Kit Number	Name (example)																																						
1000	Able	13	25	14	11	11	13	12	12	12	14	14	29	18	9	10	11	11	25	15	18	30	15	16	17	17	11	11	19	23	17	16	21	18	37	41	12	12
2000	Baker	13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	16	11	11	19	24	17	16	19	17	37	40	13	12
3000	Charlie	13	26	14	11	11	13	12	12	12	13	14	29	18	9	10	11	11	24	15	18	30	16	16	16	17	11	13	19	23	16	16	18	18	38	41	12	12
5000	Dog	13	24	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	17	12	11	19	23	16	16	18	17	38	39	12	12
2567	Easy	13	25	14	11	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	30	15	16	16	16	11	11	19	23	16	16	18	17	40	40	12	12
etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc	etc

CHECK LIST

I suggest you form a separate Excel file, not just enter values on this file.
I prefer an Excel file ==> .xlsx, NOT .xls.

The current code I use, written by Fred Schwab, can produce RCC trees and matrices of any number of DYS values, but the marker lengths must all be the same for each RCC tree and RCC matrix.
    You can send me results that mix marker lengths, and I can separate them into individual runs here.
In the template, Row 1 shows the DYS values for all 111 markers. For each haplotype, beginning in Column C, insert marker values to the right in the exact same sequence that FTDNA reports them.
Put haplotype strings in Columns C to AM for 37 marker entries, Columns C to BQ for 67 marker entries, and Columns C to DI for 111 marker entries. Make sure they are numbers, not text.
Insert testee results in rows down the page. The order of the haplotypes does not matter.
Do not include anything in rows UNDER the last row of haplotypes you insert into the spreadsheet.
Insert up to 500-600 testee results, row by row. Sometimes the program can take ~ 2000 entries.
Put Kit No in Column A. Put any other indicator in Column B. TRY TO KEEP COLUMN B AS SHORT AS POSSIBLE.
The columns to the right of the column that contains the last marker entry are not used by the program. You are encouraged to further identify the haplotypes by inserting other information there.
    Make liberal use of the columns to the right of the last marker so that all the data will be on one spreadsheet. You or I can decide which info will go into Column B.
    Suggestions include: Testee name, earliest known ancestor, country of origin, haplotype, SNP designation, FTDNA or administrator group designation, your own identification, comments

Be sure your entries are all numbers and not text. If they are text they will show a little triangle in the upper left side of the entry. Be sure only numbers are in the Excel sheet.
The RCC time scale was calibrated using 37 markers. When other marker lengths are analyzed, the organization of the haplotypes in the tree will be valid, but the time-equivalent of the RCC scale will
    If marker lengths are not the same on the haplotypes you send, I will separate them into equal marker lengths which must be the same for each run.

Don't enter rows that are not haplotypes. When you are finished, the entries in the columns and rows to be analyzed should look like a number matrix.
Make sure that there are no null or zero entries anywhere in the marker value entries you send.
Insert the marker values in the same order as FTDNA reports them. Do NOT rearrange the multimarker values like 464. Do not include 464e or 464f if they are reported. Merely erase them.
    In the case of DYS 464 where there are markers a, b, c, d, and sometimes e and f, use only markers a through d. Do not reorder them.
Please also check and be sure that the values in the DYS column marked in yellow, above, are in the high range, not the lower values that are sometimes reported.
Check to see that all hyperlink references are omitted.
In your version of Excel that develops the worksheet that you will sending me, be sure that the Workbook calculation option should be set to Automatic, not to Manual. On my Mac, it is found in Prefere