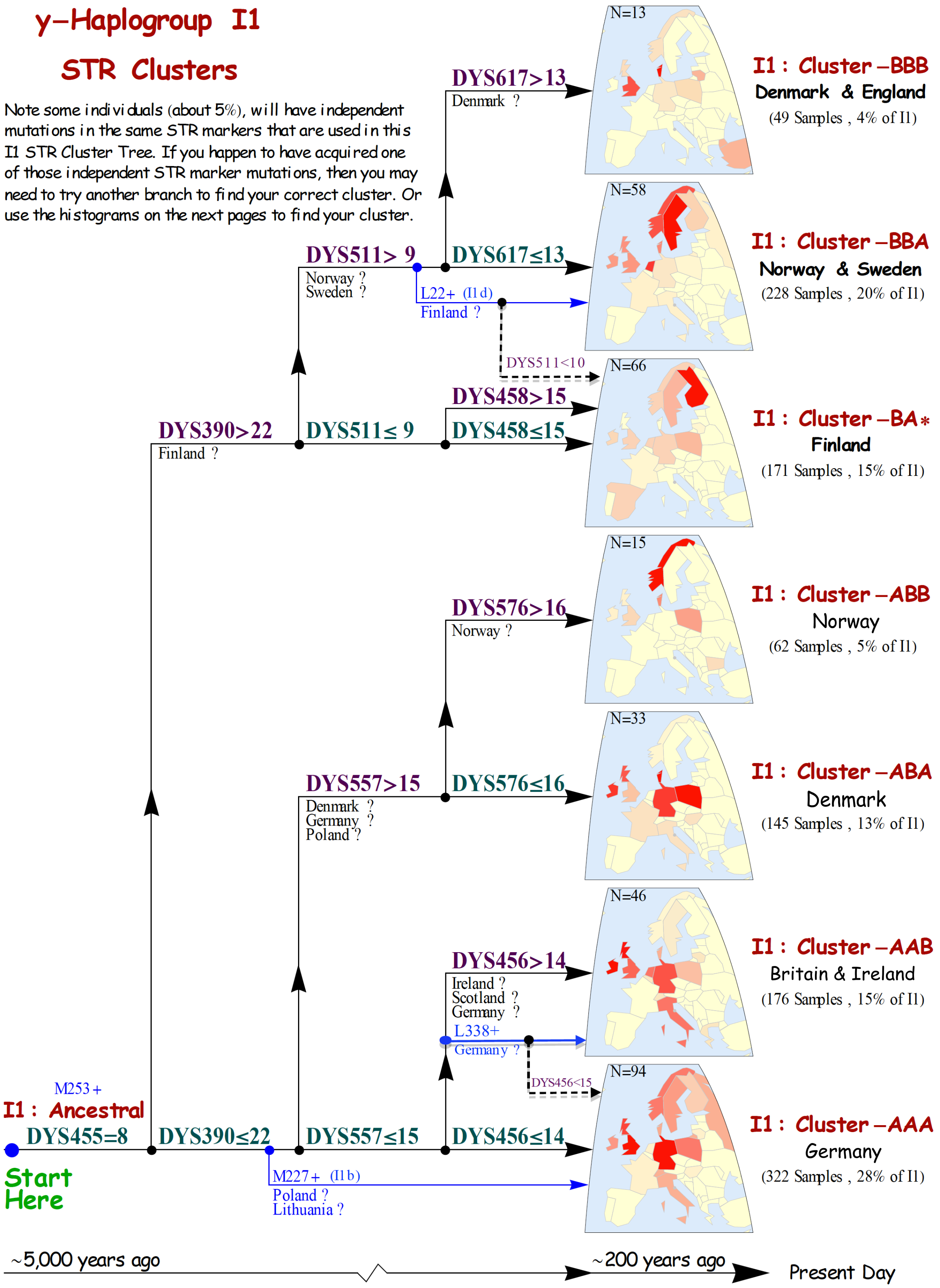
y-Haplogroup I1

STR Clusters

Note some individuals (about 5%), will have independent mutations in the same STR markers that are used in this I1 STR Cluster Tree. If you happen to have acquired one of those independent STR marker mutations, then you may need to try another branch to find your correct cluster. Or use the histograms on the next pages to find your cluster.



M253+

I1 : Ancestral

DYS455=8

Start Here

DYS390>22
Finland ?

DYS390≤22

M227+ (I1b)
Poland ?
Lithuania ?

DYS511> 9
Norway ?
Sweden ?

DYS511≤ 9

DYS617>13
Denmark ?

DYS617≤13

L22+ (I1d)
Finland ?

DYS511<10

DYS458>15

DYS458≤15

DYS557>15
Denmark ?
Germany ?
Poland ?

DYS557≤15

DYS576>16
Norway ?

DYS576≤16

DYS456>14
Ireland ?
Scotland ?
Germany ?

L338+
Germany ?

DYS456<15

DYS456≤14

N=13

I1 : Cluster – BBB
Denmark & England
(49 Samples , 4% of I1)

N=58

I1 : Cluster – BBA
Norway & Sweden
(228 Samples , 20% of I1)

N=66

I1 : Cluster – BA*
Finland
(171 Samples , 15% of I1)

N=15

I1 : Cluster – ABB
Norway
(62 Samples , 5% of I1)

N=33

I1 : Cluster – ABA
Denmark
(145 Samples , 13% of I1)

N=46

I1 : Cluster – AAB
Britain & Ireland
(176 Samples , 15% of I1)

N=94

I1 : Cluster – AAA
Germany
(322 Samples , 28% of I1)

~5,000 years ago

~200 years ago

Present Day

Start at the bottom left, then follow the branch corresponding to your particular STR marker values.
That will give you your I1 STR Cluster, which will indicate where your male-line ancestors may have originated.
Brighter reds in the map represent the locations of the most-distant male-line ancestor reported by members of the cluster.

TDR, June 2010 (updated December 2010)

I1 STR Clan "AAB" splits into "AABA" with Y-GATA-H4 ≥ 10, and "AABB" with Y-GATA-H4 < 10. "AABB" people are mostly L338+.

Note DYS459a=7 is a completely separate branch, that by chance convergence ends up in "BA*". It has peak density in Poland.

The sub-clans "AABA", "AABB", "BABA", and "BABB", represent 9%, 6%, 4%, and 2% respectively of people tested as I1.

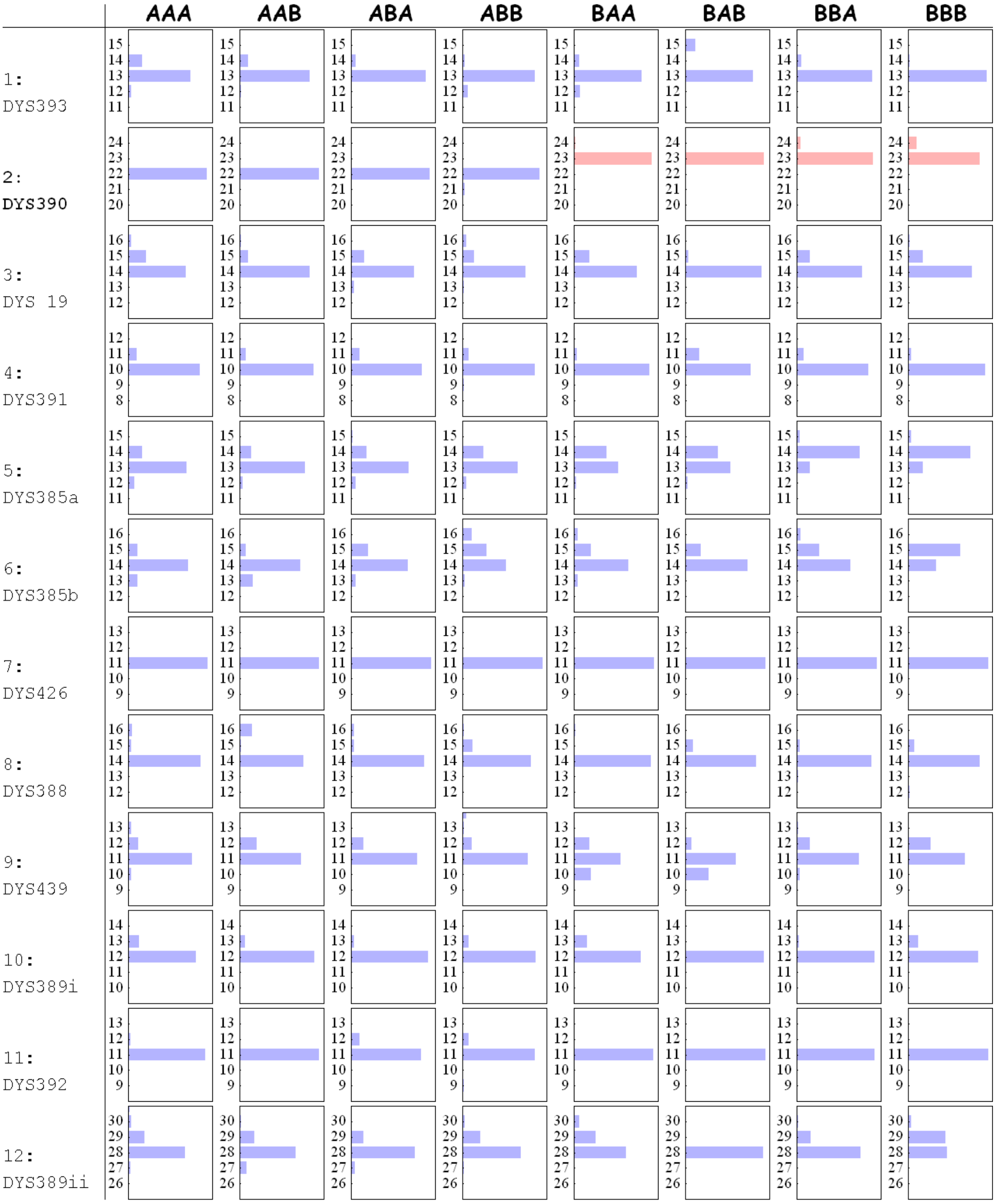
Within Finland, I1-"BAB" is more likely in eastern areas. (Note DYS459a=7 should be excluded from I1-"BA*".)
Within Finland, I1-"BAA" is more likely in western areas (and even across to Sweden/Norway).
I1-"AABB" is relatively high in Ireland, Scotland, England, and the Netherlands/Belgium.
I1-"AABA" is particularly high in Wales, but occurs commonly elsewhere.

y-Haplogroup I1 STR Clusters - Marker Modal Values

Marker	(mutate)	AAA	AAB	ABA	ABB	BAA	BAB	BBA	BBB
1: DYS393	(1320g)	13	13	13	13	13	13	13	13
2: DYS390	(320g)	22	22	22	22	23	23	23	23
3: DYS 19	(660g)	14	14	14	14	14	14	14	14
4: DYS391	(380g)	10	10	10	10	10	10	10	10
5: DYS385a	(440g)	13	13	13	13	13	13	14	14
6: DYS385b	(440g)	14	14	14	14	14	14	14	15
7: DYS426	(11000g)	11	11	11	11	11	11	11	11
8: DYS388	(4500g)	14	14	14	14	14	14	14	14
9: DYS439	(210g)	11	11	11	11	11	11	11	11
10: DYS389i	(540g)	12	12	12	12	12	12	12	12
11: DYS392	(1920g)	11	11	11	11	11	11	11	11
12: DYS389ii	(410g)	28	28	28	28	28	28	28	29
13: DYS458	(120g)	15	15	15	15	15	16	15	15
14: DYS459a	(760g)	8	8	8	8	8	8	8	8
15: DYS459b	(760g)	9	9	9	9	9	9	9	9
16: DYS455	(6200g)	8	8	8	8	8	8	8	8
17: DYS454	(6200g)	11	11	11	11	11	11	11	11
18: DYS447	(380g)	23	22	23	23	23	23	23	23
19: DYS437	(1010g)	16	16	16	16	16	16	16	16
20: DYS448	(740g)	20	20	20	20	20	20	20	20
21: DYS449	(120g)	28	28	29	28	28	29	28	28
22: DYS464a	(180g)	12	12	12	12	12	12	12	12
23: DYS464b	(180g)	14	14	14	14	14	14	14	14
24: DYS464c	(180g)	15	15	15	15	15	15	15	15
25: DYS464d	(180g)	16	16	16	16	15	15	16	16
26: DYS460	(250g)	10	11	10	10	10	10	10	10
27: Y-GATA-H4	(480g)	10	10	10	10	10	10	10	10
28: Y-CA-IIa	(810g)	19	19	19	19	19	19	19	19
29: Y-CA-IIb	(810g)	21	21	21	21	21	21	21	21
30: DYS456	(140g)	14	15	14	14	14	14	14	14
31: DYS607	(240g)	14	14	14	14	14	14	14	14
32: DYS576	(100g)	16	16	16	17	16	16	17	17
33: DYS570	(130g)	19	19	20	20	20	20	20	20
34: CDYa	(30g)	35	35	35	35	35	35	35	35
35: CDYb	(30g)	37	36	37	38	37	37	37	37
36: DYS442	(310g)	12	12	12	12	12	12	12	12
37: DYS438	(1820g)	10	10	10	10	10	10	10	10
38: DYS531	(2700g)	11	11	11	11	11	11	11	11
39: DYS578	(12500g)	8	8	8	8	8	8	8	8
40: DYS395a	(3200g)	15	15	15	15	15	15	15	15
41: DYS395b	(3200g)	15	15	15	15	15	15	15	15
42: DYS590	(1850g)	8	8	8	8	8	8	8	8
43: DYS537	(1750g)	11	11	11	11	11	11	11	11
44: DYS641	(5600g)	10	10	10	10	10	10	10	10
45: DYS472	(100000g)	8	8	8	8	8	8	8	8
46: DYS406	(650g)	9	9	9	9	9	9	9	9
47: DYS511	(780g)	9	9	9	9	9	9	10	10
48: DYS425	(5600g)	12	12	12	12	12	12	12	12
49: DYS413a	(500g)	22	22	23	23	23	22	23	23
50: DYS413b	(500g)	25	25	25	25	25	24	25	25
51: DYS557	(310g)	15	15	16	16	15	15	15	15
52: DYS594	(3400g)	10	10	10	10	10	10	10	10
53: DYS436	(5600g)	12	12	12	12	12	12	12	12
54: DYS490	(5300g)	12	12	12	12	12	12	12	12
55: DYS534	(120g)	16	16	16	16	16	16	16	17
56: DYS450	(5000g)	8	8	8	8	8	8	8	8
57: DYS444	(310g)	13	13	13	13	13	13	13	12
58: DYS481	(180g)	25	25	25	25	25	26	25	25
59: DYS520	(410g)	20	20	20	20	20	20	20	20
60: DYS446	(1050g)	13	13	13	13	13	13	13	13
61: DYS617	(2400g)	13	13	13	13	13	13	13	14
62: DYS568	(1900g)	11	11	11	11	11	11	11	11
63: DYS487	(1030g)	12	12	12	12	12	12	12	12
64: DYS572	(470g)	11	11	11	11	11	11	11	11
65: DYS640	(2900g)	11	11	11	11	11	11	11	11
66: DYS492	(2400g)	12	12	12	12	12	12	12	12
67: DYS565	(1100g)	11	11	11	11	11	11	11	11

y-Haplogroup I1 STR Clusters – Allele Histograms

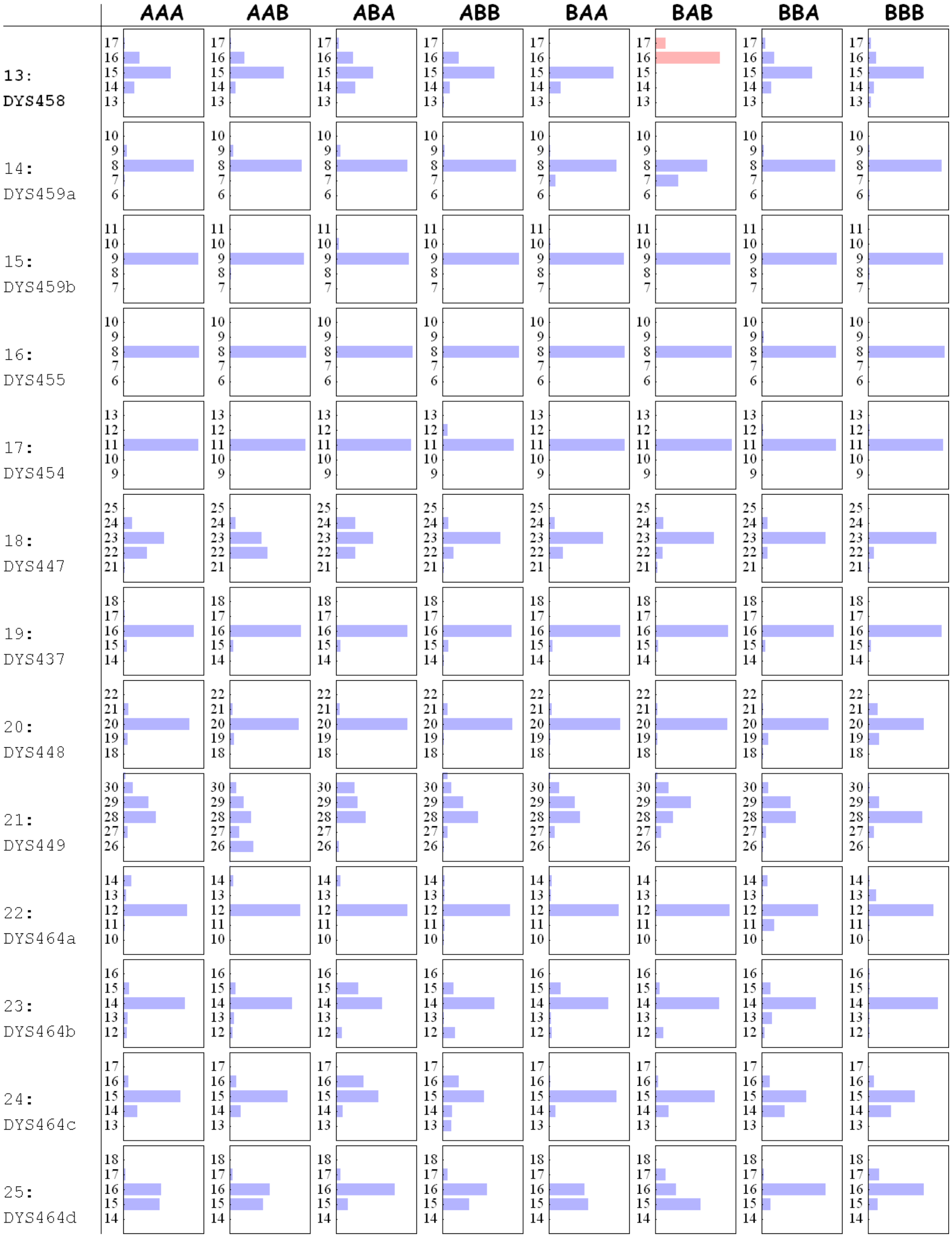
(for FTDNA markers 1 to 12)



Here the STR marker **DYS390** can be used to separate the "A**" and "B**" clusters. In addition, the "B**" cluster members often have increased allele values for the STR markers **DYS385a,b** compared to the "A**" cluster members. The Kittler order is important for **DYS385a,b** and that information is not given here.

y-Haplogroup I1 STR Clusters – Allele Histograms

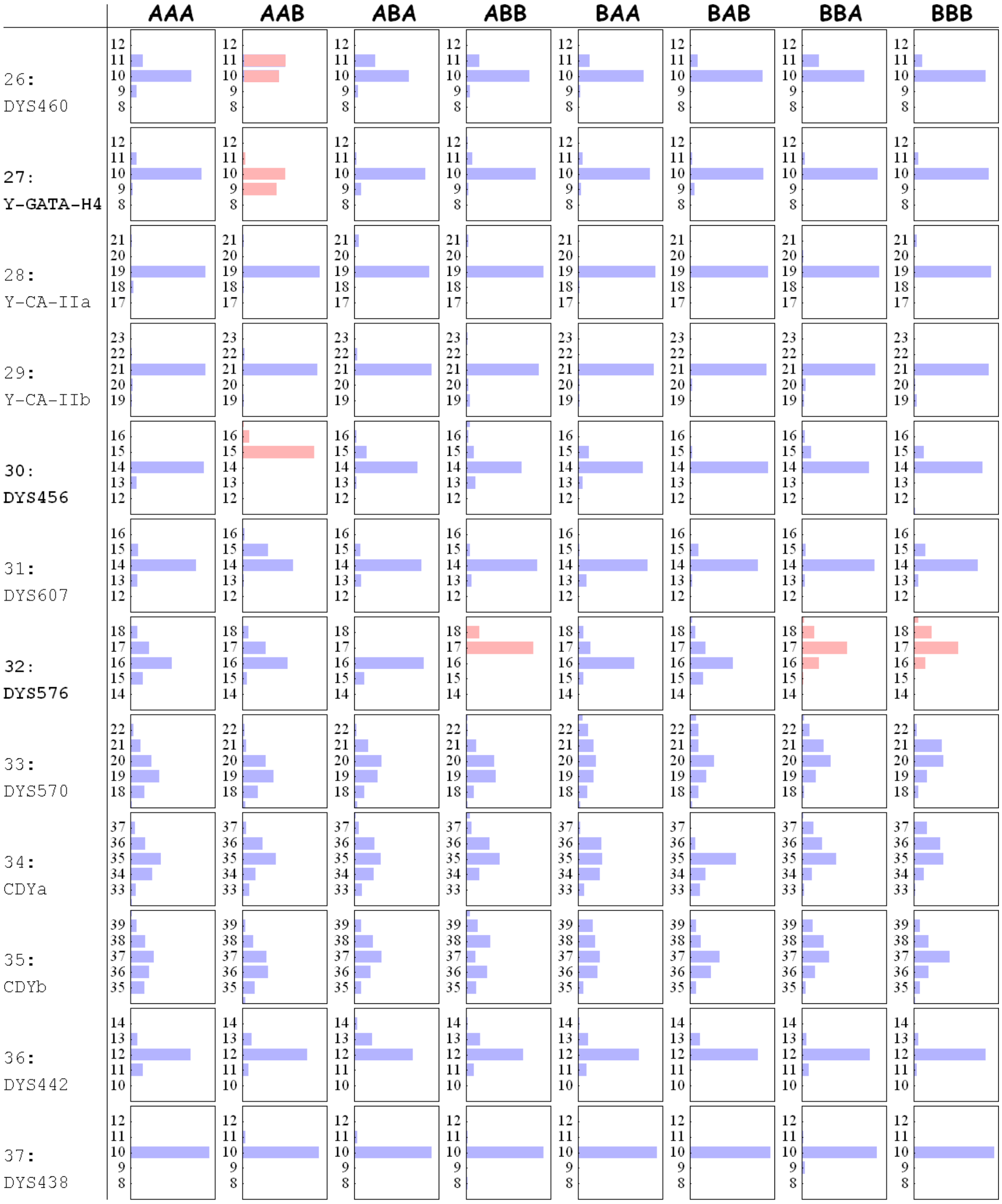
(for FTDNA markers 13 to 25)



Here the STR marker **DYS458** can be used to separate the "BAA" and "BAB" clusters – it is a weak separation however, as that marker has a high mutation rate. Some members of the "BAB" cluster have acquired a decreased allele value for the STR marker **DYS459a**.

y-Haplogroup I1 STR Clusters – Allele Histograms

(for FTDNA markers 26 to 37)

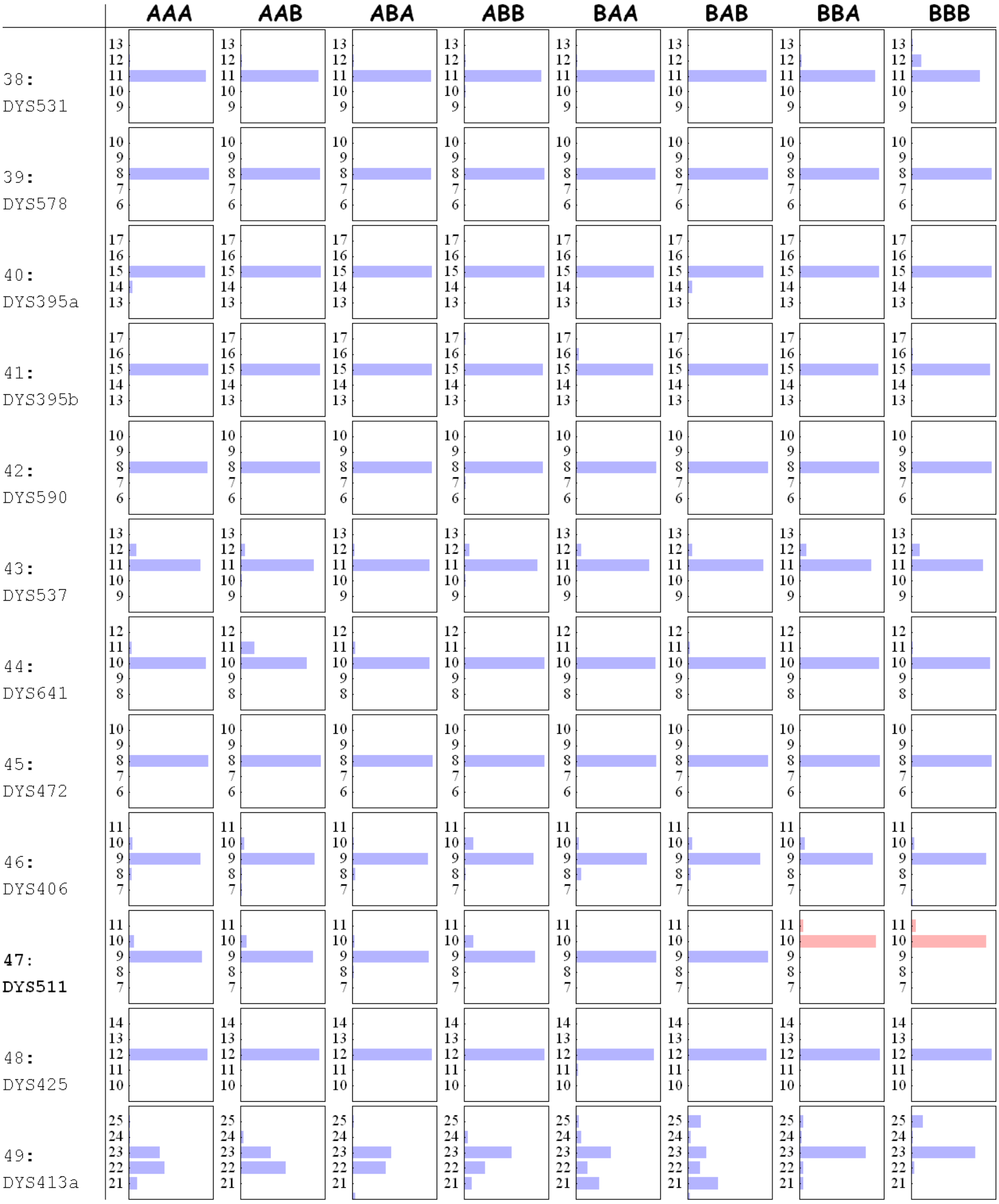


Here the STR marker **DYS456** can be used to separate the "AAA" and "AAB" clusters. In addition, the STR marker **DYS576** can be used to separate the "ABA" and "ABB" clusters - it is a weak separation however, as that marker has a particularly high mutation rate*. Some members of the "AAB" cluster have acquired a decreased allele value for the STR marker **Y-GATA-H4**, and an increased allele value for the STR markers **DYS460** and **DYS607**.

* One mutation in **DYS576** is expected to occur about every 100 generations. Equivalently, one child in every 100 male births can be expected to have a different **DYS576** allele than its father. So using the fast mutating **DYS576** to split clusters will fail in some cases.

y-Haplogroup I1 STR Clusters – Allele Histograms

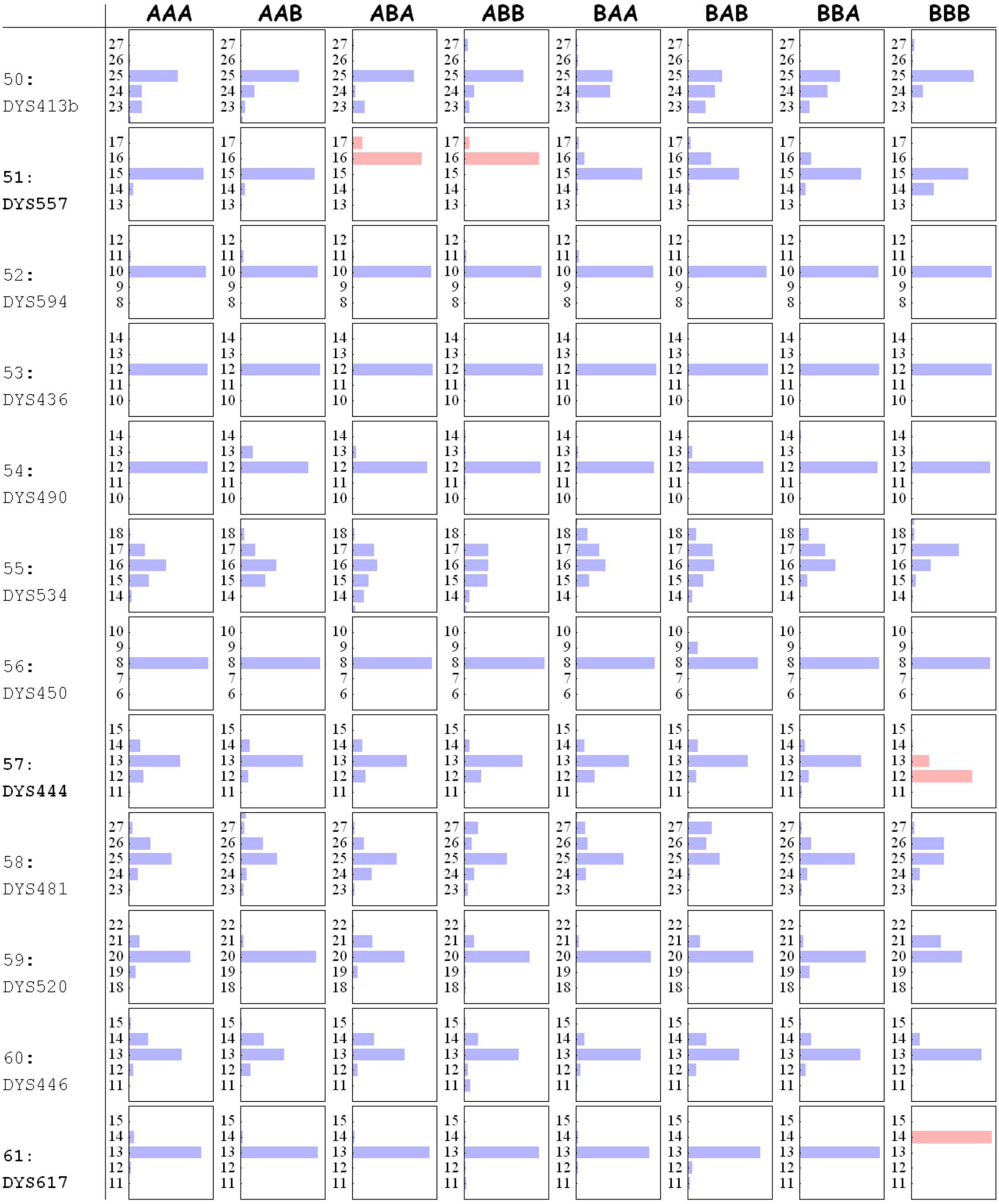
(for FTDNA markers 38 to 49)



Here the STR marker **DYS511** can be used to separate the “BA*” and “BB*” clusters - but be careful, as a small number of “ABB” cluster members have independently acquired the same mutation.

y-Haplogroup I1 STR Clusters – Allele Histograms

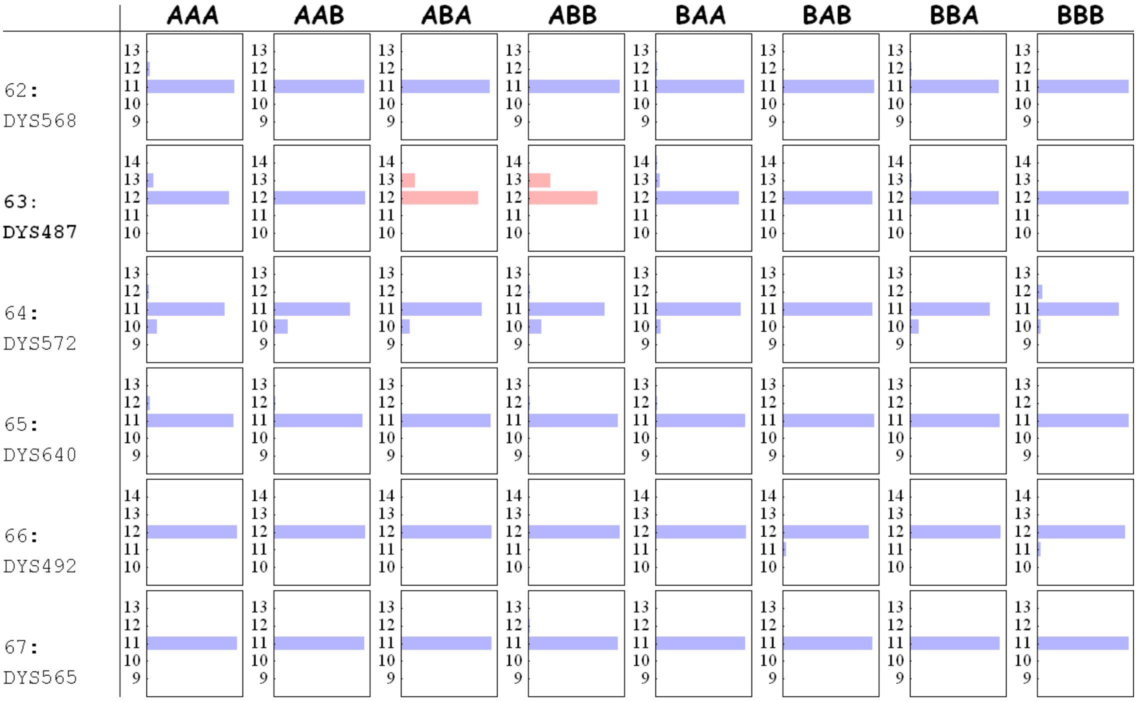
(for FTDNA markers 50 to 61)



Here the STR marker **DYS557** can be used to separate the "AA*" and "AB*" clusters. In addition, the STR marker **DYS617** can be used to separate the "BBA" and "BBB" clusters – but be careful, as a very small number of "AAA" cluster members have independently acquired the same mutation. The STR marker **DYS444** can also indicate the split between the clusters "BBA" and "BBB" in some individuals.

y-Haplogroup I1 STR Clusters – Allele Histograms

(for FTDNA markers 62 to 67)



Some members of the "AB*" clusters have an increased allele value for **DYS487**.

Additional STR markers, such as **DYS462** are not given here. A mutation in the **DYS462** marker (from an ancestral 12 repeats to 13 repeats) has probably occurred within the "BB*" clusters, and so it is a useful marker to have tested. Insufficient data was available to plot an allele histogram plot of **DYS462** for each of the eight clusters.

SNP mutations, such as **L22** (which defines the I1d sub-clade) and **M227** (which defines the I1b sub-clade) have been included in the y-Haplogroup I1 STR Cluster Tree.

The above histograms, and the "y-Haplogroup I1 STR Cluster Tree", are based on an analysis of nearly 1200 individuals who are members of y-Haplogroup I1 and who supplied their 67 FTDNA marker values. An additional 800 individuals supplied just their 37 FTDNA marker values. Nearly a third of the individuals also provided usable information about the geographic location of their most-distant known male-line ancestor. The data was divided up, using a clustering method, into eight clusters – additional sub-clusters could also be determined in some cases, but then the sample size for those sub-clusters is smaller and so less useful for establishing geographic origin. There was sufficient data, however, to generate an acceptable indication of the geographic distribution of the most-distance known ancestors for each of the eight main clusters.

TDR, June 2010