tkp The blog for science & politics

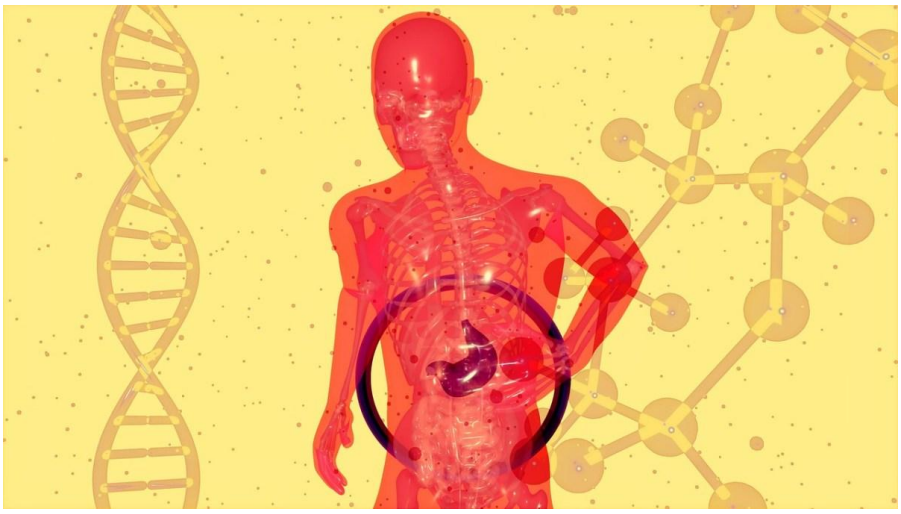


Image by Julien Tromeur on Pixabay

The greatest crime in human history?

January 21, 2026 by Em. O. Univ.Prof. Dr. med. Hartmut Glossmann 12.9 minute read

When it became clear to me some time ago that the so-called modmRNA injections against Covid-19 were by no means safe and effective, and that the NSA and Pentagon (according to Robert F. Kennedy Jr.) were significantly involved, I acquired a book on the history of killing by Peter Schuster: Criminals, Victims, Saints: A History of Killing 1200-1700 , in order to familiarize myself with the barbaric methods of medieval courts of justice.

It is obviously impossible and also unnecessary to punish all those actively involved with any of these methods. Many of these "followers" are themselves victims: The spectrum of side effects ranges from long-term COVID, myocarditis , sudden cardiac death, blindness, stroke, kidney damage, dementia, etc., to accelerated cancer . To this day, many doctors are unaware that these injections were manufactured using a different method (Process 2) than in the Pfizer/BionTech approval study (Process 1).

We now understand why the placebo group was eliminated (for ethical reasons?) by administering the active drug: in my opinion, it was to be made impossible to detect long-term effects of Process 1 injections in both groups. Therefore, observational studies are necessary for the individuals injected using Process 2.

One of these studies (currently only available as a preprint) can be found here . Sometimes it's possible to publish important findings outside of top journals. This can then be used, for example, as an argument in court.

Observers of the events are noticing increasing aggression against the US Secretary of Health and Human Services because of his "vaccine policy." High-ranking scientists like Professor Rolf Marschalek are not hesitant to attack Kennedy on social media (@rolfmarschalek.bsky.social). The content of this defamation is not quoted here, as it falls under German criminal law, in my opinion.

Marschalek is mentioned because he also acted against the authors of the publication discussed below (see @Kevin_McKernan).

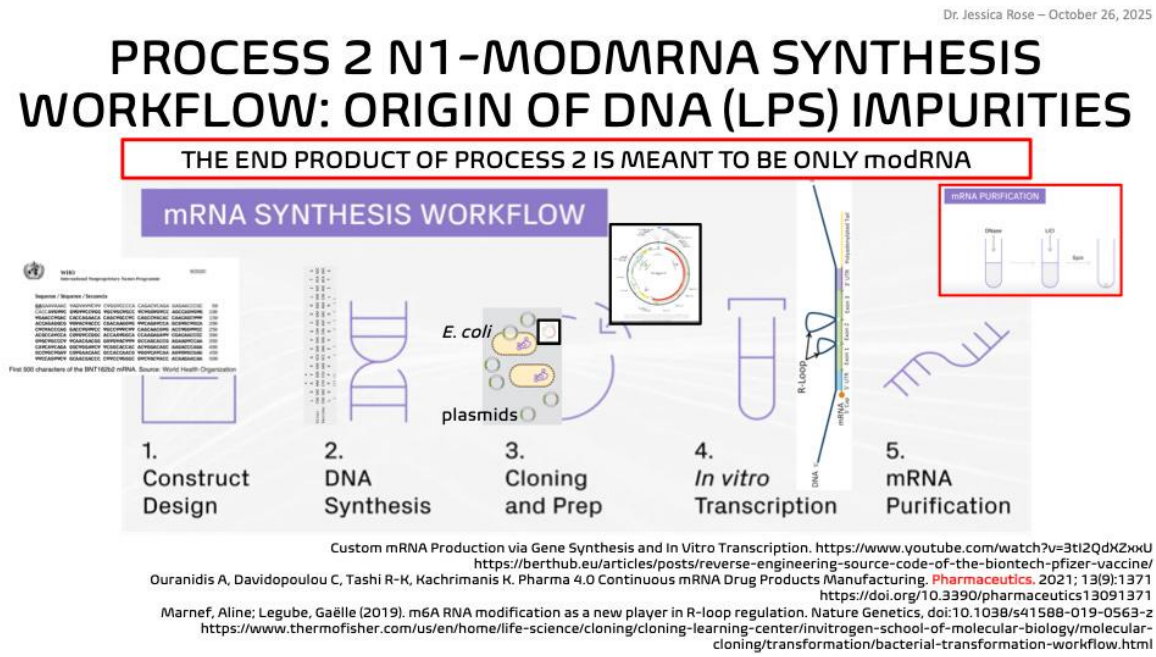
on Substack on January 16, 2026, written in layman's terms Dr. Jessica Rose published a text about her publication . It was translated and proofread using Claude.AI Pro.

RNA:DNA hybrids survive digestion during the production of mRNA vaccines.

The paper, entitled " *RNA:DNA Hybrids Survive Digestion in mRNA Vaccine Manufacturing* ", was published on January 13, 2026 in the Journal of Independent Medicine[1] and deals with DNA in the vials of the nucleoside-modified RNA-LNP COVID vaccines (Pfizer/BioNTech and Moderna).

It verifies our hypothesis that the DNA in the vials escaped enzymatic degradation during the production process because the wrong enzyme was used to remove the DNA at the end of the process. This incorrect enzyme, called DNase1, could never degrade RNA:DNA hybrids—which inevitably form during the in vitro transcription (IVT) process—and the manufacturers knew this.

Here is a reminder of the modRNA synthesis process, which is used as part of Process 2.



Custom mRNA Production via Gene Synthesis and In Vitro Transcription. https://www.youtube.com/watch?v=3tI2QdXZxxU
https://berthub.eu/articles/posts/reverse-engineering-source-code-of-the-biontech-pfizer-vaccine/
Ouranidis A, Davidopoulou C, Tashi R-K, Kachrimanis K. Pharma 4.0 Continuous mRNA Drug Products Manufacturing. Pharmaceutics. 2021; 13(9):1371 https://doi.org/10.3390/pharmaceutics13091371
Marnef, Aline; Legube, Gaëlle (2019). m6A RNA modification as a new player in R-loop regulation. Nature Genetics, doi:10.1038/s41588-019-0563-z
https://www.thermofisher.com/us/en/home/life-science/cloning/cloning-learning-center/invitrogen-school-of-molecular-biology/molecular-cloning/transformation/bacterial-transformation-workflow.html

The DNA template is the exact complement of the RNA produced (newly synthesized) during the IVT process, so the RNA strand can naturally politely ask the non-template strand of the double-stranded DNA to move aside to replace it. When the RNA and DNA strands stick together, which they inevitably do, they stick tightly. This is because the N1 methylpseudouridines have a high melting point (Tm) , and therefore high temperatures are required to separate them. They are sticky.[2]

And by the way, when I say that the manufacturers knew this, I mean it.

"However, the specific activity of DNase I for RNA:DNA hybrids is ***at least 100 times lower*** than that for dsDNA (Sutton et al., 1997).[34]

BioNTech SE, Mainz, Germany.

Wait a minute, what? A BioNTech team published this in July 2024?

the authors of this paper worked ***In fact, all*** for BioNTech.

The authors declare that this study was funded by BioNTech SE. The funder's involvement in the study is as follows: **All authors** are current employees of BioNTech SE.

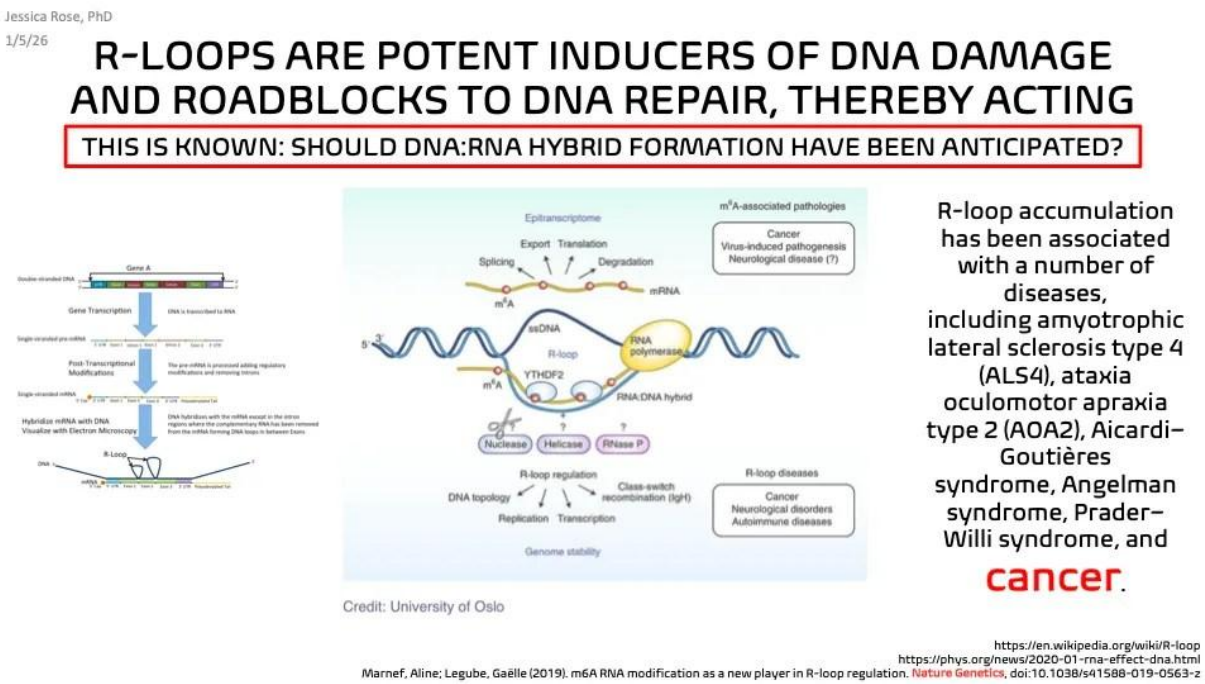
I would like to remind you that this is another point during the manufacturing/production process where the manufacturers made more than one major mistake. The substitution of N1-methylpseudouridines at every single U-position (there are 801)[5] was a major error that led to many problems such as frameshifting , and as proposed in our work, codon optimization for the deposition of coding material in humans via LNPs leads to a significant enrichment of GC content.[678]

The reason why it is so significant that they used DNase1 instead of, for example, DNase-XT to degrade potential RNA:DNA hybrids is twofold:

1. They knew that DNase1 would not efficiently degrade potential hybrids and that all hybrids would inevitably be packaged into the LNPs, and

2. This would lead to the inevitable import of these cancer-causing foreign molecules into the cytoplasm and perhaps even the nucleus of cells.

Were they unaware of the effects of introducing foreign RNA:DNA hybrids into human cells through transfection? Did they not fully understand that R-loops directly cause disease in humans when they accumulate?



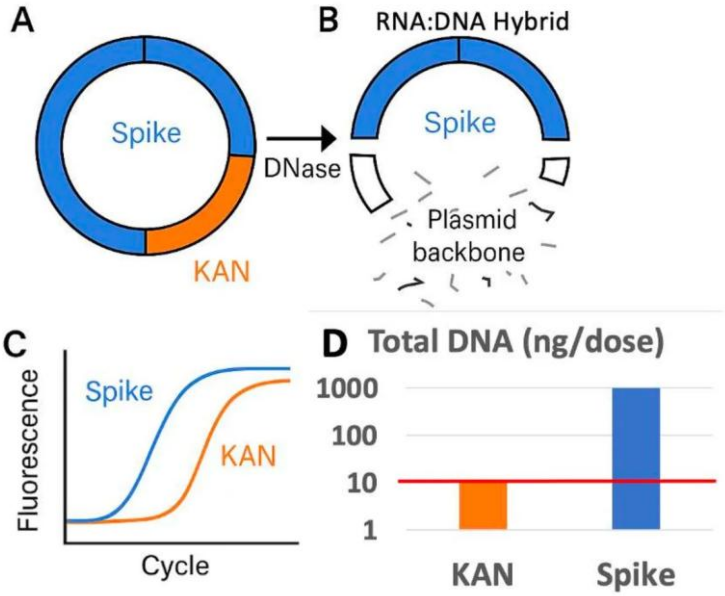
R-loops occur naturally in our cells (mostly during transcription) and can perform physiological roles such as supporting gene regulation or replication, but they can also be pathological if they are persistent (or cumulative), leading to DNA damage (cancer), replication stress, or inflammation.[9] So, can you imagine—in addition to the normal, ongoing physiological processes—what your poor cells have to contend with when confronted with hordes of these extra foreign molecules? Wouldn't anyone with half a brain anticipate R-loop accumulation that could lead to disease states like cancer?

The other Pandora's box that clearly illustrates our work is how manufacturers had tests for spike DNA detection[10], but only used tests to find KAN DNA. It's like a game of hide-and-seek—on a massive scale. But this isn't a game, is it?

A little about the KAN gene

The KAN antibiotic resistance gene is the gene that encodes neomycin phosphotransferase II, (which confers resistance to [the aminoglycoside] antibiotic kanamycin and is often used as a selectable marker in molecular biology plasmids to identify successfully transformed cells → such as our infamous E. coli colonies grown on kanamycin-containing medium during the N1-modRNA-IVT synthesis/production process).

Figure 1. Depiction of differential nuclease sensitivity with RNA:DNA hybrids



As you can see from Figure 1 in our paper, these DNase1 enzymes, which they used at the end of the IVT synthesis process, did not function with RNA:DNA hybrids. However, they did function with the other DNA elements from the plasmid that were not designed to produce modRNA—such as the KAN DNA.

Do you see the problem?

Here's a quiz for you: If you were an evil genius and wanted to hide potentially high DNA levels from regulators, what would you do and what kind of tests would you run to show low DNA levels? You might even want to show high RNA levels.

I'll give you an important clue: According to a Therapeutic Goods Administration (TGA) document (Residual DNA Quantitation in Moderna mRNA Vaccines by qPCR), Moderna developed and used a qPCR detection method for KAN DNA.[11] They also have one for Spike, so why didn't they use that one?[12] My guess would be because they knew the KAN DNA results would be low to zero, allowing them to claim there was no DNA in the vials. Presto magico!

Original In-Process Control Method – Moderna SOP-1020

The following is unmodified presentation of the original Moderna SOP-1020, which was provided under commercial in confidence arrangements and is not to be distributed beyond the HPRG.

1.0 PURPOSE

The purpose of this procedure is to detect and quantify residual plasmid DNA in mRNA Drug Substance (DS) or mRNA Product intermediate (MPI) using a real time quantitative PCR (qPCR) assay designed to amplify the kanamycin resistance gene in the plasmid.

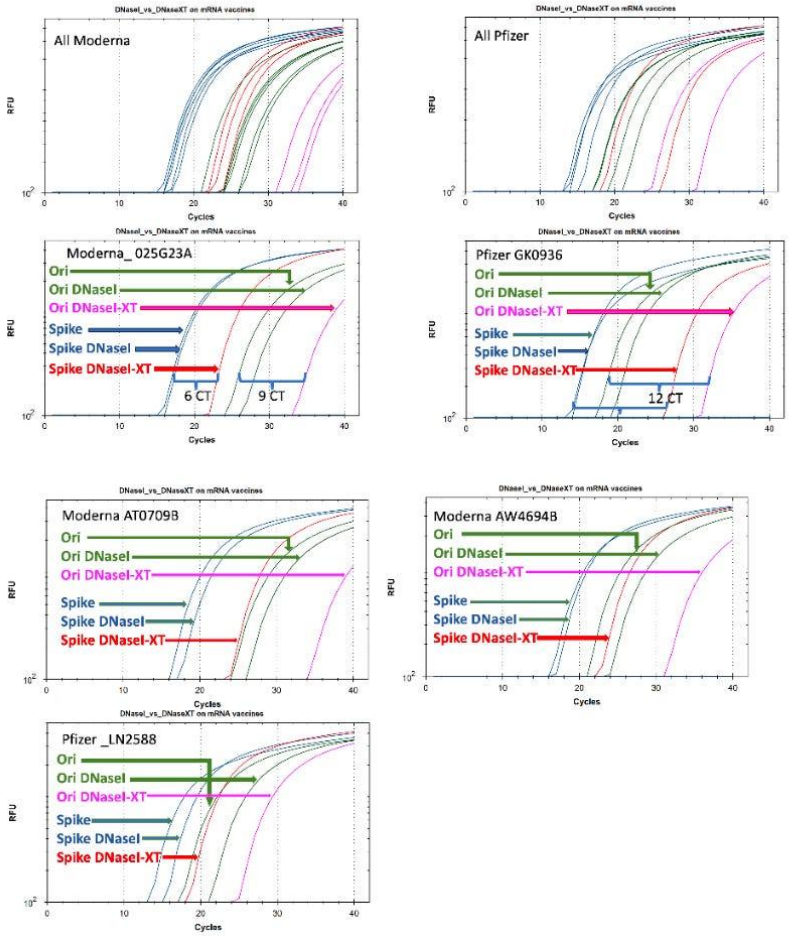
The Moderna SOP-1020 can be found here , and please note that it was written on October 9, 2020.

This document describes the method for quantifying residual DNA in Spikevax mRNA vaccines using qPCR.

Residual DNA, yes? Well, not ALL residual DNA, right?

Why would Moderna explicitly test only for the promoter/enhancer of the kanamycin resistance gene, which is a tiny part of the DNA in the vials? Well, because the use of DNase1 resulted in the KAN DNA being correctly degraded, but the DNA that produces what the products were actually supposed to produce—the spike protein—was not degraded. This spike DNA wasn't detected because the manufacturers didn't test for it. This is one of the points Kevin and I first demonstrated in May 2023.[13]

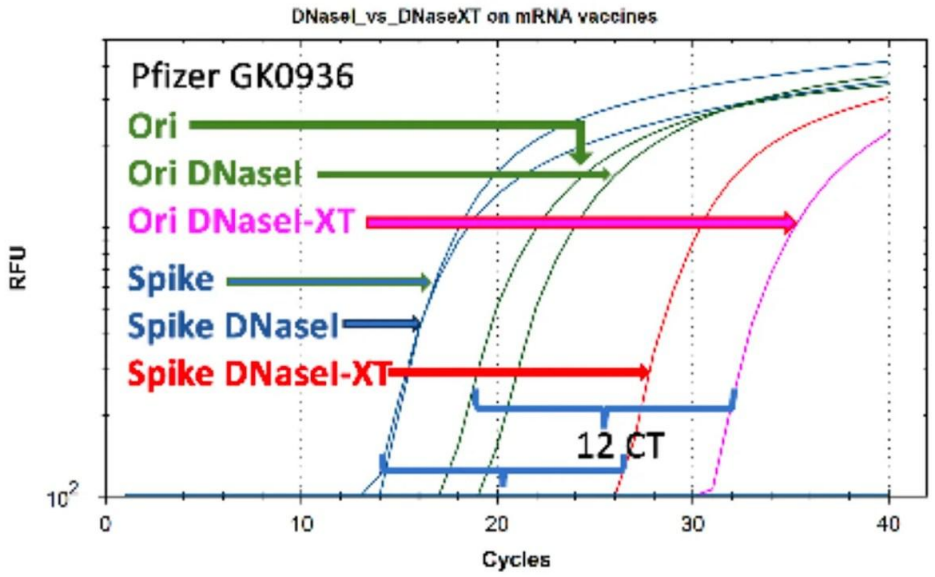
Figure 3. DNaseI/DNaseI-XT qPCR demonstrate differential nuclease sensitivity at 2 different loci in the plasmid (Spike, Ori)



And here's another important point. The New England Biolabs (NEB) website for DNase-XT states:

“ *DNase-XT efficiently removes both double-stranded and single-stranded DNA contamination from RNA samples, thus preventing false-positive results in downstream assays such as qRT-PCR. Unlike DNase I, DNase-XT also digests RNA:DNA hybrids, providing a more optimal solution for removing DNA from RNA.* ”

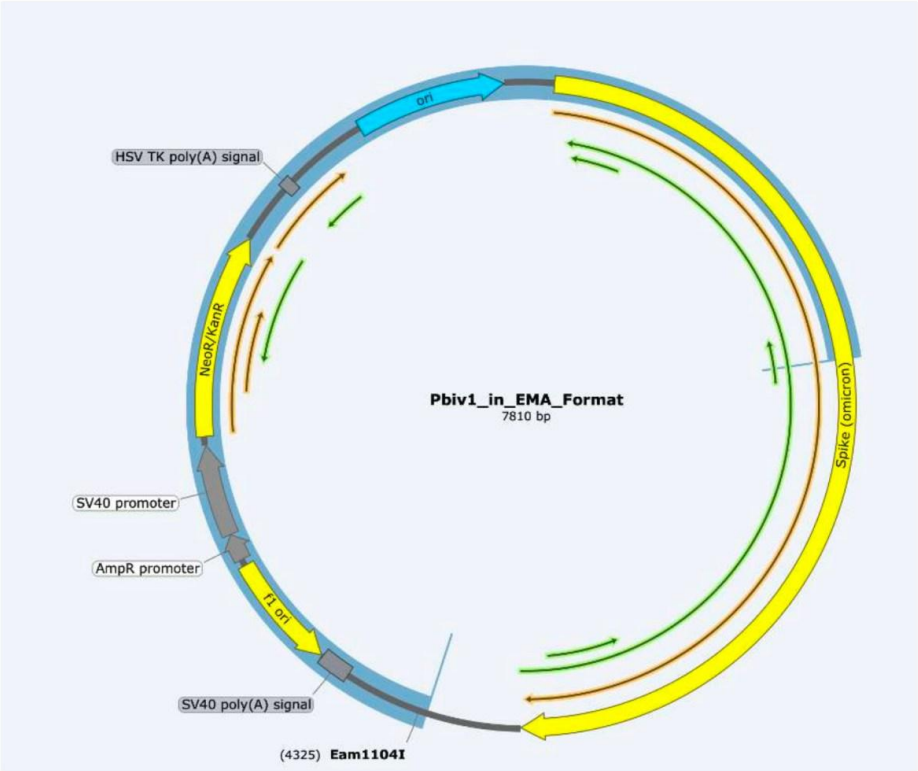
They should have used DNase-XT for DNA removal from the modRNA, not DNase1. They should have performed a qPCR for Spike, not KAN. At worst, they should have performed assays for both. Charles, Kevin, and I conducted a direct comparison between DNase1 and DNase-XT treatment of the Pfizer and Moderna vials in our work. Take a look at Figures 2 and 3.



The distinguishing feature of these results is that DNase1 did not act on the spike **because it is present in hybrid form** . These blue lines show virtually the same trajectory after treatment with DNase1; this is not the case after treatment with DNase-XT. **These are not small differences. They represent a 100- to 1000-fold increase in the degradation of spike DNA.**

Well, it's worth repeating (I've said this several times in interviews) that Charles, Kevin, and I completed this work in two days (on Veterans Day, mind you—Charles is a veteran)—meaning each of us did the following: 1. qPCR with three primer sets (we also did SV40 in addition to Spike and Ori), 2. Fluorometry (to quantify ALL DNA—not just the primer-focused DNA), and 3. Oxford Nanopore sequencing to see the complete sequences that come out of those vials! Please read the paper to find out what we found! Note: The Oxford Nanopore (ONT) sequencing also revealed numerous fragments over 200 bp, including a 5,284 bp read that covered a large portion of the Spike gene.

Figure 6. 5,283 base pair Oxford Nanopore read (blue highlight) from Pfizer lot



Do you believe that? Well done, Charles. That's why it's important to use techniques other than a KAN-qPCR assay to search for DNA.

We accomplished an incredible amount of work in two days, and it was virtually flawless because: 1. we had an excellent understanding of the problem before we even touched our pipettes, 2. we precisely defined the problem in advance as three separate experiments to be performed, and 3. we were guided by Kevin, who carefully walked us through the protocols—he is very experienced and knows his own lab and pipettes inside and out. I would especially like to thank Kevin for giving up his free time to show us these protocols, and Children's Health Defense for helping with some of the reagent costs. I also want to thank Kevin for the dirty work of opening the Pfizer/Moderna vacuum-sealed modRNA vials in the bio-hood: they are quite tricky to open because they have metal caps and you can cut yourself.

It still strikes me as insane that people were repeatedly vaccinated (and still are!) with this stuff, which should be treated and handled as a biohazard. Moderna's SOP for determining residual DNA by qPCR in mRNA in the SECURITY AREA (7.0) recommends that all personnel handling these modRNA materials (for qPCR assay preparation) wear appropriate PPE.

But it's okay to inject this stuff directly into you. And into small children.

[redacted]

7.0 SAFETY

7.1. Wear proper PPE (lab coat, gloves, safety glasses). Use Moderna Safety Manual as a reference. Follow all safety information provided on material SDSs.

All in all, I think the two main messages of our work are:

1. That we have (ONCE AGAIN) proven that there is DNA in abundant quantities (above the already excessively high EMA limit of 10 ng/dose, which is designed for naked DNA) in the Pfizer and Moderna COVID-19 "vaccine" vials, and
2. Why DNA is abundant → easily predictable RNA:DNA hybrids due to improper choice of DNA enzyme for product purification during modRNA synthesis.

We also argue irrefutably why there would never be a way to actually show that there is a lot of DNA in the vials: The manufacturers have pre-designed the wrong assays for potential use in detection.

This is not ignorance – this is malice.

Please read the paper and share it with everyone. It's not a long read and is written for laypeople to understand.

References

[1] McKernan K, Rixey C, Rose J. RNA:DNA hybrids survive digestion in mRNA vaccine manufacturing. J Independent Med. 2026;2(1). doi:10.71189/JIM/2026/V02N01A04

[2] Parr C. J. C., Wada S., Kotake K., Kameda S., Matsuura S., Sakashita S., et al. (2020). N 1-Methylpseudouridine Substitution Enhances the Performance of Synthetic mRNA Switches in Cells. Nucleic Acids Res. 48, e35. 10.1093/nar/gkaa070

[3] Lenk R, Kleindienst W, Szabó GT, et al. Understanding the impact of in vitro transcription byproducts and contaminants. Front Mol Biosci. 2024;11:1426129. doi:10.3389/fmolb.2024.1426129

[4] Sutton, D. H., Conn, G. L., Brown, T., and Lane, A. N. (1997). The dependence of DNase I activity on the conformation of oligodeoxynucleotides. Biochem. J. 321 (Pt 2), 481–486. doi:10.1042/bj3210481

[5] "The RNA does not contain uridine; instead of uridine, the modified N1-methylpseudouridine is used in RNA synthesis." COVID-19 mRNA vaccine (nucleoside modified) Rapporteur's Rolling Review assessment report. EMA/198107/2020. Page 12/67

[6] Stephanie Seneff, Greg Nigh, Anthony M. Kyriakopoulos, Peter A. McCullough, Innate immune suppression by SARS-CoV-2 mRNA vaccinations: The role of G-quadruplexes, exosomes, and MicroRNAs, Food and Chemical Toxicology, Volume 164, 2022, 113008, ISSN 0278-6915, https://doi.org/10.1016/j.fct.2022.113008

[7] S.A. Shabalina, N.A. Spiridonov, A. Kashina. Sounds of silence: synonymous nucleotides as a key to biological regulation and complexity. Nucleic Acids Res., 41 (4) (2013), pp. 2073-2094, 10.1093/nar/gks1205

[8] McKernan K, Kyriakopoulos AM, McCullough PA (2021) Differences in Vaccine and SARS-CoV-2 Replication Derived mRNA: Implications for Cell Biology and Future Disease. doi: 10.31219/osf.io/bcsa6

[9] For the record: They are not the cut-out introns themselves or their lariats.

[10] Speicher, D. J., Rose, J., & McKernan, K. (2025). Quantification of residual plasmid DNA and SV40 promoter-enhancer sequences in Pfizer/BioNTech and Moderna modRNA COVID-19 vaccines from Ontario, Canada. Autoimmunity, 58(1). https://doi.org/10.1080/08916934.2025.2551517

[11] Therapeutic Goods Administration. FOI 5286 – TGA KAN PCR documents. 2024. Page 5. Available from: https://www.tga.gov.au/sites/default/files/2024-09/FOI%205286.PDF

[12] There is a spike-specific qPCR assay that was developed or used by Pfizer/BioNTech (for BNT162b2/Comirnaty).

[13] https://www.neb.com/en-us/products/m0570-dnase-i-xt