

What Is This DNA Stuff and Why Should I Care?

Part 8: Using GedMatch to Find Additional Autosomal DNA Cousin Matches

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So, you've read about DNA testing and decided to take an autosomal DNA (atDNA) test from one of the major testing companies. After researching the companies, you order the test, send in your sample, wait anxiously for the results, and then start receiving your cousin matches. Perhaps you find some interesting new information about several new cousins, but you didn't identify as many potential people as you had hoped. Now what? There are two options to help identify additional cousin matches: 1) upload your raw DNA data to another testing company and look for potential matches on their website using their tools, and 2) upload your raw DNA to GedMatch and use the tools they provide to search for additional matches. Both options will potentially identify new matches. I will briefly discuss the first option, but most of the article will focus on the second option.

All the companies allow export of your raw DNA data files, but as shown in **Table 1**, only FTDNA, MyHeritage, and Living DNA support the upload of the other company's DNA files to their website. This allows test takers to look for additional cousin matches without having to pay for new tests. Furthermore, only some versions of those tests are supported depending on which bead chip version the testing company used for your analysis. The chip version used for your DNA analysis is usually found near the top of your raw DNA data file. Although FTDNA, MyHeritage, and Living DNA offer free DNA data uploads and free cousin matching, they do charge a small fee (\$19 for FTDNA and Living DNA; \$29 for MyHeritage) to use some of their more advanced tools such as the chromosome browser or to get your complete ethnicity estimate. However, this is still a good deal as it allows you to cast a wider net and find more potential cousins.

		DNA Can Be Imported By This Company					
		Ancestry	FTDNA	MyHeritage	23&Me	LivingDNA	GedMatch
DNA Exported from this Company	Ancestry	-	Y	Y	N	Y	Y
	FTDNA	N	-	Y	N	Y	Y
	MyHeritage	N	Y	-	N	Y	Y
	23&Me	N	Y	Y (v5 only)	-	Y	Y
	LivingDNA	N	N	Y	N	-	Y

Table 1. Comparison of the Five Leading DNA Testing Companies: Raw DNA Upload

Source: Autosomal DNA testing comparison chart: https://isogg.org/wiki/Autosomal_DNA_testing_comparison_chart (International Society of Genetic Genealogy) and the DNA Testing Companies Websites

You may be wondering, since the testing companies use their own customized microarray bead chips and they have also used different versions of the chips over time, how reliable are the comparisons between companies and different bead chip versions? This is a valid concern and the comparison between the testing companies and their two most recent bead chip versions are shown in Table 2. The table contains a great deal of information that is summarized from the Autosomal SNP Comparison Chart found

on the International Society of Genetic Genealogy (ISOGG) website. The blue column headings identify the testing company and bead chip version used. The blue row headings show the testing company and chip version the be compared with. The orange diagonal is where the column and row represent the same testing company. The bold numbers running down along the orange diagonal are the number of autosomal SNPs tested on each company's chip. For example, in the upper left-hand corner, the 23andMe chip version 4 (v4) tested 585,327 SNPs for their autosomal test.

The numbers in yellow cells in the upper half of the table are the number of SNPs that each testing company (and chip version) share between them. For example, looking at the column heading for FTDNA v2 chip and comparing how many of their SNPs are also tested by the Ancestry v1 chip (along the row), gives a value of 207,661. In other words, of the 610,832 autosomal SNPs tested on the FTDNA chip, only 207,661 are also tested by the Ancestry v1 chip. The corresponding percentage is found in the lower half of the table in the rose-colored cells by comparing the FTDNA v2 row with the Ancestry v1 column which gives a value of 34.0% shared SNPs. Although only 34.0% of the SNPs are shared, the length of shared DNA strands between cousins is often very large, over 10 million base pairs even for 4th-6th cousins which still leads to a valid comparison. However, a higher percentage of shared SNPs between different company's tests does lead to a more robust comparison. This is the case whether comparing an Ancestry test uploaded to MyHeritage or between tests from different companies uploaded to GedMatch.

Shared Autosomal SNPs	23andMe v4	23andMe v5	Ancestry v1	Ancestry v2	FTDNA v1	FTDNA v2	LivnigDNA v1	LivingDNA v2	MyHeritage v1	MyHeritage v2
23andMe v4	585,327	108,248	300,373	300,923	305,626	137,380	108,786	254,074	304,948	134,750
23andMe v5	17.6%	613,462	159,881	155,163	162,100	538,746	585,639	394,732	161,529	504,668
Ancestry v1	44.0%	23.4%	682,549	426,760	680,544	207,661	163,476	282,607	676,049	204,740
Ancestry v2	47.2%	24.4%	24.4%	636,942	432,423	191,769	156,931	267,813	431,431	185,754
FTDNA v1	43.2%	22.9%	96.2%	61.1%	707,254	212,252	165,742	284,132	702,440	208,221
FTDNA v2	22.5%	88.2%	34.0%	31.4%	34.7%	610,832	541,654	385,521	211,907	561,788
LivingDNA v1	18.0%	97.1%	27.1%	26.0%	27.5%	89.8%	603,129	401,315	165,159	508,732
LivingDNA v2	37.2%	57.8%	41.3%	39.2%	41.6%	56.4%	58.7%	683,503	283,253	386,023
MyHeritage v1	43.4%	23.0%	96.2%	61.4%	99.9%	30.2%	23.5%	40.3%	702,442	207,848
MyHeritage v2	23.4%	87.5%	35.5%	32.2%	36.1%	97.4%	88.2%	66.9%	36.0%	576,690

Table 1. Shared Autosomal SNP Comparison Chart Between the Various Testing Companies and the Bead Chip Versions Used (Values in yellow and orange cells are expressed in Thousands of SNPs; values in red cells are expressed as percentages)
 Source: Autosomal SNP Comparison Chart: https://isogg.org/wiki/Autosomal_SNP_comparison_chart
 (International Society of Genetic Genealogy); Rounded SNP numbers and percentages determined by the author.

To give you an analogy, suppose there is a picture on a wall that has a resolution of 3 billion pixels, and this picture represents the human genome, all 3 billion base pairs along the DNA stands. If you could see all the pixels in the picture, then you would have a very complete picture. Now imagine the light in the room is turned off and you are given about 700 thousand tiny flashlights to shine on the entire picture, one flashlight per pixel. This would represent only 0.023% of the 3 billion pixels but they shine enough light to recognize the picture. These tiny flashlights represent the SNPs the testing companies measure when you take an autosomal DNA test. Although you cannot see the entire picture in detail, you can get some idea about what the picture looks like, albeit at a much lower resolution. Now suppose a friend of yours is given 600 thousand tiny flashlights. When she turns these on, some of these will shine on the same pixels as yours did and some will shine on different pixels. Her tiny flashlights

represent the SNPs tested by another testing company. She will get a similar idea about what the actual picture looks like. Both are correct even though slightly different from each other; however, the strength of your comparison will improve the more your flashlights shine on the same pixels.

The second method to find additional cousin matches is to use GedMatch.com. GedMatch is a third-party website designed specifically to compare autosomal results from different testing companies. Before using GedMatch you first need to download your raw DNA file from the company website where you tested. For Ancestry, go to the DNA tab, select Your DNA Results Summary, and then select Settings. Scroll down to the bottom of the page under Test Management>Actions and download the DNA zip file to your computer. For MyHeritage, hover over the DNA tab and then select Manage DNA Kits. On the right side of the page, click on the 3 vertical dots and then select Download Kit to download a txt file. For 23andMe, at the far right of the Home page, select the up carrot next to your name and then select Browse Raw Data. Near the top of the page select Download, read the necessary information, click the I Understand... box, and then select Submit. An email with a link to the DNA txt file will be sent to you when the results are ready. For FTDNA, hover over the Results & Tools tab and then Autosomal DNA and select Download Raw DNA. Download the Build 37 Autosomal Raw Data (GZIP,CSV) file. And finally, for Living DNA, on the main dashboard page, select Profiles on the left-hand side and select the download icon (a down arrow above a horizontal bracket). Click the consent box and download the Family Ancestry file. If you have any problems with the raw data downloads use Google or YouTube to search for directions.

When you first sign into GedMatch (www.gedmatch.com) you have the choice to sign into the Classic version or the New version. The New version is much more user friendly, looks much more like the major genealogy websites, and is easier to navigate so I would highly recommend signing into this version. All the screen shots used in this article are from the New version. After signing in you will need to register with a User ID and password. Once registered, the first task is to upload the raw data file that you previously downloaded. GedMatch can open the txt file, zip file, or Gzip file directly, so you do not need to unzip any of the files before uploading. On the GedMatch Home page, select Upload DNA on the upper tab list. Enter the information Donor Name, Alias (optional), Haplogroup (optional if known from another test), Testing Company your data comes from, Sex (M or F), Raw Data Type (typically Your DNA), your Privacy Options, and then navigate to the location of your downloaded DNA file and select Upload. This may take up to 10 minutes to upload and you may see little or no activity while it does. Once uploaded, the Home page will now show your profile information along with your assigned DNA kit number under the Your DNA Resources heading. GedMatch now needs to compare your information with all the other people in its database and this can take 1-2 days. Once the comparison is complete, they will send an email informing you that you can now log onto GedMatch to look for new cousin matches. There is one more item to complete before you begin using GedMatch - uploading a gedcom file of your ancestors to the website, just like you have hopefully done on the testing company's website. This will help you identify how your DNA matches are related to you, assuming your matches have also uploaded gedcom files of their ancestors. Hover over the Family Trees tab and then select Upload GEDCOM (Fast) and follow the instructions. If you have a very large family tree you may need to split the gedcom file and then use Upload GEDCOM (Alternate) instead.

GedMatch offers a set of limited Free Tools and a fully functional set of Tier 1 Tools that can be used to analyze your data and compare it with other people's results. The free tools will show your cousin matches, but you will not be able to use any of the visualization and advanced analysis tools without a subscription. The Tier 1 tools cost \$10/month or \$100/year for a subscription. If you start with the Free Tools, hovering over the tab at the top of the Home page will show a drop down menu with the following headings, *One-to-Many - Limited Version, One-to-One Autosomal, One-to-One X, Admixture (heritage), Admixture/Oracle, Match Both or 1 of 2, DNA File Diagnostics, Are Your Parents Related, 3D Chromosome Browser, Archaic DNA Matches, and Ancestor Projects.*

A brief explanation of these free tools follows. The *One-to-Many - Limited Version* is the same as your cousin matches from the testing companies. The *One-to-One Autosomal* compares your information to one other person's autosomal DNA and the *One-to-One X* compares your X-DNA information to one other person's X-DNA. The *Admixture (heritage)* and *Admixture/Oracle* are like the Ethnicity Estimate given by the testing companies, but there are multiple possible models to choose from and I find them confusing. The *Match Both or 1 of 2* tool is the same as finding shared matches between you and another person on the testing company's websites. *File Diagnostics* just gives you some information about your uploaded DNA file. *Are Your Parents Related* does an analysis of your DNA to see if there is any familial relationship between your parents, i.e., were your parents first or second cousins or similarly related. The *3D Chromosome Browser* is like the chromosome browser at 23andMe, MyHeritage, and FTDNA but in 3D. Personally, I find this 3D view more confusing than the standard 2D view. The *Archaic DNA Matches* compares your DNA to a collection of ancient DNA from fossilized remains found across the world. And finally, the *Ancestor Projects* are a list of the available ancestor projects you can join based on regions of the world. Personally, I find the *One-to-Many - Limited Version* and *Match Both or 1 of 2* to be the most useful of these free tools. A more detailed description of these two tools is given below.

One-to-Many - Limited Version: After selecting the *One-to-Many - Limited Version* tool from the drop-down menu, you will need to enter your kit number. Every person who uploaded their DNA to GedMatch is given a unique kit number and every tool in GedMatch is based on these kit numbers. This can be copied from the home page and pasted into the box. There are also some filters which you can also select. I usually leave these as the defaults, but I do increase the match Limit to 500 individuals and increase the shared centimorgan Size to 10 cM which gives me the most relevant matches. Figure 1 shows a screen shot of the *One-to-Many - Limited Version* showing my first 12 cousin matches in order of decreasing centimorgans (cM).

Select	Kit	Name (* => alias)	Email	GED WikiTree	Age(days)	Type	Sex	Mt	Y	Total cM	Largest	Gen	X-DNA Total cM	X-DNA Largest	Source	Overlap
<input type="checkbox"/>	DY5437351	Marguerite Anne Adams (n)	grayed out		795	2	F			216.5	59.7	3.03	0	0	FTDNA	315044
<input type="checkbox"/>	A350873	*BevArk	grayed out		1394	2	F			79.5	28.2	3.75	0	0	Migration - F2 - A	183874
<input type="checkbox"/>	A843754	F. L. Powell	grayed out		1843	2	F	I4a1		53	35.4	4.04	0	0	Migration - F2 - A	304596
<input type="checkbox"/>	A215694	Colleen Myers	grayed out		2183	2	F			52.5	37.6	4.05	0	0	Migration - F2 - A	305261
<input type="checkbox"/>	A458080	*MapleSugar	grayed out		1192	2	F			48.8	30	4.10	0	0	Migration - F2 - A	181414
<input type="checkbox"/>	FP2260895	*Genesee19	grayed out		797	2	M			48	38	4.11	0	0	23andMe	72671
<input type="checkbox"/>	H952654	*Tiffany Walker Martin B	grayed out		1454	2	F			45.6	35.6	4.15	0	0	Migration - F2 - H	306629
<input type="checkbox"/>	A757381	Donald P Schwert	grayed out		1744	2	M			44.6	36.7	4.16	0	0	Migration - F2 - A	302950
<input type="checkbox"/>	A950936	Cathy Joy Guinn	grayed out		2281	2	F			43.4	25.5	4.18	0	0	Migration - F2 - A	304938
<input type="checkbox"/>	RA9008468	*JLC	grayed out		1109	2	F	J2b1		40.4	24	4.24	0	0	23andMe	72265
<input type="checkbox"/>	KU8778022	*Thomas S	grayed out		569	2	M	H1n	R-5660	39.8	18.4	4.25	0	0	23andMe	73373
<input type="checkbox"/>	A837158	*CJW	grayed out		1200	2	F			39.7	22.5	4.25	0	0	Migration - F2 - A	302854

Figure 1. A view of the *One-to-Many - Limited Version* tool showing the first twelve cousin matches for the author. The emails in the 4th column have been grayed out for privacy concerns. Source: www.GedMatch.com

The first column, Select, is grayed out and is only available in the advanced subscription-based Tier 1 Tools. I will discuss these a little later. The second column of blue numbers contain the kit numbers of people matching you. The closer to the top of the page, the closer the cousin match. The third column

contains the name or User ID of the match and the fourth column a corresponding email, which for this article has been grayed out for privacy concerns. The Age(days) column show how many days since that individual uploaded their DNA to GedMatch. Sex is of course the whether the person is male of female. The Haplogroup information (Mt and Y) is only displayed if the individual tested for this separately and manually entered the information when they first registered. As you can see from the figure, most people have not entered this information. Under Autosomal, the Total cM and Largest are the amount of DNA and longest region of matching DNA between you and your match and the Gen column is a calculation of the closeness of the match. A value of 3.00 would indicate a common great grandparent and a value of 4.00 would indicate a common great great-grandparent. This is the same as a label of 3rd or 4th cousin estimated by the major testing companies. The X-DNA columns show any matches to your X-DNA as well. Since the X-DNA has a unique inheritance pattern, which limits who can contribute to your DNA, this will help narrow down how you may be related to a match. The Source is the testing company each matching person used. You should specifically look for new matches from people who uploaded their information from a different testing company than you used because you will already find their information on the website of the company you tested with. In other words, if you tested at Ancestry, you would specifically want to look for the people who tested at 23andMe, FTDNA, MyHeritage, or Living DNA not at Ancestry because you can just go to Ancestry website to see those matches. Finally, the Overlap is the number of SNPs that are being used to compare the two kits. The larger the number of SNPs, the better. If cell is white with black text, that indicates a good comparison. If the cell color is pink or red, the shared match is not as good a comparison. The reason for this was explained in the first half of this article which discussed the number shared SNPs between each company's testing method.

Match Both or 1 of 2: The *Match Both or 1 of 2* tool allows you to compare two different kits and see who matches with both kits. It is the same as the Shared Matches from the testing companies. After selecting the *Match Both or 1 of 2* tool, you will need to enter two different kit numbers. Most likely this will be your kit number and one of your close match's kit numbers. When I select my kit number and the first match from the One-to-Many Tool, I get the information shown in Figure 2.

Kit 1: QW9004439 (David Neithamer)
 Kit 2: DY5437351 (Marguerite Anne Adams (née Sharpe))
 Found 334 matches that match both kit QW9004439 and kit DY5437351.

Select 3 or more from '✓' column, and click this button for additional display and processing options.

Match	✓	Name	QW9004439			DY5437351			Generations Difference	Ged/Wiki	Email
			Shared	Largest	Gen	Shared	Largest	Gen			
A458080	<input type="checkbox"/>	*MapleSugar	48.8	30.0	4.1	82.9	33.7	3.7	0.4		maplesugartart@gmail.com
A839105	<input type="checkbox"/>	*ElizabethPH	31.2	22.8	4.4	28.0	28.0	4.5	0.1	GED	lizhenberry@gmail.com
RU8903879	<input type="checkbox"/>	*Eleonora	30.3	22.2	4.4	25.0	25.0	4.6	0.1		familypieces372@gmail.com
TV5303976	<input type="checkbox"/>	Tammy Fox	28.9	28.9	4.5	32.0	32.0	4.4	0.1		tamfox0410@gmail.com
UN3943374	<input type="checkbox"/>	Elizabeth Henderson	28.7	10.4	4.5	12.4	12.4	5.1	0.6		libbyt54@gmail.com
A434681	<input type="checkbox"/>	*JCasey	26.4	18.5	4.5	10.3	10.3	5.2	0.7		jamilahcasey71@gmail.com
M107454	<input type="checkbox"/>	*DBliss	26.3	26.3	4.5	26.3	26.3	4.5	0.0		blucker@aol.com
RL3222974	<input type="checkbox"/>	Vincenzo Martina	26.0	26.0	4.6	29.8	29.8	4.5	0.1		bitenbytes81@hotmail.com
G195832	<input type="checkbox"/>	*MWhitebread	25.0	13.7	4.6	12.3	12.3	5.1	0.5		nichelwhitebread@yahoo.com
A358830	<input type="checkbox"/>	*DSize3018	24.8	17.1	4.6	25.8	18.4	4.6	0.0		rx033@yahoo.com
M109170	<input type="checkbox"/>	Liza Derk	24.4	24.4	4.6	32.4	32.4	4.4	0.2	Wiki	elizabethderkac2@gmail.com
DB9881475	<input type="checkbox"/>	*Scott B	23.4	23.4	4.6	23.4	23.4	4.6	0.0		scottbeat@gmail.com

Figure 2. Match Both or 1 of 2 tool showing the first twelve shared cousin matches between both of us. The emails in the last column have been grayed out for privacy concerns. Source: www.GedMatch.com

In the first column you will see the shared matches kit number and User ID name. Then you will see two sets of columns with Shared, Largest, and Gen for each kit number, the first kit (most likely yours) and the second one (one of your closet matches). These show the matching criteria used to match the shared match with each of the kits. The Generations Difference is the difference in the two Gen numbers and gives an indication of how closely related each match is to the shared match. Now that you have your closet matches from the *One-to-Many – Limited Version* tool and the shared matches from the *Match Both or 1 of 2* tool, the next course of action would be to compare your family trees (if they uploaded a gedcom file) or to contact these people by email and see if you can determine how you are related. However, if you choose to pay for the Tier 1 tools, you can do some more analysis which may help determine how you are related.

Hovering over the Tier 1 Tools tab at the top of the Home page will show a drop down menu with the following headings, *One-to-Many - Full Version*, *One-to-Many - Classic*, *Q Matching One-to-One*, *Segment Search*, *Phasing*, *Triangulation*, *AutoSegment*, *AutoKinship*, *Multiple Kit Analysis (MKA)*, *Lazarus*, *My Evil Twin*, *Combine Multiple Kits into 1 Super Kit*, *AutoTree Clustering*, *MRCA from DNA Matches*, and *Surname Matches from DNA Matches*.

The *One-to-Many - Full Version* is identical to the free *One-to-Many - Limited Version* tool, except that the first column, Select, (shown in Figure 1) is now active and the Visualization Options button at the top left is green and active. The *One-to-Many - Classic* is the same as the *One-to-Many - Full Version*, but without the final two columns, Source and Overlap. I suggest using the full version for your research. The *Q Matching One-to-One* tool is a comparison of your DNA with the DNA of a match, like other one-to-one tools, but with an algorithm to examine the quality of shared segments. The *Segment Search* tool is a search of your top matches for overlapping segments so you can research groups of matches that likely share most recent common ancestors (MRCA). The tool gives the beginning and ending segment locations, cM lengths, and the number of SNPs along each chromosome for your matches. The *Phasing* tool determines which of your DNA segments came from which of your parents. You will need to upload at least one of your parent's DNA to GedMatch to be able to use this tool, however, knowing which segments come from which parent will help narrow down how your cousin matches are related. The *Triangulation* tool is like the *Match Both or 1 of 2* free tool but is more advanced. It is used to confirm descent between 3 or more matches from a common ancestor and assign a specific segment of DNA to that ancestor, even if that ancestor has not yet been identified. There are several good tutorials on how to use this tool on YouTube. The *AutoSegment* tool is a newer tool that auto-clusters your matches to show how your different matches are related. This is basically an automated version of the *Triangulation* tool. Once the analysis is run, a .zip file will be sent to your email with the results. The *AutoKinship* tool predicts trees based on shared DNA between DNA matches from clusters identified by the AutoCluster tool. In addition, it also identifies common ancestors in shared genealogical trees from these matches and identifies segment clusters by triangulating segments using AutoSegment. Both the reconstructed trees from AutoTree and the segment clusters from AutoSegment are integrated into the AutoKinship reports.

The *Multiple Kit Analysis* tool does exactly what it says. It allows you to analyze multiple kits at one time and consists of five specific tools - Segment Search, Triangulation, a 2D Chromosome Browser, a 3D Chromosome Browser, and a Compact Segment Mapper. I will not go into this in depth here, but these are very powerful analysis tools. The *Lazarus* tool attempts to generate a DNA profile of a deceased person using the DNA from various descendant's DNA tests. The *My Evil Twin* tool is a way to take your kit, compare it with a parent, and create a phased kit of the DNA you didn't get. This isn't the most useful tool, but if you are curious about how each of your parents contributed to your DNA strands, you may find this interesting. *Combine Multiple Kits into 1 Super Kit* allows you to combine up to four uploaded kits in your account into one GEDmatch superkit. The defined reason to do this is to improve the accuracy of how you match with other GEDmatch users and to reduce false matches at the lower centimorgan ranges. I do not really understand this tool very well.

The last three Tier 1 tools are useful for matches that have also uploaded a gedcom file of their family tree. The *AutoTree Clustering* tool attempts to identify common ancestors and reconstruct family trees based on the uploaded trees of DNA matches. This will only be successful for closer DNA matches with extensive family trees. The *MRCA from DNA Matches* tool analyzes your DNA matches and provides a list of your matches with the most recent common ancestor (MRCA) for each match. Finally, the *Surname Matches from DNA Matches* tool automates the process of searching through family trees of your DNA matches to see if there are shared surnames or specific ancestors. These are all potentially very useful tools. Unfortunately, only about 15% of my matches have uploaded their family trees and in many cases the trees do not contain many individuals, so I have found this to be of limited use so far.

In addition to the Free Tools and the Tier 1 Tools, there is a Genealogy Comparisons/Searches tab which is available whether or not you have paid for the Tier 1 Tools. Opening this tab reveals five additional tools: *1 GEDCOM to All*, *2 GEDCOMS Comparison*, *Search All GEDCOMS*, *GEDCOM + DNA Matches*, and *Find GEDCOMS by Kit*. The *1 GEDCOM to All* tool compares any gedcom (based on a gedcom number which is assigned when it is first uploaded) to all the other uploaded gedcoms in the database which at the time of writing of this article was 153,100 gedcoms. The *2 GEDCOMS Comparison* tool does just that - it compares two uploaded gedcoms for common ancestors. The *Search All GEDCOMS* tool, searches all the uploaded gedcoms for a specific person with information about them and their parents. The *GEDCOM + DNA Matches* tool pulls together all your DNA matches who have also uploaded a gedcom file. Finally, *Find GEDCOMS by Kit* number will find any gedcom associated with a particular DNA kit number.

Since very good tutorials are available for each of these tools on YouTube and more extensive articles describing these have been written, I will not go into any further description here. There are some very powerful analysis tools available in GedMatch, beyond the typical tools seen on the testing company's websites. This alone should be a good reason to try GedMatch and specifically the Tier 1 tools. Unless you plan to do extensive research over many individuals, I would suggest paying monthly, as opposed to an annual subscription, particularly if this is your first time using it. If you find it particularly helpful you can upgrade at any time.

This concludes the series on DNA. Hopefully the 8 articles presented over the last two years have given you more information about the structure of DNA, the testing procedures used by the major testing companies, the different types of DNA tests available and how they are useful for your genealogical research, the differences between each major testing company, and finally how to find more cousin matches using GedMatch. I hope you have enjoyed reading these tutorials as much as I have enjoyed researching and presenting them to you. Due to space limitations, abridged versions of the articles have been printed in the AFAOA newsletters, but the full versions, with more detail, are available on the AFAOA website under the Austin DNA Project link under the sub-heading DNA Tutorial. If you have any questions about any of the DNA article topics, please contact me at database.chair@afaoa.org. I look forward to seeing you at an upcoming AFAOA conference. Until then, happy genealogical hunting!