



Nipah PCR Forward Primer Matches Human Genome—A Built-In Pathway to False Positives as Media Hypes 'Deadly Outbreak'

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Are PCR tests showing positive results for human genetics, not Nipah?

JON FLEETWOOD
JAN 26



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Mainstream outlets are amplifying alarm over an alleged Nipah virus outbreak in India while confirming that the cases are being “confirmed” by RT-PCR testing.

But the PCR test at the center of that confirmation relies on a forward primer sequence that aligns to the human genome across numerous loci, creating a straightforward mechanism for false positives: amplification of human genetic material rather than viral RNA.

Are these tests showing positive results for human genetics, not Nipah?

Is this a false outbreak?

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BLAST Results Confirm Nipah PCR Primer Matches Human Genetics

The sequence in question is published in the [World Organisation for Animal Health \(OIE\) Terrestrial Manual](#), which describes a TaqMan real-time RT-PCR assay targeting the Nipah virus N gene as a primary diagnostic method for confirming clinical cases.

- The original TaqMan 5' nuclease PCR chemistry patent ([U.S. Patent 5,210,015](#)) explicitly states that a detectable positive signal can be generated from polymerase binding to a single primer alone—through probe cleavage—without requiring full target amplification.
- In plain terms, the chemistry used in PCR testing can produce a “positive” signal simply because a primer sticks to genetic material—even if the virus the test claims to detect is not there—raising the possibility that outbreaks defined by these tests can be created by the assay itself rather than by real infections.

The OIE manual lists the Nipah N-gene forward primer as: NiV_N_1198F:
TCA-GCA-GGA-AGG-CAA-GAG-AGT-AA.

Table 2. Real-time RT PCR (Taqman) assays for the detection of HeV and NiV

Assay	Oligo	Name	Primer sequence (5'–3')	Probe label (5'–3')
HeV_TQM_M	Forward	HeV M 5755F	CTT-CGA-CAA-AGA-CGG-AAC-CAA	
	Reverse	HeV M 5823R	CCA-GCT-CGT-CGG-ACA-AAA-TT	
	Probe	HeV M 5778P	TGG-CAT-CTT-TCA-TGC-TCC-ATC-TCG-G	FAM-TAMRA
HeV_TQM_N	Forward	HeV N119F	GAT-ATI-TTT-GAM-GAG-GCG-GCT-AGT-T	
	Reverse	HeV N260R	CCC-ATC-TCA-GTT-CTG-GGC-TAT-TAG	
	Probe	HeV N198-220P	CTA-CTT-TGA-CTA-CTA-AGA-TAA-GA	FAM-MGBNFQ
NiV_TQM_N	Forward	NiV_N_1198F	TCA-GCA-GGA-AGG-CAA-GAG-AGT-AA	
	Reverse	NiV_N_1297R	CCC-CTT-CAT-CGA-TAT-CTT-GAT-CA	
	Probe	NiV_N_1247comp	CCT-CCA-ATG-AGC-ACA-CCT-CCT-GCA-G	FAM-TAMRA

That is the primer sequence tested for in samples purportedly containing Nipah.

However, I carried out a BLAST alignment of NiV_N_1198F against the human reference genome (GRCh38) that returned high-identity matches distributed across the genome, including contiguous match lengths that meet typical priming thresholds used in PCR reactions.

In other words, the primer used to detect Nipah matches human genetics, meaning the test can amplify human DNA and generate a “positive” signal even when no virus is present.

The BLAST alignments include multiple perfect and near-perfect binding sites spanning many chromosomes.

Standard Nucleotide BLAST

blastn

blastp

blastx

tblastn

tblastx

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Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

TCAGCAGGAAGGCAAGAGAGTAA

Query subrange [?](#)

From

To

Or, upload file

No file chosen [?](#)

Job Title

NiV_N_1198F

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database

☒ Standard databases (nr etc.): ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus ☐ Experimental databases

RefSeq Genome Database (refseq genomes) [?](#)

Organism

Optional

humans (taxid:9605)

☐ exclude

[Add Organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

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(GPIPE/9606/RS_2025_08/GCF_000001405.40_top_level)
See details

Query ID
lcl|Query_6051197

Description
None

Molecule type
nucleic acid

Query Length
23

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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒ Homo sapiens chromosome 3, GRCh38.p14 Primary Assembly	Homo sapiens	34.6	474	100%	0.69	95.24%	198295559	NC_000003.12
☒ Homo sapiens chromosome 4, GRCh38.p14 Primary Assembly	Homo sapiens	33.7	637	100%	0.69	100.00%	190214555	NC_000004.12
☒ Homo sapiens chromosome 11, GRCh38.p14 Primary Assembly	Homo sapiens	33.7	412	100%	0.69	100.00%	135086622	NC_000011.10
☒ Homo sapiens chromosome 13, GRCh38.p14 Primary Assembly	Homo sapiens	33.7	318	100%	0.69	100.00%	114364328	NC_000013.11
☒ Homo sapiens chromosome 2, GRCh38.p14 Primary Assembly	Homo sapiens	32.8	664	100%	2.4	95.00%	242193529	NC_000002.12
☒ Homo sapiens chromosome 15, GRCh38.p14 Primary Assembly	Homo sapiens	32.8	349	100%	2.4	95.00%	101991189	NC_000015.10
☒ Homo sapiens chromosome 1, GRCh38.p14 Primary Assembly	Homo sapiens	31.9	725	100%	2.4	100.00%	248956422	NC_000001.11
☒ Homo sapiens chromosome 5, GRCh38.p14 Primary Assembly	Homo sapiens	31.9	498	100%	2.4	100.00%	181538259	NC_000005.10
☒ Homo sapiens chromosome 6, GRCh38.p14 Primary Assembly	Homo sapiens	31.9	669	100%	2.4	100.00%	170805979	NC_000006.12
☒ Homo sapiens chromosome 7, GRCh38.p14 Primary Assembly	Homo sapiens	31.9	469	100%	2.4	100.00%	159345973	NC_000007.14
☒ Homo sapiens chromosome 10, GRCh38.p14 Primary Assembly	Homo sapiens	31.9	526	100%	2.4	100.00%	133797422	NC_000010.11
☒ Homo sapiens chromosome 8, GRCh38.p14 Primary Assembly	Homo sapiens	31.0	494	100%	8.4	94.74%	145138636	NC_000008.11
☒ Homo sapiens chromosome 12, GRCh38.p14 Primary Assembly	Homo sapiens	31.0	318	100%	8.4	94.74%	133275309	NC_000012.12
☒ Homo sapiens chromosome 14, GRCh38.p14 Primary Assembly	Homo sapiens	31.0	464	100%	8.4	94.74%	107043718	NC_000014.9
☒ Homo sapiens chromosome 18, GRCh38.p14 Primary Assembly	Homo sapiens	34.6	295	96%	0.69	95.24%	80373285	NC_000018.10
☒ Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly	Homo sapiens	33.7	290	96%	0.69	100.00%	90338345	NC_000016.10
☒ Homo sapiens chromosome X, GRCh38.p14 Primary Assembly	Homo sapiens	32.8	441	96%	2.4	95.00%	156040895	NC_000023.11
☒ Homo sapiens chromosome 17, GRCh38.p14 Primary Assembly	Homo sapiens	31.0	343	96%	8.4	94.74%	83257441	NC_000017.11
☒ Homo sapiens chromosome 19, GRCh38.p14 Primary Assembly	Homo sapiens	31.0	116	96%	8.4	94.74%	58617616	NC_000019.10
☒ Homo sapiens chromosome 9, GRCh38.p14 Primary Assembly	Homo sapiens	29.2	227	96%	29	94.44%	138394717	NC_000009.12
☒ Homo sapiens chromosome Y, GRCh38.p14 Primary Assembly	Homo sapiens	34.6	215	91%	0.69	95.24%	57227415	NC_000024.10
☒ Homo sapiens chromosome 13 genomic patch of type FIX, GRCh38.p14 PATCHES HG2509_PATCH	Homo sapiens	30.1	30.1	91%	8.4	90.48%	409912	NW_021160012.1
☒ Homo sapiens chromosome 14 genomic patch of type FIX, GRCh38.p14 PATCHES HG2510_PATCH	Homo sapiens	30.1	30.1	91%	8.4	90.48%	399183	NW_021160013.1
☒ Homo sapiens chromosome 15 genomic patch of type FIX, GRCh38.p14 PATCHES HG2511_PATCH	Homo sapiens	30.1	30.1	91%	8.4	90.48%	396515	NW_021160018.1
☒ Homo sapiens chromosome 22 genomic patch of type FIX, GRCh38.p14 PATCHES HG2512_PATCH	Homo sapiens	30.1	30.1	91%	8.4	90.48%	412368	NW_021160026.1
☒ Homo sapiens unplaced genomic scaffold, GRCh38.p14 Primary Assembly HSCRUN_RANDOM_CTG1	Homo sapiens	30.1	30.1	91%	8.4	90.48%	182896	NT_113901.1
☒ Homo sapiens chromosome 2 genomic patch of type NOVEL, GRCh38.p14 PATCHES HSCR2_6_CTG1	Homo sapiens	32.8	32.8	87%	2.4	95.00%	284971	NW_025791763.1

PCR amplifies whatever the primer binds to.

When a primer binds host (human) DNA at scale, the assay’s output can reflect host genetics rather than a pathogen.

In practical terms, a “positive” can be created by the assay’s binding behavior

alone, depending on sample composition, amplification conditions, cycle thresholds, and contamination controls.

This primer-to-human-genome alignment issue lands in the middle of a media cycle pushing the public toward fear and potential government-imposed outbreak response.

Mainstream Nipah Reporting

[PEOPLE](#) reports that two nurses near Kolkata were identified as Nipah cases, that 180 people had been tested, and that RT-PCR testing is being used in surveillance and bat screening in West Bengal.

Those headlines leave out the technical detail that determines whether a PCR “confirmed” case is meaningful: whether the primers uniquely target Nipah virus.

A primer that repeatedly aligns to human DNA introduces a simple diagnostic problem.

It creates a pathway for false positives through ordinary lab dynamics and also expands the space for manufactured outcomes, because the assay can generate a positive signal from material already present in the patient.

Are “Nipah cases” being manufactured?

PCR Test Inventor’s Warning

Dr. Kary Mullis, the late inventor of the PCR test, said in a 1997 [interview \(here\)](#) that his test should not be used to determine whether a subject is infected with a virus.

This is because the test “can find almost anything in anybody” if its parameters are set high enough, tainting the results, according to the Nobel Prize winner.

“Anyone can test positive for practically anything with a PCR test. If you run it long enough... you can find almost anything in anybody,” Dr. Mullis said. “It doesn’t tell you that you’re sick.”

Mullis’ warning now appears directly relevant to a system where public health emergencies can be declared based on tests that do not require a virus to produce a positive result.

Bottom Line

Health agencies, laboratories, and media outlets reporting “PCR-confirmed Nipah” now face a basic burden: publish the primer specificity analysis, disclose the cycle threshold and control strategy used to rule out host-genome amplification, and demonstrate that the reported positives are tied to viral targets rather than to human sequence overlap.

Until that specificity question is addressed in the open, PCR-confirmed Nipah claims rest on a test design that can produce its own signal.

Public fear, quarantine measures, and international headlines are now being driven by a test that cannot be assumed to distinguish between human genetic material and the virus it is supposed to identify.

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