

YSearch Macro_67_markers_20111103C.txt

67 marker Y-Search macro using DNA fingerprints (generic L21 baseline search - add & modify for DNA fingerprint):

```
http://www.ysearch.org/search_search.asp?fail=2&uid=&freeentry=true&L1=13&L2=0&L3=14&L4=0&L5=0&L6=11&L7=0&L8=12&L9=12&L10=0&L11=13&L12=13&L13=0&L14=0&L15=9&L16=0&L17=11&L18=11&L19=0&L20=15&L21=0&L22=0&L23=15&L24=0&L25=0&L26=17&L27=0&L28=0&L29=0&L30=0&L31=0&L32=19&L33=23&L34=0&L35=0&L36=0&L37=0&L38=0&L39=0&L40=0&L41=12&L42=12&L43=0&L44=0&L45=0&L46=0&L47=0&L48=0&L49=0&L50=0&L51=0&L52=0&L53=0&L54=11&L55=9&L56=15&L57=16&L58=8&L59=10&L60=10&L61=8&L62=0&L63=10&L64=0&L65=23&L66=0&L67=10&L68=12&L69=12&L70=0&L71=8&L72=0&L73=20&L74=12&L75=11&L76=13&L77=11&L78=11&L79=12&L80=12&L81=0&L82=0&L83=0&L84=0&L85=0&L86=0&L87=0&L88=0&L89=0&L90=0&L91=0&L92=0&L93=0&L94=0&L95=0&L96=0&L97=0&L98=0&L99=0&min_markers=38&mismatches_max=0&mismatch_type=sliding&mismatches_sliding_starting_marker=33&haplo=&region=
```

Number	Marker	% of L21	Macro ID	
Markers 1 to 37				
L1	393=13	93	L21 Baseline	N
L2	390			N
L3	19=14	91	L21 Baseline	N
L4	19b			Exception
L5	391			N+1
L6	385a=11	90	L21 Baseline	N+1
L7	385b			N+1
L8	426=12	98	L21 Baseline	N+1
L9	388=12	97	L21 Baseline	N+1
L10	439			N+1
L11	389-1=13	82	L21 Baseline	N+1
L12	392=13	77	L21 Baseline	N+1
L13	389-2			N+1
L14	458			N+1
L15	459a=9	89	L21 Baseline	N+1
L16	459b			N+1
L17	455=11	95	L21 Baseline	N+1
L18	454=11	96	L21 Baseline	N+1
L19	447			N+1
L20	437=15	88	L21 Baseline	N+1
L21	448			N+1
L22	449			N+1
L23	464a=15	79	L21 Baseline	N+1
L24	464b			N+1
L25	464c			N+1
L26	464d=17	77	L21 Baseline	N+1
L27	464e			Exception
L28	464f			Exception
L29	464g			Exception
L30	460			N+4

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L31	GATA-H4			N+4
L32	YCAIIa=19	91	L21 Baseline	N+4
L33	YCAIIb=23	78	L21 Baseline	N+4
L34	456			N+4
L35	607			N+4
L36	576			N+4
L37	570			N+4
L38	CDYa			N+4
L39	CDYb			N+4
L40	442			N+4
L41	438=12	90	L21 Baseline	N+4

Note: Markers 1 to 37 are very consistent, however, they include 19b, 464e, 464f and 464g (4 additional marker values).

Markers 38 to 67

L42	425=12	94	L21 Baseline	N-6
L43	461	NA		(68+)
L44	462	NA		(68+)
L45	GATA-A10	NA		(68+)
L46	635	NA		(68+)
L47	GAAT-1B07	NA		(68+)
L48	441	NA		(68+)
L49	444	NA		N-8
L50	445	NA		(68+)
L51	446	NA		N-9
L52	452	NA		(68+)
L53	463	NA		(68+)
L54	531=11	88	L21 Baseline	N+16
L55	578=9	98	L21 Baseline	N+16
L56	395S1a=15	94	L21 Baseline	N+16
L57	395S1b=16	98	L21 Baseline	N+16
L58	590=8	98	L21 Baseline	N+16
L59	537=10	96	L21 Baseline	N+16
L60	641=10	98	L21 Baseline	N+16
L61	472=8	100	L21 Baseline	N+16
L62	406S1	NA		N+16
L63	511=10	87	L21 Baseline	N+16
L64	413a	NA		N+15
L65	413b=23	90	L21 Baseline	N+15
L66	557	NA		N+15
L67	594=10	99	L21 Baseline	N+15
L68	436=12	99	L21 Baseline	N+15
L69	490=12	99	L21 Baseline	N+15
L70	534	NA		N+15
L71	450=8	98	L21 Baseline	N+15
L72	481	NA		N+14
L73	520=20	88	L21 Baseline	N+14
L74	617=12	78	L21 Baseline	N+13
L75	568=11	98	L21 Baseline	N+13

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L76	487=13	94	L21 Baseline	N+13
L77	572=11	88	L21 Baseline	N+13
L78	640=11	89	L21 Baseline	N+13
L79	492=12	98	L21 Baseline	N+13
L80	565=12	89	L21 Baseline	N+13
L81	434	NA		(68+)
L82	435	NA		(68+)
L83	485	NA		(68+)
L84	494	NA		(68+)
L85	495	NA		(68+)
L86	505	NA		(68+)
L87	522	NA		(68+)
L88	533	NA		(68+)
L89	549	NA		(68+)
L90	556	NA		(68+)
L91	575	NA		(68+)
L92	589	NA		(68+)
L93	636	NA		(68+)
L94	638	NA		(68+)
L95	643	NA		(68+)
L96	714	NA		(68+)
L97	716	NA		(68+)
L98	717	NA		(68+)
L99	726	NA		(68+)

Note: CDYa and CDYb are always excluded from all searches as the mutation rates of these markers are so much faster than all other markers that they are not reliable for searches.

Note: 389-1 and 389-2 are difficult to analyze since mutations in 389-1 can show up redundantly as false hits in 389-2. Adjustments are made due to this unique issue.

After the setup and execution of the 67 marker search, another 37 marker search is very easy to conduct by just turning off marker values for markers 38 to 67.

111 marker searches are currently not supported in Y-Search due to the 99 marker limitation of Y-Search. Additionally, for the smaller breadth Y-SNPs being analyzed, it is not very common to find enough 111 markers submissions to analyze for these smaller SNPs.

The DNA fingerprint (L21 off modal mutations) are based on the MRCA haplotype for all known submissions that test positive for the SNP - not just the WTY submission. As more positive results are found, the DNA fingerprint will change over time.

Genetic Distance only includes one mutation for each marker. Multiple step mutations are counted only as one mutation which is consistent with MRCA calculator methodology.

For most Y-SNPs that are not widely tested, it is assumed that a 70 % match of the DNA fingerprint warrants testing. This percentage could be adjusted in either direction as testing reveals the actual breadth of each Y-SNP.

In order to reduce false hits and maximize positive hits, many "baseline" values are

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added for L21. All markers that have over 75 % of the same marker value are included in this baseline. When adding off modal mutations that are specific to the Y-SNP, it may be required to override the existing baseline value with the off modal value.

The URL macro must be one line in order to function properly. Notepad and Wordpad tend to turn on and turn off word wrap at random times. If the URL is multiple lines, just turn off word wrap and will correct the URL to one line.

Baseline percentages are derived from Mike Walsh's L21 spreadsheet. A total of 16 baseline markers are included in markers 1 to 37 and another 23 markers are included from markers 38 to 67. This reduces false hits from improper haplogroups to less than five percent of matches found and usually catches around 90 % of submissions found in surname project lists.

Comments for enhancing the accuracy of the Y-Search baseline and DNA fingerprint methodology are always welcome. Improving the format the spreadsheets are also welcomed, however, these spreadsheets must remain somewhat simple in order to cover the maximum number of SNPs.

Below is a summary of markers included in the L21 baseline:

Markers 1 to 37

1)	426=12	98	L8
2)	388=12	97	L9
3)	454=11	96	L18
4)	455=11	95	L17
5)	393=13	93	L1
6)	19=14	91	L3
7)	YCAIIa=19	91	L32
8)	385a=11	90	L6
9)	438=12	90	L41
10)	459a=9	89	L15
11)	437=15	88	L20
12)	389-1=13 82		L11
13)	464a=15	79	L23
14)	YCAIIb=23	78	L33
15)	392=13	77	L12
16)	464d=17	77	L26

Markers 38 to 67

1)	472=8	100	L52
2)	436=12	99	L59
3)	490=12	99	L60
4)	594=10	99	L58
5)	492=12	98	L70
6)	578=9	98	L46
7)	395S1b=16	98	L48
8)	590=8	98	L49
9)	641=10	98	L51

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10)	450=8	98	L62
11)	568=11	98	L66
12)	537=10	96	L50
13)	395S1a=15	94	L47
14)	425=12	94	L42
15)	487=13	94	L67
16)	413b=23	90	L56
17)	640=11	89	L69
18)	565=12	89	L71
19)	531=11	88	L45
20)	520=20	88	L64
21)	572=11	88	L68
22)	511=10	87	L54
23)	617=12	78	L65

Sample search for L96 (10/18/2011):

http://www.ysearch.org/search_search.asp?fail=2&uid=&freeentry=true&L1=13&L2=0&L3=14&L4=0&L5=10&L6=11&L7=0&L8=12&L9=12&L10=0&L11=13&L12=13&L13=28&L14=0&L15=9&L16=0&L17=11&L18=11&L19=24&L20=15&L21=0&L22=29&L23=15&L24=0&L25=0&L26=17&L27=0&L28=0&L29=0&L30=0&L31=0&L32=18&L33=23&L34=0&L35=0&L36=19&L37=19&L38=0&L39=0&L40=0&L41=12&L42=12&L43=0&L44=0&L45=0&L46=0&L47=0&L48=0&L49=0&L50=0&L51=0&L52=0&L53=0&L54=11&L55=9&L56=15&L57=16&L58=8&L59=11&L60=10&L61=8&L62=0&L63=10&L64=0&L65=23&L66=17&L67=10&L68=12&L69=12&L70=0&L71=8&L72=23&L73=21&L74=12&L75=11&L76=13&L77=11&L78=11&L79=12&L80=12&L81=0&L82=0&L83=0&L84=0&L85=0&L86=0&L87=0&L88=0&L89=0&L90=0&L91=0&L92=0&L93=0&L94=0&L95=0&L96=0&L97=0&L98=0&L99=0&min_markers=38&mismatches_max=0&mismatch_type=sliding&mismatches_sliding_starting_marker=3&haplo=®ion=

Sample search for L144 (11/1/2011):

[Sample search for L371 \(11/3/2011\):](http://www.ysearch.org/search_search.asp?fail=2&uid=&freeentry=true&L1=13&L2=0&L3=14&L4=0&L5=10&L6=11&L7=0&L8=12&L9=12&L10=0&L11=13&L12=13&L13=0&L14=0&L15=9&L16=0&L17=11&L18=11&L19=0&L20=15&L21=0&L22=0&L23=15&L24=0&L25=16&L26=17&L27=0&L28=0&L29=0&L30=0&L31=0&L32=19&L33=23&L34=0&L35=0&L36=17&L37=18&L38=0&L39=0&L40=0&L41=12&L42=12&L43=0&L44=0&L45=0&L46=0&L47=0&L48=0&L49=0&L50=0&L51=12&L52=0&L53=0&L54=11&L55=10&L56=15&L57=16&L58=8&L59=10&L60=10&L61=8&L62=0&L63=10&L64=16&L65=23&L66=0&L67=10&L68=12&L69=12&L70=0&L71=8&L72=0&L73=20&L74=10&L75=11&L76=13&L77=11&L78=11&L79=12&L80=12&L81=0&L82=0&L83=0&L84=0&L85=0&L86=0&L87=0&L88=0&L89=0&L90=0&L91=0&L92=0&L93=0&L94=0&L95=0&L96=0&L97=0&L98=0&L99=0&min_markers=38&mismatches_max=0&mismatch_type=sliding&mismatches_sliding_starting_marker=33&haplo=®ion=</p>
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http://www.ysearch.org/search_search.asp?fail=2&uid=&freeentry=true&L1=13&L2=0&L3=14&L4=0&L5=0&L6

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=12&L7=0&L8=12&L9=12&L10=0&L11=13&L12=13&L13=0&L14=0&L15=9&L16=0&L17=11&L18=11&L19=0&L20=15&L21=17&L22=0&L23=15&L24=0&L25=0&L26=17&L27=0&L28=0&L29=0&L30=0&L31=0&L32=19&L33=23&L34=14&L35=0&L36=17&L37=0&L38=0&L39=0&L40=0&L41=12&L42=12&L43=0&L44=0&L45=0&L46=0&L47=0&L48=0&L49=0&L50=0&L51=0&L52=0&L53=0&L54=11&L55=9&L56=16&L57=16&L58=8&L59=10&L60=10&L61=8&L62=0&L63=10&L64=22&L65=23&L66=0&L67=10&L68=12&L69=12&L70=16&L71=10&L72=23&L73=20&L74=13&L75=11&L76=13&L77=11&L78=11&L79=12&L80=12&L81=0&L82=0&L83=0&L84=0&L85=0&L86=0&L87=0&L88=0&L89=0&L90=0&L91=0&L92=0&L93=0&L94=0&L95=0&L96=0&L97=0&L98=0&L99=0&min_markers=38&mismatches_max=0&mismatch_type=sliding&mismatches_sliding_starting_marker=33&haplo=®ion=