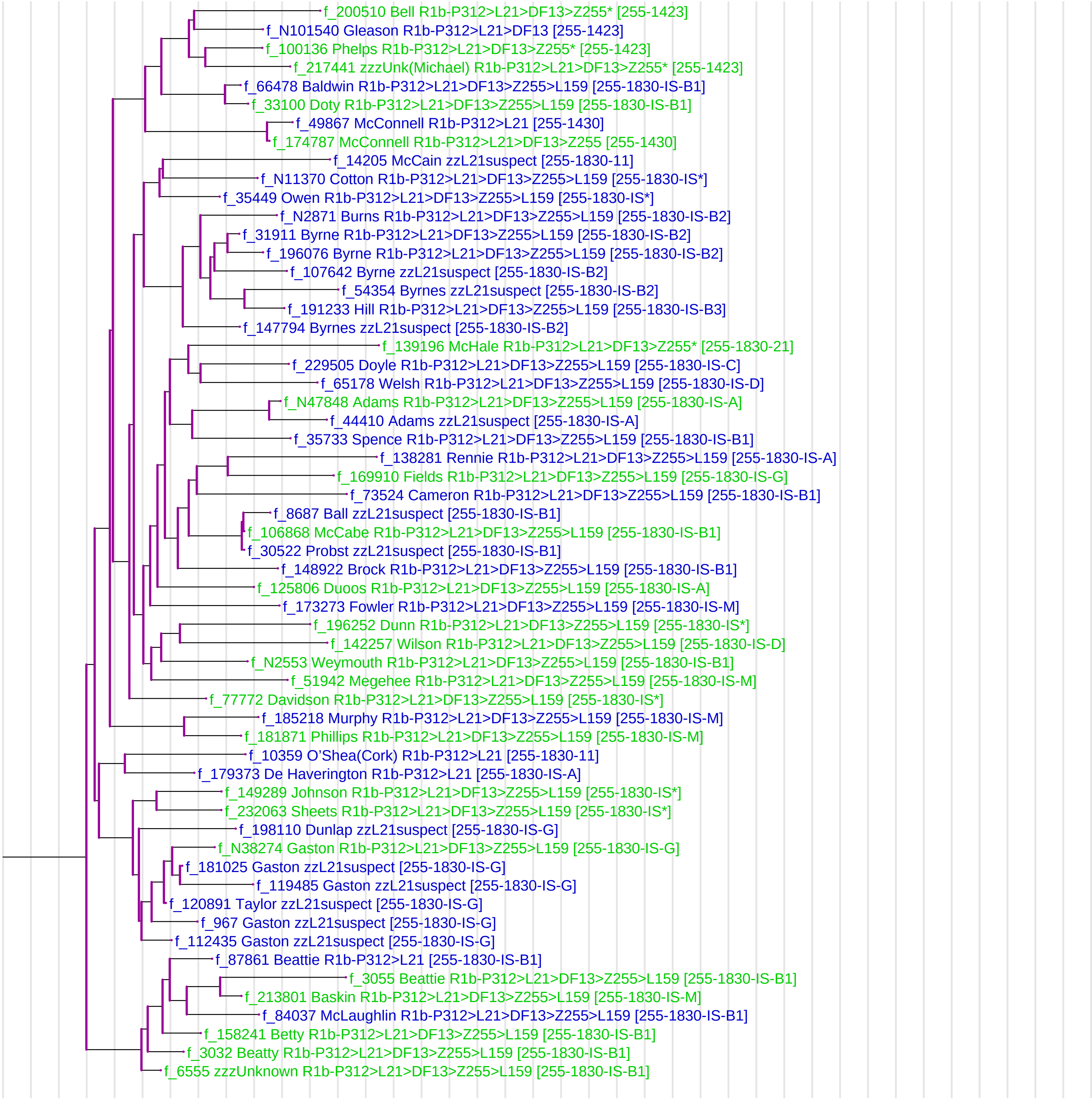
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	12	25	26	19	12	11	13	12	12	9	13	12	10	11	11	30	12	13	23	13	10	11	20	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

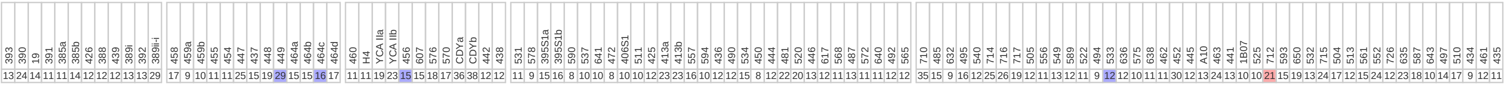
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
58	3886	420	10.81%	57.12±5.79	1428.1±203.403



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	16	17

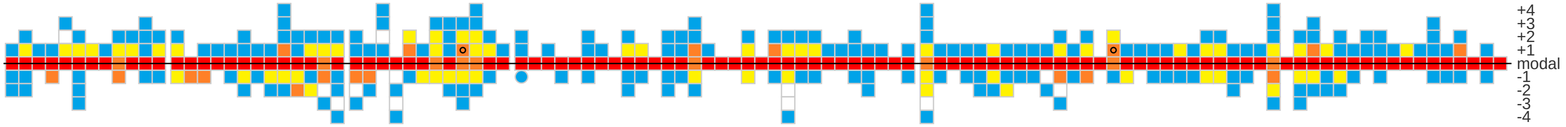
460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	15	15	18	17	36	38	12	12

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
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

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10
35	15	9	16	12	25	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13

463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
24	13	10	10	21	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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)
119	7973	1720	21.57%	120.85±12.18	3021.22±428.907

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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	11	13	13	29

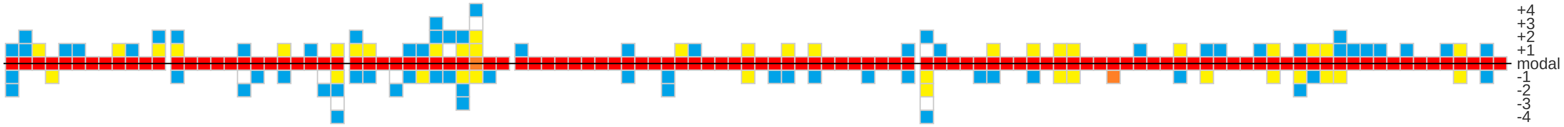
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	8	9	11	11	25	15	19	29	13	13	15	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	15	15	18	17	36	38	12	12

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
11	9	15	16	8	10	10	8	10	10	12	23	23	15	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

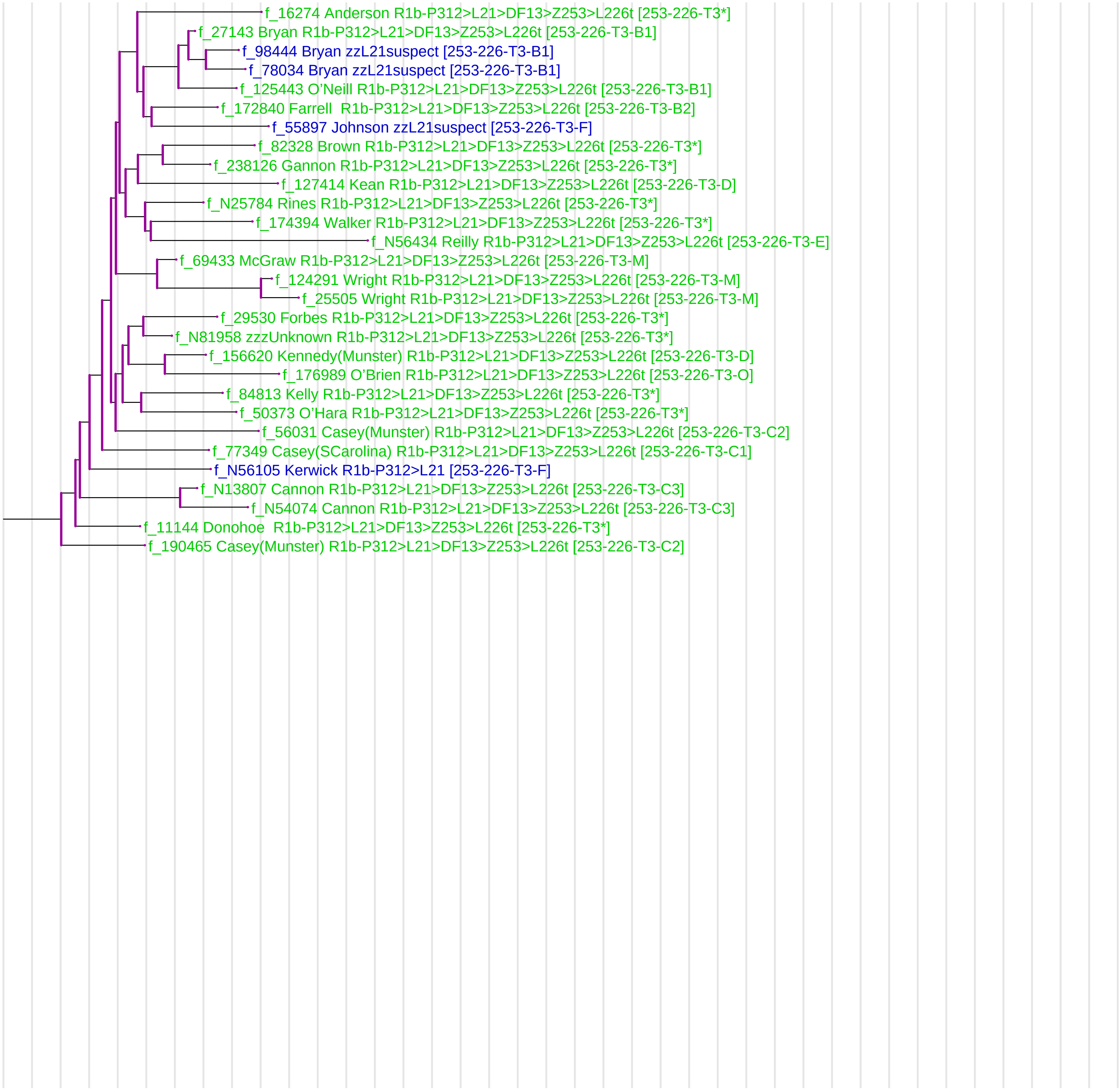
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	24	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	25	13	10	10	21	15	19	13	24	17	12	15	24	12	23	18	10	14	18	9	12	11

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



Age Analysis

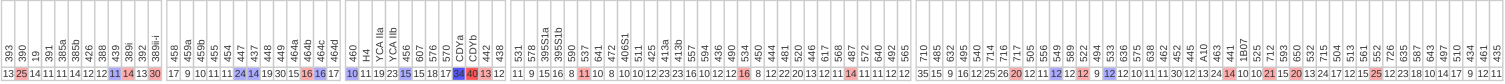
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
29	1943	181	9.32%	48.85±5.02	1221.28±175.132



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	389ii-i
13	25	14	11	11	14	12	12	11	14	13	30

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	24	14	19	30	15	16	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
10	11	19	23	15	15	18	17	34	40	13	12

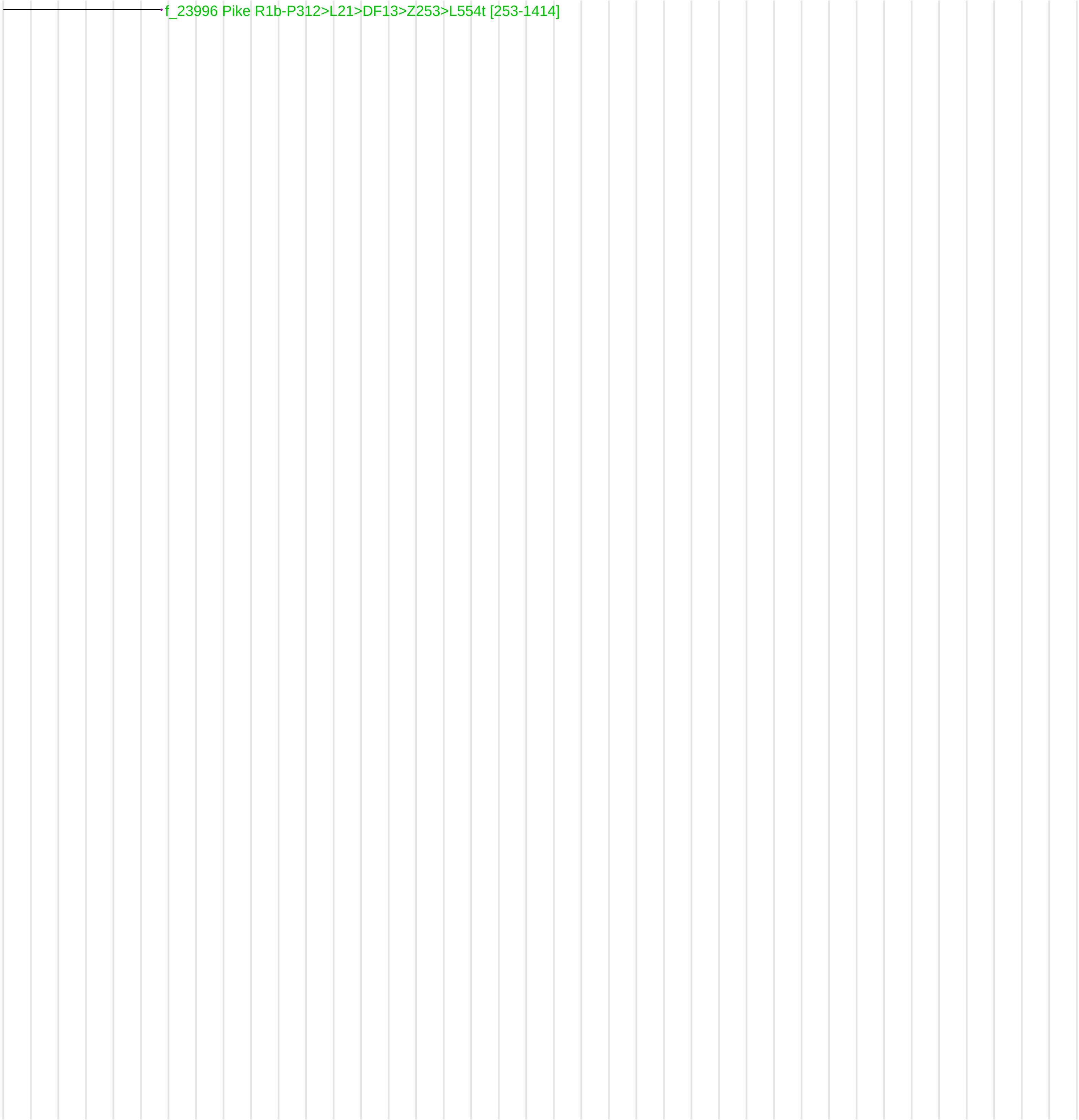
531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
11	9	15	16	8	11	10	8	10	10	12	23	23	16	10	12	12	16	8	12	22	20	13	12	11	14	11	11	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	20	12	11	12	12	12	9	12	12	10	11	11	30	12	13	24	14	10	10	21	15	20	13	24	17	12	15	25	12	23	18	10	14	17	9	12	11

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)
1	67	0	0.00%	0.00±0.00	0±0



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	10	11	15	12	12	12	13	13	29

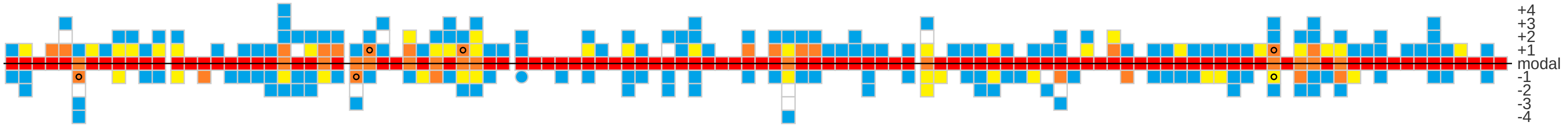
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	23	15	15	18	17	36	38	12	12

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
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

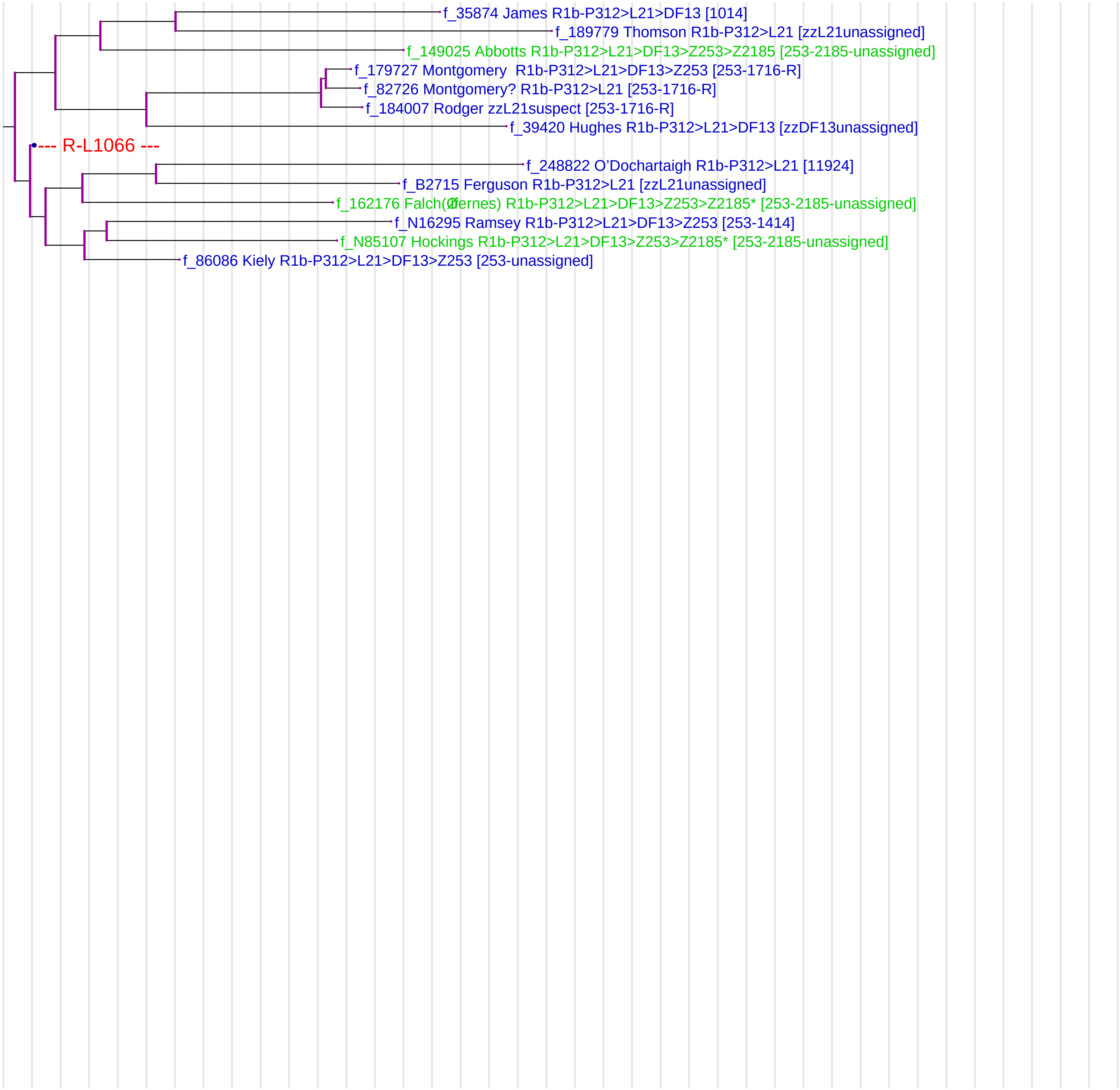
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	19	12	11	13	12	10	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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)
52	3484	812	23.31%	131.83±13.42	3295.64±470.224



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	10	11	15	12	12	12	13	13	29

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	16	17

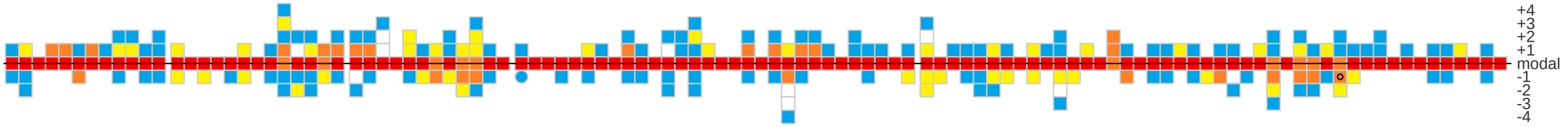
460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
10	10	19	23	15	15	18	17	37	38	12	12

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
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

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10
35	15	9	16	12	25	26	19	12	11	13	12	10	9	12	12	10	11	11	30	12	13

463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
24	13	10	10	21	15	19	14	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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)
39	2613	556	21.28%	119.00±12.18	2975.11±425.644

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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

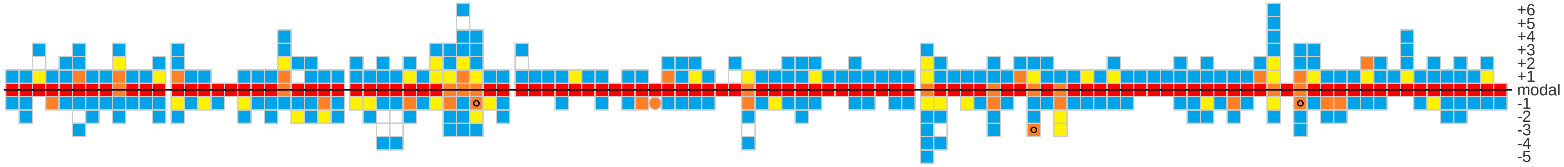
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	28	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	18	36	38	12	12

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
11	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12

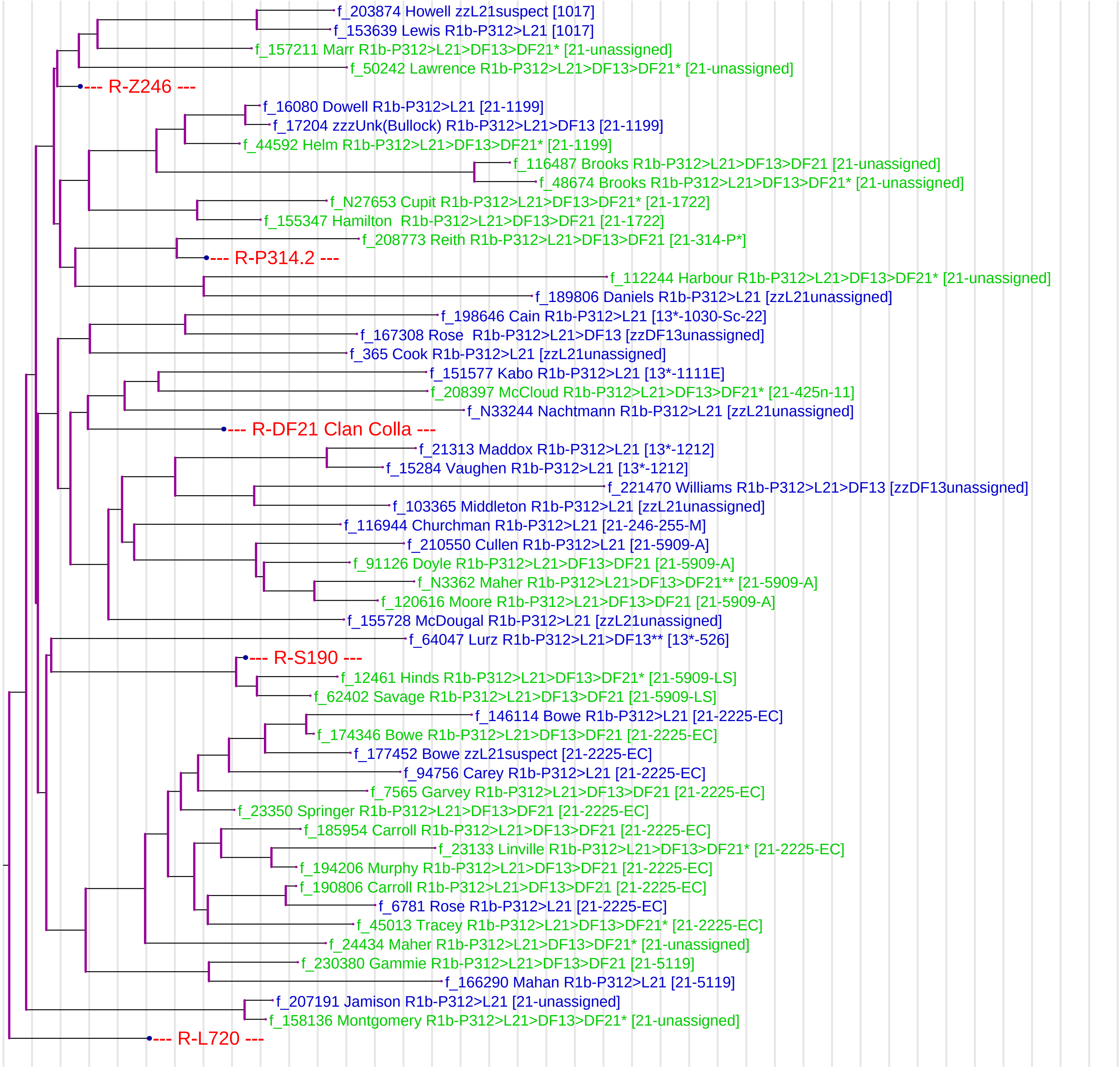
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	26	26	19	12	11	14	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

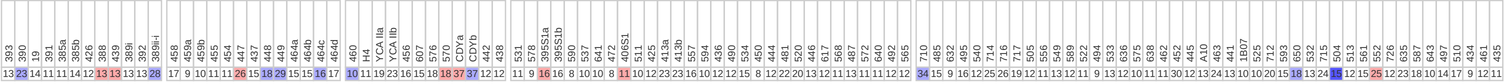
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
227	15209	3043	20.01%	111.12±11.16	2777.97±393.645



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	389ii-i
13	23	14	11	11	14	12	13	13	13	13	28

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	26	15	18	29	15	15	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
10	11	19	23	16	15	18	18	37	37	12	12

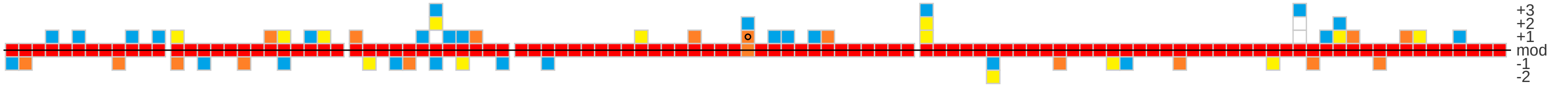
531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594
11	9	16	16	8	10	10	8	11	10	12	23	23	16	10

436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441
34	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13

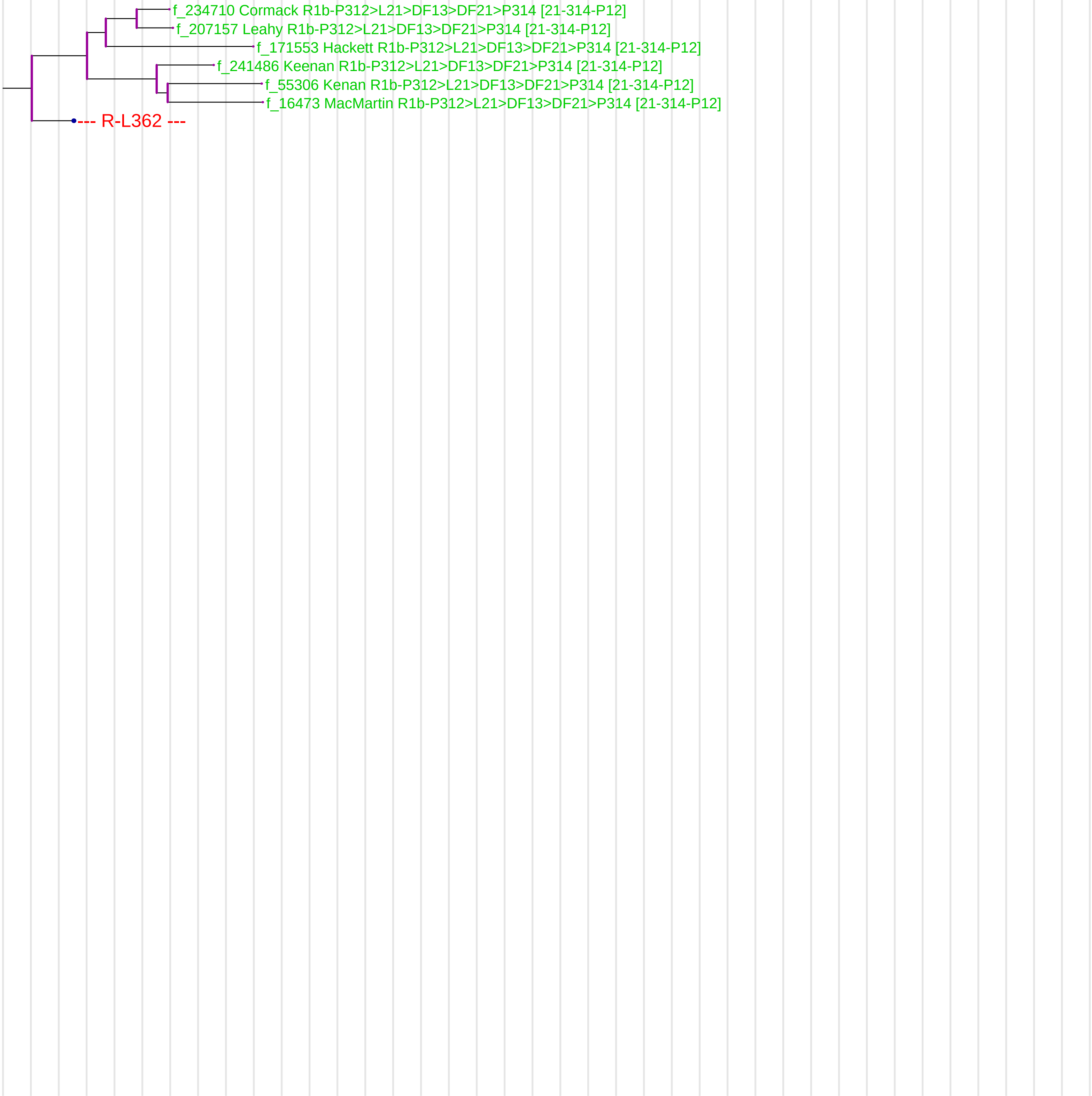
1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
10	10	20	15	18	13	24	15	12	15	25	12	23	18	10	14	17	9	12	11

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)
11	737	86	11.67%	61.96±6.65	1548.88±227.215



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	23	14	11	11	14	12	13	13	13	13	28

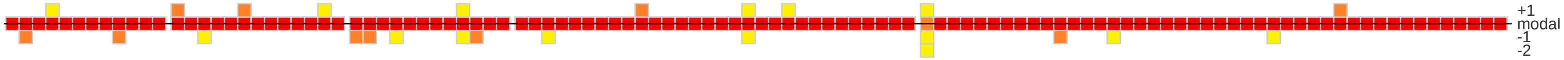
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	18	37	38	12	12

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
11	9	16	16	8	10	10	8	11	10	12	23	23	17	10	12	12	16	8	12	22	20	13	13	11	13	11	11	12	12

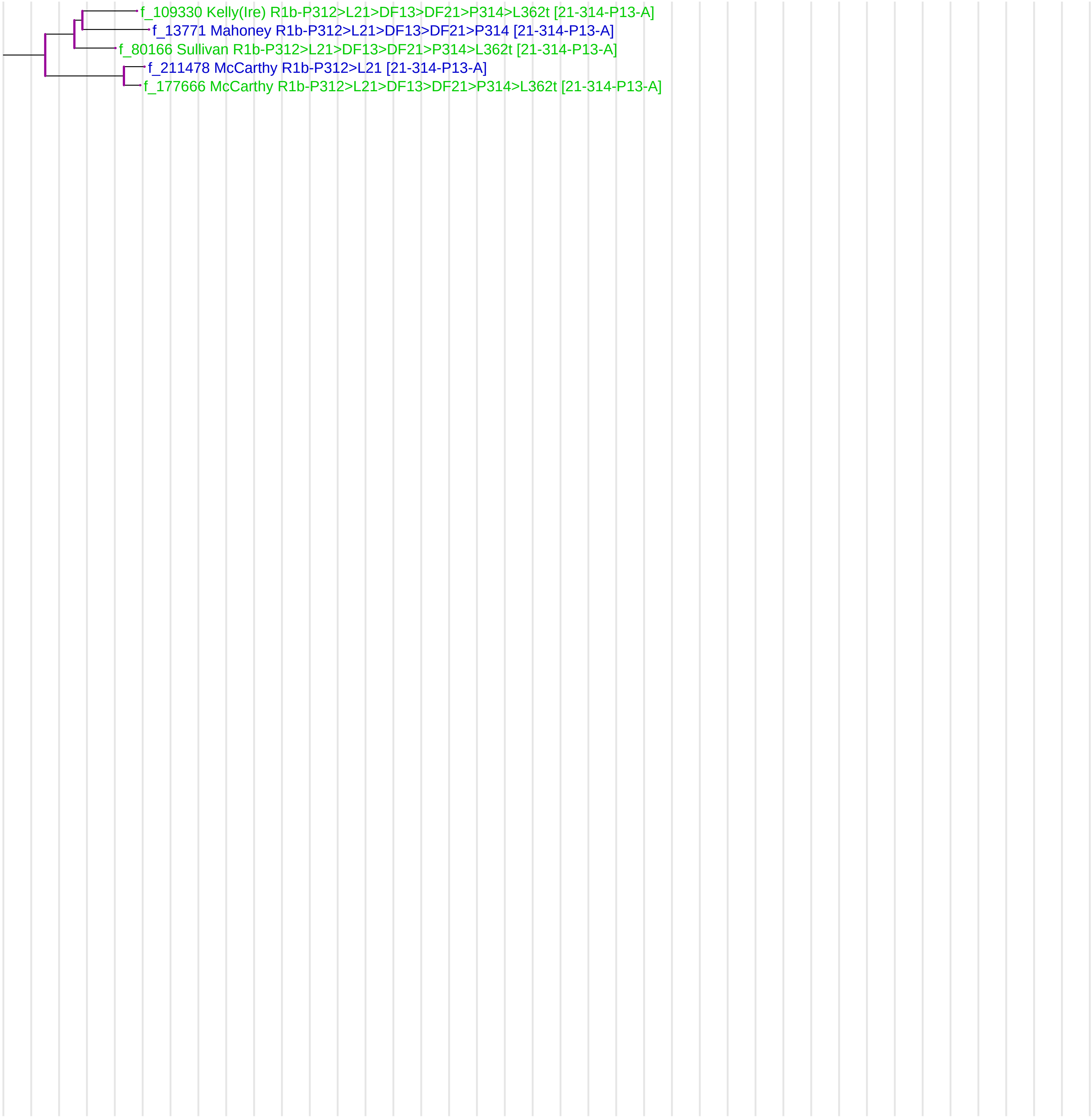
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	15	13	15	25	12	23	18	10	14	17	9	12	11

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)
5	335	26	7.76%	40.37±4.64	1009.3±153.802



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	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

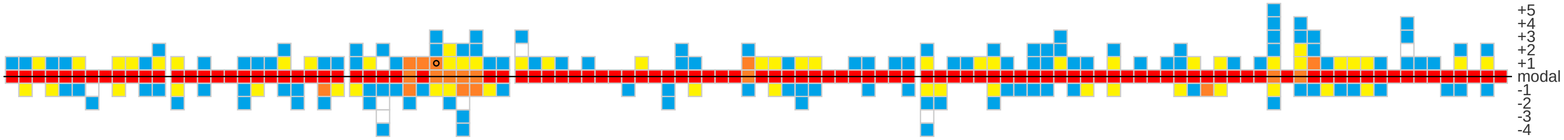
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	37	38	12	12

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
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

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11

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



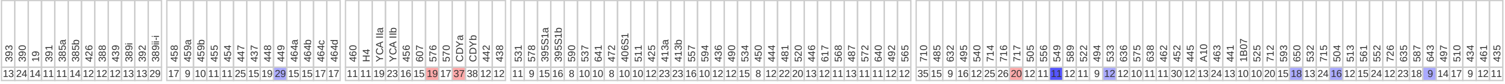
Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
48	3216	606	18.84%	103.98±10.59	2599.61±371.047

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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

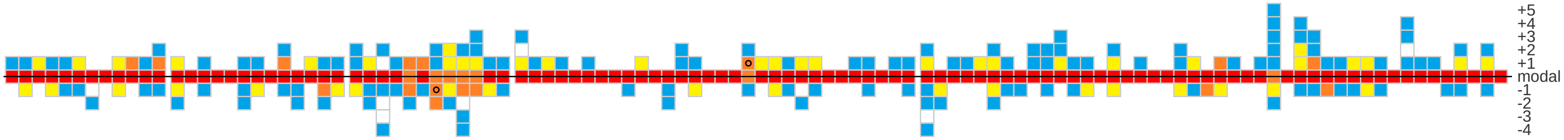
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	19	17	37	38	12	12

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
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

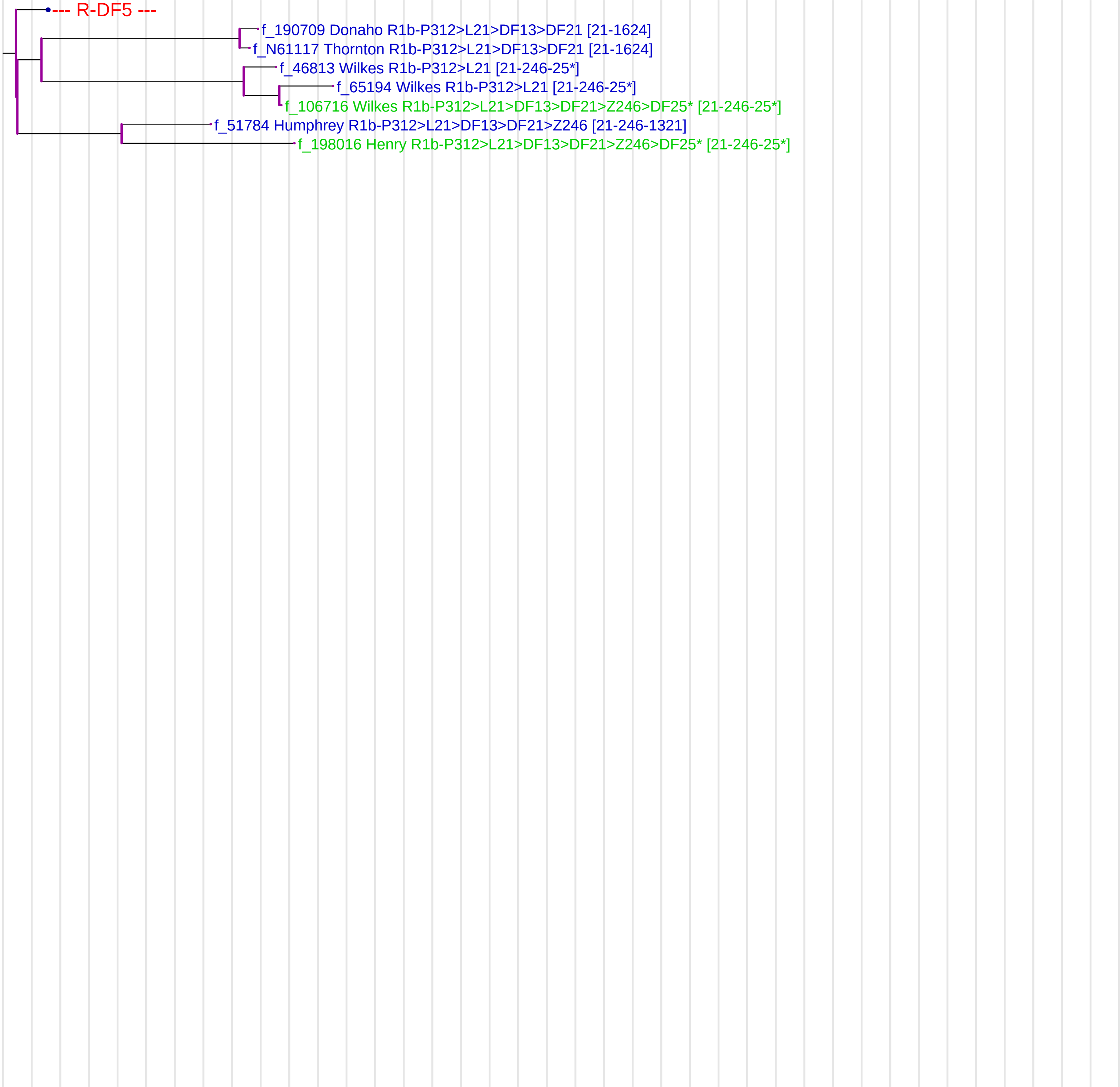
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11

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)
47	3149	602	19.12%	105.65±10.76	2641.36±377.087



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

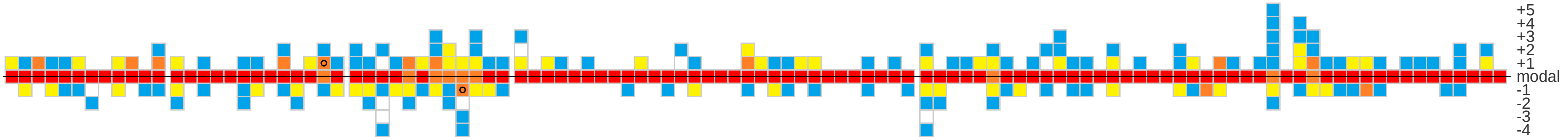
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	37	38	12	12

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
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

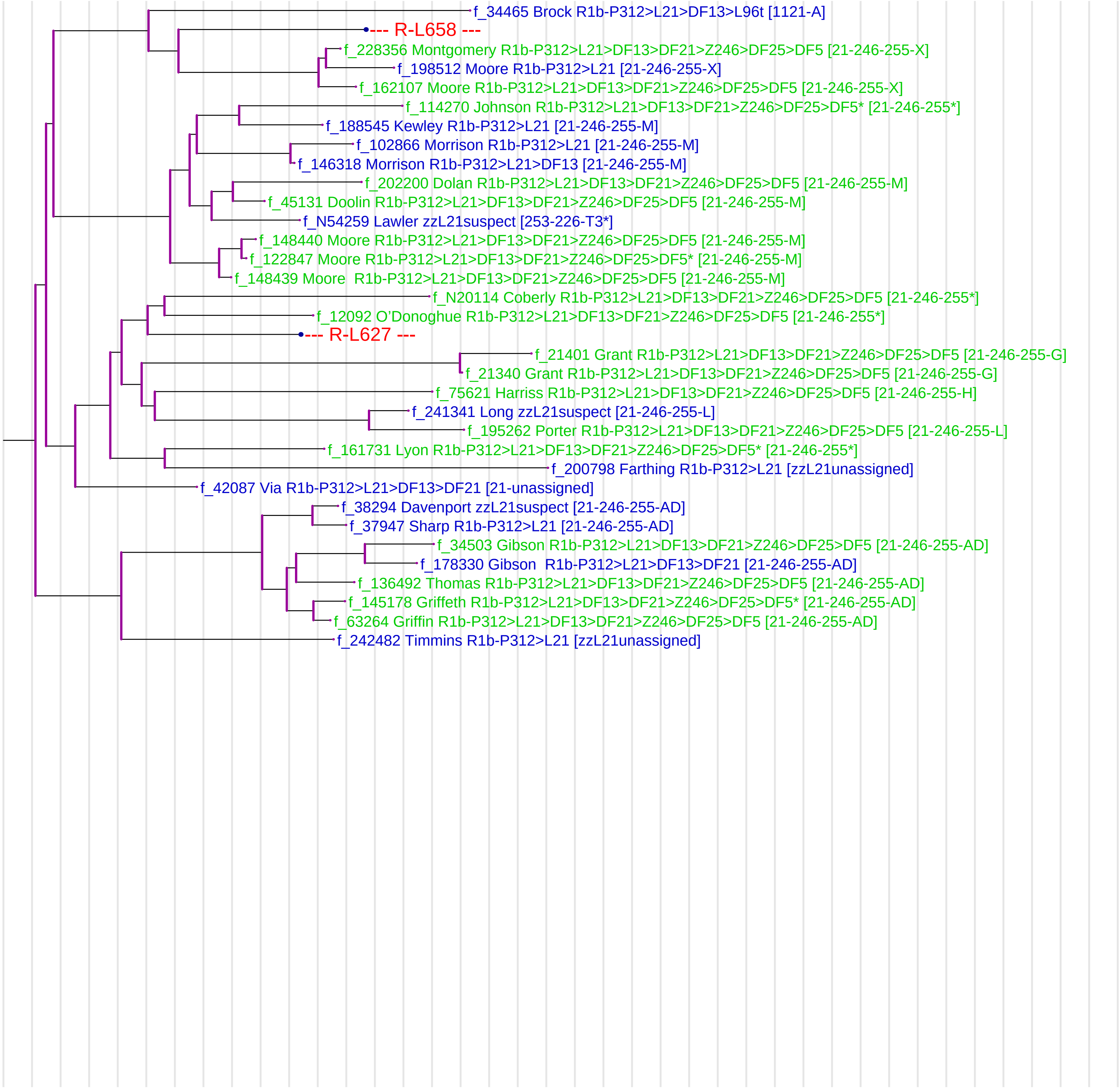
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11

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



Age Analysis

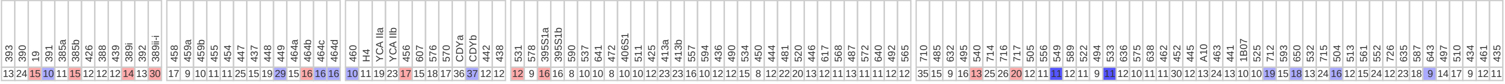
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
40	2680	504	18.81%	103.76±10.60	2593.94±370.911



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	389ii-i
13	24	15	10	11	15	12	12	12	14	13	30

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	16	16	16

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
10	11	19	23	17	15	18	17	36	37	12	12

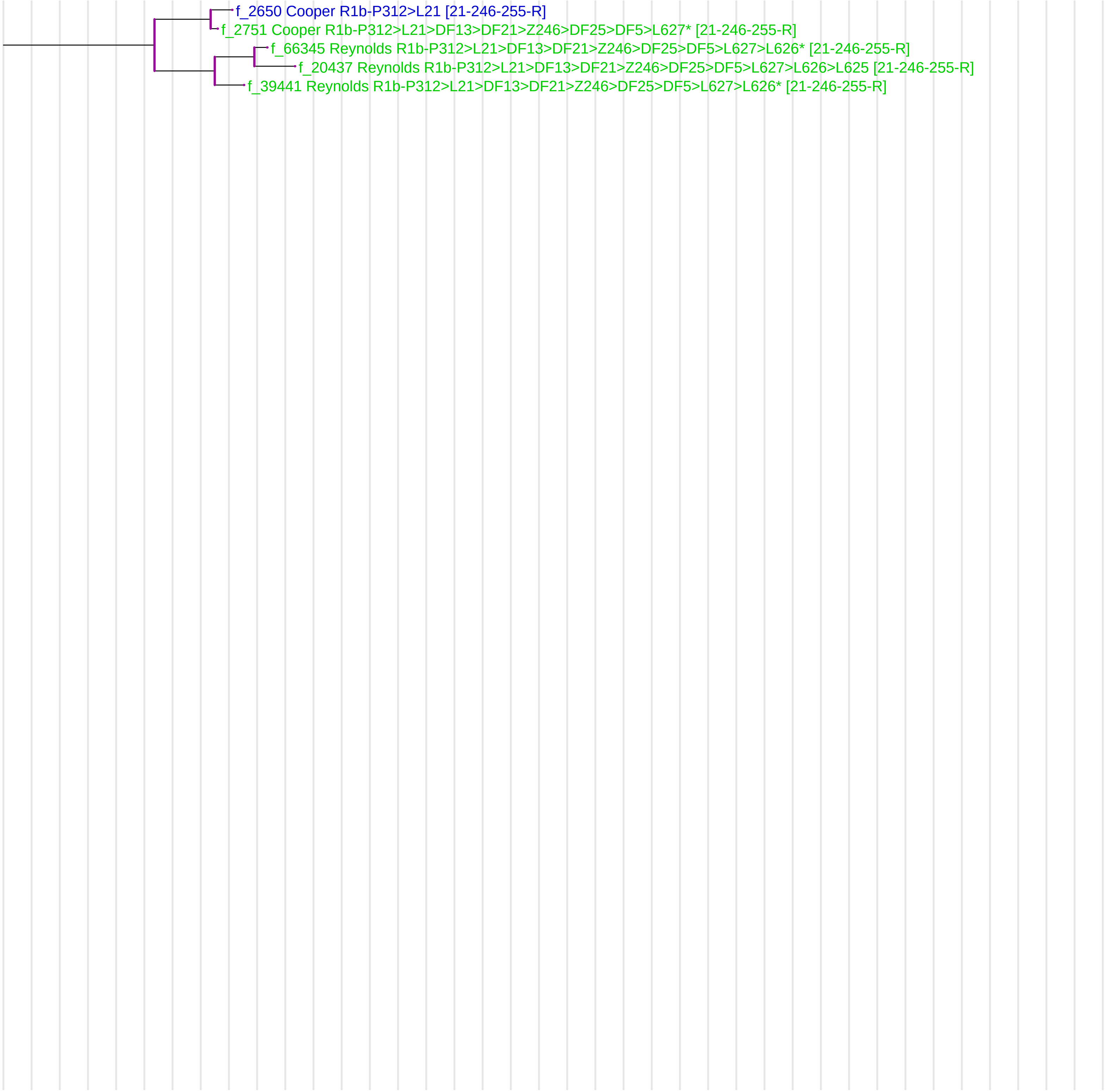
531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
12	9	16	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	13	25	26	20	12	11	11	12	11	9	11	12	10	11	11	30	12	13	24	13	10	10	19	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11

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

Age Analysis

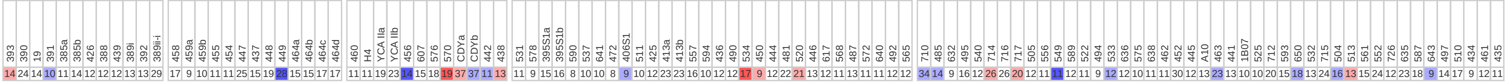
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
5	335	23	6.87%	35.55±4.08	888.705±135.345



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
14	24	14	10	11	14	12	12	12	13	13	29

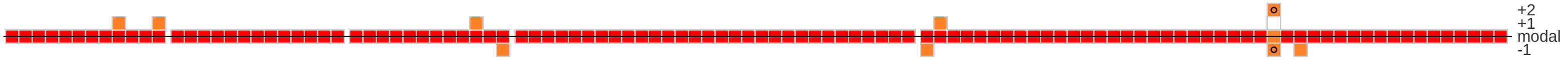
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	28	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	14	15	18	19	37	37	11	13

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
11	9	15	16	8	10	10	8	9	10	12	23	23	16	10	12	12	17	9	12	22	21	13	12	11	13	11	11	12	12

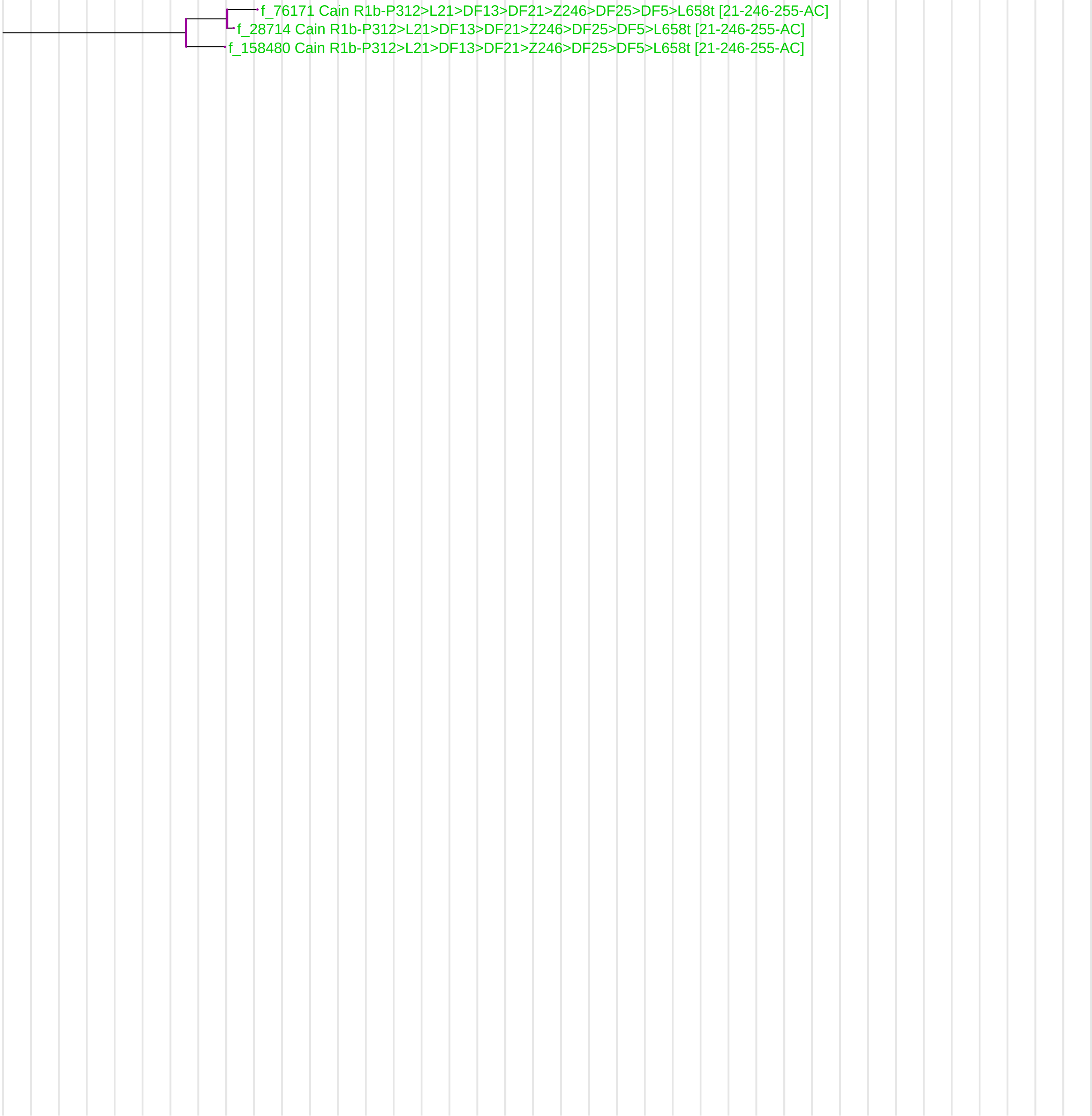
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
34	14	9	16	12	26	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	23	13	10	10	20	15	18	13	24	16	13	15	24	12	23	18	9	14	17	9	12	11

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



Age Analysis

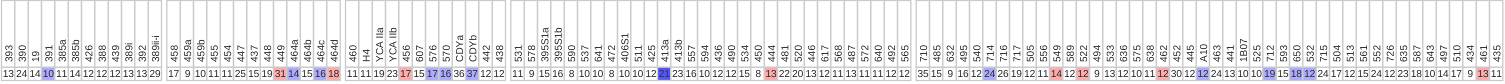
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	4	1.99%	10.05±1.23	251.256±39.7863



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	389ii-i
13	24	14	10	11	14	12	12	12	13	13	29

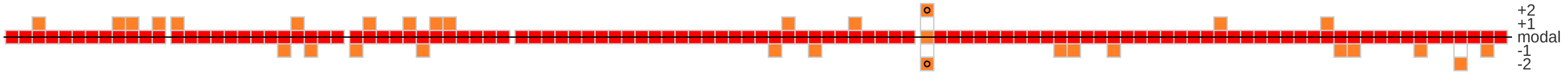
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	31	14	15	16	18

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	17	15	17	16	36	37	12	12

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
11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	13	22	20	13	12	11	13	11	11	12	12

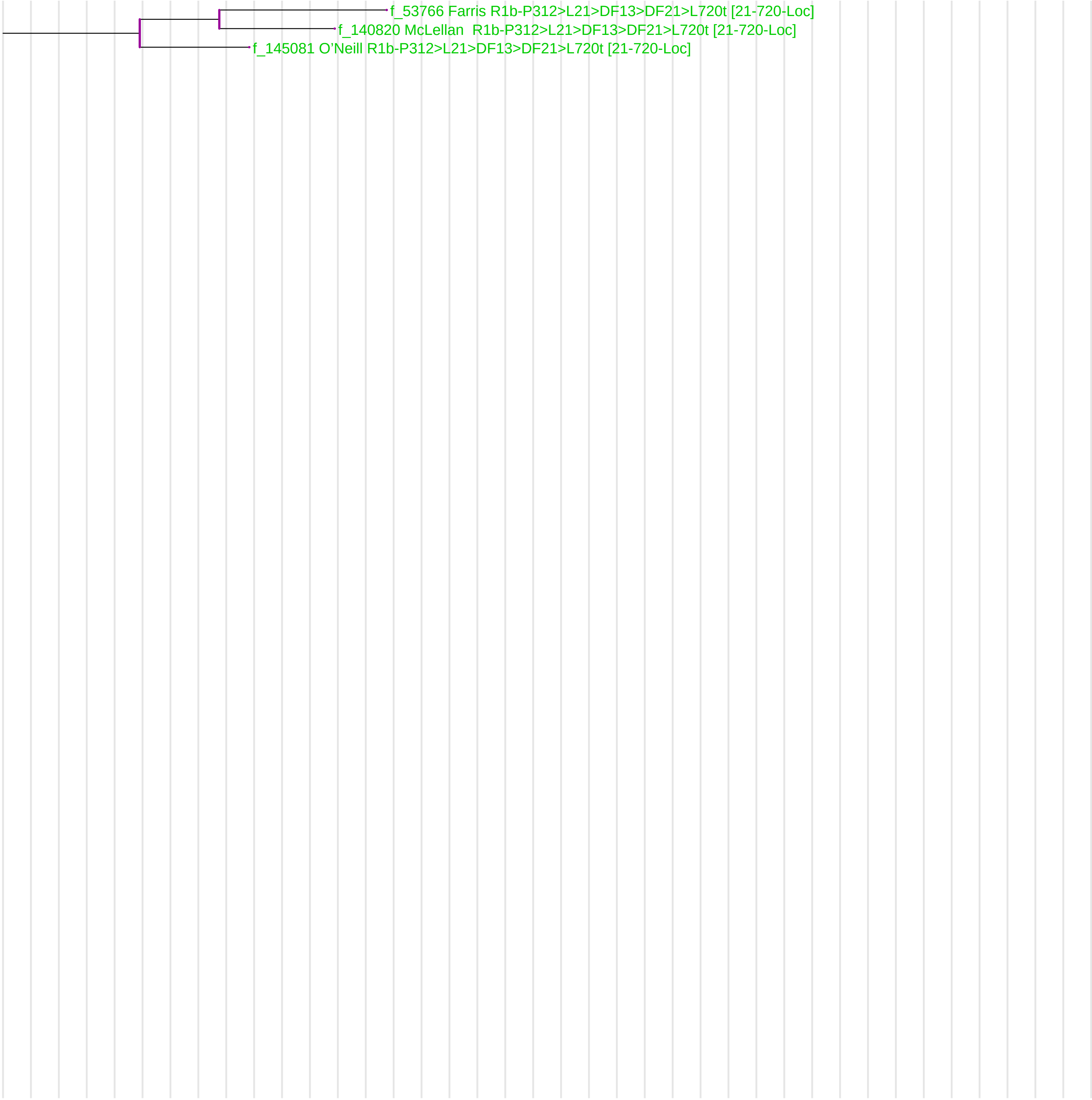
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	24	26	19	12	11	14	12	12	9	13	12	10	11	12	30	12	12	24	13	10	10	19	15	18	12	24	17	12	15	24	12	23	18	10	14	17	9	13	11

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)
3	201	18	8.96%	46.87±5.82	1171.84±186.873



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	10	11	14	12	12	12	13	13	29

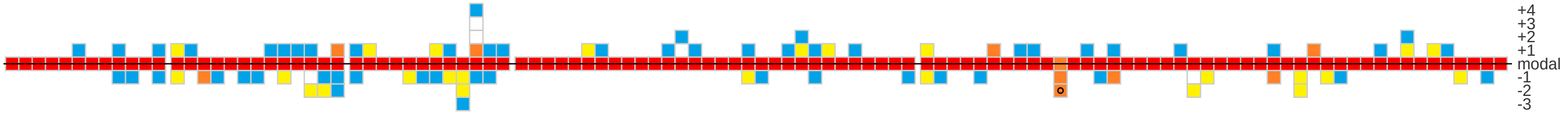
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
18	9	10	11	11	25	15	19	30	13	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	23	16	15	18	18	38	38	12	12

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
11	9	15	16	9	10	10	8	10	10	12	22	23	16	10	12	12	15	8	11	22	20	14	12	11	13	11	11	12	12

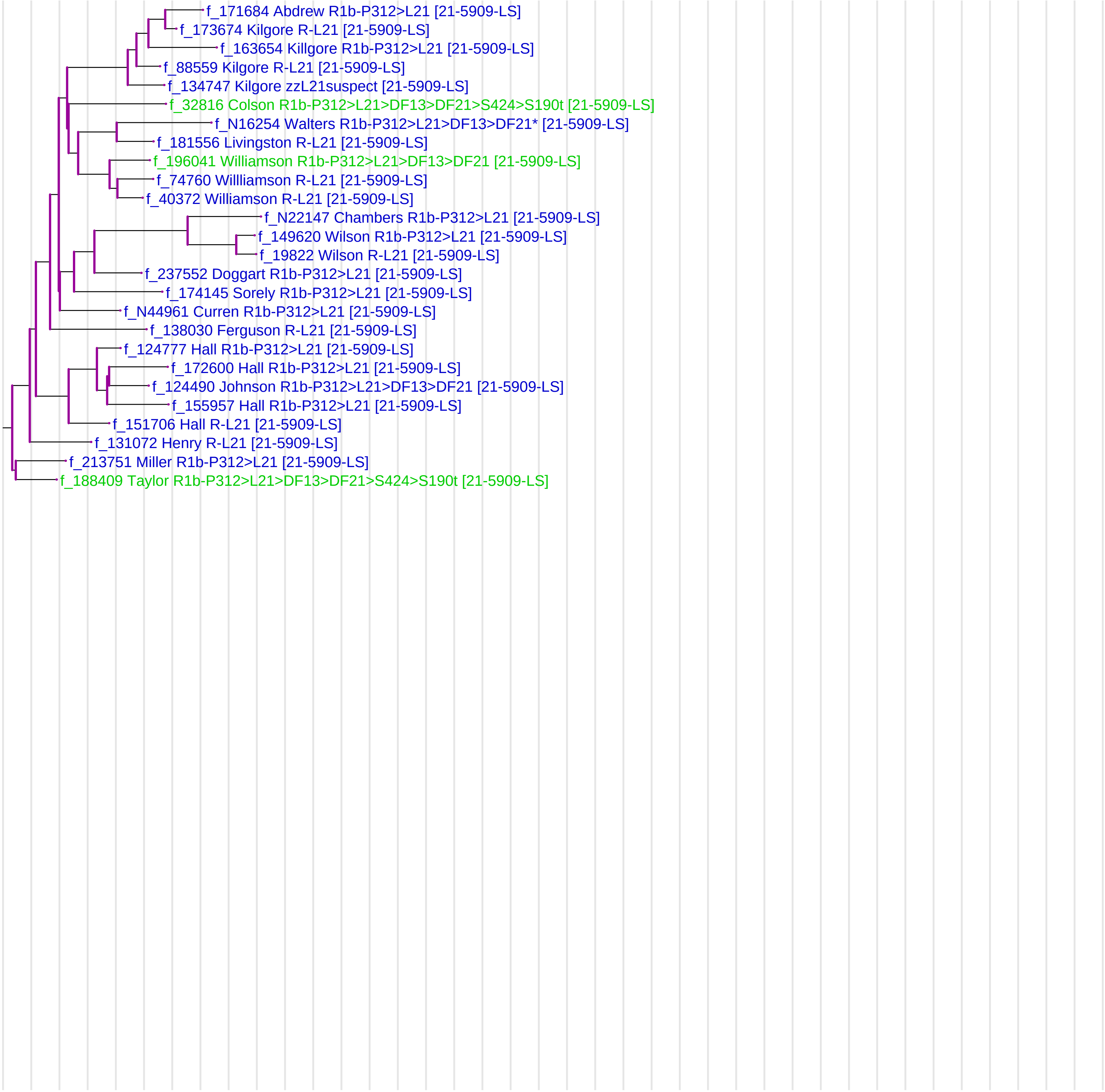
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
31	15	9	15	12	25	26	20	13	11	14	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	23	17	12	15	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

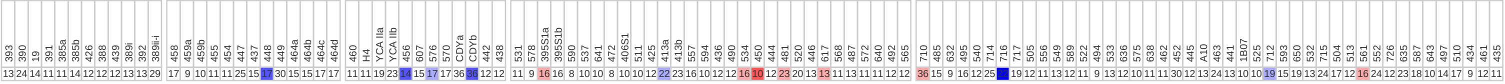
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
26	1742	144	8.27%	43.11±4.44	1077.82±154.78



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

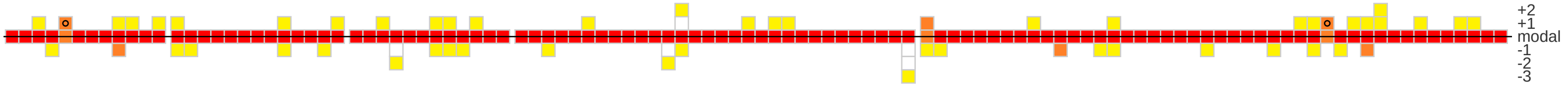
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	17	30	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	14	15	17	17	36	36	12	12

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
11	9	16	16	8	10	10	8	10	10	12	22	23	16	10	12	12	16	10	12	23	20	13	13	11	13	11	11	12	12

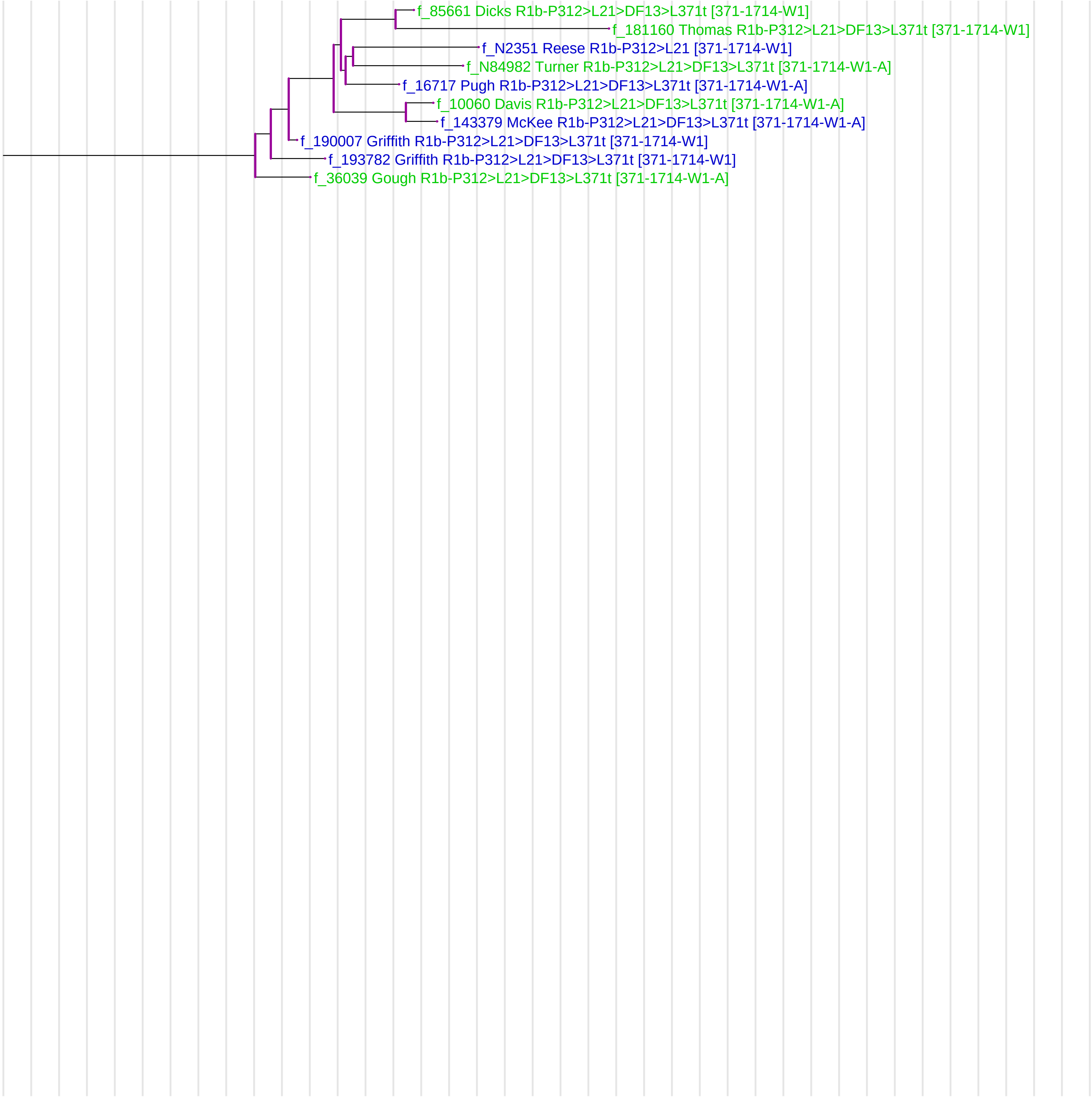
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	12	25	22	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	19	15	19	13	24	17	12	16	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

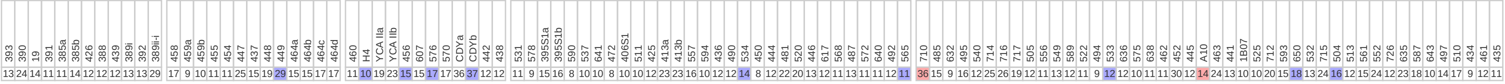
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
10	670	50	7.46%	38.76±4.18	968.975±142.429



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

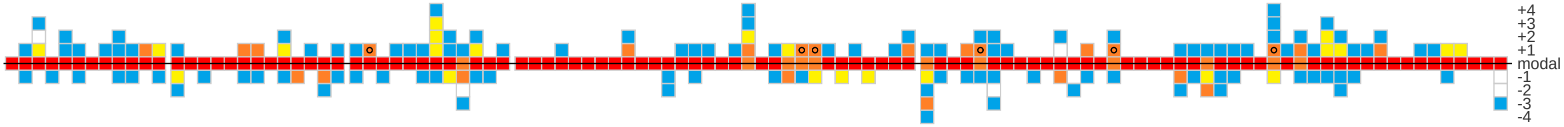
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	23	15	15	17	17	36	37	12	12

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
11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	14	8	12	22	20	13	12	11	13	11	11	12	11

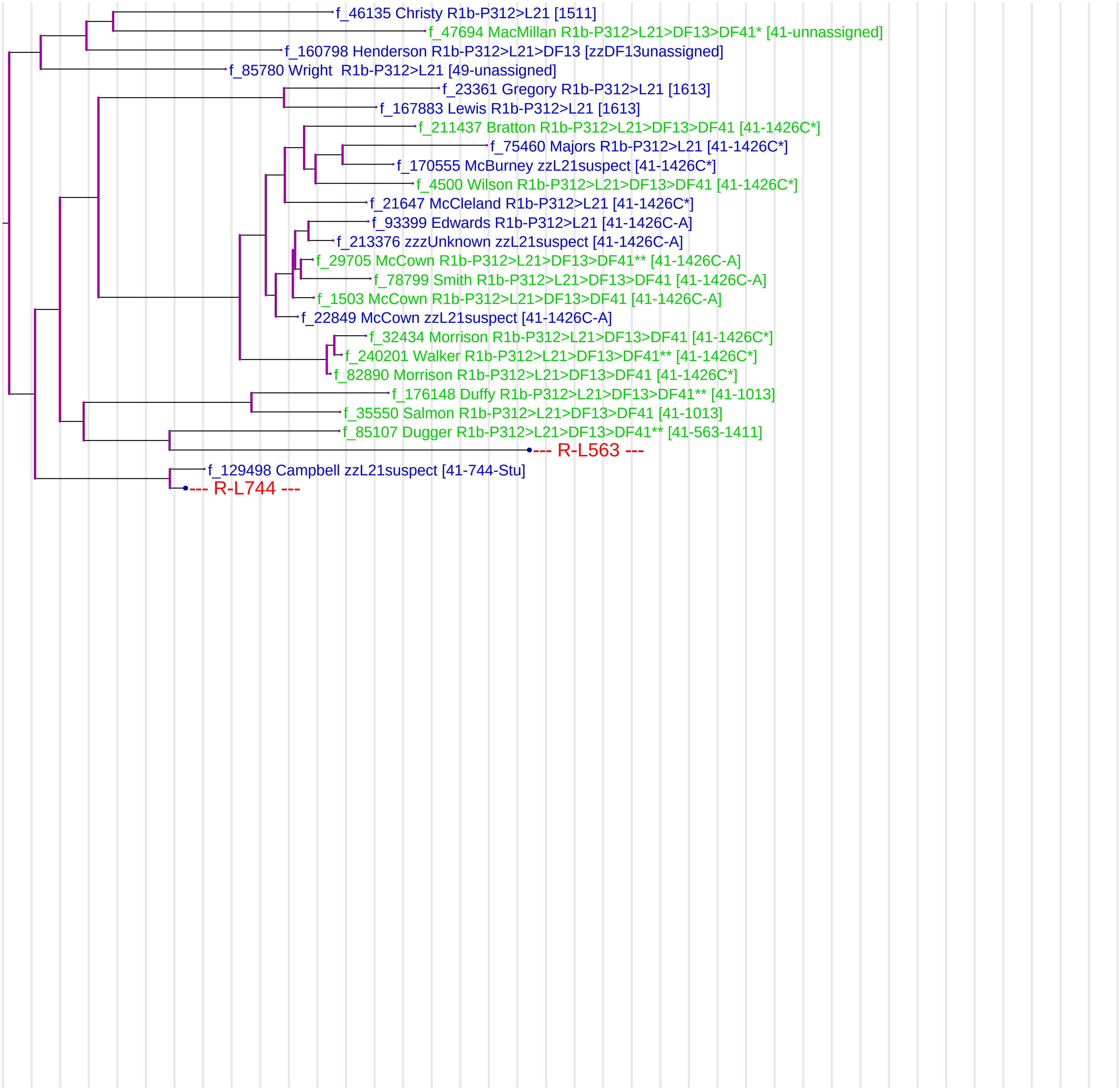
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	12	25	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	14	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	10	14	17	9	12	11

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)
42	2814	476	16.92%	92.37±9.43	2309.28±329.976



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	389ii-i
13	24	14	11	12	14	12	12	12	14	13	30

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	14	19	29	15	16	16	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	24	15	15	17	17	36	37	12	12

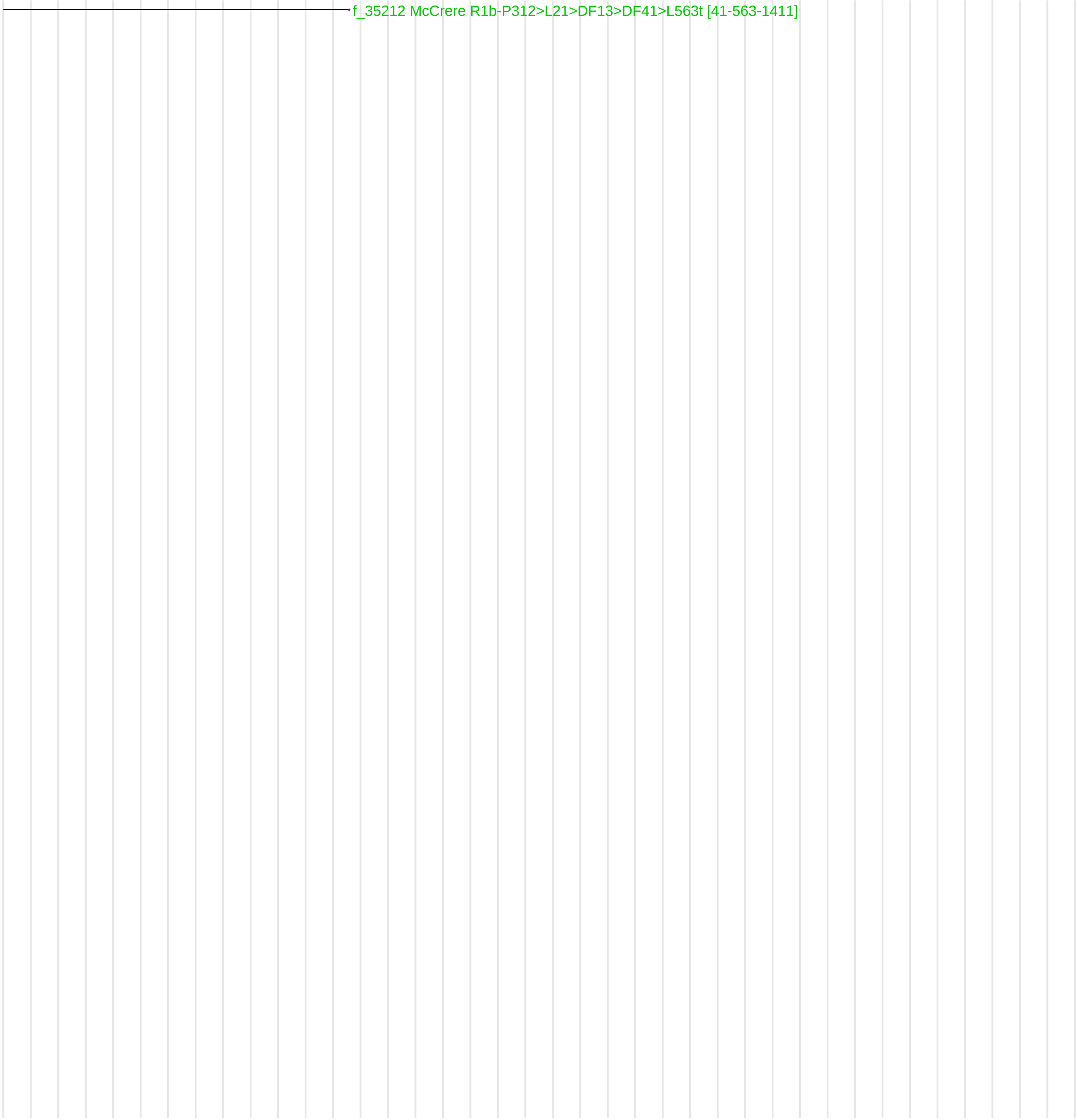
531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
11	9	15	16	8	10	10	8	10	10	12	21	23	16	11	12	12	14	8	12	21	20	12	12	11	14	11	11	12	12

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	14	25	26	19	12	11	15	12	11	9	13	12	10	11	11	30	12	13	24	12	10	10	19	15	19	13	24	14	11	16	25	12	23	18	10	14	17	9	12	11

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)
1	67	0	0.00%	0.00±0.00	0±0



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	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

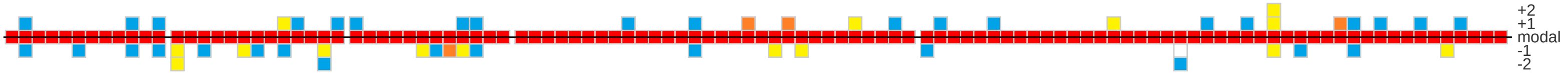
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	14	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	23	15	15	17	17	36	37	12	12

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
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	12	22	21	14	12	11	13	11	11	12	11

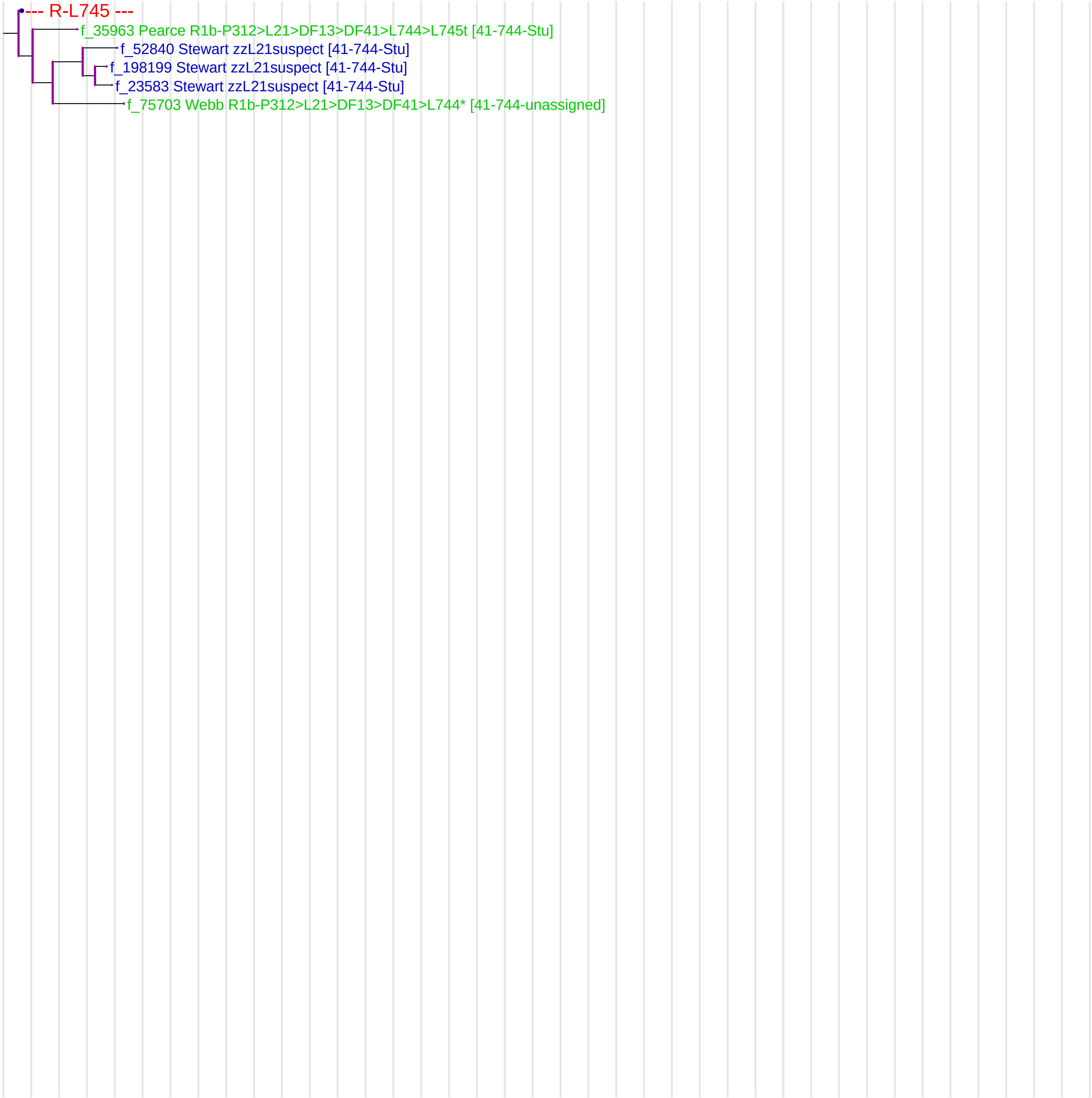
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	13	25	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	14	24	13	10	10	21	15	18	13	24	16	12	15	25	12	23	18	10	14	17	9	12	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)
17	1139	69	6.06%	31.24±3.27	780.889±112.978



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.

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	14	12	12	12	13	13	29

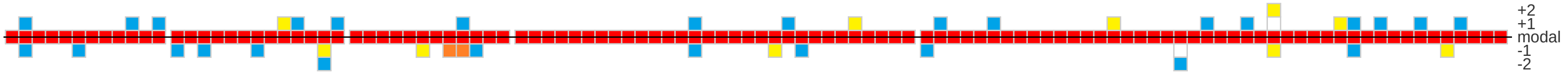
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	14	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	10	19	23	15	15	17	17	36	37	12	12

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
11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	12	22	21	14	12	11	13	11	11	12	11

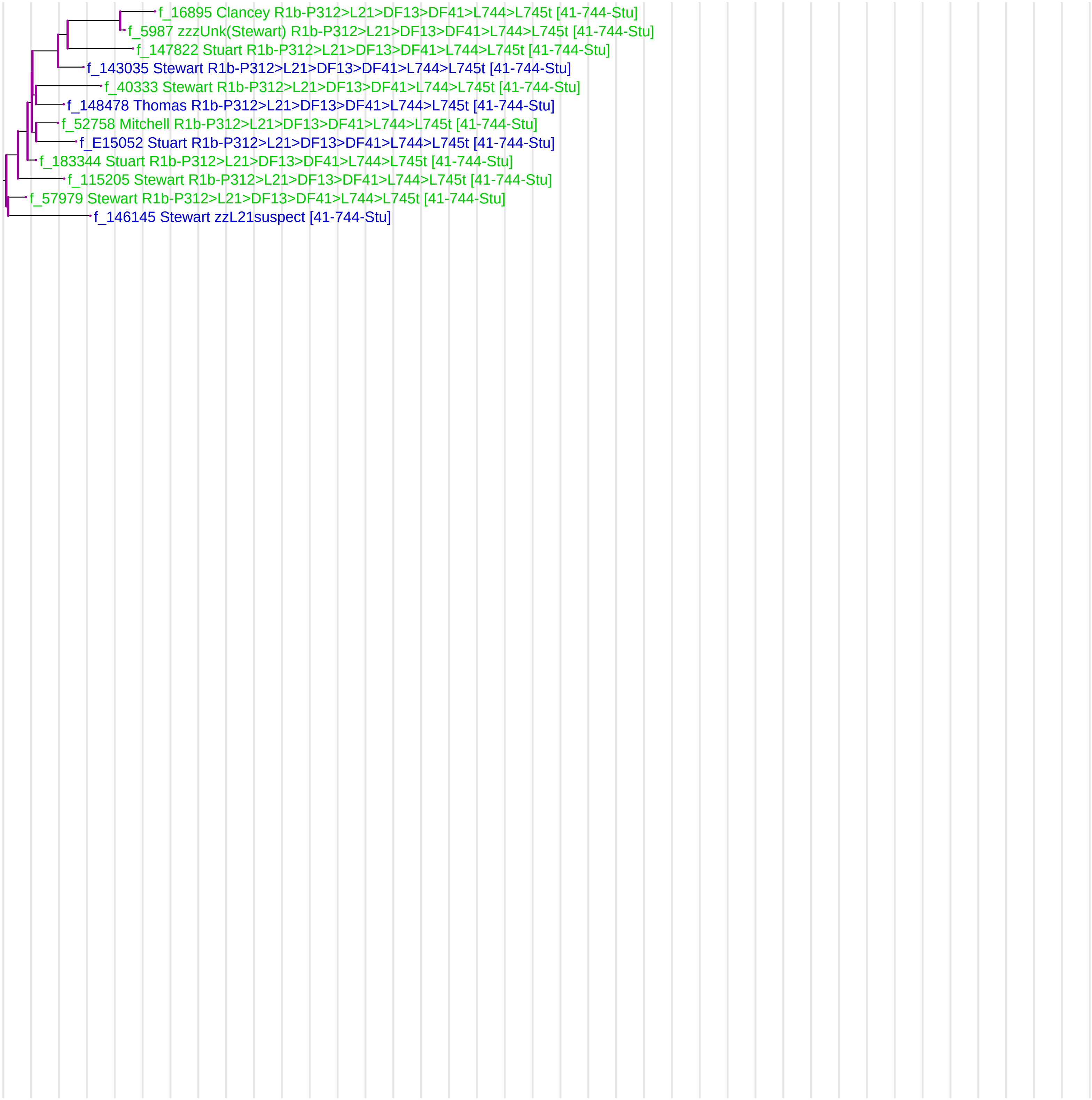
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	13	25	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	14	24	13	10	10	21	15	18	13	24	16	12	15	25	12	23	18	10	14	17	9	12	11

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



Age Analysis

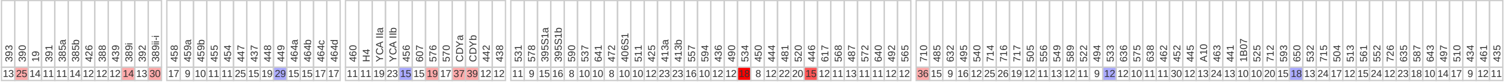
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
12	804	37	4.60%	23.55±2.50	588.794±85.9351



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.



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	25	14	11	11	14	12	12	12	14	13	30

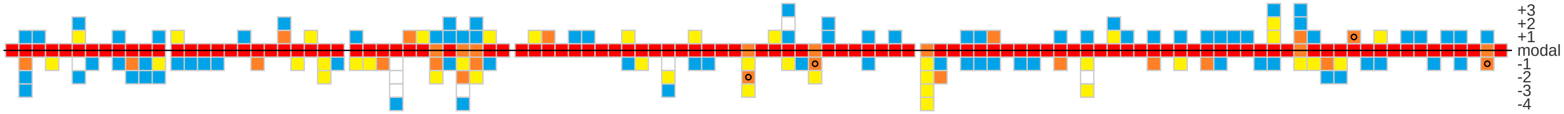
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	15	15	19	17	37	39	12	12

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
11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	18	8	12	22	20	15	12	11	13	11	11	12	12

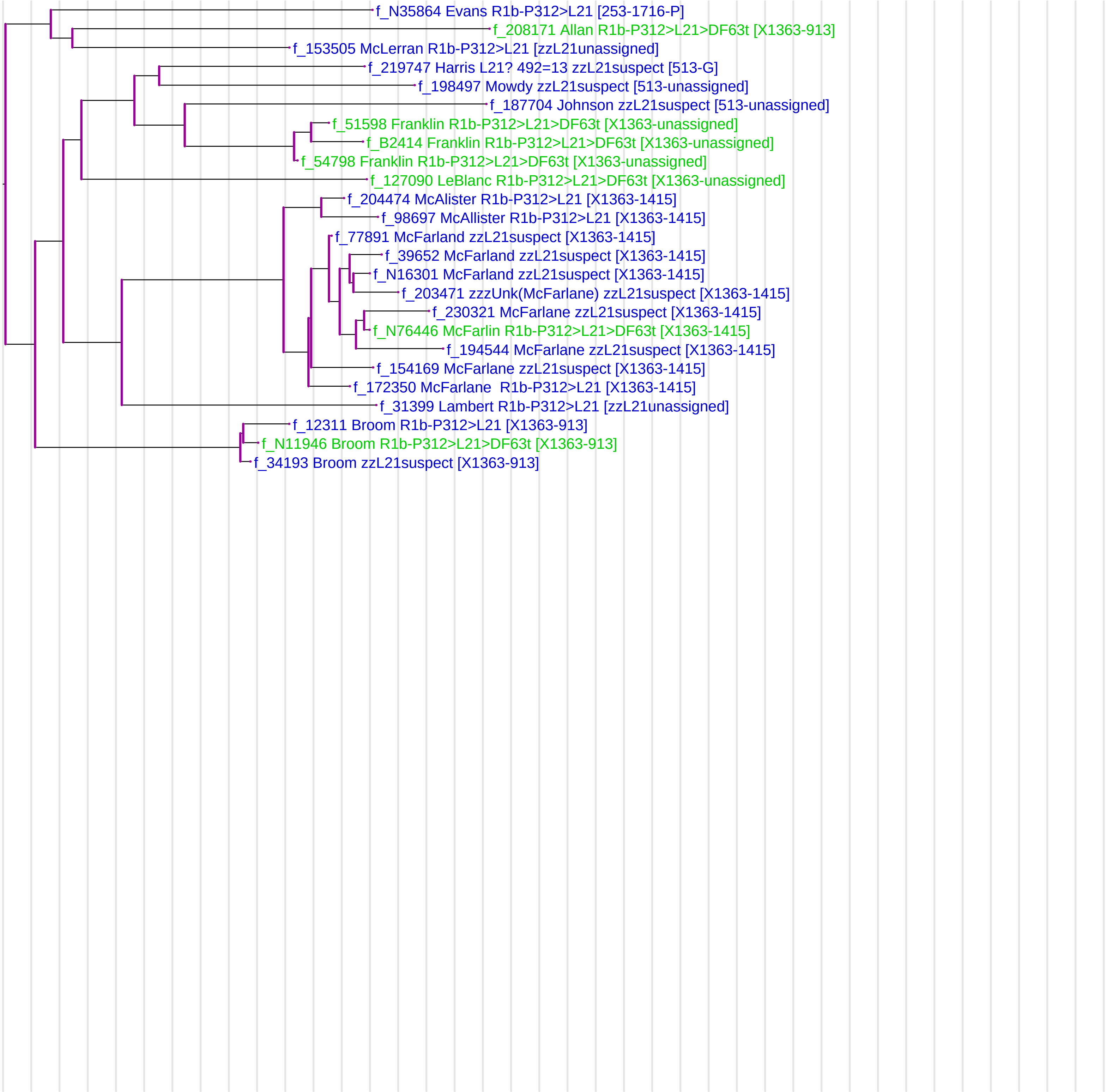
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	12	25	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

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



Age Analysis

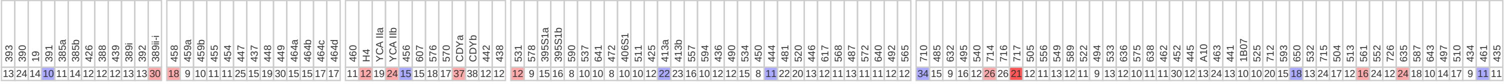
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
25	1675	329	19.64%	108.87±11.27	2721.66±391.768



The vertical grey lines are separated 10 generations apart.

R-DF13 Scots Cluster

This is the modal haplotype for R-DF13 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	389ii-i
13	24	14	10	11	14	12	12	12	13	13	30

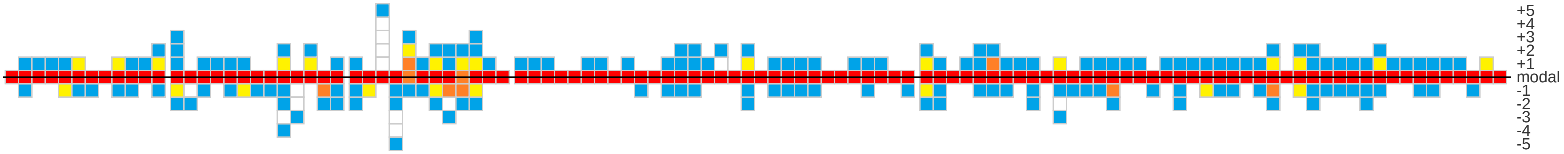
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
18	9	10	11	11	25	15	19	30	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	12	19	24	15	15	18	17	37	38	12	12

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
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	11	12	12

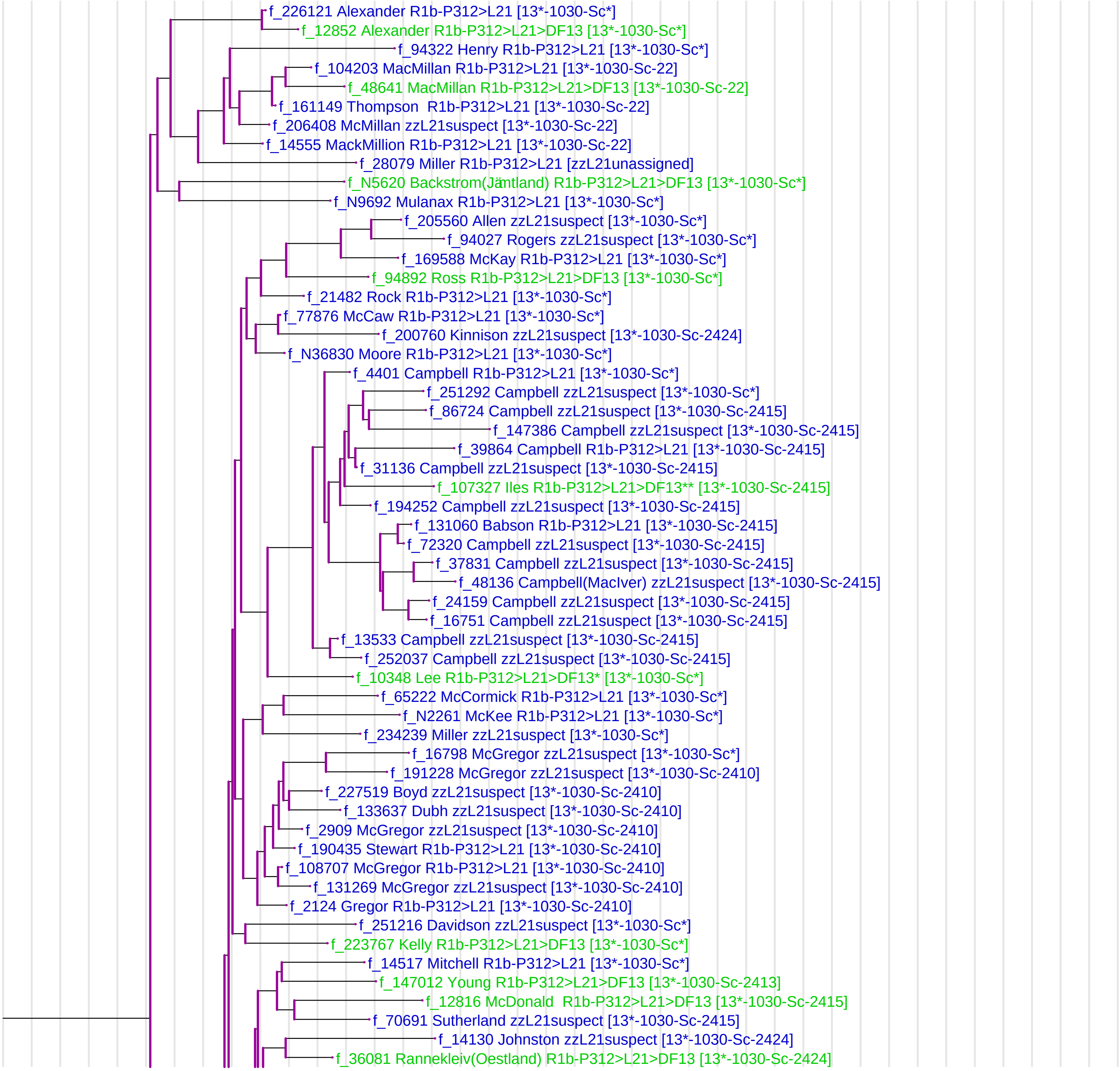
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
34	15	9	16	12	26	26	21	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	17	12	16	24	12	24	18	10	14	17	9	11	11

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

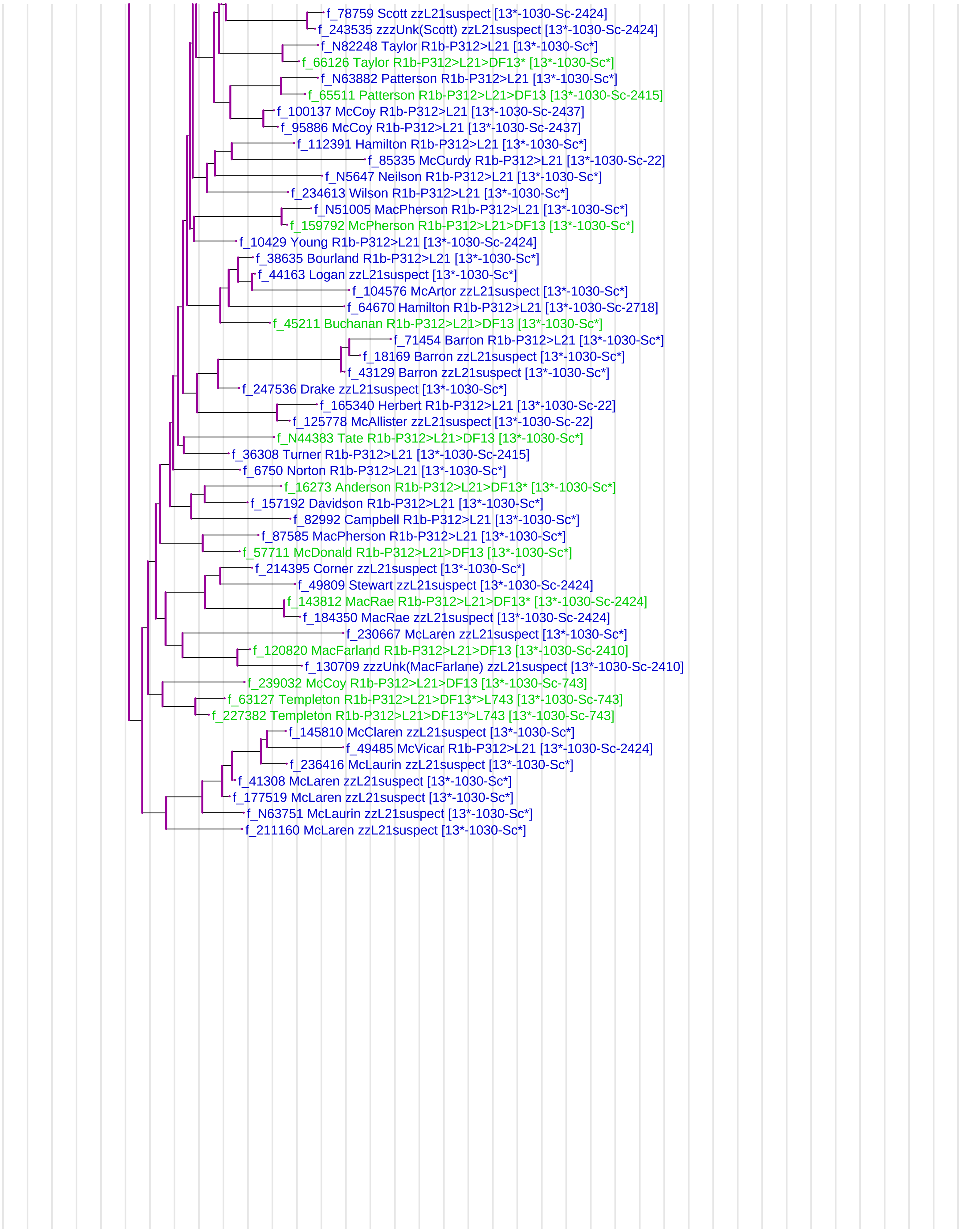


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
107	7169	785	10.95%	57.92±5.84	1447.94±205.562



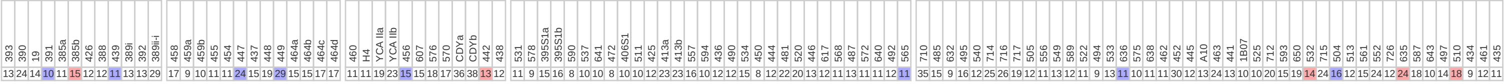
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

R-DF13 South Irish

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



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	10	11	15	12	12	11	13	13	29

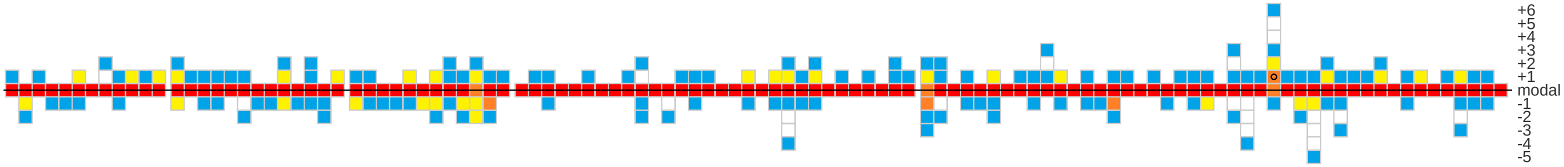
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	24	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	15	15	18	17	36	38	13	12

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
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	11

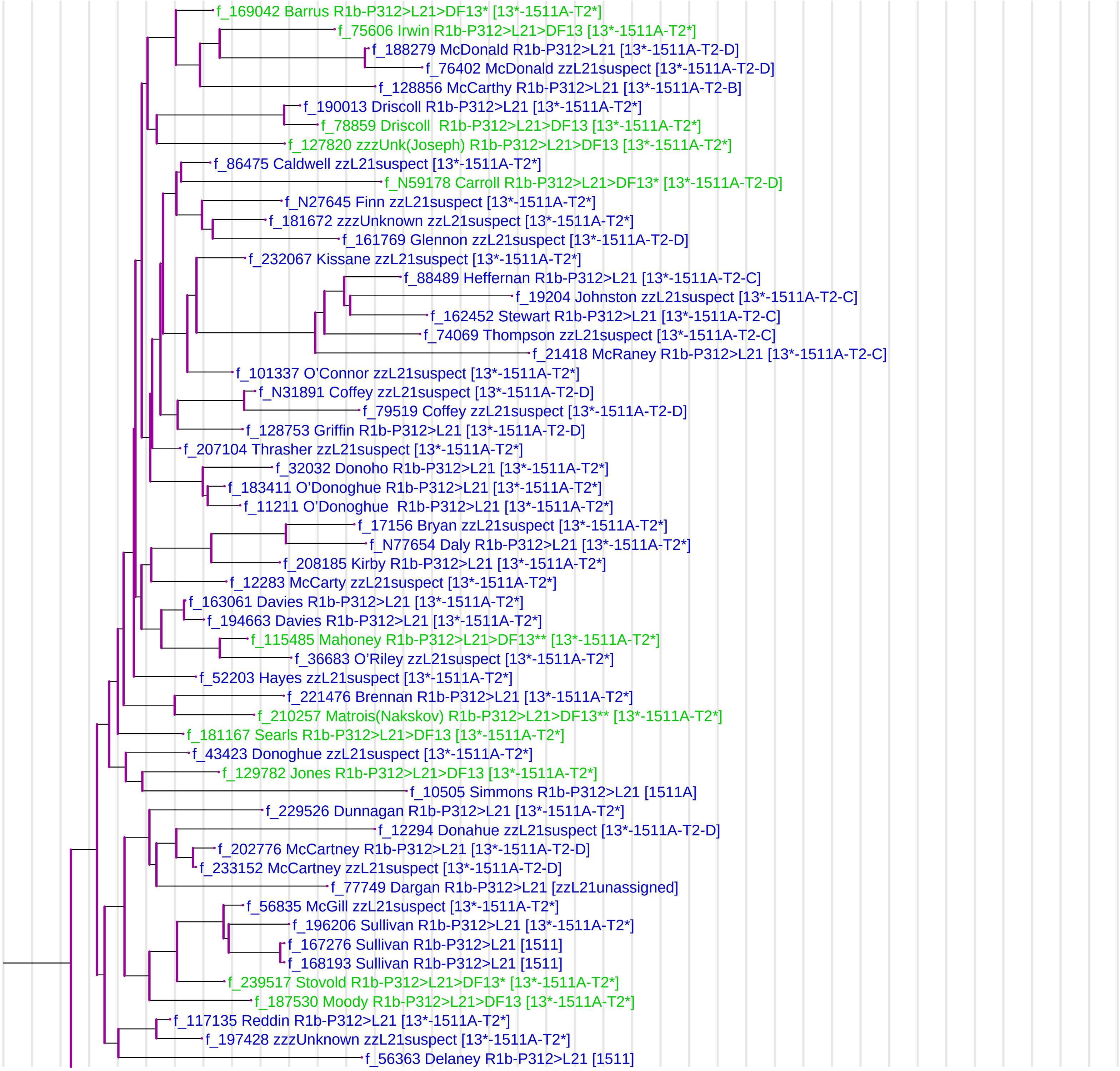
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	19	12	11	13	12	11	9	13	11	10	11	11	30	12	13	24	13	10	10	20	15	19	14	24	16	12	15	24	12	24	18	10	14	18	9	12	11

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

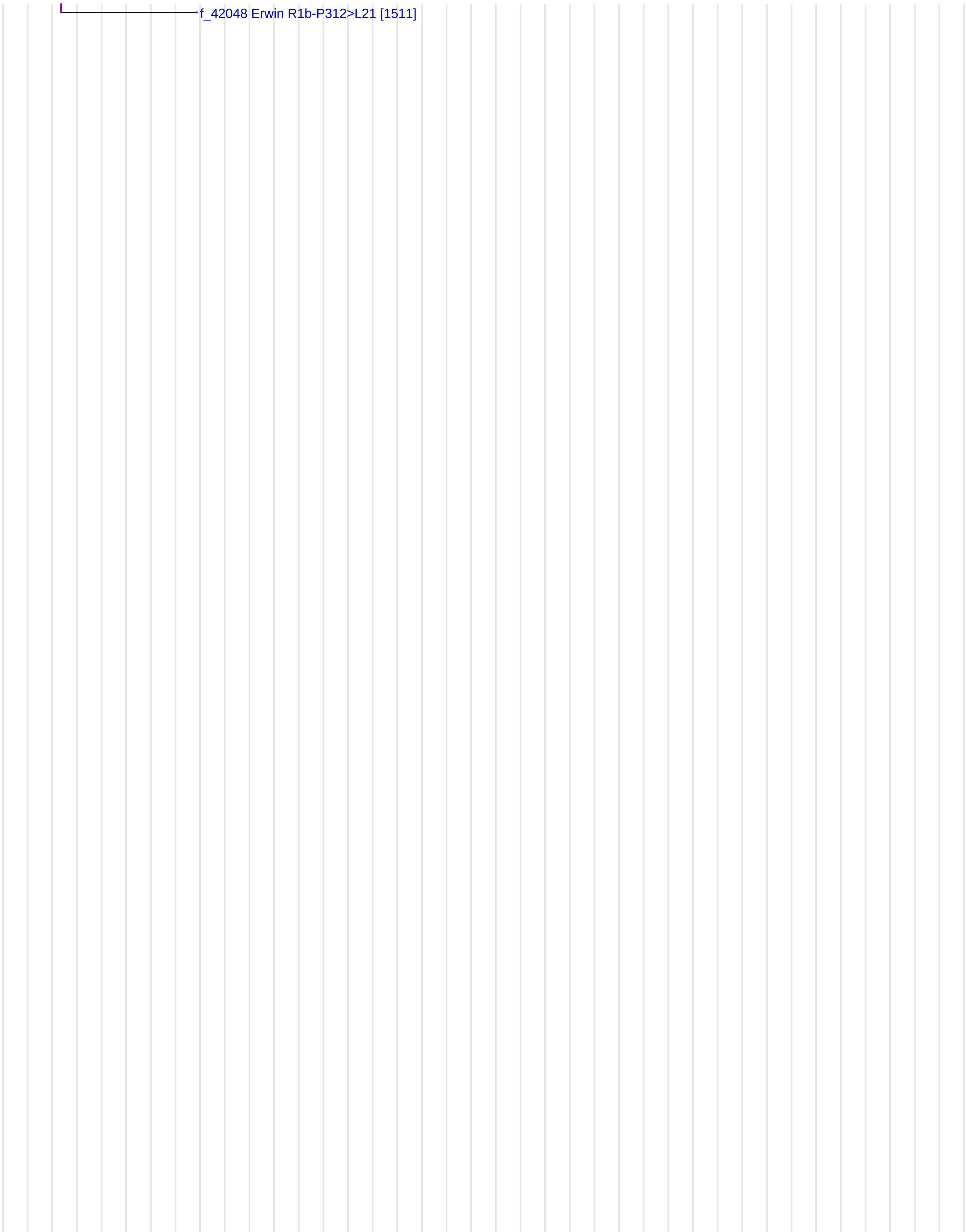


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
57	3819	394	10.32%	54.39±5.52	1359.68±193.675



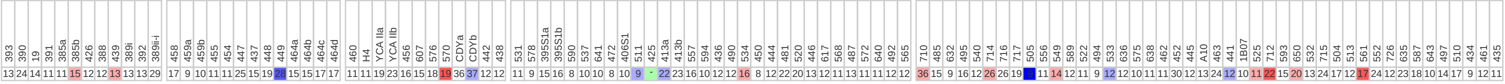
The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

R-DF21 Clan Colla

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



393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	11	11	15	12	12	13	13	13	29

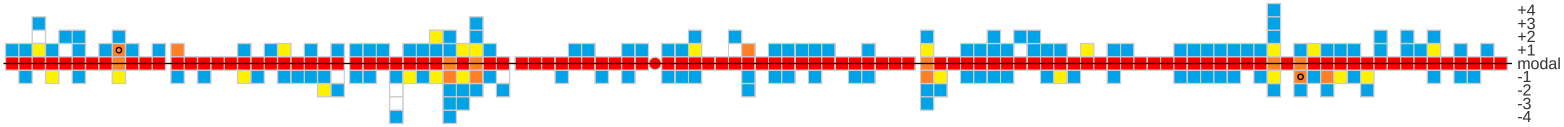
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	28	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	19	36	37	12	12

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
11	9	15	16	8	10	10	8	10	9	-	22	23	16	10	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12

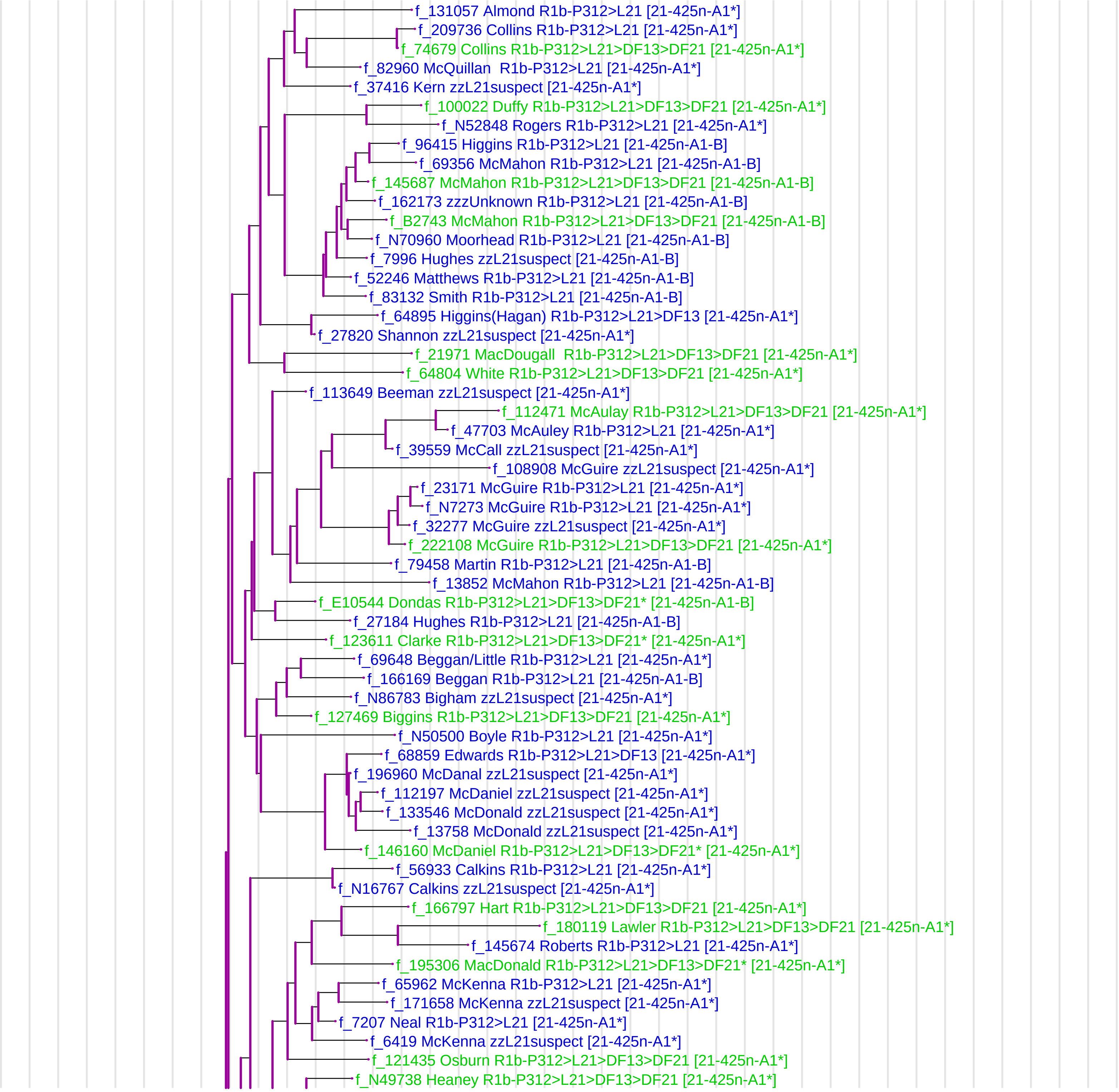
710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
36	15	9	16	12	26	26	19	9	11	14	12	11	9	12	12	10	11	11	30	12	13	24	12	10	11	22	15	20	13	24	17	12	17	24	12	23	18	10	14	17	9	12	11

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

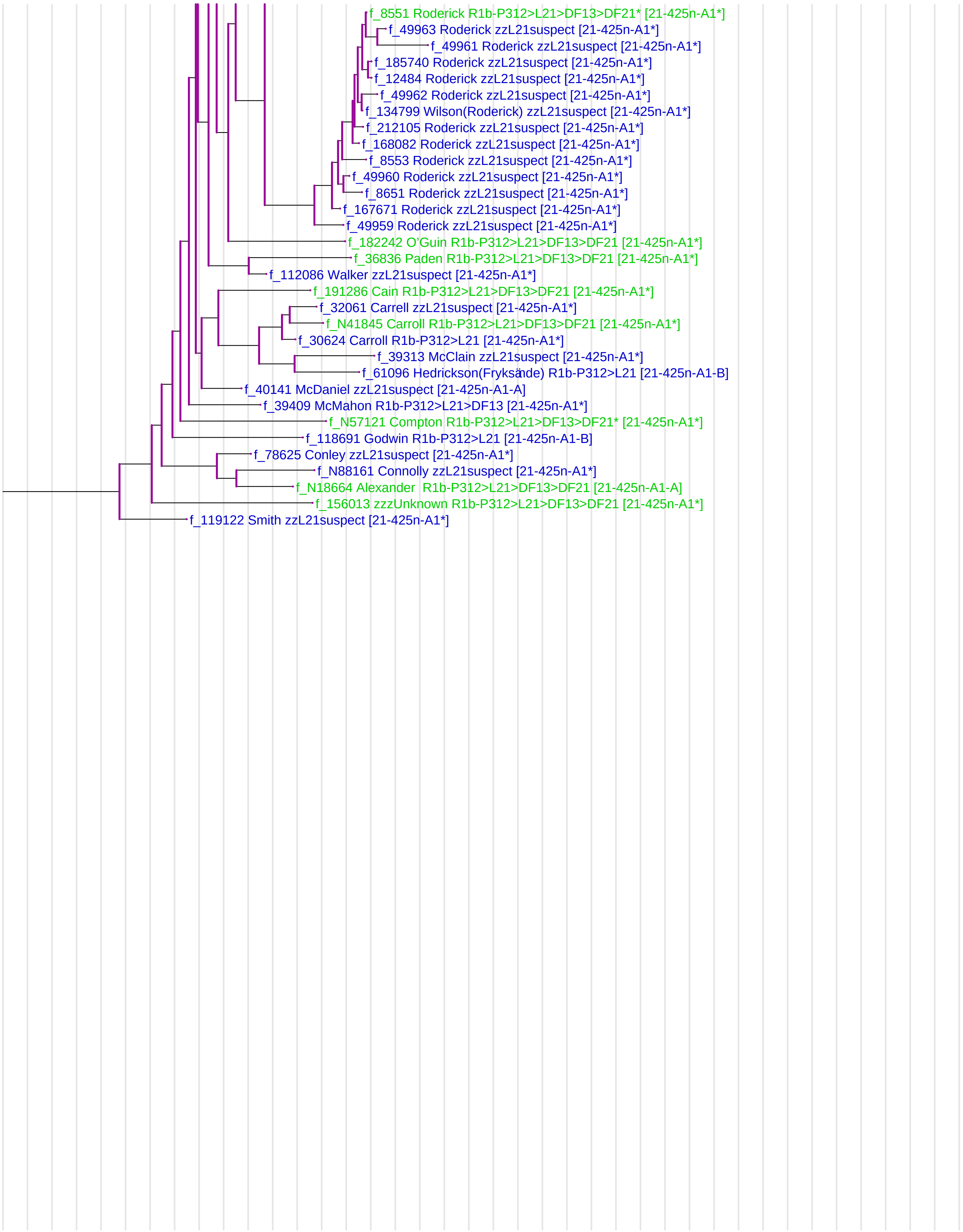


Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
89	5963	598	10.03%	52.79±5.33	1319.68±187.492



The vertical grey lines are separated 10 generations apart.



The vertical grey lines are separated 10 generations apart.

Cluster Modals

Cluster	Age	393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
Full Tree (R-L21)	Age: 3410±482.428 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	30	15	15	17	17
R-DF13	Age: 3412.03±482.719 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	30	15	15	17	17
R-DF49	Age: 1940.34±274.91 years	13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17
R-DF23	Age: 1709.1±242.169 years	13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17
R-M222	Age: 1471.3±208.499 years	13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17
R-L513	Age: 2819.52±399.736 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17
R-P66	Age: 187.97±29.7502 years	13	25	14	11	11	14	12	12	12	13	13	29	15	9	10	11	11	25	16	18	29	15	16	17	18
R-L193	Age: 1120.83±159.577 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17
R-L706.2	Age: 968.975±141.947 years	13	24	15	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	31	15	15	17	17
R-L705.2	Age: 797.572±119.012 years	13	24	15	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	31	15	15	17	17
R-L555	Age: 408.401±59.4434 years	13	24	14	11	11	15	12	12	12	13	13	29	17	9	10	11	11	25	15	20	30	15	16	17	17
R-Z255	Age: 1428.1±203.403 years	13	24	14	11	11	14	12	12	12	14	13	30	17	9	10	11	11	25	15	18	30	15	15	17	17
R-Z253	Age: 3021.22±428.907 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17
R-L226	Age: 1221.28±175.132 years	13	24	14	11	11	14	12	12	11	13	13	29	17	8	9	11	11	25	15	19	29	13	13	15	17
R-L554	Age: 0±0 years	13	25	14	11	11	14	12	12	11	14	13	30	17	9	10	11	11	24	14	19	30	15	16	16	17
R-Z2185	Age: 3295.64±470.224 years	13	24	14	10	11	15	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17
R-L1066	Age: 2975.11±425.644 years	13	24	14	10	11	15	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17
R-DF21	Age: 2777.97±393.645 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	28	15	15	17	17
R-P314.2	Age: 1548.88±227.215 years	13	23	14	11	11	14	12	13	13	13	13	28	17	9	10	11	11	26	15	18	29	15	15	16	17
R-L362	Age: 1009.3±153.802 years	13	23	14	11	11	14	12	13	13	13	13	28	17	9	10	11	11	25	15	19	29	15	15	16	17
R-Z246	Age: 2599.61±371.047 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17
R-DF25	Age: 2641.36±377.087 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17
R-DF5	Age: 2593.94±370.911 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	16	17
R-L627	Age: 888.705±135.345 years	13	24	15	10	11	15	12	12	12	14	13	30	17	9	10	11	11	25	15	19	29	15	16	16	16
R-L658	Age: 251.256±39.7863 years	14	24	14	10	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	28	15	15	17	17
R-L720	Age: 1171.84±186.873 years	13	24	14	10	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	31	14	15	16	18
R-S190	Age: 1077.82±154.78 years	13	24	14	10	11	14	12	12	12	13	13	29	18	9	10	11	11	25	15	19	30	13	15	17	17
R-L371	Age: 968.975±142.429 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	17	30	15	15	17	17
R-DF41	Age: 2309.28±329.976 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	15	15	17	17
R-L563	Age: 0±0 years	13	24	14	11	12	14	12	12	12	14	13	30	17	9	10	11	11	25	14	19	29	15	16	16	17
R-L744	Age: 780.889±112.978 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	14	15	17	17
R-L745	Age: 588.794±85.9351 years	13	24	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	14	15	17	17
R-DF63	Age: 2721.66±391.768 years	13	25	14	11	11	14	12	12	12	14	13	30	17	9	10	11	11	25	15	19	29	15	15	17	17
R-DF13 Scots Cluster	Age: 1447.94±205.562 years	13	24	14	10	11	14	12	12	12	13	13	30	18	9	10	11	11	25	15	19	30	15	15	17	17

Cluster	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
Full Tree (R-L21)	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
R-DF13	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
R-DF49	11	11	19	23	17	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12
R-DF23	11	11	19	23	17	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12
R-M222	11	11	19	23	17	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12
R-L513	11	11	19	23	16	15	18	17	38	39	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	11	12	12	12
R-P66	11	11	19	23	18	15	17	17	35	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	24	20	13	13	11	13	11	12	12	12
R-L193	11	11	19	23	16	16	18	17	38	39	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	12	12	12	12
R-L706.2	11	11	18	23	16	15	18	18	37	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12
R-L705.2	11	11	18	23	16	15	18	18	37	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12
R-L555	11	10	19	24	15	15	18	16	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12
R-Z255	11	11	19	23	16	15	18	18	39	40	11	12	11	9	15	16	8	10	10	8	10	10	12	23	23	17	10	12	12	15	8	12	22	20	14	12	11	13	11	11	12	12
R-Z253	11	11	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L226	11	11	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	15	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L554	10	11	19	23	15	15	18	17	34	40	13	12	11	9	15	16	8	11	10	8	10	10	12	23	23	16	10	12	12	16	8	12	22	20	13	12	11	14	11	11	12	12
R-Z2185	11	10	19	23	15	15	18	17	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L1066	10	10	19	23	15	15	18	17	37	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-DF21	11	11	19	23	16	15	18	18	36	38	12	12	11	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12
R-P314.2	10	11	19	23	16	15	18	18	37	37	12	12	11	9	16	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L362	11	11	19	23	16	15	18	18	37	38	12	12	11	9	16	16	8	10	10	8	11	10	12	23	23	17	10	12	12	16	8	12	22	20	13	13	11	13	11	11	12	12
R-Z246	11	11	19	23	16	15	18	17	37	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-DF25	11	11	19	23	16	15	19	17	37	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-DF5	11	11	19	23	16	15	18	17	37	38	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L627	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	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12
R-L658	11	11	19	23	14	15	18	19	37	37	11	13	11	9	15	16	8	10	10	8	9	10	12	23	23	16	10	12	12	17	9	12	22	21	13	12	11	13	11	11	12	12
R-L720	11	11	19	23	17	15	17	16	36	37	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	13	22	20	13	12	11	13	11	11	12	12
R-S190	11	10	19	23	16	15	18	18	38	38	12	12	11	9	15	16	9	10	10	8	10	10	12	22	23	16	10	12	12	15	8	11	22	20	14	12	11	13	11	11	12	12
R-L371	11	11	19	23	14	15	17	17	36	36	12	12	11	9	16	16	8	10	10	8	10	10	12	22	23	16	10	12	12	16	10	12	23	20	13	13	11	13	11	11	12	12
R-DF41	11	10	19	23	15	15	17	17	36	37	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	14	8	12	22	20	13	12	11	13	11	11	12	11
R-L563	11	10	19	24	15	15	17	17	36	37	12	12	11	9	15	16	8	10	10	8	10	10	12	21	23	16	11	12	12	14	8	12	21	20	12	12	11	14	11	11	12	12
R-L744	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	12	12	15	8	12	22	21	14	12	11	13	11	11	12	11
R-L745	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	12	12	15	8	12	22	21	14	12	11	13	11	11	12	11
R-DF63	11	11	19	23	15	15	19	17	37	39	12	12	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	18	8	12	22	20	15	12	11	13	11	11	12	12
R-DF13 Scots Cluster	11	12	19	24	15	15	18	17	37	38	12	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	11	12	12

Cluster	710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
Full Tree (R-L21)	35	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-DF13	35	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-DF49	35	15	9	16	12	24	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	22	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11
R-DF23	35	15	9	16	12	24	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	22	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11
R-M222	35	15	9	16	12	24	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	22	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11
R-L513	35	15	9	16	12	26	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	14	24	16	12	15	24	12	23	18	10	14	17	9	12	11
R-P66	34	15	9	16	12	24	26	19	13	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	9	20	15	19	13	24	16	12	15	24	12	23	18	10	13	17	9	13	11
R-L193	35	15	9	16	12	26	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	19	15	18	14	24	15	12	15	24	12	23	18	10	14	16	9	12	11
R-L706.2	34	15	9	16	12	26	26	19	12	12	13	12	11	9	12	12	10	11	11	30	12	13	23	13	10	10	20	15	17	13	25	15	12	15	24	12	23	18	10	14	16	9	12	11
R-L705.2	34	15	9	16	12	26	26	19	12	12	13	12	11	9	12	12	10	11	11	30	12	13	23	13	10	10	20	15	17	13	25	15	12	15	24	12	23	18	10	14	16	9	12	11
R-L555	34	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	21	13	24	16	12	14	24	12	26	18	10	14	17	9	12	11
R-Z255	36	15	9	16	12	25	26	19	12	11	13	12	12	9	13	12	10	11	11	30	12	13	23	13	10	11	20	15	19	13	24	17	13	15	24	12	23	18	10	14	17	9	12	11
R-Z253	35	15	9	16	12	25	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	21	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-L226	35	15	9	16	12	25	24	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	25	13	10	10	21	15	19	13	24	17	12	15	24	12	23	18	10	14	18	9	12	11
R-L554	35	15	9	16	12	25	26	20	12	11	12	12	12	9	12	12	10	11	11	30	12	13	24	14	10	10	21	15	20	13	24	17	12	15	25	12	23	18	10	14	17	9	12	11
R-Z2185	35	15	9	16	12	25	26	19	12	11	13	12	10	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-L1066	35	15	9	16	12	25	26	19	12	11	13	12	10	9	12	12	10	11	11	30	12	13	24	13	10	10	21	15	19	14	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-DF21	35	15	9	16	12	26	26	19	12	11	14	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-P314.2	34	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	15	12	15	25	12	23	18	10	14	17	9	12	11
R-L362	36	15	9	16	12	25	26	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	15	13	15	25	12	23	18	10	14	17	9	12	11
R-Z246	35	15	9	16	12	25	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11
R-DF25	35	15	9	16	12	25	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11
R-DF5	35	15	9	16	12	25	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11
R-L627	35	15	9	16	13	25	26	20	12	11	11	12	11	9	11	12	10	11	11	30	12	13	24	13	10	10	19	15	18	13	24	16	12	15	24	12	23	18	9	14	17	9	12	11
R-L658	34	14	9	16	12	26	26	20	12	11	11	12	11	9	12	12	10	11	11	30	12	13	23	13	10	10	20	15	18	13	24	16	13	15	24	12	23	18	9	14	17	9	12	11
R-L720	35	15	9	16	12	24	26	19	12	11	14	12	12	9	13	12	10	11	12	30	12	12	24	13	10	10	19	15	18	12	24	17	12	15	24	12	23	18	10	14	17	9	13	11
R-S190	31	15	9	15	12	25	26	20	13	11	14	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	23	17	12	15	24	12	23	18	10	14	17	9	12	11
R-L371	36	15	9	16	12	25	22	19	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	19	15	19	13	24	17	12	16	24	12	23	18	10	14	17	9	12	11
R-DF41	36	15	9	16	12	25	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	14	24	13	10	10	20	15	18	13	24	16	12	15	24	12	23	18	10	14	17	9	12	11
R-L563	36	15	9	16	14	25	26	19	12	11	15	12	11	9	13	12	10	11	11	30	12	13	24	12	10	10	19	15	19	13	24	14	11	16	25	12	23	18	10	14	17	9	12	11
R-L744	36	15	9	16	13	25	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	14	24	13	10	10	21	15	18	13	24	16	12	15	25	12	23	18	10	14	17	9	12	11
R-L745	36	15	9	16	13	25	26	19	12	11	12	12	11	9	13	12	10	11	11	30	12	14	24	13	10	10	21	15	18	13	24	16	12	15	25	12	23	18	10	14	17	9	12	11
R-DF63	36	15	9	16	12	25	26	19	12	11	13	12	11	9	12	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11
R-DF13 Scots Cluster	34	15	9	16	12	26	26	21	12	11	13	12	11	9	13	12	10	11	11	30	12	13	24	13	10	10	20	15	18	13	24	17	12	16	24	12	24	18	10	14	17	9	11	11

Cluster Modals (continued...)

R-DF13 South Irish

Age: 1359.68±193.675 years

393	390	19	391	385a	385b	426	388	439	389i	392	389ii-i
13	24	14	10	11	15	12	12	11	13	13	29

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	24	15	19	29	15	15	17	17

460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	15	15	18	17	36	38	13	12

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
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	11

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	A10	463	441	1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	19	12	11	13	12	11	9	13	11	10	11	11	30	12	13	24	13	10	10	20	15	19	14	24	16	12	15	24	12	24	18	10	14	18	9	12	11

R-DF21 Clan Colla

Age: 1319.68±187.492 years

13	24	14	11	11	15	12	12	13	13	13	29

17	9	10	11	11	25	15	19	28	15	15	17	17

11	11	19	23	16	15	18	19	36	37	12	12

11	9	15	16	8	10	10	8	10	9	-	22	23	16	10	12	12	16	8	12	22	20	13	12	11	13	11	11	12	12

36	15	9	16	12	26	26	19	9	11	14	12	11	9	12	12	10	11	11	30	12	13	24	12	10	11	22	15	20	13	24	17	12	17	24	12	23	18	10	14	17	9	12	11

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 2012-11-09, while the SNP data came primarily from the L21+, Scottish, and Irish FTDNA projects. Only members with 111 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. The 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%	

Tree and analysis completed by Alexander R. Williamson on October 15, 2012.