

REFUTING NESTED HIERARCHIES AND HOMOLOGY AS EVIDENCE FOR COMMON ANCESTRY

CHAPTER THREE

THE NON-DISCRIMINATORY EVIDENCE

By Donny Budinsky

Featured in *The Endogenous Retrovirus Handbook*
(Dismantling the Best Evidence for Common Ancestry)

Defenders of evolution have boldly claimed that the existence of shared endogenous retroviruses between humans and chimpanzees provides irrefutable evidence for common descent. There is no question in their minds—endogenous retroviral sequences refute Biblical creation and separate ancestry.

The Endogenous Retrovirus Handbook: Dismantling the Best Evidence for Common Descent presents a compelling scientific case that the presence of shared ERV elements are no longer good evidence for common descent. The evolutionary community maintains that these intriguing genomic elements are the ancient remains of viral invasions over millions of years.

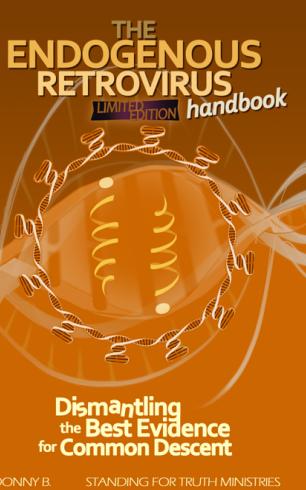
The author of the book, Donny, refutes ERVs as evidence for common descent by utilizing the highest quality arguments available. This was accomplished through a comprehensive investigation into the best evidence for evolution and common ancestry. Donny also presents directly from the scientific literature that the argument from ERVs has been invalidated. This handbook thoroughly counters the best arguments the critics have to offer and demonstrates overwhelmingly that ERV-like sequences should now be understood as designed units of DNA function.

DONNY ANSWERS QUESTIONS SUCH AS:

- What best explains why ERVs from different species are found in the same locations in the genomes of different organisms?
- Why do ERV elements resemble viral genetic material?
- What is the best explanation for the nested hierarchical distribution of endogenous retroviral elements?
- Can the separate ancestry model explain endogenous retroviruses better than common descent?

The amazing evidence presented in this must-read book has massive implications for the question of ancestry. The conclusions are underwhelming and they point us to common design rather than common descent.

THE ENDOGENOUS RETROVIRUS
LIMITED EDITION handbook



NESTED HIERARCHIES

It is obvious that God created the biological world hierarchically. We observe nested hierarchical patterns all throughout the living world. All we must do to see this is focus specifically on humans and chimpanzees. We as humans are far more like chimpanzees (and other great apes) than we are to dogs and fish. There is no doubting the fact that the creation order can be grouped into a hierarchy. Even though the Biblical model of ancestry (which I have written numerous books on that covers these topics in detail) would reject the notion that humans and chimpanzees are related—we should have no problem admitting that humans do share more with the chimpanzees than other creatures like cats and whales. Humans and chimpanzees would belong to different created kinds, and yet we find more in common with chimpanzees (when comparing humans) than with any other form of life. Every creature on this planet will have to be more like one creature than to another. This just comes down to classification systematics. The animals don't really care where you classify them—but we as humans like to classify things. We classify man-made things all the time, such as modes of transportation and tools.

Proponents of common descent point to the nesting patterns in life, and this includes the nested hierarchical pattern of distribution we find these ERV sequences fall into. Therefore, it is important that we deal with this argument here before we continue into the importance of DNA function when differentiating the two models, creation and evolution. Can these groups within groups patterns evolutionists point to as evidence for descent with modification only be explained by

the common descent model? As I mentioned in the above paragraph, nested hierarchies in DNA, anatomy, and physiology are also predicted by Biblical creationists based on the design model. The classification of life can be compared to the classification of modes of transportation on how different companies manufacture cars based on their similarities, which form hierarchies. Sedans are more like an SUV than they are to a tractor. And a sedan, SUV, and tractor are all more similar to each other than they are to a boat or an airplane. This is much like how humans are more like a chimpanzee than they are to a fish or a bird. It turns out that human designers build and design things in nested hierarchical patterns. It doesn't take long to see that groups within groups patterns also emerge in designed modes of transportation. Nested hierarchical patterns are simply a hallmark of design and reflective of God's hierarchical nature. God created life in hierarchical patterns in the same way we design things in these types of patterns.

Why wouldn't God create kinds of creatures in the beginning that are different from us as humans, and also create kinds of creatures that are more like us? Evolutionists miss the bigger picture. Yes, we can find hierarchies in all biological life, including humans and the great apes (taxonomists would categories humans as human apes and the other apes as non-human apes), but apes don't build airplanes, apes don't write books, apes don't start YouTube channels and host interviews with people from across the planet, and apes certainly don't compose symphonies. Chimpanzees and other animals don't do any of these things. Mankind has built the space shuttle and have accomplished many incredible wonders that animals simply don't have the capabilities of doing. An excerpt from a well-written technical article by Biblical

creationists (Dr. Nathaniel Jeanson and Dr. Jeffrey Tomkins) sums up this issue of nested hierarchies found in the biological world adequately:

However, it doesn't take much reflection to see that YEC and evolution make the same prediction about the relative genetic hierarchies found in nature. Under the YEC model, God designed the entire universe, including the various kinds of biological life that exist in it, and we would expect to find that life fits a design pattern. Since humans are made in God's image, we can get a sense for what kinds of design patterns God might have used by examining the patterns that result from human designs. Examples of nested hierarchies abound among the designed things in our world.

For example, designed means of transportation easily fit a relative hierarchical pattern. This fact is unequivocal. Sedans resemble SUVs more than they resemble tractor trailers, and all three vehicles have more in common than do sedans and amphibious assault vehicles. The latter two vehicles have more in common with one another than with submarines, and this simple pattern matches the type of hierarchy that we see in biology.²³

SOURCE: Jeanson, N. T., and J. P. Tomkins. 2016. "Genetics Confirms the Recent, Supernatural Creation of Adam and Eve." In *Searching for Adam: Genesis & the Truth About*

Man's Origin. Edited by T. Mortenson. Green Forest, Arkansas: Master Books.

<https://answersingenesis.org/adam-and-eve/genetics-confirms-recent-supernatural-creation-adam-and-eve/>

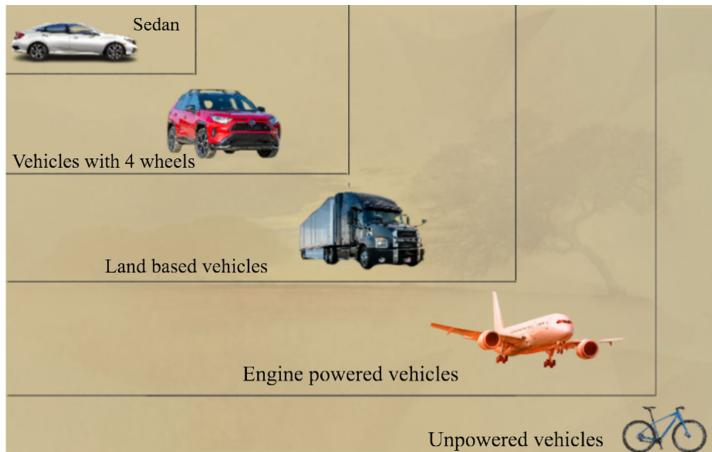


Image - The groups within groups patterns that emerge from examining the various modes of transportation man has designed

HOMOLOGOUS PATTERNS

The same thing is also true when it comes to homologous patterns (similarities between different creatures). Human designers also build in homologous patterns. Similarities in anatomy, morphology, physiology and genetics are not the best way to differentiate between the creation and evolution models. Shared ERV elements between various creatures are only convincing evidence for common descent if only evolution can explain this data. This also goes for the nested hierarchical

distribution of these unique DNA elements. The reader can probably already see where I am going with the information presented in this chapter—if ERVs are created units of DNA function, the similarities, and the nested hierarchical distribution of these DNA sequences become evidence for common design, as creationists have predicted. Let's deal with homology in greater detail before we move on. Dr. Nathaniel Jeanson explains in his book **“Replacing Darwin”** why homology is an agnostic (non-discriminatory) line of evidence to the greater debate of ancestry:

The biological phenomena that we've explored parallel the properties of family trees. But they also have strong parallels to another concept. In other words, a competing explanation exists for all the evidence we've just discussed. This competing explanation becomes clear with an example. For instance, humans have extended considerable effort for thousands of years in attempting to move themselves from one place to another—and at faster rates. In doing so, they have produced characteristic patterns in their designs.

Take the sedan as an example. Whether sedans are manufactured by automakers based in Asia, North America, or Europe, all share a common set of features (Figure 5.6). You won't find cars without wheels, engines, doors, or windshields. Despite the geographic distance separating their locations, sedans made by Honda, Chevrolet, and Mercedes have four

wheels, doors on the side, windshields in the front, brake lights in the back, and a host of other shared characteristics.

The reason for this similarity is not common ancestry. Honda, Chevys, and Mercedes did not evolve from a common sedan ancestor in the Arctic. Rather, because these cars were designed for similar functions, these purposes put constraints on the final product.

For example, when the purpose is transportation of several individuals and their luggage, four wheels are superior to either three or five.* Conversely, without windshields in the front, the passengers would be accosted with an unending attack of bugs and debris when traveling at high speeds. In addition, climbing into these cars from the top is challenging. Having doors on the side makes entry and exit far easier. Thus, human designers naturally produce similar patterns—due to shared functional purposes, not common ancestry.

SOURCE: Replacing Darwin (The New Origin of Species), Chapter 5, Pages 135-136. Dr. Nathaniel T. Jeanson

As has been demonstrated, Biblical creationists and Intelligent Design advocates would expect a human and a chimpanzee to be more like each other in overall similarity than if we were comparing a human and a fish. Even before we had genetic sequencing capabilities, you could easily stand back, and based merely on the outward appearance, expect

greater similarity in terms of genetics with a human and a chimpanzee, than between a human and another form of life.

Humans must be more similar to some creatures, and less similar to other creatures, in the same way sedans have to be more similar to some vehicles and less similar to others. Even if chimpanzees and bonobos did not exist—we would still be more similar to a particular animal than to other animals. If chimpanzees and bonobos did not exist—we would be most similar to a gorilla. And if none of the great apes existed, we would still be most similar to a type of monkey. The evolutionary community will always look to this as evidence for common descent. Life sharing relationships is their basic starting point. Either way you look at it, there will always be a degree of hierarchy.

The next time you take your children to the zoo, have them pick out what they believe is the animal that most closely resembles humans. It wouldn't be long before they came back with a chimpanzee, or a monkey. Biblical creationists do not need to fear similarity. Similarity simply demonstrates common design. Modes of transportation share thousands of similarities, and fall into hierarchical patterns, not because of common ancestry—but because of common design. The features are shared for functional reasons. With ERVs being the focus of this book, we know that since ERV's are functional DNA elements—the reason we share many with chimpanzees is because of common design and shared purpose. But we will touch on more of that later.

CLASSIFICATION SYSTEMS

Evolutionists put a significant amount of confidence in the classification of animals as supporting evidence for common descent. Since the law of monophyly tells us we can never outgrow our ancestry, evolutionists would say humans and pine trees are related simply because they are both eukaryotes (organisms whose cells consist of a nucleus inside a membrane), and both cats and dogs are related because they are both carnivores. If we draw a circle big enough, we can add just about everything into it. We could draw a circle and label it “living things”. And just because everything could be grouped into that circle does not mean everything within that circle is related.

We could draw a circle and call it “modes of transportation”. Does this mean all modes of transportation including sedans, hatchbacks, vans, bikes, skateboards, and airplanes are related? Of course not.



Image - Classifying things based on their ability to breath



Image - Classification system based on motorized transportation

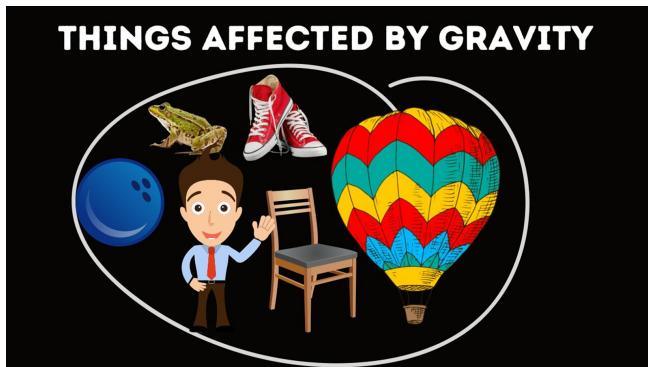


Image - Classifying things that are affected by gravity

SHARED ERV ELEMENTS

I wouldn't be surprised if every form of life shared endogenous retroviral-like DNA. Since life depends on these various classes of DNA elements, we should expect various forms of life to share many things in common. I bet the chimpanzee requires functional DNA elements to work in embryological

development, determining cell types, and acting as antiviral protectors (just to name a few of the many known functional and essential roles of these amazingly intricate DNA elements) in similar ways that humans do. Chevys and Hondas both build their cars with windshields, doors, a steering wheel, and even tires. Many modes of transportation have four tires, and those tires are even made of rubber! This must mean that Chevys, Hondas, Mercedes, and Fords, all share a common ancestor (I am confident the reader can sense my sarcasm). Perhaps they inherited these features from a common sedan ancestor in the arctic millions of years ago.

Vehicles these days are even designed and built (one could say front-loaded) with control features such as lane control, adaptive headlights, back-up cameras, and navigation systems. This is all evidence of forward thinking that comes directly from the mind of the human engineer who designed these features in these modes of transportation. You'll also find many vehicles have airbags in common, require gas, and are used to move from one place to another. There are countless similarities between all forms of modes of transportation. And again, it's not because of common ancestry. It's because of common design. Therefore, the question pertaining to endogenous retroviruses as evidence for common descent, or common design, comes down to "**are these really the ancient remnants of viral infections, or are these created units of DNA function?**" And this is precisely why DNA function is the best way to help us determine which model best explains the existence of these viral-like sequences—creation or evolution? Are nested hierarchies a reflection of descent, or design? Chapter four will comprehensively answer all of the important questions on this topic.

DIFFERENCES BETWEEN HUMANS AND CHIMPANZEES

I do want to touch on a few final details (details that dismantle the evolutionary story of common descent) before we wrap up this chapter, and move into the major differentiating lines of evidence for ERVs. Let us cover a few powerful lines of evidence that strongly invalidate ape-to-man evolution, and common descent. We are now finding out that even in the regions of the genome where there exists significant similarity, there exists considerable differences in gene expression:

Studies show that gene expression in humans is significantly different from the expression found in chimpanzees, especially in the brain, where one study showed that 90% of the human genes were turned on at significantly higher levels than chimpanzee genes. Another study showed the brain DNA sequences of both species didn't match evolutionary descent predictions for a common ancestor.

SOURCE: [Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution \(ICR In Depth Science\)](#) – Dr. Jeffrey P. Tomkins (Page 98)

Please see: Cáceres, M. et al. 2003. Elevated gene expression levels distinguish human from non-human primate brains. *Proceedings of the National Academy of Sciences*. 100 (22): 13030-13035.

Enard, Wolfgang et al. "Intra- and interspecific variation in primate gene expression patterns." *Science (New York, N.Y.)* vol. 296,5566 (2002): 340-3. doi:10.1126/science.1068996

In addition to differences in gene expression, we find alternative splicing differences:

Genes are encoded in pieces by the Creator to increase their utility and functionality. The segments that code for protein are called exons, while the intervening regions are called introns. Before being used to make a protein, the messenger RNA copied from a gene is processed by complex cellular machinery that involves the splicing out of the introns in the RNA and the joining together of the exons. During this process, exons can be omitted, doubled, or even added in from another gene. As a result, a single gene can produce many different variants like a Swiss army knife. This whole process is called alternative splicing and is tightly regulated according to the specific needs of the cell.

Alternative splicing for a single gene can generate many protein variants depending on the gene. See Figure 1 for a graphic illustration of alternative splicing. These splice variations fall under very complex regulatory genetic control mechanisms. In fact, the first such research in 2007 showed that alternative splicing differs significantly between humans and chimps. The

authors of the paper state. “Surprisingly, 6-8% of profiled orthologous (similar) exons display pronounced splicing level differences in the corresponding tissues from the two species.” In such cases of distinct differences, the typical explanation is always rapid evolution. The researchers go on to say, “These layers of regulation have evolved rapidly.¹

SOURCE: Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution (ICR In Depth Science) – Dr. Jeffrey P. Tomkins (Page 100)

Please see: Calarco, J. et al. 2007. Global analysis of alternative splicing differences between humans and chimpanzees. *Genes & Development.* 21: 2963-2975.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2049197/>

And:

In a 2018 paper using even more advanced technology and also throwing Rhesus macaque in the mix, the researchers found that “in total, 1526 exons and exon sets from 1236 genes showed significant splicing differences among primates.”² The uniqueness of human was especially profound in that “the increase in isoform inclusion levels [gene variants], showed a 2-fold acceleration on the human evolutionary lineage when compared with the chimpanzee lineage.”² Once again, such so-called rapid “2-fold” evolution expressed in human

uniqueness of alternative splicing for genes previously determined to be highly evolutionarily similar does not support the Darwinian paradigm.

SOURCE: Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution (ICR In Depth Science) – By Dr. Jeffrey P. Tomkins (Pages 100-101)

Please see: Jieyi Xiong, Xi Jiang, Angeliki Ditsiou, Yang Gao, Jing Sun, Elijah D Lowenstein, Shuyun Huang, Philipp Khaitovich, Predominant patterns of splicing evolution on human, chimpanzee and macaque evolutionary lineages, *Human Molecular Genetics*, Volume 27, Issue 8, 15 April 2018, Pages 1474–1485, <https://doi.org/10.1093/hmg/ddy058>

<https://academic.oup.com/hmg/article/27/8/1474/4857231>

Dr. Jeffrey Tomkins continues in his book “**Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution**” to discuss these important differences between humans and chimpanzees with a focus on the vast differences in gene expression in the brain between humans and chimpanzees:

One of the first studies undertaken along the lines of reasoning was in 2003, in which 169 different brain genes were found to be expressed in a markedly different manner in human, chimp, and macaque cerebral cortices.⁵ Of these genes, 90% were turned on at significantly higher levels in humans compared to chimp. The researchers reported, “The human brain

displays a distinctive pattern of gene expression relative to non-human primates, with higher expression levels for many genes belonging to a wide variety of functional classes.”⁵

SOURCE: Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution (ICR In Depth Science) – By Dr. Jeffrey P. Tomkins (Pages 101-102)

As you can see, the significant differences between humans and chimpanzees in gene expression, alternative splicing, and even differences in regulatory sequences are far too immense to be explained by common descent:

Not only are genes regulated in networks and differently between humans and chimps, so are the non-protein-coding sequences in the genome that regulate the genes. In fact, interesting data have also been produced from the analysis of differences in regulatory sequences that are DNA features that control how genes are expressed.

One such study of regulatory DNA sequences compared the control regions of genes called promoters that were similar in human, chimp, and macaque. Promoters are the regions of DNA that immediately precede the gene and play a large role in controlling its level and rate of expression. Of those examined, 55 human gene promoters were found to be markedly different from those in chimps.¹¹ Many of these promoter differences were

associated with genes that control nerve cell development. However, many others were connected to genes associated with more basic metabolic activities like carbohydrate metabolism. Differences in regulatory DNA sequence, even minor variations, can result in large effects.

SOURCE: Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution (*ICR In Depth Science*) – By Dr. Jeffrey P. Tomkins (Page 105)

Don't forget to read: Haygood, Ralph et al. “Promoter regions of many neural- and nutrition-related genes have experienced positive selection during human evolution.” *Nature genetics* vol. 39,9 (2007): 1140-4. doi:10.1038/ng2104

<https://pubmed.ncbi.nlm.nih.gov/17694055/>

Babbitt, Courtney C et al. “Both noncoding and protein-coding RNAs contribute to gene expression evolution in the primate brain.” *Genome biology and evolution* vol. 2 67-79. 18 Jan. 2010, doi:10.1093/gbe/evq002

We discussed the epigenome earlier in this book, and pointed out how this extra layer of amazingly complicated information points us right back to the forward thinker (God). Well—it turns out that we have significant differences in epigenetics between humans and our so-called closest cousin (the only way evolutionists attempt to explain the evolution of

these huge differences are through a lot of fanciful storytelling and imagination):

Genetic tags that make chemical changes to genes are known as epigenetic mechanisms. Epigenetic tags regulate DNA sequence. Studies show that epigenetic differences in human and chimpanzee brain genes are far too great to indicate an evolutionary connection but rather reflect the creature-kind distinctiveness creationists would predict. A study on comparative epigenetics showed orangutans and gorillas had more similar patterns to humans than chimpanzees—a result completely backward to evolutionary predictions.

SOURCE: Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution (ICR In Depth Science) – Dr. Jeffrey P. Tomkins (Page 108)

Please see: Zeng, J, et al. 2012. Divergent Whole-Genome Methylation Maps of Human and Chimpanzee Brains Reveal Epigenetic Basis of Human Regulatory Evolution. *American Journal of Human Genetics*. 91 (3): 455-465.

Martin, D. I. K. et al. 2011. Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states. *Genome Research*. 21 (12): 2049-2057.

Dr. Jeffrey Tomkins counters the argument from DNA similarity indisputably here in this excerpt from his article titled “**Human-Chimp Similarities: Common Ancestry or Flawed Research?**”

Here are a number of key points that counter the evolutionary claims of close human-chimp similarity:

- The chimp genome is 10 to 12 percent larger than the human genome and is not in a near-finished state like the human genome; it is considered a rough draft.
- When large regions of the two genomes are compared, critical sequence dissimilarities become evident.
- Extremely large blocks of dissimilarity exist on a number of key chromosomes, including marked structural differences between the entire male (Y) chromosomes.
- Distinct differences in gene function and regulation are now known to be a more significant factor in determining differences in traits between organisms than the gene sequence alone. Research in this area has clearly demonstrated that this is the case with humans and apes, where marked dissimilarities in expression patterns are evident.

SOURCE: Tomkins, J. 2009. Human-Chimp Similarities: Common Ancestry or Flawed Research? *Acts & Facts*. 38 (6): 12.

The last thing I want to point out before we conclude this chapter is how the overall structure of the human and

chimpanzee (I am focusing on chimpanzees because proponents of common descent purport chimpanzees are our closest cousin and living relative) genomes are vastly different:

All plant and animal genomes studied so far exhibit complex and distinct three-dimensional (3-D) structures in their chromosome configurations depending on the type of cell (e.g., heart, liver, brain, etc.). Given the incredible variability among genome configurations within a single type of creature, let alone that which exists between creatures (e.g., human vs. chimpanzee), this area of evolutionary comparison has been difficult for secular researchers. Now a new study published in Trends in Genetics evaluates research in this emerging field that shows the human 3-D genome is distinctly unique to humans, confirming previous research that showed it is as different compared to chimp as it is to mouse.¹

SOURCE: *3-D Human Genome Radically Different from Chimp.* (n.d.). [Www.icr.org](http://www.icr.org/article/human-genome-radically-different-from-chimp). Retrieved May 5, 2022, from <https://www.icr.org/article/human-genome-radically-different-from-chimp>

Please see: Eres, I. E. and Y. Gilad. A TAD Skeptic: Is 3D Genome Topology Conserved? *Trends in Genetics*, published online November 14, 2020

This is just the very tip of the iceberg when it comes to the overwhelming amount of genetic related data that

dismantles common ancestry. The evidence for separate ancestry and independent origins is stronger than ever. The evolutionary community, and the critics of Young Earth Creation have failed to provide any real sophisticated counter response. You will also notice that all of the above arguments and data points come directly from secular literature, and primary sources. I am invalidating common descent right from the primary source data. The evolutionary community ignores the obvious conclusion of this fascinating data. These are not points and arguments that Biblical creationists are making up. These are straight out of the scientific literature.

I like to focus on common ancestry with the great apes, because oftentimes you will find the apologists of evolution accusing creationists of ignoring common ancestry with the apes (specifically evolution with chimpanzees) while choosing to focus on what is assumed to be distantly related organisms (human and a strawberry). By showing exactly why humans are not related to chimpanzees, with strong scientific based arguments, the entire universal phylogenetic tree crumbles to pieces. If we are not related to chimpanzees, and the great apes, then common descent is false. If we are not related to chimpanzees—we are then unquestionably not related to strawberries, and mosquitos. Common descent requires that humans have their place in the tree of life, with the great apes being our closest relatives. This handbook's main focus is endogenous retroviruses, and for that reason we must move on. But I have written extensively on the separate ancestry model in previous books. I have also had roughly 100 debates with PhD evolutionists and serious students of common descent. I could cover more significant differences between the genetics of humans and the great apes, such as in the Y

chromosome and mitochondrial DNA, but a greater amount of time has been devoted to this in my book “**Special Creation - Dismantling Evolution and Confirming Independent Origins**”.

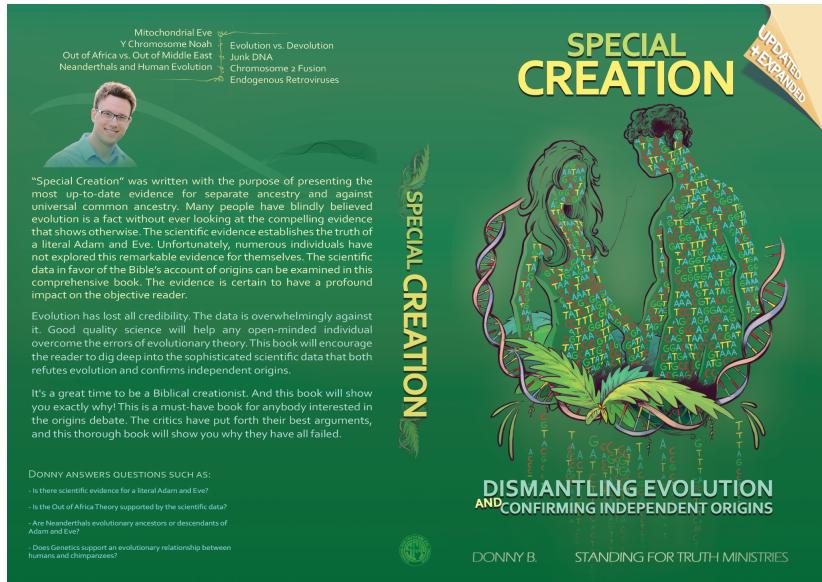


Image - Special Creation (By Donny Budinsky)



RECOMMENDED BOOKS BY THIS AUTHOR

The Endogenous Retrovirus Handbook (Dismantling the Best Evidence for Common Descent):

Black and White version -

<https://www.amazon.com/dp/B0B14KHL8G>

Full Color Version plus Variant Cover -

<https://www.amazon.com/dp/B0B1B1N8F6>

Special Creation UPDATED and EXPANDED:

Black and White -

<https://www.amazon.com/dp/B08R64MPQ7>

Full Color - <https://www.amazon.com/dp/B0BD55T5FQ>



CHAPTER THREE REFERENCES

Jeanson, N. T., and J. P. Tomkins. 2016. "Genetics Confirms the Recent, Supernatural Creation of Adam and Eve." In *Searching for Adam: Genesis & the Truth About Man's Origin*. Edited by T. Mortenson. Green Forest, Arkansas: Master Books.

Replacing Darwin (The New Origin of Species) Nathaniel T. Jeanson

Cáceres, M. et al. 2003. Elevated gene expression levels distinguish human from non-human primate brains. *Proceedings of the National Academy of Sciences*. 100 (22): 13030-13035.

Enard, Wolfgang et al. "Intra- and interspecific variation in primate gene expression patterns." *Science (New York, N.Y.)* vol. 296,5566 (2002): 340-3. doi:10.1126/science.1068996

Calarco, J. et al. 2007. Global analysis of alternative splicing differences between humans and chimpanzees. *Genes & Development*. 21: 2963-2975.

Jieyi Xiong, Xi Jiang, Angeliki Ditsiou, Yang Gao, Jing Sun, Elijah D Lowenstein, Shuyun Huang, Philipp Khaitovich, Predominant patterns of splicing evolution on human, chimpanzee and macaque evolutionary lineages, *Human*

Molecular Genetics, Volume 27, Issue 8, 15 April 2018, Pages 1474–1485, <https://doi.org/10.1093/hmg/ddy058>

Haygood, Ralph et al. "Promoter regions of many neural- and nutrition-related genes have experienced positive selection

during human evolution.” *Nature genetics* vol. 39,9 (2007): 1140-4. doi:10.1038/ng2104

Babbitt, Courtney C et al. “Both noncoding and protein-coding RNAs contribute to gene expression evolution in the primate brain.” *Genome biology and evolution* vol. 267-79. 18 Jan. 2010, doi:10.1093/gbe/evq002

Zeng, J, et al. 2012. Divergent Whole-Genome Methylation Maps of Human and Chimpanzee Brains Reveal Epigenetic Basis of Human Regulatory Evolution. *American Journal of Human Genetics*. 91 (3): 455-465.

Martin, D. I. K. et al. 2011. Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states. *Genome Research*. 21 (12): 2049-2057.

[Chimps and Humans: A Geneticist Discovers DNA Evidence That Challenges Evolution \(ICR In Depth Science\)](#) – Dr. Jeffrey P. Tomkins

Tomkins, J. 2009. Human-Chimp Similarities: Common Ancestry or Flawed Research? *Acts & Facts*. 38 (6): 12. <https://www.icr.org/article/human-genome-radically-different-from-chimp>

Eres, I. E. and Y. Gilad. A TAD Skeptic: Is 3D Genome Topology Conserved? *Trends in Genetics*, published online November 14, 2020