BREAKING: Integration of corona vaccine-contaminated DNA into the human cell line genome

2ND SMARTEST GUY IN THE WORLD

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This important article further establishes that the Modified mRNA “vaccines” integrate into the cells. While these contaminated cells do not express the entire spike protein, but, rather, only part of it, the net effect is that the DNA of the “vaccinated” is irrevocably altered.

Any type of integration into the genome, especially when being assaulted by millions of different random sequences from the “vaccine,” will inevitably cause mutations and other damage to the genome, irrespective if the entire spike protein is expressed, or not.

This DNA contamination ultimately results in the plethora of slow kill bioweapon adverse events that we are now seeing in surging amounts, not limited to prion diseases, turbo cancers, SADS, and so on and so forth.

The below is translated from Japanese, and it is a rather technical read, but well worth your time.

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by Mao Arakawa (Okudo Hirokushi)

The essence of the corona vaccine contaminated DNA problem is the possibility of altering the human genome. To validate this possibility, Dr. Ulrike Kaemmerer conducted an experiment to administer the corona vaccine to MCF7 and OVCAR-3 cancer cell lines. Dr. McKernan, consulted by Dr. Kaemmerer, conducted an experiment to detect contaminated DNA from these cell lines. He reports on his blog the first case of contaminated DNA integration into the cancer cell line genome. (2SG: yesterdays article

entitled, [UPDATE: Doctors Warn mRNA "Vaccines" Could Spur Epidemic of Prion Brain Diseases] addresses this.)

I was interested, so I attempted to recreate the DNA recombinant event that Dr. McKernan identified. In this article, I will show the results of my analysis.

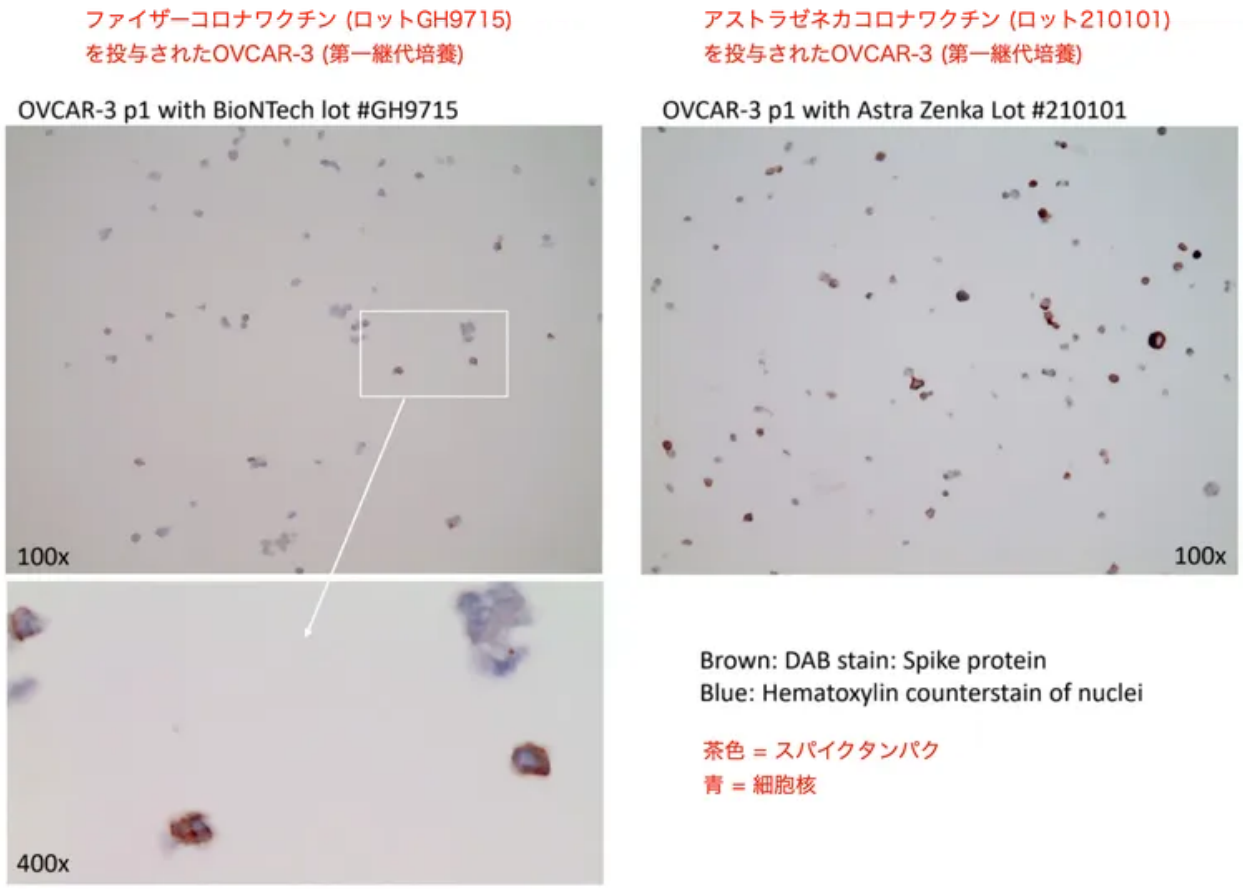

Figure 1

Dr. Kaemmerer administered the corona vaccine from Pfizer and AstraZeneca to the ovarian tumor cell line OVCAR-3 and, after subculture, confirmed the expression of the spikutanpak by immunohistochemical staining. Deep Sequencing comes at a high cost; therefore, preliminary experiments are required in advance to perform DNA detection experiments. Dr. McKernan first screened post-vaccination cells with qPCR and targeted qPCR-positive cells for deep sequencing.

Contaminated DNA that is not integrated into the genome is diluted with subculture. In fact, the Ct value of the vector was Ct 30.28 in the first generation, but it was 34.72 in the second generation. The difference in 4Ct is 16 times the difference, and that is the lower concentration in the second passage. Dr. McKernan extracted DNA from two cells subcultured and performed deep sequencing. Sequence data detected SV40, replication origin and spiked DNA. Spike DNA was detected in the full genomic shotgun library of vaccine-treated samples with 3000x coverage. (Coverage means the percentage of the total base pair or locus of the genome covered by sequencing.) Since the coverage in the

human genome was 30 times, we can see that the DNA with a large number of copies of the genome was invading the cell.

As a result, strangely, SNP (monobasic polymorphism) was detected in deep sequencing at the origin of the vaccine plasmid replication (F1 and SV40). This SNP does not exist in the vaccine. In other words, it seems that plasmids are mutating in cells. Also, the coverage of deep sequencing in the replication origin area is higher than average, and the number of copies observed is relatively high, which means that the DNA embedded in the cell may be duplicated and mutated. I mean. Originally, plasmids and SV40 DNA replication require specific enzymes not owned by human cells. Experiments such as the introduction of large amounts of microDNA fragments containing replication points into cells are not usually performed in molecular genetics. It is possible that unexpected DNA replication is occurring within the cell.

A total of two genomic integrations were observed in the vaccinated cell line from the analysis of Deep Sequencing by Dr. McKernan. Individual arrays of deep sequencing are called「leads」. It was very interesting data, so I tried to re-parse the lead myself.

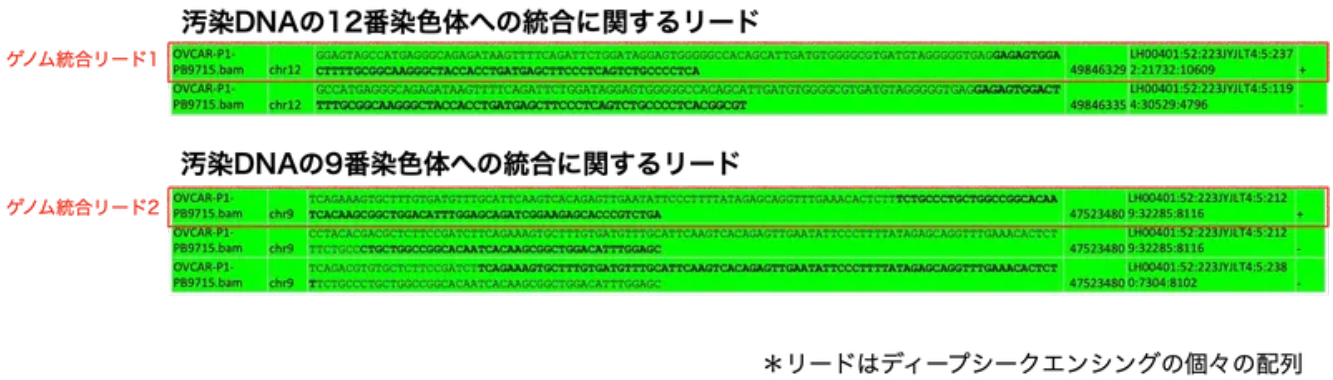

Figure 2

Figure 2 is a lead showing genomic integration in Dr. McKernan's Deep Sequencing Analysis. The subject of the analysis is Genome Integration Leads 1 and 2. You can also read a lot of information from short array data. This time in comparison with the human genomeblat searchTo find homologyblast searchI used it.

Now, after that, it will be my own re-parse.

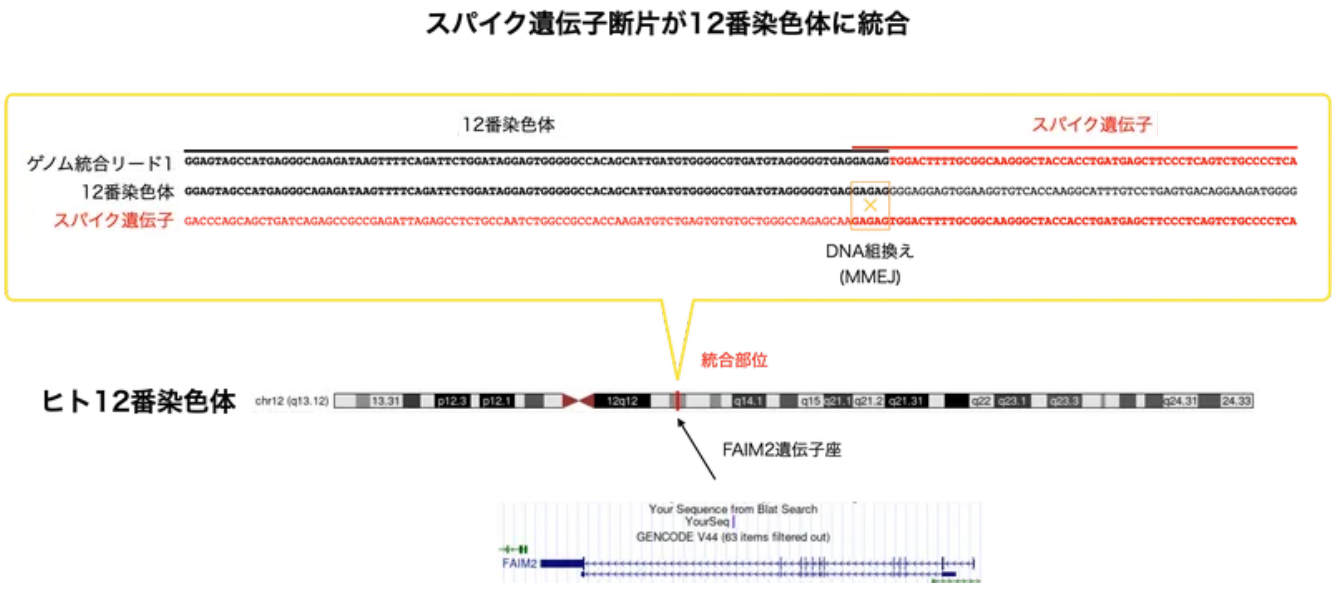

Figure 3

The top of the array in Figure 3 is the lead. As you can tell by aligning this lead with the 12th chromosome (black) and the spike gene (red) of the Pfizer Corona vaccine, the 12th chromosome (black) is on the way to the spike gene (red). I am switching. And there is a short identical array (here GAGAG) in the place of switching. You can see that the end-recombination (MMEJ, Microhomology-mediated end joining) mediated by microhomology (microhomology) recombinates the contaminated DNA and human genome. Since MMEJ involves multiple intracellular DNA repair enzymes, this recombination is an artifact (mistake product) in the test tube. Instead, gene recombination may have occurred in cells.

Genome integration occurs on the long arm of chromosome 12, and the FAIM2 gene is present at this locus. FAIM2 is a gene that has been suggested to be associated with cancer malignancy. Recombinations occur on introns (arrays that do not encode proteins), but I do not know how such mutations also affect gene expression.

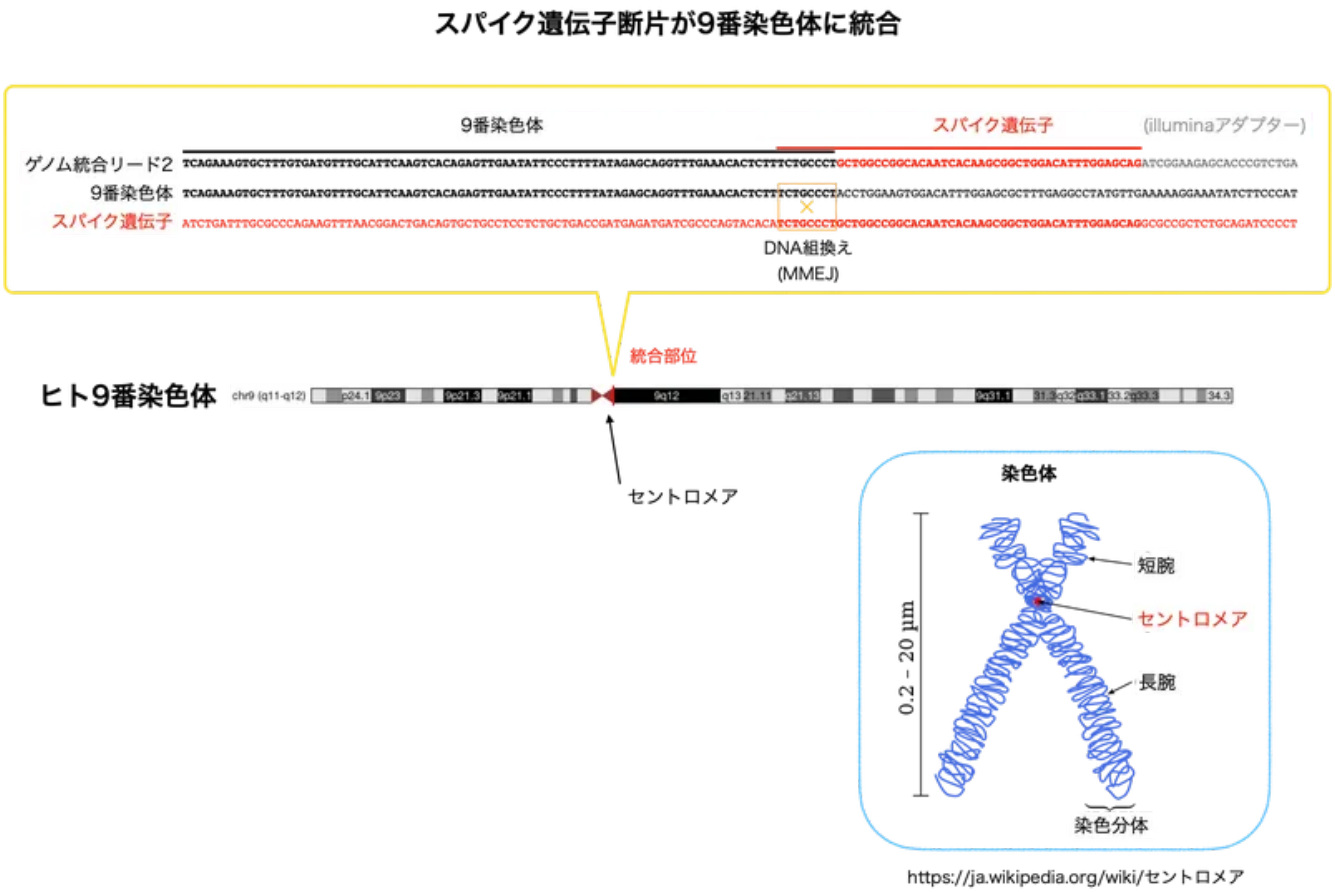

Figure 4

Another example of genomic integration is Figure 4. If you align this lead with chromosome 9 (black) and spike gene (red), you can see that in the lead, chromosome 9 (black) is switching to the spike gene (red) on the way. There is a short identical array (here TCTGCCCT) in the place where this example also switches. After all, it is believed that the contaminated DNA and the human genome were recombined using microhomology. Since there are multiple pathways for DNA repair, which repair pathway is used when foreign DNA is taken into the genome is case-by-case.

Part of the lead had an Illumina adapter array left. Adapter arrays are arrays granted to PCR amplify and sequence DNA for deep sequencing. Originally, the adapter array is removed during parsing, but often the removal is inadequate and remains in the lead.

Integration of contaminated DNA into the genome is occurring near Centromea. Let's talk a little about Centromea. Two chromosomes with the same genetic information that can be done after DNA replication are chromatids (sister chromatids). The chromatids are connected until the chromosomes are distributed during cell division, but the region

on the connected DNA is Centromea. As such, Centromea is an important area for chromosome separation and distribution.

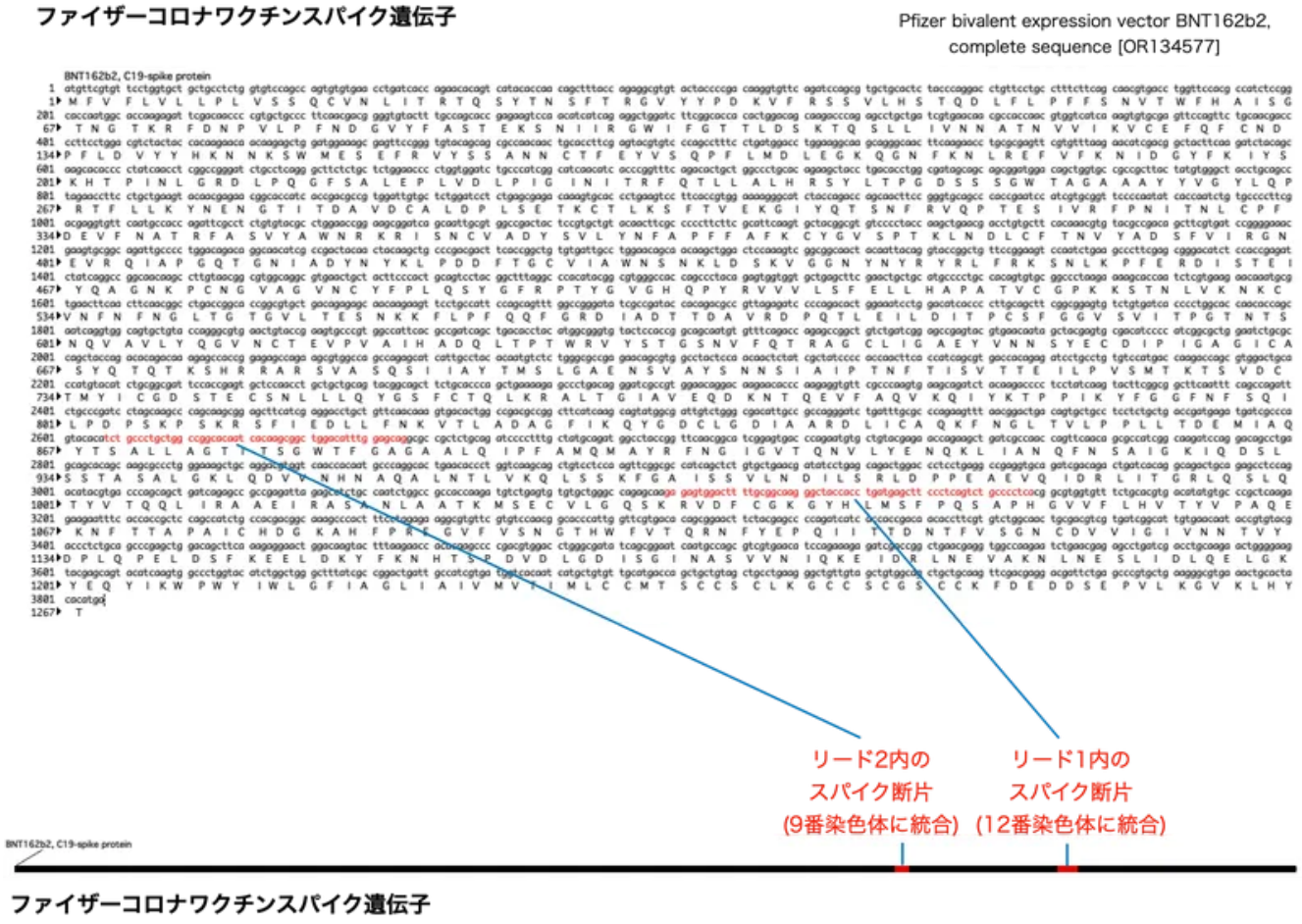

Figure 5

Figure 5 is about the DNA fragments of the spike gene integrated into the genome. On the Pfizer Corona vaccine spike gene, the sequence found in the genome integrated lead was written in red. Due to lead length limitations, the actual integrated array will be even larger. The integrated sequence is part of the spike gene, and it is not possible to make a full-length spike sequence. However, it is unpredictable how contaminated DNA will be inserted into any area of the genome and have any effect.

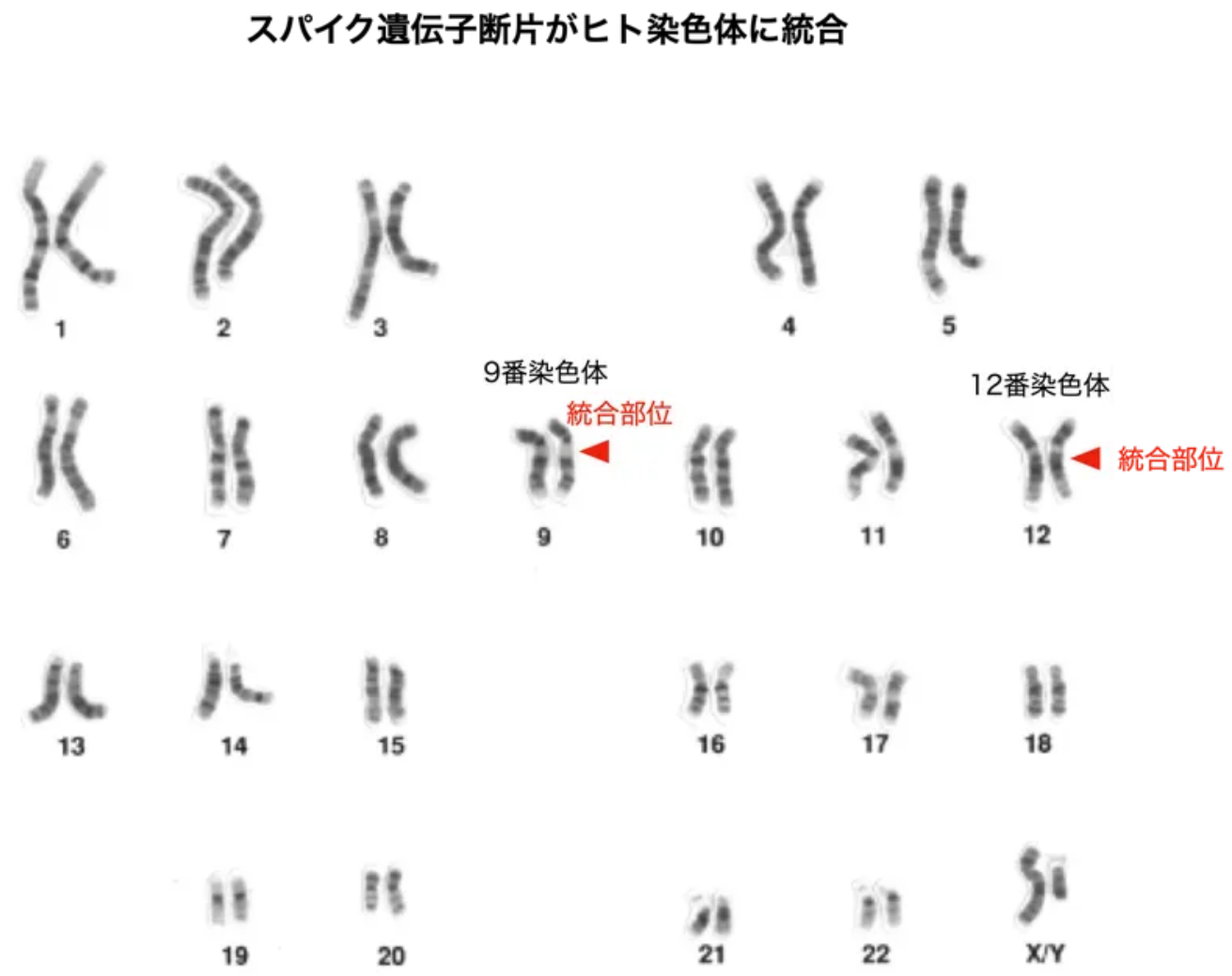

Figure 6

Nucleotype (cario type) means the size, shape, and number of chromosomes. Human chromosomes consist of a total of 46 22 pairs of autosomal and one pair of sex chromosomes. The autosomal is assigned the number 1 chromosome, number 2 chromosome,, number 22 chromosome and number in order of size. The integrated site of contaminated DNA is the FAIM2 locus on the long arm of chromosome 9 and near Centromea on chromosome 12.

The genomic integration observed this time is the first two cases in cultured cell experiments, but the specific identification of recombinant sequences with the human

genome of contaminated DNA is a major advance. Further verification experiments will be advanced in the future. Genome integration, as in Figure 6, does not know which locus actually occurs on the genome. This is exactly the「 shotgun attack on the genome 」. What happens in cultured cells can also occur in normal cells, with a wide variety of alterations depending on the site of genomic integration. The first predicted catabolism is cancer induction and malignancy. And then, the ones that manifest themselves over time are various genetic diseases.

What is known as a factor that causes genomic damage is, for example, radiation exposure, but genomic modification by contaminated DNA is different in that it is due to fragments of artificially created genes, and random mutations which are akin to radiation. But it is fundamentally different in nature. This experiment in cultured cells epitomizes genomic integration of contaminated DNA. This is a real problem that a large number of humans around the world, under the name of vaccination, are now experiencing a「 transfection human body experiment 」of contaminated DNA.

The genomic modification of humanity is a direct consequence of the largest experiment in history of mRNA drug substance harm, and in the future it may be etched in history as the「 **original sin** 」of humanity.

They want you dead.

Do NOT comply.