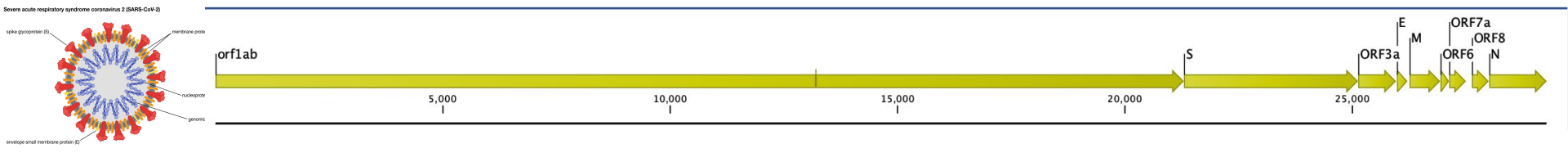
Molecular verification tools to enhance public trust during pandemic response

Phillip Buckhaults, Ph.D.
Professor, Department of Drug Discovery and Biomedical Sciences
Director, Cancer Genetics Lab
University of South Carolina
phillip.buckhaults@SC.EDU

Verba volant, scripta manent

SARS-CoV2 virus has unusual sequence features

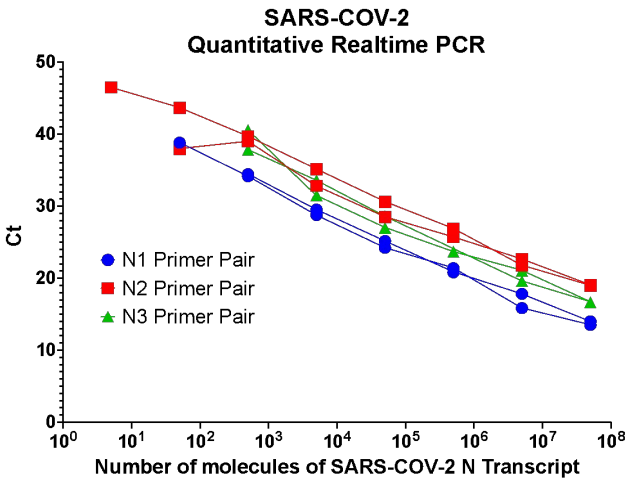


The SPIKE gene has more nonsynonymous changes relative to MRCA than predicted by standard evolutionary theory.

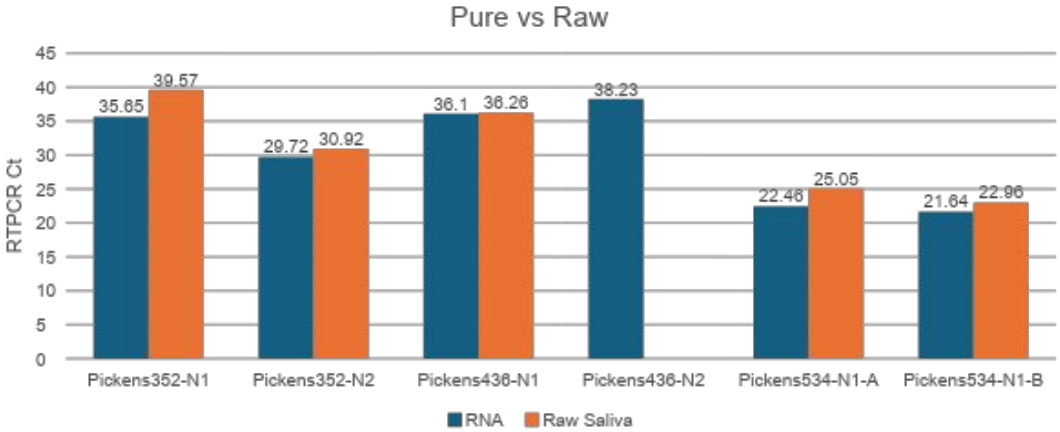
We made our own PCR primers and protocols and could detect this novel virus in sick people.

The Virus Is Real

Realtime qPCR to detect Sars-CoV-2



Ct values vary inversely with the amount of virus present. Higher virus = lower Ct value



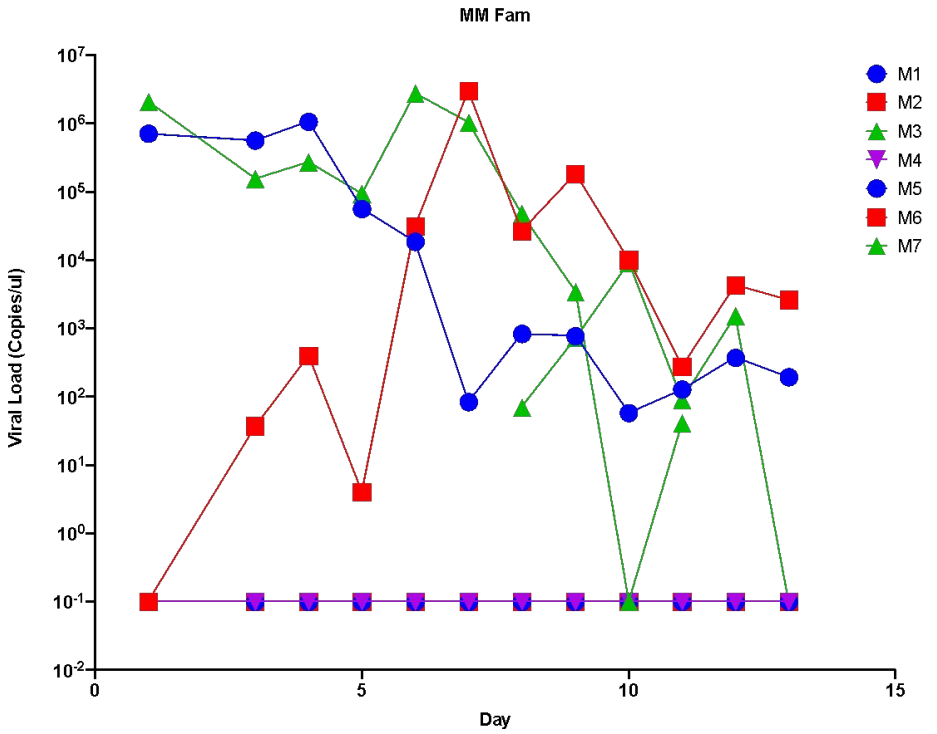
An experiment that should not have worked

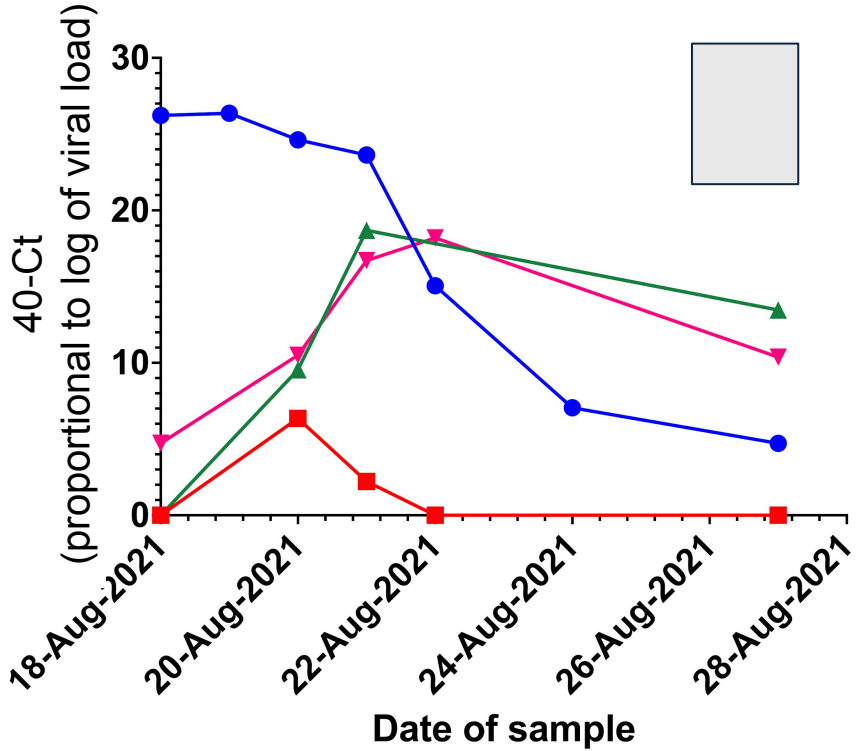
(done because we ran out of nasal swabs and mRNA purification reagents)

PCR from raw saliva works ***BETTER*** than it does purified nasal swab RNA.

This was kind of hilarious given all the regulatory gatekeeping around NP swabs

Tracking Symptoms and Transmission within Families



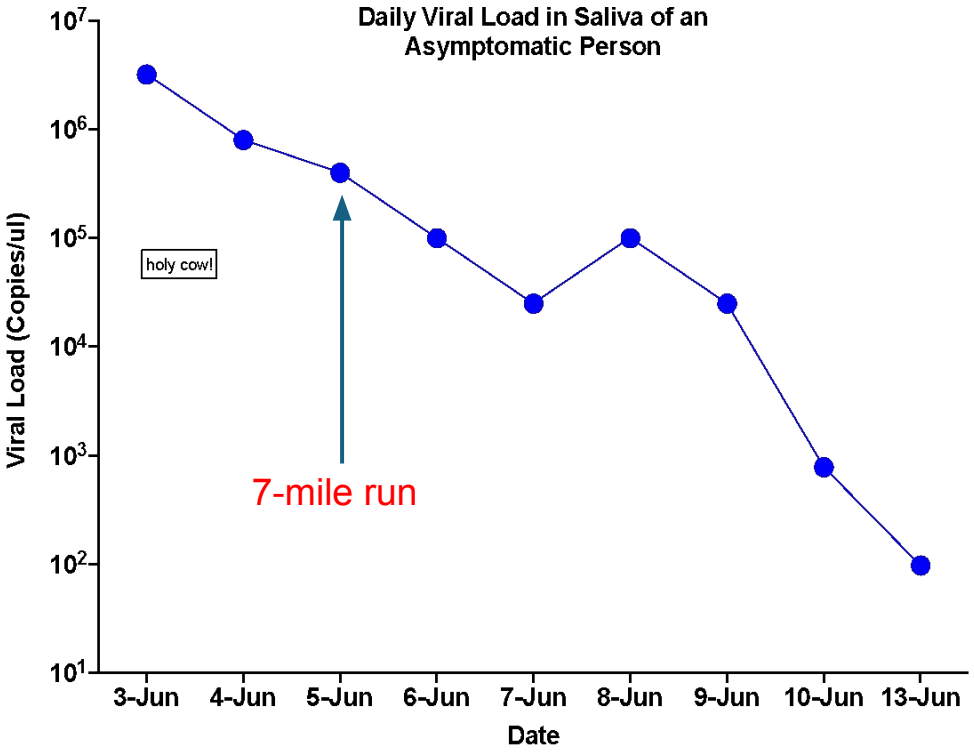


I know this is real.

Most people do not have access to this kind of “verification” and so the levels of trust in PCR diagnostic vary substantially.

Important....

Some Asymptomatic people can have huge viral loads



This guy went on his usual 7 mile run on June 5 and clocked his normal time!!

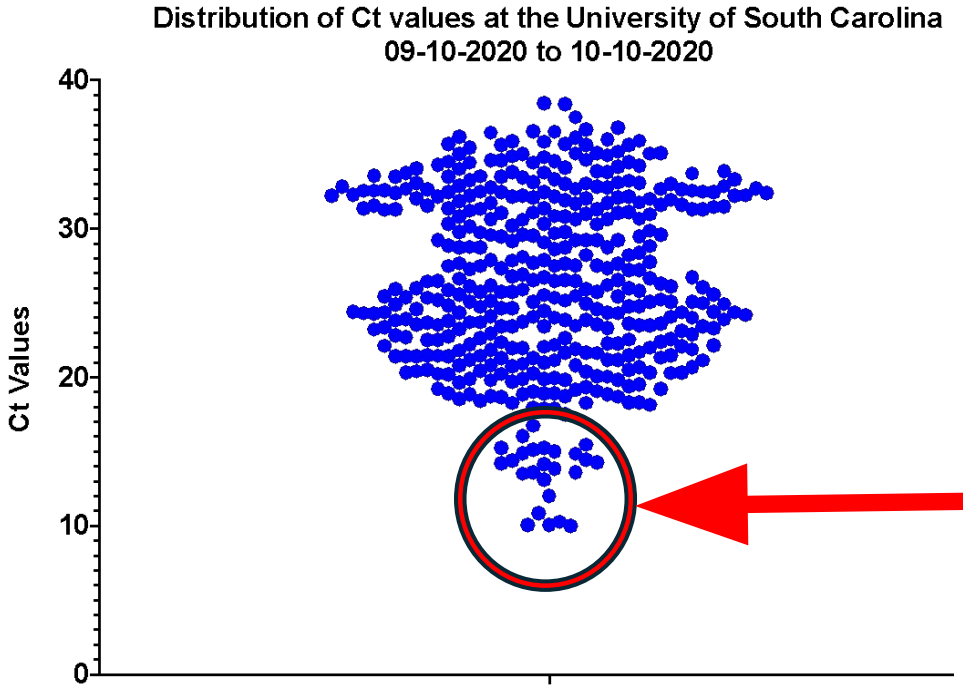
This phenomenon is how the virus spread so well throughout the community.

Silent superspreaders walked among us and spread the virus. Reasonable people grew suspicious.

Future pandemic response needs to deal with this in a verifiable way.

Quantitative analysis of 437 positives picked up during a 1-month window of time

Remember, in PCR, Ct is inversely related to the LOG(2) of viral load.



Superspreaders have 1 billion times more virus than do average people.

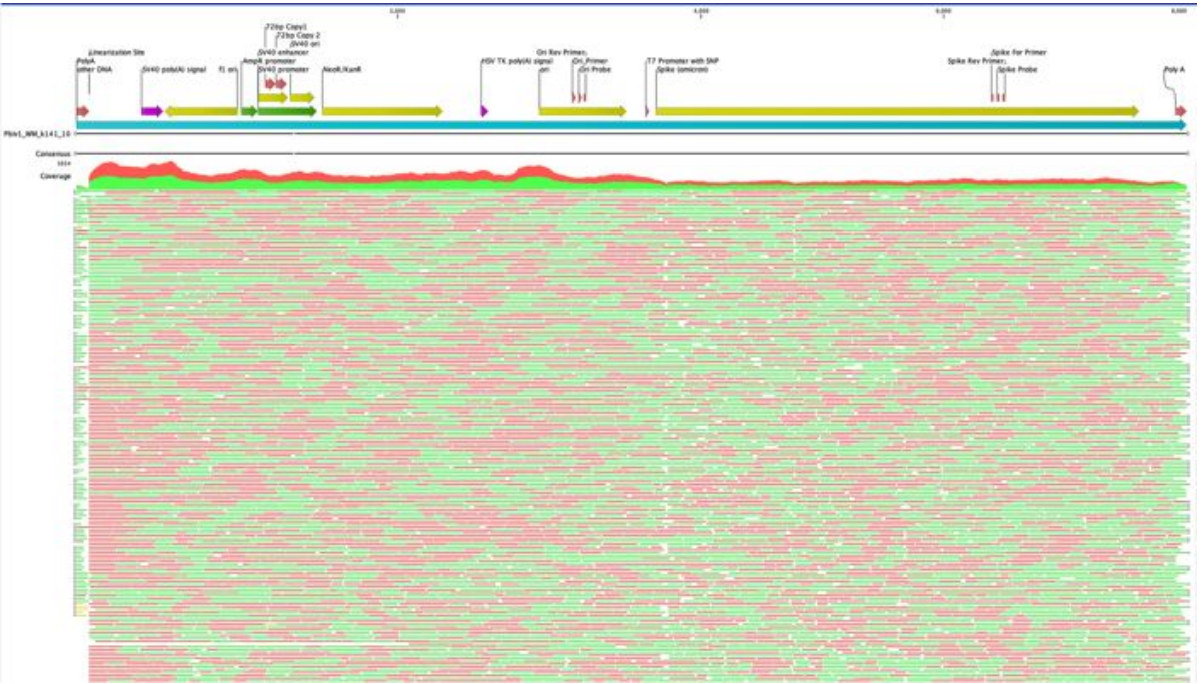
We measured lots of people at the university of south Carolina. Over 300,000 tests in a two-year period More than 95% of positives were or became symptomatic. PCR does NOT have a huge false positive problem.

The silent superspreaders were documented to transmit. Sneaky virus. Causes mistrust to develop.

mRNA Vaccines

- Deployed under emergency. No time for public trust to develop organically.
- Most analyses show 80% protection from death. *This point is debated*.
- Many reports of side effects are currently unexplained. Flippant dismissal of these adverse events has seriously eroded public trust in science, medicine, and public health.
- Sequencing by me and others has identified bits of process DNA contaminating the final products. This DNA could be the cause of some of the rare but serious side effects. Public deserves proper investigation.
- The public has a right to know what is in any product that they consume, vaccines included.

Sequencing analysis of mRNA vaccine



Lots of little pieces of DNA. Easy to to reconstruct the full sequence of where they came from. (molecular forensics). the pieces of DNA are small and could damage the human genome.

With modern DNA sequencing technologies, you do not need to know what you are looking for to find it.

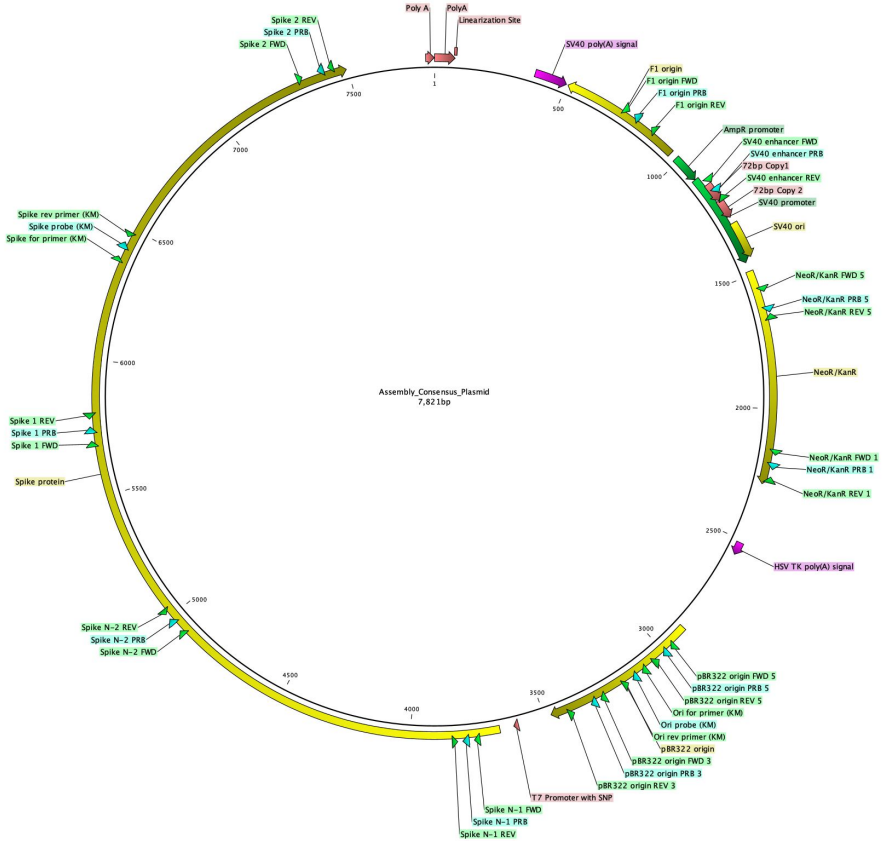
What's in your saliva, what's in your vaccine, what's in your food, what's in your environment,

All such questions can all be answered by sequencing.

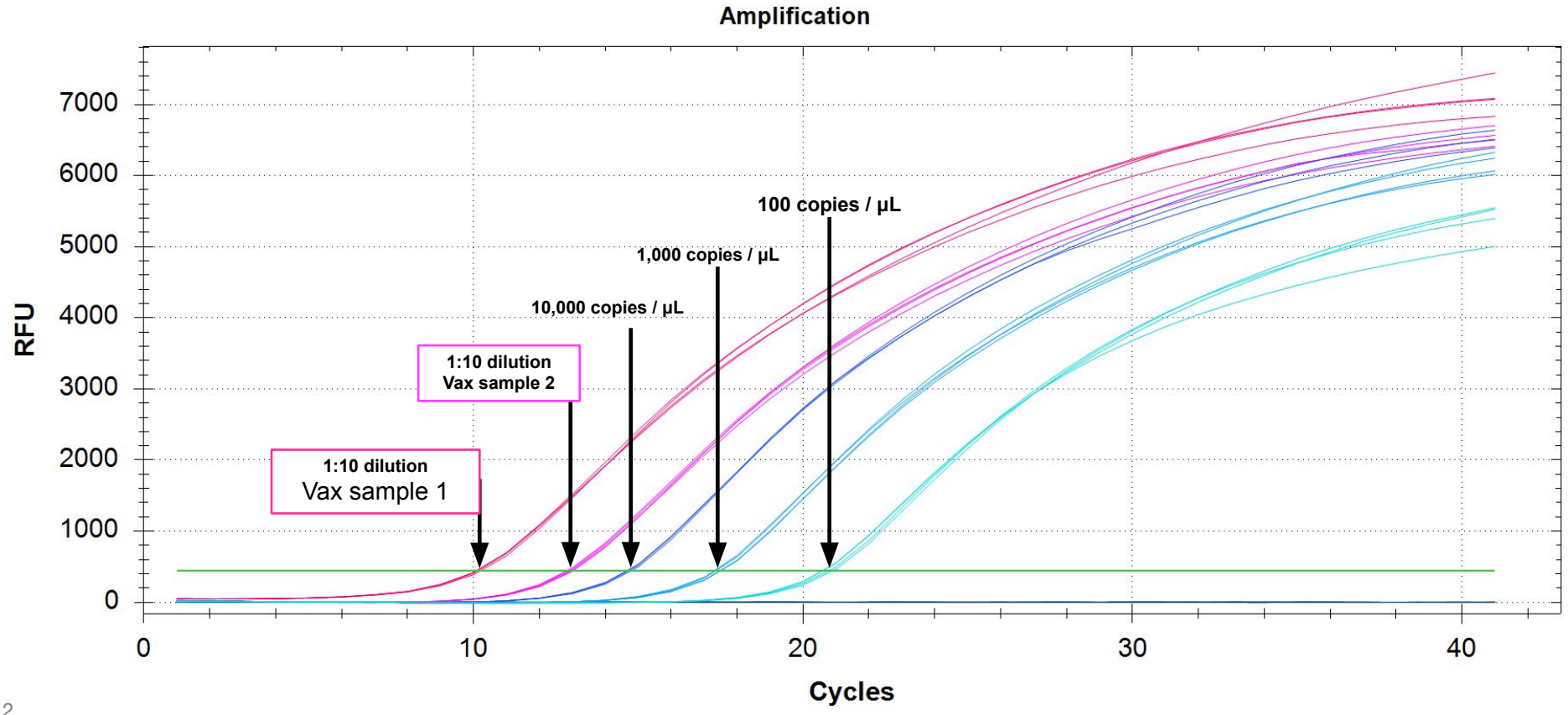
Used properly, deployed decentralized testing can enhance public trust in society and mitigate psychological damage caused by pandemics.

its important to monitor genome integrity of vaccinated people to see if genome modification is happening
The public should have access to results of sequencing hundreds of vaccinated people.

We designed primers and protocols to detect this DNA in any type of sample

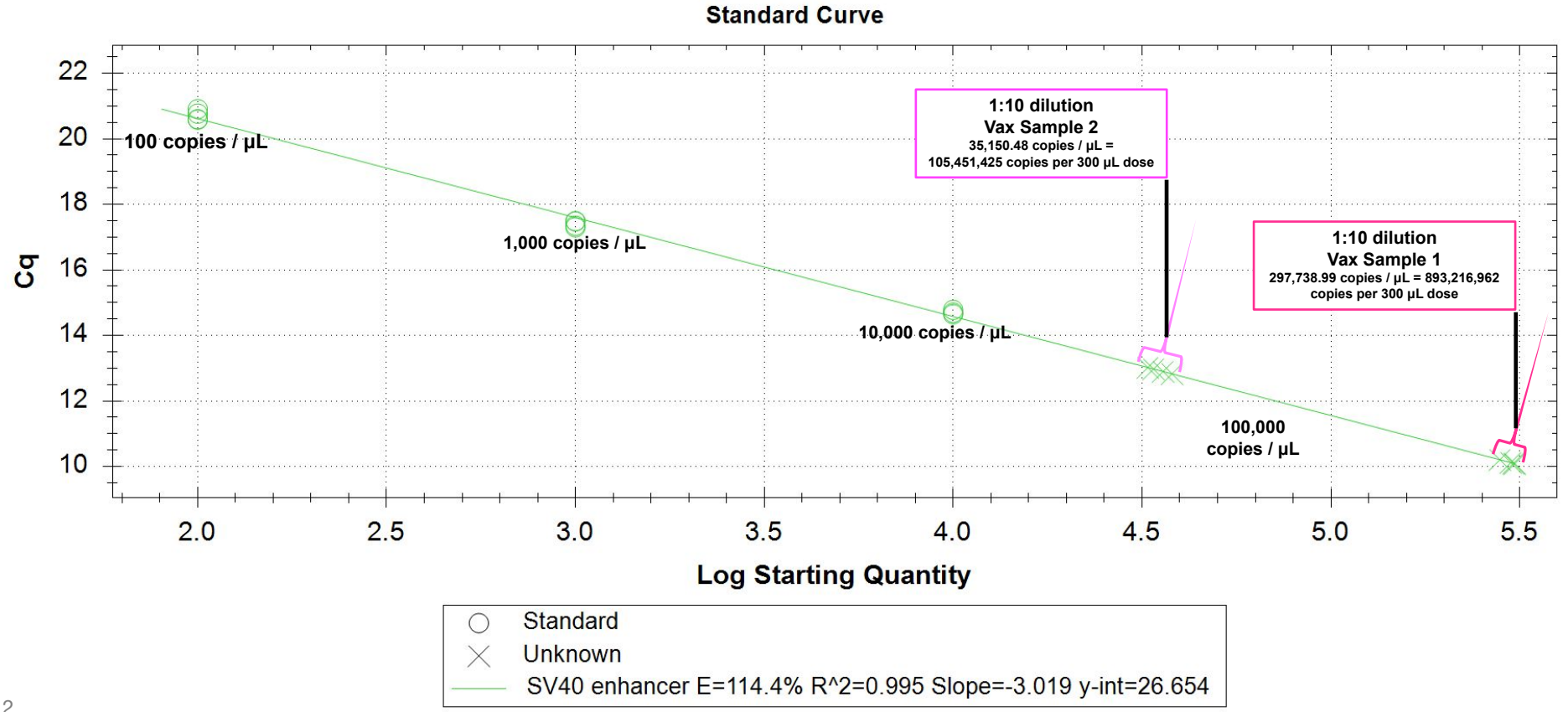


PCR detection of SV40 Promoter/Enhancer region



2024/03/27 data

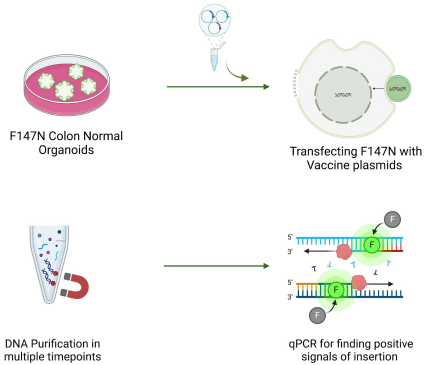
PCR detection of SV40 Promoter/Enhancer region



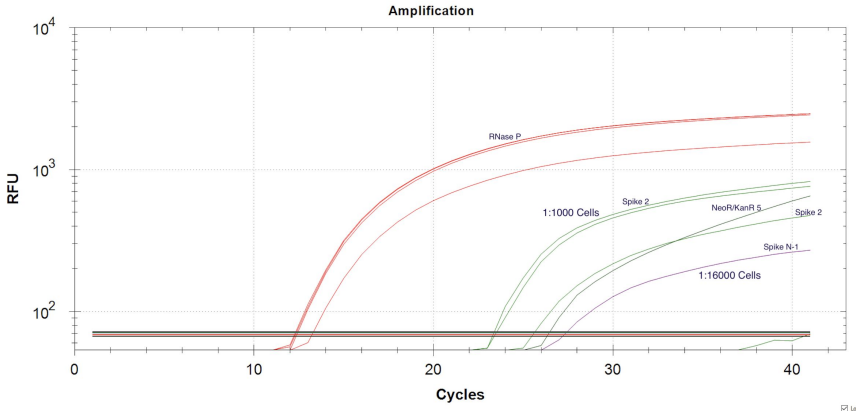
2024/03/27 data

Proof Plasmid DNA in mRNA vaccine modifies human genome. “Vaccination” of a normal colon organoid avatar

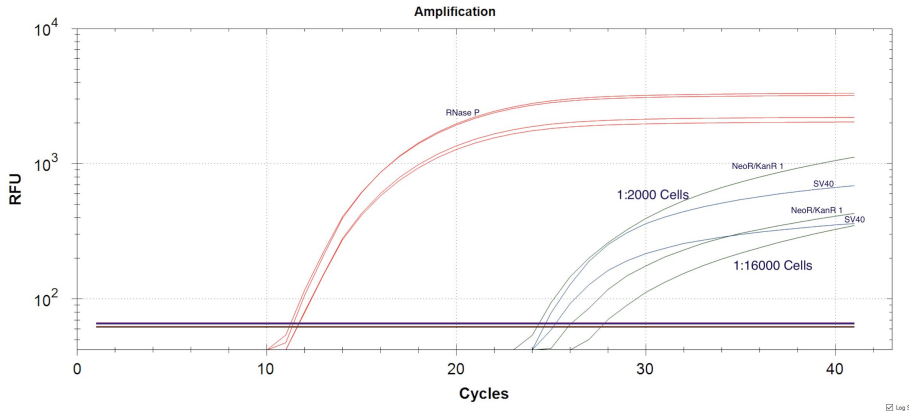
- **Vaccination** of normal colon epithelial cells with mRNA vaccine (we just added it to the media).
- Growth for one month with three washings and replating.
- Isolated genomic DNA and perform PCR to detect presence of plasmid DNA



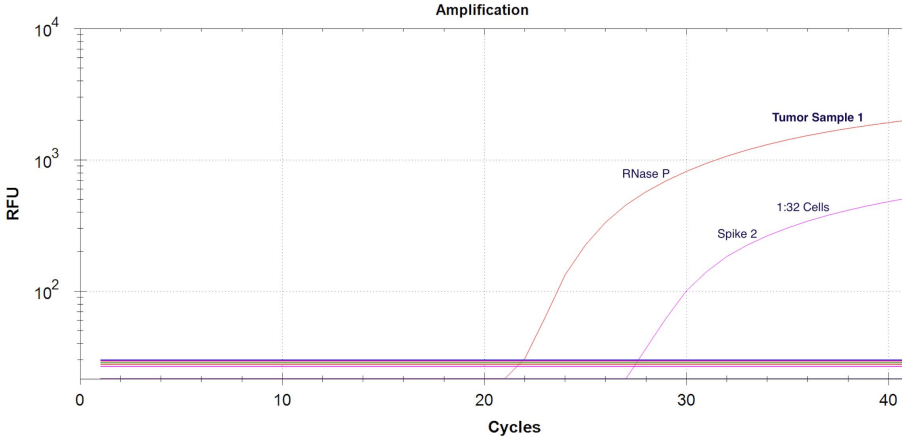
PCR detection of persistent Plasmid DNA

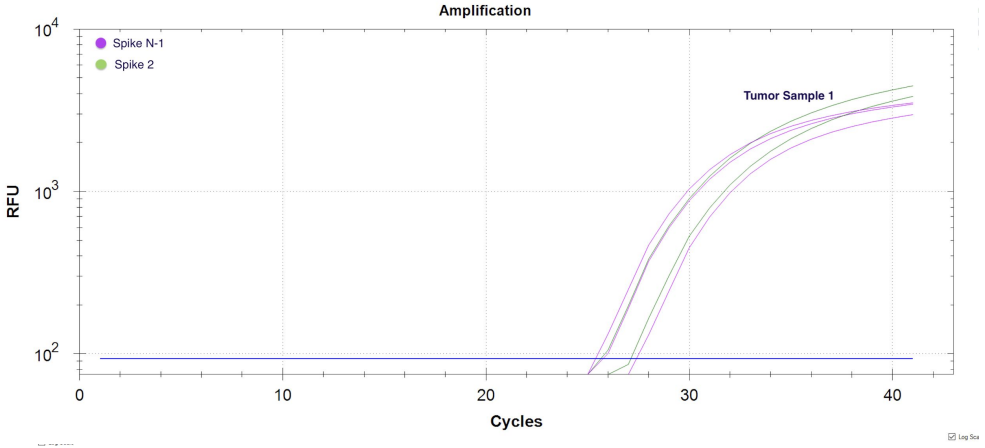


PCR detection of persistent Plasmid DNA



Identification of a tumor sample positive for SPIKE DNA





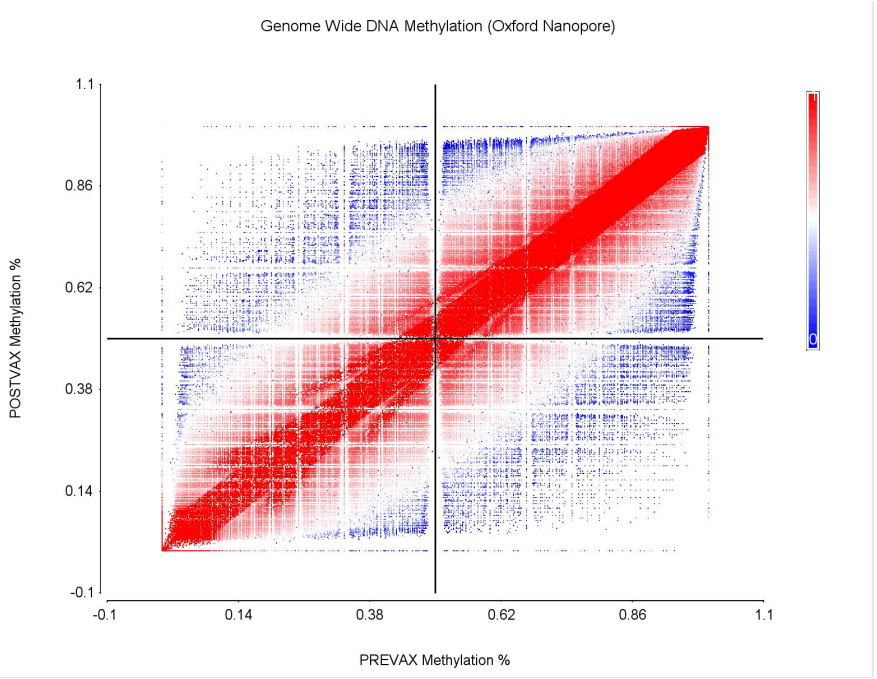
We have checked about 50 unselected tumors that developed in last 3 years and found two potential positives.

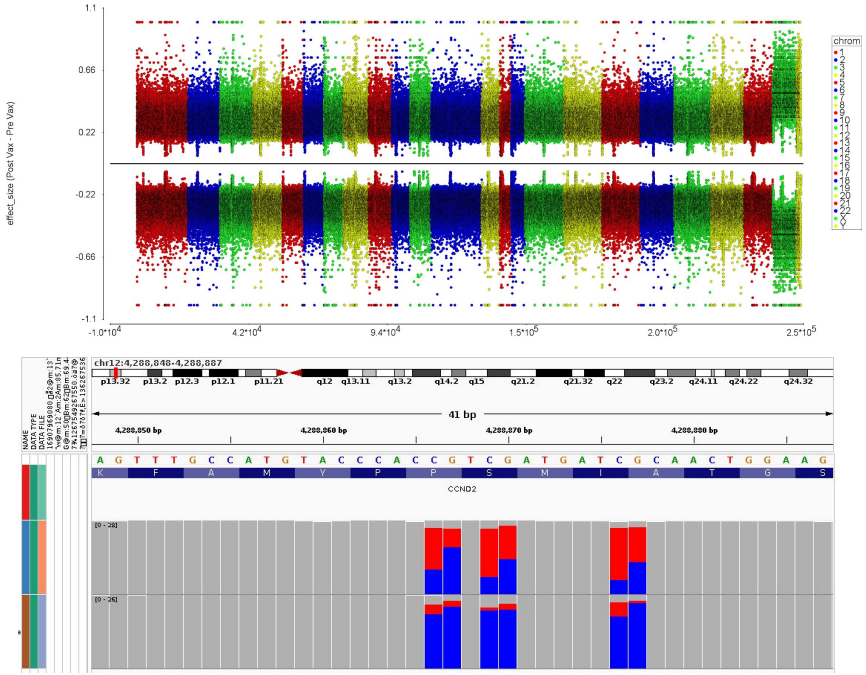
Ongoing work will determine if the vaccine DNA was a driver or passenger event.

DNA methylation determinants of human cellular aging

- DNA can be modified by changing the sequence (insertional mutagenesis of foreign DNA for example)
- DNA is naturally modified as we age by the addition and removal of methyl groups on Cytosine residues.
- DNA methylation closely tracks with and may cause organismal aging.
- Sequence analysis of normal blood cells can agnostically monitor for both types of modifications and serve as an early warning sign of mutagenesis (cancer risk) or accelerated aging.

DNA Methylation Pre-and Post Vaccination





I did this on myself. (i also did it pre and post covid).

One sample is scientifically meaningless, its just to illustrate the power of the technology.

Molecular testing of large numbers of samples from people suffering from long COVID, or taking mRNA vaccines can serve as an early warning indicator of either good long term immunity or unanticipated harm.

Once you know what you are looking for, it's very cheap and easy to survey different kinds of samples for specific changes.

- Virus in human samples : COVID PCR TEST
- Gene fragments in vaccines : PLASMID DNA PCR TEST
- Food products : Pathogen Metagenomic Sequencing
- Environmental samples (dairy farm wastewater) : BIRD FLU PCR TEST
- Specific loci with altered DNA methylation. (DNAMAGE)

Results uploaded to an information blockchain will make such surveys verifiable and improve public trust.

Molecular genetics records the past and can predict the future

- DNA sequence of SARS-COV2 records its unusual evolutionary history
- SC2 RNA sequences in a person predicts sickness (hours).
- Vaccine DNA fragments record past process purity / contamination.
- Vaccine DNA fragments in human DNA can predict future cancer risk (years).
- DNA methylation changes may predict future organ system aging (years).

Final Thoughts

- Pandemics stress test the trust people have in each other and reveal pre-existing lack of social trust.

- Low trust societies fare worse than do high trust societies.

- Molecular biology tools can be used to
- identify (sequence) and detect (PCR) viruses in the environment or asymptomatic people
- identify (sequence) and detect contaminants in medicines, food, or anything else.
- survey people for cancer causing mutations or increases in methylation aging

- Molecular biology tools can best increase public trust and future pandemic preparedness if protocols are decentralized, independent and redundant testing sites are distributed, and all results made public.

- Much of the decentralized pandemic response was ad-hoc, from cowboy labs around the world.

- The public could have benefitted from a molecular biology / public health / medical records Blockchain to enhance trust.

- We should do this now.