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ARTICLE

**Refuting Gutsick Gibbon's video titled "Donny Botches Human Chromosome 2 Again"**

By Donny Budinsky

*\*For a full dismantling of the chromosome 2 fusion, please see this article written by Donny Budinsky:*

**OVERTURNING THE CHROMOSOME 2 FUSION**

<https://drive.google.com/file/d/1dJghXsEkARBD-Gr2dvsnuqeujNb1Tjhi/view?usp=sharing>

In her video titled “*Human Chromosome 2 VS Creationism | Bite-Sized Busts*” (1), Erika (known as *Gutsick Gibbon* on YouTube) claims the human chromosome 2 (specifically at the purported fusion site) is the only place in the entire genome where we find the signature telomeric repeats in both forwards and in reverse (TTAGGG/CCCTAA). She does not reference any additional incidence within the human genome where we observe the same sequences found at the presumed fusion site in a head-to-head organization. The reader can see this argument for themselves in the previously referenced video starting at the timestamp 18:55.

I should clarify—while Erika does not mention other occurrences in the genome encompassing telomeric repeats in a head-to-head arrangement (not just in isolation with a sequence of TTAGGG and another independent occurrence of CCCTAA), she does complete her dispute with an appeal to the high-density nature of the reputed fusion site (in chromosome 2). She argues the density is half the argument. Unfortunately for protagonists of evolution, the density (which is claimed to be half the argument) is of no help. It is arbitrary—as I will cover later in this section.

## **CONFIRMED PREDICTION**

Telomeres (a wide-spread genetic feature found at the end of chromosomes) have respective calling cards (2). These are specific sequences found in the genome—and they comprise the DNA letters TTAGGG in forwards and CCCTAA in reverse (reverse complement). These base pairs occur in this

specific order at telomere sites. These telomere-specific sequences are found repeatedly at telomere locations.

Since we have discovered interstitial telomeric-repeats all throughout the genome that are in spots not specific to telomeres, defenders of common descent can't look to these sequences of repetitive DNA as evidence for an ancient fusion. As a counter to this, Erika, and other critics of separate ancestry, have argued that the only place in the human genome where we find the telomeric calling cards in both forwards and in reverse (TTAGGG and CCCTAA) is at the alleged fusion site.


I suspected this was not the case. I have engaged in many discussions and debates with champions of common descent (including at least 1 PhD evolutionary biologist) (3). I have also participated in a formal podcast debate on the topic of chromosome 2 with a serious student of evolution (4). I have made it clear that this claim was thought-provoking—but that it might not actually be the case. At these points in time, there had not yet been a thorough search performed to verify whether this argument was true or not. A friend of mine (Christopher Rupe) whom I co-authored a technical article with (on genetic entropy) agreed that it would be unusual to not find telomeric calling cards (not just the sequences found independently in either forward or reverse) elsewhere in the human genome. He was firmly against this. We both predicted that if our arguments against a human fusion event were valid, we should find other instances of these DNA signatures within human chromosomes that are not the chromosome 2 (in a head-to-head arrangement). This was a novel prediction not yet tested.

Christopher Rupe and I worked on this issue to authenticate the prediction. Chris exclusively ran the BLASTn analysis. He performed comprehensive analyses using this useful program. It turns out there is compelling evidence for the telomeric repeats (interstitial or internal telomeric sequences) in both forwards and in reverse being found on multiple chromosomes (1, 2, 6, 9, 10, 15, 16, 18, 20). And this is based on innovative research done by Christopher Rupe and Donny Budinsky.

We also discovered a similar signature in chromosome 9. The telomeric-like hexamer sequence and its reverse complement are arranged head-to-head in a similar fashion to the purported fusion site. Was the reputed fusion site cherry-picked? It appears so. It is important to note that chromosome 2 is moreover the second largest chromosome in the human genome. Chromosome 9 is much smaller, and yet it contains fewer gaps between the telomeric repeats, with the chromosome 2 site containing numerous gaps. The asserted fusion site is only 798 bases in length. If this really was the mark of an ancient fusion event, this region should be much larger than 798 bases. There are only 10 intact TTAGGG telomere sequences that exist at the site. And there are only 43 of the reverse complement telomere sequences that are recovered intact.

*\*Chromosome 9 visual on next page*

Chromosome 9 with head-to-head telomeric sequences  
(TTAGGG/CCCTAA)

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**Homo sapiens chromosome 9, GRCh38.p14 Primary Assembly**

Sequence ID: [NC\\_000009.12](#) Length: **138394717** Number of Matches: **55**

Range 1: 128154271 to 128154325 [GenBank](#) [Graphics](#)

▼ Next Match

▲ Previous Match

Score	Expect	Identities	Gaps	Strand
87.8 bits(96)	4e-16	54/57(95%)	2/57(3%)	Plus/Plus

Features:

1152 bp at 5' side: [neutrophil gelatinase-associated lipocalin precursor](#)

6083 bp at 3' side: [bublin coiled-coil protein](#)

Query 2

taggggttaggggttaggggttaggggttaggggttagggCCCTAACCCCTAACCCCTAACCCCT 58

Sbjct 128154271 TAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTT---TAACCCCTAACCCCTAACCCCT 128154325

AGCCCCCTGGTCATCACCAGCAGCTTTGTGGCTGACCACCCTGAG  
TCCTTCCCACGTGGTGTAACACCGTCCTCCCTCCTGCTGTGACAT  
GGCGCCCAGCCCCAGAGCAGCGGCAGTTCTCACATTCCCCTGCC  
TAGGAGGGTGCCCCAGTCCATCGCAGACACGGTGGGGCCACACCCC  
ATCAGAGTGCGACAGGGGCATGCACAGCTGGAGGCTGTTCCAG  
GCAGAGGGTTCGGCTCGGCGGGGATGGTCCCCCTGCCCTCTGCCA  
GCCCACTGTGGGCCCCGTGGGTGAGGGGGCCATGTCCATGCTAAC  
CCCGTTTCAGAGCGTGCTGCCCTTACCCCCACACCTCCCCGCCTG  
ATGACATCCAGGCCACCTTGGGGGTGCATTCTGAAGCCAGGGGC  
AGGGCCAGGGGGAAGTGAGGAGGGGCTGTGCCGCCAAGAATCC  
AATCCCCAGGACTCAGAGGGCTCCAGGCCTGCACTTATCACTT  
GGCTGCCTGTGTCAGGCCTGACAAGCCCCTGGTCCCCCACTGGC  
CGCAGAGGCAACCTCTCCAGGTCCGCATCATGCACAGGCACTCC  
CTCCCCAGCCCCCTTCTCCCCGTGCAAGTTCAGAGGCCAGAGTGG  
GTGGGGTTCTGAGGAAACCCCATGGACAGACACACCACCCCGTT  
CACCCCTCGGC**TAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTA**  
**GGGTTAACCCTAACCCTAACCCCT**CGTTCACCCTCGGCTGGGCT  
AAGGAGAGATGCTGGCACTGTGAACCAGCCCCAGCCTCGGACC  
CCAAGGAGCAGGACAGGCCTGAGACCCAGGCCACCAAATGCT  
GCCAAAGCCTCGGAAAGTCTGGTCCAGACTCCCGGAAGAGGCCA  
GCTTGGTGCAGCCCCAGCTTTGAGAGAGGGATGGGACTGTTCCC  
AAGCCCAGAGAGGCTCAGGCTGAGAAAGTCACCCAGGGACTGC  
TAGCTGGCCAAGGGGGTGGAAAGTGCACCCAGCACGCCTGGCC



respectively. The hypothetical head-to-head fusion site has a yellow background. (5)

## **WHY THE CHROMOSOME 2 FUSION ARGUMENT FAILS**

Finding head-to-head telomeric repeats cannot be strongly interpreted as being the result of a fusion, since these DNA elements are found within the human genome at locations not applicable to a fusion. They simply represent functional stretches of DNA fulfilling a purpose to the overall management of the human genome. If these telomeric calling cards (in a head-to-head arrangement) were only found at the reputed fusion site, the evolutionary community may have a point, and for a while this was thought to be the case. But with this novel encounter of locating these sequences in a head-to-head arrangement at other locations within the genome not pertinent to an ancient fusion, this line of evidence has been removed as supporting evidence for a chromosome fusion in humans.

It's not only that we find telomeric repeats scattered all throughout the genome, with many of these repeats having evidence for functional activity (in gene expression), it's that we also find them in both forwards and in reverse. The head-to-head arrangement of repetitive telomeric DNA (TTAGGG/CCCTAA) has now been demonstrated to not be unique to the so-called fusion site—as these DNA elements have been found in other places within the human genome. This finding (by Christopher Rupe and myself) completely

shatters the challenge put out by Erika (Gutsick Gibbon) and repeated by other defenders of evolution.

## **THE RESCUE DEVICE**

Apologists of common descent will now want to only focus on the high-density nature of the purported fusion site—which means they have lost half of their argument. But the other half (the density portion of the challenge) is no help to the chromosome 2 fusion argument. This rescue mechanism assumes the telomeric marks are indeed characteristic of an archaic fusion incident. But if one assumes (correctly) that these are functional units of DNA, the density of the area is not a challenge. Protagonists of evolution still can't explain why the reputed fusion site is exceedingly degenerate. The site itself is small and insignificant. As I mentioned earlier, the human chromosome 2 is also the second largest chromosome in the genome—and therefore it should not be a huge astonishment to find a greater degree of these telomeric repeats within this chromosome.

These repeats are found within other chromosomes that aren't nearly as large as chromosome 2. Interstitial telomeric repeats are found in varying degrees of density—with the chromosome 2 location comprising the highest density. But since these internal telomeric repeats simply represent functional DNA elements important to the operation of the cell, the chromosome 2 location is only high density when compared to other instances of these internal DNA elements—which is why it is relative. It is also no

surprise that the so-called fusion site comprises more of these elements since the location itself is a hotspot for genomic activity and function. If we were to assume this location within the human chromosome 2 was actually representative of an ancient fusion event, the area should not be considered high density, since it is far too corrupt to be a fusion signature. The density argument is arbitrary. It is, as a matter of fact, relative.

## **GUTSICK GIBBON'S RESPONSE TO THE FINDINGS**

Erika put out a video reacting to an open mic debate I engaged in (specifically dealing with the interstitial telomeric repeats found all throughout the genome—including areas that are not in the chromosome 2—and are found in both forwards and reverse) (6). The video did not tackle the significance of our findings. To our surprise, she did not even acknowledge the telomeric repeats (in a head-to-head arrangement) that were discovered within other chromosomes. She assumed this was not the case—and that it was another variation of the “internal telomeric repeats found scattered throughout the genome” argument.

As I have covered, Christopher Rupe specifically ran the BLASTn analysis as we researched Erika's false claims. We discovered the internal telomeric repeats (supposedly the signature of a fusion in the chromosome 2) elsewhere in the genome—and this includes chromosome 9 (which can be seen in the video that she reacted to).

## **THE FACTS**

The fact is—we find the repeats in many chromosomes (with a large signature in chromosome 9) in both forwards and in reverse. These signatures have nothing to do with an ancient fusion. The part where the repeats (TTAGGG and CCCTAA) meet head-to-head is actually more pristine in chromosome 9. Christopher Rupe and I found 9 hexamers in a head-to-head array. These signatures are not only unique to chromosome 2. Erika has claimed that there is no other place in the human genome where these sequences are found in mirror image. This has been demonstrated to be false.

## **THE REALITY**

The suggested fusion site turns out to not be a fusion site. It is a key genomic switch within a highly competent gene. The gene that crosses the alleged fusion location is a long noncoding RNA gene. The action of this gene has been tracked (using public databases) to numerous significant human tissues. The gene is associated or connected with several important networks in other crucial genes in the human body. And the internal telomeric sequences represent functional units important to genes.

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