

The Pan-SL-CoV/GD sequences may be from contamination.

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ABSTRACT

Recently, There were much hype about an alleged SARS-like coronavirus being found in samples of Malayan pangolins (*Manis Javanica*) possessing nearly identical RBD to the SARS-CoV-2 coronavirus. Prominent journals cite the alleged discovery to claim that pangolins may be one of a possible intermediate host for the zoonotic transmission of SARS-CoV-2 to humans.

Here, we report that all databases used to support such a claim, upon which metagenomic analysis was possible, contained unexpected reads and was in serious risk of contamination. Here we also report that the presence of unexpected reads are directly related to the presence of coronavirus reads. Finally, we deduced the actual causative agent of the death of the pangolins sampled in GuangDong 2019 where the claim of coronavirus detections was made.

METHODS

The NCBI Trace tool

The NCBI SRA archive come with it's own tool called Trace, which identifies the origin or reads within the SRA dataset through the recognition of unique K-mers within the nucleotide sequence. Multiple reads of 32 nucleotides is taken from each read to identify the reads toward an origin by comparison with a large database of reference sequences, which produces a classification signal. Then read of 64 nucleotides are taken from each of the read for definitive mapping toward species in the reference database. If any one of the 32nt or 64nt K-mers are found in more than one reference sequence, the reads are instead classified at the lowest phylogenetic classification node where reference sequences containing such a K-mer is found.

The 32nt TRACE generate a "strong signal" classification of sequence origin useful for the deduction of the content of the sample by organism of origin, accessed via the NCBI Krona charting tool,

While the 64nt TRACE generate a definitive classification signal used for the exact tracing of reads to the origin from a specific Species/Taxon, used for the exact classification of reads.

Both the 32nt and 64nt TRACE analysis classify their reads according to the lowest common taxonomical node where K-mers from said read are present in the reference sequence database, a strategy known as "lowest non-ambiguous mapping". Such a strategy avoids the problem with RNA degradation or sequencing errors by excluding potential errors in reads, without introducing potential ambiguous classification by clustering ambiguous reads under the lowest common classification node such ambiguity is found.

Therefore, if TRACE gives an identification to a specific taxonomical node for a sequence read, it could be from any of the taxonomical nodes and species classified under the node, but it could not be from a taxonomical node or species that is not under said node. E.g. if TRACE says hominoidea which was classified under Catarrhini; Simiiformes; Haplorrhini; Primates; Euarchontoglires, Then it can't be from a pangolin since pangolins (Manis Spp.) are classified under Pholidota; Laurasiatheria. The lowest common classification node between Primates and Pangolins is Boreoeutheria—reads from parts of the genomes shared between Primates and Pangolins will only be classified to Boreoeutheria, but not further classified down toward either Laurasiatheria or Euarchontoglires. And definitely will not be classified individually toward Pholidota or Primates, or any child nodes or phylogenetic nodes under them.

Specific BLAST analysis

Whenever a genus or species is provided by analysis, a specific BLAST analysis is performed to confirm the presence of reads toward the exact species by a search of the database in question with representative reference sequences of the specific species in question in look for matches that is either: 100% match, or: contained no 100% matches on BLAST when queried against the Pangolin reference sequences available on GanBank.

RESULTS

The Accession numbers and contents of all Pan-SL-CoV/GD related sequencing experiments are listed under the following table.

Table 1: List of available GD Pangolin sample datasets as provided under NCBI GenBank. By Accession number, size and citation by thesis (if claimed to have SARS-CoV-2 related reads by paper).

| Accession number | Size | SARS-CoV-2-like Coronavirus Identified and Cited? |
|----------------------------|------------|---|
| SRX6893158 | 16,491,648 | |
| SRX6893157 | 9,275,501 | Lung12 [3] SRR10168374 |
| SRX6893156 | 22,220,187 | Lung11 [1] |
| SRX6893155 | 18,067,615 | Lung09 [1] [3] SRR10168376 |
| SRX6893154 | 16,414,925 | Lung08 [1] [3] [4] SRR10168377 |
| SRX6893153 | 19,045,923 | Lung07 [1] [3] [4] SRR10168378 |
| SRX6893152 | 13,527,964 | |
| SRX6893151 | 16,068,654 | |
| SRX6893150 | 12,967,281 | |
| SRX6893149 | 12,590,769 | |
| SRX6893148 | 15,273,939 | |

| | | |
|----------------------------|---------------------------|------------------------|
| SRX6893147 | 15,975,904 | |
| SRX6893146 | 19,038,817 | |
| SRX6893145 | 19,055,973 | |
| SRX6893144 | 15,350,468 | |
| SRX6893143 | 11,527,782 | |
| SRX6893142 | 20,045,443 | |
| SRX6893141 | 18,903,834 | |
| SRX6893140 | 19,986,780 | |
| SRX6893139 | 39,738,679 | Lung02 [3] SRR10168392 |
| SRX6893138 | 22,900,426 | |
| SRX7756769 | 107,267,359 PRJNA607174** | M1[2]*** |
| SRX7756766 | 273,651,431 PRJNA607174** | |
| SRX7756765 | 196,761,202 PRJNA607174** | |
| SRX7756764 | 222,286,763 PRJNA607174** | |
| SRX7756763 | 212,161,250 PRJNA607174** | |
| SRX7756762 | 232,433,120 PRJNA607174** | M6[2]*** |
| SRX7756761 | 113,900,941 PRJNA607174** | |
| SRX7732094 | 2,633* | "P2S"[3] |

*: "Design: This dataset contains coronavirus-like sequence reads, based on BLAST search."

** : All available SRA datasets from PRJNA607174

***: Actual SRA datasets identified from the "Extended Data Table 3" of [2]

Article

Extended Data Table 3 | Identification of SARSr-CoV sequence reads in metagenomes from the lung of pangolins using the SARS-CoV-2 sequence (GenBank accession No. MN908947) as the reference

| Sample ID | Animal species | Total reads* | No. mapped |
|-----------|------------------|--------------|------------------------------|
| M1 | Malayan pangolin | 107,267,359 | 496 ←SRX7756769 "pangolin 9" |
| M2 | Malayan pangolin | 38,091,846 | 302 |
| M3 | Malayan pangolin | 79,477,358 | 14 |
| M4 | Malayan pangolin | 32,829,850 | 1,100 |
| M5 | Malayan pangolin | 547,302,862 | 56 |
| M6 | Malayan pangolin | 232,433,120 | 10 ←SRX7756762 "pangolin 2" |
| M8 | Malayan pangolin | 44,440,374 | 12 |
| M10 | Malayan pangolin | 227,801,882 | 0 |
| Z1 | Chinese pangolin | 444,573,526 | 0 |

Not available

Not available

Fig.1 the "Extended Data Table 3" of [2]. SRA datasets identified in the available database is pointed out by an arrow, while SRA "runs" that failed to be identified in known datasets are outlined in a red square.

Analysis of reads from The Available datasets using NCBI Trace.

Table 2. The Trace result of Known GD Pangolin datasets when examined using NCBI Trace SRA.

| Accession number and registration date | Primary Mammalian Trace results and percentage | Primate-related results in Krona and read size by Kbp | Identification of "Coronaviridae" as by Trace and total read size |
|---|--|---|---|
| SRX6893158 20-Sep-2019 | Manis javanica: 14.66% | N/D | N/D |
| SRX6893157 20-Sep-2019 | Boreoeutheria: 1.24% | Catarrhini 644546 | N/D*** |
| SRX6893156 20-Sep-2019 | Manis javanica: 7.51% Homo sapiens: 0.03% | Homo sapiens 81948 | Pangolin coronavirus 2Kbp |
| SRX6893155 20-Sep-2019 | Homo sapiens: 0.37% | Homininae 3534150 | Pangolin coronavirus 5Kbp |
| SRX6893154 20-Sep-2019 | Homo sapiens: 0.02% | Hominoidea 356003 | Pangolin coronavirus 154Kbp |
| SRX6893153 20-Sep-2019 | Homo sapiens: 0.01% | Homo sapiens 162180 | Pangolin coronavirus 41Kbp |
| SRX6893152 20-Sep-2019 | Manis javanica: 2.87% Euarchontoglires: 1.37% | N/D | N/D |
| SRX6893151 20-Sep-2019 | Manis javanica: 7.47% | N/D | N/D |
| SRX6893150 20-Sep-2019 | Boreoeutheria: 1.91% | N/D | N/D |
| SRX6893149 20-Sep-2019 | Manis javanica: 1% | Simiiformes 313069 | N/D |
| SRX6893148 20-Sep-2019 | Manis javanica: 0.4% | Catarrhini 194320 | N/D |
| SRX6893147 20-Sep-2019 | Manis javanica: 2.71% | Catarrhini 69937 | N/D |
| SRX6893146 20-Sep-2019 | Boreoeutheria: 1.72% | Hominoidea 231755 | N/D |
| SRX6893145 20-Sep-2019 | Homininae: 0.27% Manis javanica: 1.01% | Homininae 2536765 | N/D |
| SRX6893144 20-Sep-2019 | Manis javanica: 0.62% | Hominoidea 166628 | N/D |
| SRX6893143 20-Sep-2019 | Manis javanica: 1.63% | N/D | N/D |
| SRX6893142 | Manis javanica: 1.28% | Simiiformes 57084 | N/D |

| | | | |
|---|-------------------------------|----------------------------|---|
| 20-Sep-2019 | | | |
| SRX6893141 20-Sep-2019 | Boreoeutheria: 1.41% | N/D | N/D |
| SRX6893140 20-Sep-2019 | Boreoeutheria: 1.56% | N/D | N/D |
| SRX6893139 20-Sep-2019 | Homo sapiens: 0.01% | Homo sapiens 491120 | Pangolin coronavirus 2Kbp |
| SRX6893138 20-Sep-2019 | Boreoeutheria: 1.67% | Homininae 2761176 | N/D |
| SRX7756769 18-Feb-2020 | Homo sapiens: 0.03% | Homo sapiens 5457929 | Bat SARS-like coronavirus 2Kbp Wuhan seafood market pneumonia virus 2Kbp |
| SRX7756766 18-Feb-2020 | Manis javanica: 78.6% | Cercopithecidae 3116 | Betacoronavirus 2Kbp** |
| SRX7756765 18-Feb-2020 | Manis javanica: 87.17% | Cercopithecinae 11339 | N/D**** |
| SRX7756764 18-Feb-2020 | Manis javanica: 48.39% | Cercopithecidae 22600 | N/D |
| SRX7756763 18-Feb-2020 | Manis javanica: 94.95% | Cercopithecidae 5076 | N/D |
| SRX7756762 18-Feb-2020 | Manis javanica: 95.37% | Catarrhini* 2831 | Nidovirales 0Kbp |
| SRX7756761 18-Feb-2020 | Manis javanica: 13.63% | Chlorocebus sabaeus 498506 | N/D |
| SRX7732094 15-Feb-2020 | N/A*** | N/A | Pangolin coronavirus*** |

*: Chlorocebus Sabaeus

** : Not claimed as being SARS-CoV-2 related in the original publication. Likely unrelated.

*** Not analyzable. All Non-Coronavirus data filtered out. Leaving only 2,633 reads, all of which can be mapped to the SARS-CoV-2 reference genome.

**** 8 reads as claimed by [10]

Specific BLAST analysis

In order to determine the authenticity of the Primate-related reads in the datasets, Specific BLAST analysis is carried out for all datasets that possessed claimed or analyzed reads of coronavirus-related viruses. An 100% full-length match that does not map to non-primates confirms Authenticity of read.

select all 100 sequences selected

[Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|---|
| <input checked="" type="checkbox"/> SRX7756762 | 279 | 1047 | 0% | 4e-68 | 100.00% | SRA-SRR11119766.160125840.2 |
| <input checked="" type="checkbox"/> SRX7756762 | 279 | 1366 | 0% | 4e-68 | 100.00% | SRA-SRR11119766.138036805.1 |
| <input checked="" type="checkbox"/> SRX7756762 | 279 | 967 | 0% | 4e-68 | 100.00% | SRA-SRR11119766.101239747.1 |
| <input checked="" type="checkbox"/> SRX7756762 | 279 | 1624 | 0% | 4e-68 | 100.00% | SRA-SRR11119766.46413326.2 |

Chlorocebus sabaeus isolate 1994-021 unplaced genomic sca ...
dna
1339488
[Distance tree of results](#) [MSA viewer](#)

Fig.2a Specific BLAST analysis on the PRINA607174 dataset, [SRX7756762](#), that contained claimed SARS-CoV-2 related coronavirus reads. The 100% full-length matches clearly indicate presence of Primate-derived material.

select all 100 sequences selected

[GenBank](#) [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|----------------------------|
| <input checked="" type="checkbox"/> Macaca mulatta isolate Rh22777_5890-1b major histocompatibility complex genomic sequence | 279 | 279 | 100% | 2e-71 | 100.00% | KT332833.1 |
| <input checked="" type="checkbox"/> Macaca mulatta isolate Rh22335_5775-3 major histocompatibility complex genomic sequence | 279 | 279 | 100% | 2e-71 | 100.00% | KT332608.1 |
| <input checked="" type="checkbox"/> Macaca mulatta isolate Rh22335_5725-2 major histocompatibility complex genomic sequence | 279 | 279 | 100% | 2e-71 | 100.00% | KT332521.1 |
| <input checked="" type="checkbox"/> Macaca mulatta isolate Rh22335_5702-1a major histocompatibility complex genomic sequence | 279 | 279 | 100% | 2e-71 | 100.00% | KT332463.1 |

>gn|SRA|SRR11119766.160125840.2 160125840 (Biological)
TAATCCTTTGGGTATATACCCAGTAATGGGATGGCTGGGTCATATGGTACATCTAGTTCF
AGATCCTTGAGGAATCGCCATACTGTTTTCCATTAATGGTTGAAGTACTTACAATCCAC
CAACAGTGTAAAGTGTTCCTATTTCTCCAC

Fig.2b BLAST result on the returned sequence revealed it as a Primate-derived MHC complex gene, confirming Primate origin.

select all 100 sequences selected

[Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|---|
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.269072261.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.255768440.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.255768440.1 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.255318754.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.254520929.1 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 6344 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.251645135.1 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.234036838.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.211208832.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 9108 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.199583624.1 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.198110623.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.196936636.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.196936636.1 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.133631622.2 |
| <input checked="" type="checkbox"/> SRX7756766 | 279 | 279 | 0% | 5e-67 | 100.00% | SRA-SRR11119762.108819247.2 |

Description Macaca mulatta isolate AG07107 chromosome 3 genomic sca ...
Molecule type dna
Query Length 17855752
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.3a Specific BLAST analysis of [SRX7756766](#) revealed large amount of 100% full-length matches with Macaca Mulatta.

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments Download Manage Columns Show 1000

select all 18 sequences selected GenBank Graphics Distance tree of results

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|---|-----------|-------------|-------------|---------|------------|------------|
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-461L13 from chromosome 7, complete sequence | 279 | 279 | 100% | 2e-71 | 100.00% | AC198296.4 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone RP43-31117 from chromosome 7, complete sequence | 279 | 279 | 100% | 2e-71 | 100.00% | AC146248.2 |
| <input checked="" type="checkbox"/> Canis lupus familiaris breed Labrador retriever chromosome 06a | 274 | 274 | 100% | 8e-70 | 99.34% | CP050586.1 |
| <input checked="" type="checkbox"/> Canis lupus familiaris breed Labrador retriever chromosome 06b | 274 | 274 | 100% | 8e-70 | 99.34% | CP050622.1 |

Description gn|SRA|SRR11119762.133631622.2 133631622 (Biological)
Molecule type dna
Query Length 151
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.3b More intriguing—many of the reads showed only 100% matches to hominids—Chimpanzees and also clearly Macaca Mulatta itself. This indicate that [SRX7756766](#) also contained significant amount of material derived from primates.

select all 100 sequences selected Graphics Distance tree of results

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|----------------------------|
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 278 | 0% | 9e-69 | 100.00% | SRA-SRR11119759.99831231.2 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 278 | 0% | 9e-69 | 100.00% | SRA-SRR11119759.99831231.1 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 4814 | 1% | 9e-69 | 100.00% | SRA-SRR11119759.88019245.2 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 5178 | 2% | 9e-69 | 100.00% | SRA-SRR11119759.82130976.2 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 278 | 0% | 9e-69 | 100.00% | SRA-SRR11119759.70689253.2 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 278 | 0% | 9e-69 | 100.00% | SRA-SRR11119759.70689253.1 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 278 | 0% | 9e-69 | 100.00% | SRA-SRR11119759.57405658.2 |
| <input checked="" type="checkbox"/> SRX7756769 | 278 | 278 | 0% | 9e-69 | 100.00% | SRA-SRR11119759.57405658.1 |

[AC073210.8](#)
Homo sapiens BAC clone RP11-460N20 from 7, complete seq ...
nucleic acid
203396

Fig.4a Similarly, [SRX7756769](#) contained large amount of reads that are 100% full-length matches to Human genomic DNA.

select all 0 sequences selected GenBank Graphics Distance tree of results

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|-------------|
| <input type="checkbox"/> Homo sapiens chromosome 22 clone ABC11_00047178300_E22, complete sequence | 278 | 456 | 100% | 6e-71 | 100.00% | AC279316.1 |
| <input type="checkbox"/> Homo sapiens actin related protein 2 pseudogene (LOC284441) on chromosome 19 | 278 | 278 | 100% | 6e-71 | 100.00% | NG_022927.2 |
| <input type="checkbox"/> Homo sapiens TBC1 domain containing kinase (TBCK), RefSeqGene on chromosome 4 | 278 | 2140 | 100% | 6e-71 | 100.00% | NG_034057.3 |
| <input type="checkbox"/> Homo sapiens chromosome 15 clone VMRC59-280I06, complete sequence | 278 | 2291 | 100% | 6e-71 | 100.00% | AC279072.1 |
| <input type="checkbox"/> Homo sapiens chromosome 2 clone VMRC59-389K09, complete sequence | 278 | 3905 | 100% | 6e-71 | 100.00% | AC279037.1 |
| <input type="checkbox"/> Homo sapiens chromosome 15 clone VMRC59-359A02, complete sequence | 278 | 3589 | 100% | 6e-71 | 100.00% | AC278991.1 |
| <input type="checkbox"/> Homo sapiens chromosome 16 clone VMRC59-453B14, complete sequence | 278 | 2239 | 100% | 6e-71 | 100.00% | AC278975.1 |

Description gn|SRA|SRR11119759.88019245.2 88019245 (Biological)
Molecule type dna
Query Length 150
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.4b A BLAST analysis on reads sampled from the 100% hit results confirmed that it was found only in humans. Once again confirming human origin.

select all 100 sequences selected Graphics Distance tree of results

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|---------------------------|
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA-SRR10168375.5045789.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA-SRR10168375.5964.1 |

Description Homo sapiens BAC clone RP11-460N20 from 7, complete seq
Molecule type nucleic acid
Query Length 203396
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.5a [SRX6893156](#) also returned 100% matched results from the human Genome.

| select all 14 sequences selected | | GenBank | Graphics | Distance tree of results | | |
|---|-----------|-------------|-------------|--------------------------|------------|----------------------------|
| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
| <input checked="" type="checkbox"/> Homo sapiens BAC clone RP11-460N20 from 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC073210.8 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-623C19 from chromosome 7, complete sequence | 267 | 267 | 100% | 1e-67 | 98.67% | AC184799.2 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-2015 from chromosome 7, complete sequence | 267 | 267 | 100% | 1e-67 | 98.67% | AC174000.3 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-565C10 from chromosome 7, complete sequence | 267 | 267 | 100% | 1e-67 | 98.67% | AC148313.3 |

Description gnl|SRA|SRR10168375.5045789.1.5045789 (Biological)
Molecule type dna
Query Length 150
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.5b BLAST search on the result returned 100% match only found in humans. Confirming origin in human-derived material.

| select all 100 sequences selected | | Graphics | Distance tree of results | | | |
|--|-----------|-------------|--------------------------|---------|------------|--|
| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.17339580.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.17013625.2 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.17013625.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.16930714.2 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.16930714.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.15267479.2 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.15267479.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.13985702.2 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.13985702.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.13353823.2 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.13353823.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.11109740.1 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.9343845.2 |
| <input checked="" type="checkbox"/> SRX6893156 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA_SRR10168376.9232549.2 |

Description Homo sapiens BAC clone RP11-460N20 from 7, complete seq ...
Molecule type nucleic acid
Query Length 203396
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.6a Similarly, BLAST research on [SRX6893155](#) gives large number of full length 100% matches to the human genome.

| select all 57 sequences selected | | GenBank | Graphics | Distance tree of results | | |
|--|-----------|-------------|-------------|--------------------------|------------|--------------------------------|
| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
| <input checked="" type="checkbox"/> Homo sapiens FOSMID clone ABC13-48840700E15 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC242196.4 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-340I24 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC185242.2 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-623C19 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC184799.2 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-114G16 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC183835.2 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-2015 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC174000.3 |
| <input checked="" type="checkbox"/> Homo sapiens BAC clone RP11-479O9 from 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC073107.7 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-565C10 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC148313.3 |
| <input checked="" type="checkbox"/> Homo sapiens BAC clone RP11-460N20 from 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC073210.8 |
| <input checked="" type="checkbox"/> PREDICTED: Cebus capucinus imitator small integral membrane protein 11A (SMIM11A), transcript variant X6, mRNA | 87.9 | 87.9 | 49% | 1e-13 | 88.00% | XM_017526193.1 |

Description gnl|SRA|SRR10168376.15267479.2.15267479 (Biological)
Molecule type dna
Query Length 150
Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.6b The results, when put through BLAST, confirms that the 100% matches are in fact derived from a Hominid origin.

Description Homo sapiens BAC clone RP11-460N20 from 7, complete seq ...
 Molecule type nucleic acid
 Query Length 203396
 Other reports [Distance tree of results](#) [MSA viewer](#)

Percent Identity to E value to Query Coverage to

Descriptions Graphic Summary Alignments

Sequences producing significant alignments Download Manage Columns Show 100

select all 100 sequences selected [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|---------------------------|
| <input checked="" type="checkbox"/> SRX6893153 | 278 | 278 | 0% | 2e-69 | 100.00% | SRA.SRR10168378.1832954.1 |

Fig.7a [SRX6893153](#) have also returned 100% match full-length read on this tiny part of the human genome.

Description gnl|SRA|SRR10168378.1832954.1 1832954 (Biological)
 Molecule type dna
 Query Length 150
 Other reports [Distance tree of results](#) [MSA viewer](#)

Percent Identity to E value to Query Coverage to

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download Manage Columns Show 1000

select all 170 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|----------------------------|
| <input checked="" type="checkbox"/> Homo sapiens FOSMID clone ABC18-862111 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC245205.1 |
| <input checked="" type="checkbox"/> Homo sapiens FOSMID clone ABC13-48840700E15 from chromosome 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC242196.4 |
| <input checked="" type="checkbox"/> Homo sapiens BAC clone RP11-460N20 from 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC073210.8 |
| <input checked="" type="checkbox"/> Pan troglodytes BAC clone CH251-487D11 from chromosome 7, complete sequence | 272 | 272 | 100% | 3e-69 | 99.33% | AC182733.3 |

Fig.7b Similarly, the read is only found in humans—indicating the Homo Sapiens Trace result is accurate.

Description Homo sapiens FOSMID clone ABC12-46670400J18 from chro ...
 Molecule type nucleic acid
 Query Length 40058
 Other reports [Distance tree of results](#) [MSA viewer](#)

Percent Identity to E value to Query Coverage to

Descriptions Graphic Summary Alignments

Sequences producing significant alignments Download Manage Columns Show 100

select all 100 sequences selected [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|----------------------------|
| <input checked="" type="checkbox"/> SRX6893154 | 278 | 278 | 0% | 3e-70 | 100.00% | SRA.SRR10168377.15657119.2 |

Fig.8a One read from the Human MHC gene is recovered from [SRX6893154](#) with a query sequence only 40058bp in length.

Human PAC clone DJ149P21 complete sequence
 Human Cosmid g0771a233 complete sequence
 Human Cosmid g0771a222 from Tg31.3 complete sequence
 Pan troglodytes BAC clone CH251-59TE5 from chromosome X complete sequence
 Pan troglodytes BAC clone CH251-134K23 from Y complete sequence
 Pan troglodytes BAC clone CH251-511H17 from Y complete sequence
 Pan troglodytes BAC clone CH251-663H18 from Y complete sequence
 Pan troglodytes BAC clone CH251-571G18 from chromosome Y complete sequence
 Pan troglodytes BAC clone RP43-48C7 from chromosome Y complete sequence
 Pan troglodytes BAC clone CH251-94F1 from chromosome Y complete sequence
 Pan troglodytes BAC clone CH251-346F2 from chromosome Y complete sequence
 Pan troglodytes BAC clone CH251-416C12 from chromosome Y complete sequence
 Pan troglodytes chromosome Y clone PTB-547B05 complete sequences
 Pan troglodytes BAC clone CH251-358H21 from chromosome 2 complete sequence
 Pan troglodytes BAC clone CH251-231L11 from chromosome 2 complete sequence
 Homo sapiens chromosome 8 clone RP11-91J19 complete sequence
 Homo sapiens BAC clone RP11-651C2 from 4 complete sequence
 Homo sapiens chromosome 8 clone RP11-63E5 complete sequence
 Homo sapiens chromosome 8 clone CTA-366D10 complete sequence
 Pan paniscus chromosome 20 clone VMRC74-188E6 complete sequence
 Homo sapiens protein tyrosine phosphatase receptor type T (PTPRT) RefSeqGene on chromosome 20
 Pan troglodytes chromosome 15 clone CH251-23J09 complete sequence
 Pongo abelii chromosome 16 clone CH276-83L13 complete sequence
 Homo sapiens chromosome 2 clone VMRC53-318M16 complete sequence

| | | | | | |
|-----|------|------|-------|---------|-------------|
| 278 | 1001 | 100% | 6e-71 | 100.00% | AC000112.1 |
| 278 | 278 | 100% | 6e-71 | 100.00% | AC000110.1 |
| 278 | 278 | 100% | 6e-71 | 100.00% | AC000109.1 |
| 276 | 786 | 100% | 2e-70 | 100.00% | AC195517.3 |
| 276 | 1511 | 100% | 2e-70 | 100.00% | AC147655.3 |
| 276 | 1305 | 100% | 2e-70 | 100.00% | AC147654.3 |
| 276 | 738 | 100% | 2e-70 | 100.00% | AC151848.4 |
| 276 | 738 | 100% | 2e-70 | 100.00% | AC159017.2 |
| 276 | 1517 | 100% | 2e-70 | 100.00% | AC142313.1 |
| 276 | 1522 | 100% | 2e-70 | 100.00% | AC147670.4 |
| 276 | 749 | 100% | 2e-70 | 100.00% | AC151848.4 |
| 276 | 1517 | 100% | 2e-70 | 100.00% | AC150005.3 |
| 276 | 1789 | 100% | 2e-70 | 100.00% | BS000502.1 |
| 274 | 1148 | 100% | 8e-70 | 100.00% | AC182394.2 |
| 274 | 1148 | 100% | 8e-70 | 100.00% | AC183770.3 |
| 274 | 636 | 100% | 8e-70 | 100.00% | AC083964.3 |
| 274 | 1276 | 100% | 8e-70 | 100.00% | AC093880.4 |
| 274 | 478 | 100% | 8e-70 | 100.00% | AC136777.8 |
| 274 | 478 | 100% | 8e-70 | 100.00% | AC103954.9 |
| 272 | 506 | 100% | 3e-69 | 99.33% | AC279338.1 |
| 272 | 2126 | 100% | 3e-69 | 99.33% | NG_033880.2 |
| 272 | 272 | 98% | 3e-69 | 100.00% | AC279059.1 |
| 272 | 272 | 100% | 3e-69 | 99.33% | AC278962.1 |
| 272 | 272 | 100% | 3e-69 | 99.33% | AC278616.1 |

Description: gnl|SRA|SRR10168377.15657119.2.15657119 (Biological)
 Molecule type: dna
 Query Length: 150
 Other reports: [Distance tree of results](#) [MSA viewer](#)

Fig.8b This MHC read is only found in Humans and Chimpanzees. This is clearly a contaminant from a hominid origin.

Description: Homo sapiens BAC clone RP11-611L7 from 7, complete sequence
 Molecule type: nucleic acid
 Query Length: 173967
 Other reports: [Distance tree of results](#) [MSA viewer](#)

Percent Identity: to E value: to Query Coverage: to

Descriptions | Graphic Summary | Alignments

Sequences producing significant alignments Download Manage Columns Show 100

select all 100 sequences selected [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per Ident | Accession |
|--|-----------|-------------|-------------|---------|-----------|----------------------------|
| <input checked="" type="checkbox"/> SRX6893139 | 278 | 278 | 0% | 3e-69 | 100.00% | SRA_SRR10168392.39544030.1 |
| <input checked="" type="checkbox"/> SRX6893139 | 278 | 278 | 0% | 3e-69 | 100.00% | SRA_SRR10168392.28917809.1 |
| <input checked="" type="checkbox"/> SRX6893139 | 278 | 278 | 0% | 3e-69 | 100.00% | SRA_SRR10168392.14357888.1 |
| <input checked="" type="checkbox"/> SRX6893139 | 278 | 278 | 0% | 3e-69 | 100.00% | SRA_SRR10168392.2548655.2 |

Fig.9a Similarly, multiple 100% match Full length reads were obtained from [SRX6893139](#). As this query sequence is only 173967 nucleotides in length, the real extent of Human-derived contamination is also extremely severe.

Description: gnl|SRA|SRR10168392.28917809.1.28917809 (Biological)
 Molecule type: dna
 Query Length: 150
 Other reports: [Distance tree of results](#) [MSA viewer](#)

Percent Identity: to E value: to Query Coverage: to

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments Download Manage Columns Show 1000

select all 66 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per Ident | Accession |
|---|-----------|-------------|-------------|---------|-----------|----------------|
| <input checked="" type="checkbox"/> Homo sapiens zinc finger protein 316 (ZNF316), mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | NM_001278559.2 |
| <input checked="" type="checkbox"/> PREDICTED: Homo sapiens zinc finger protein 316 (ZNF316), transcript variant X3, mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | XM_024446619.1 |
| <input checked="" type="checkbox"/> PREDICTED: Homo sapiens zinc finger protein 316 (ZNF316), transcript variant X2, mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | XM_024446618.1 |
| <input checked="" type="checkbox"/> PREDICTED: Homo sapiens zinc finger protein 316 (ZNF316), transcript variant X1, mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | XM_006715630.4 |
| <input checked="" type="checkbox"/> Homo sapiens BAC clone RP11-611L7 from 7, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC073343.6 |
| <input checked="" type="checkbox"/> PREDICTED: Pongo abelii zinc finger protein 316 (ZNF316), mRNA | 272 | 272 | 100% | 3e-69 | 99.33% | XM_024250011.1 |

Fig.9b Examining these reads revealed that they are only found in humans and apes. This is

therefore also clear evidence that there are Human/Hominid-derived contamination in [SRX6893139](#).

Description Homo sapiens chromosome 9, clone hRPK.202_H_3, comple ...
 Molecule type nucleic acid
 Query Length 187174
 Other reports [Distance tree of results](#) [MSA viewer](#)

Percent Identity to E value to Query Coverage to

Descriptions Graphic Summary Alignments

Sequences producing significant alignments Download Manage Columns Show 100

select all 100 sequences selected [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|---|
| <input checked="" type="checkbox"/> SRX6893167 | 278 | 278 | 0% | 8e-70 | 100.00% | SRA-SRR10168374.7906491.2 |

Fig.10a One read is also recovered from [SRX6893157](#). From a query sequence only 187174nt in length.

| | | | | | | | |
|-------------------------------------|---|-----|-----|------|-------|---------|--------------------------------|
| <input checked="" type="checkbox"/> | PREDICTED: Homo sapiens formin binding protein 1 (FNBP1), transcript variant X13, mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | XM_005251824.2 |
| <input checked="" type="checkbox"/> | PREDICTED: Homo sapiens formin binding protein 1 (FNBP1), transcript variant X4, mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | XM_011518402.1 |
| <input checked="" type="checkbox"/> | PREDICTED: Homo sapiens formin binding protein 1 (FNBP1), transcript variant X3, mRNA | 278 | 278 | 100% | 6e-71 | 100.00% | XM_011518401.1 |
| <input checked="" type="checkbox"/> | Homo sapiens formin binding protein 1 (FNBP1), RefSeqGene on chromosome 9 | 278 | 278 | 100% | 6e-71 | 100.00% | NG_033946.1 |
| <input checked="" type="checkbox"/> | Homo sapiens cDNA FLJ13619 fis, clone PLACE1010926, weakly similar to HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOS | 278 | 278 | 100% | 6e-71 | 100.00% | AK023681.1 |
| <input checked="" type="checkbox"/> | Human DNA sequence from clone RP11-138E2 on chromosome 9q34.11-34.3, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AL136141.13 |
| <input checked="" type="checkbox"/> | Homo sapiens formin-binding protein 17 (FBP17) mRNA, partial cds | 278 | 278 | 100% | 6e-71 | 100.00% | AF265550.1 |
| <input checked="" type="checkbox"/> | Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence | 278 | 278 | 100% | 6e-71 | 100.00% | AC006241.1 |
| <input checked="" type="checkbox"/> | Homo sapiens KIAA0554 mRNA for KIAA0554, protein | 278 | 278 | 100% | 6e-71 | 100.00% | AB011126.1 |
| <input checked="" type="checkbox"/> | PREDICTED: Nomascus leucogenys formin binding protein 1 (FNBP1), transcript variant X18, mRNA | 272 | 272 | 100% | 3e-69 | 99.33% | XM_030818029.1 |
| <input checked="" type="checkbox"/> | PREDICTED: Nomascus leucogenys formin binding protein 1 (FNBP1), transcript variant X17, mRNA | 272 | 272 | 100% | 3e-69 | 99.33% | XM_030818028.1 |
| <input checked="" type="checkbox"/> | PREDICTED: Nomascus leucogenys formin binding protein 1 (FNBP1), transcript variant X16, mRNA | 272 | 272 | 100% | 3e-69 | 99.33% | XM_030818027.1 |

Description gn|SRA|SRR10168374.7906491.2.7906491 (Biological)
 Molecule type dna
 Query Length 150
 Other reports [Distance tree of results](#) [MSA viewer](#)

Fig.10b This particular sequence is only found in humans—indicating that even the [SRX6893157](#) dataset was contaminated by material of human origin.

Description Chlorocebus aethiops BAC clone CH252-276C1 from chromos ...
 Molecule type nucleic acid
 Query Length 160189
 Other reports [Distance tree of results](#) [MSA viewer](#)

Percent Identity to E value to Query Coverage to

Descriptions Graphic Summary Alignments

Sequences producing significant alignments Download Manage Columns Show 100

select all 100 sequences selected [Graphics](#) [Distance tree of results](#)

| Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|--|-----------|-------------|-------------|---------|------------|---|
| <input checked="" type="checkbox"/> SRX7756765 | 279 | 774 | 0% | 4e-69 | 100.00% | SRA-SRR11119763.129105044.1 |
| <input checked="" type="checkbox"/> SRX7756765 | 279 | 375 | 0% | 4e-69 | 100.00% | SRA-SRR11119763.106754018.1 |
| <input checked="" type="checkbox"/> SRX7756765 | 279 | 279 | 0% | 4e-69 | 100.00% | SRA-SRR11119763.75715814.1 |
| <input checked="" type="checkbox"/> SRX7756765 | 279 | 510 | 0% | 4e-69 | 100.00% | SRA-SRR11119763.47541416.1 |
| <input checked="" type="checkbox"/> SRX7756765 | 279 | 279 | 0% | 4e-69 | 100.00% | SRA-SRR11119763.40703161.1 |
| <input checked="" type="checkbox"/> SRX7756765 | 279 | 768 | 0% | 4e-69 | 100.00% | SRA-SRR11119763.38948039.1 |

Fig.11a The presence of Reads from Somatic Chlorocebus aethiops in [SRX7756765](#) confirms the identity of the Cercopithecinae reads there.

| | | | | | | | |
|-------------------------------------|---|-----|------|------|-------|---------|--------------------------------|
| <input checked="" type="checkbox"/> | MACACA MULATTA BAC clone CH250-425F21 from chromosome 1, complete sequence | 279 | 279 | 100% | 2e-71 | 100.00% | AC198454.3 |
| <input checked="" type="checkbox"/> | Macaca mulatta chromosome UNK clone CH250-5H12, complete sequence | 279 | 279 | 100% | 2e-71 | 100.00% | AC188081.1 |
| <input checked="" type="checkbox"/> | Macaca mulatta chromosome UNK clone CH250-50H12, complete sequence | 279 | 1081 | 100% | 2e-71 | 100.00% | AC188078.1 |
| <input checked="" type="checkbox"/> | Chlorocebus aethiops clone CH252-390I5, complete sequence | 279 | 775 | 100% | 2e-71 | 100.00% | AC138437.3 |
| <input checked="" type="checkbox"/> | Chlorocebus aethiops BAC clone CH252-464J14 from chromosome 11, complete sequence | 276 | 1209 | 100% | 2e-70 | 100.00% | AC2389276.4 |
| <input checked="" type="checkbox"/> | PREDICTED: Macaca mulatta ubiquinone biosynthesis protein COQ9, mitochondrial pseudogene (LOC715179), misc. RNA | 274 | 274 | 100% | 9e-70 | 99.34% | XR_001440096.2 |
| <input checked="" type="checkbox"/> | Macaca mulatta chromosome 1 clone CH250-144H6, complete sequence | 274 | 859 | 100% | 9e-70 | 99.34% | AC277709.1 |
| <input checked="" type="checkbox"/> | Macaca mulatta isolate Rh22335_5775-3 major histocompatibility complex genomic sequence | 274 | 274 | 100% | 9e-70 | 99.34% | KT332608.1 |
| <input checked="" type="checkbox"/> | Macaca mulatta isolate Rh22335_5725-2 major histocompatibility complex genomic sequence | 274 | 274 | 100% | 9e-70 | 99.34% | KT332521.1 |
| <input checked="" type="checkbox"/> | Macaca mulatta isolate Rh22335_5702-1a major histocompatibility complex genomic sequence | 274 | 274 | 100% | 9e-70 | 99.34% | KT332463.1 |

Fig.11b the sequences from the BLAST hits indicate that they were unique to the family Cercopithecinae. Confirming Primate origin.

Analyzing the extent of contamination.

As the Specific BLAST analysis confirmed significant level of Human-derived contamination in all samples positive for SARS-CoV-2 related Coronaviruses, The TRACE result can therefore be trusted for the analysis on the extent of contamination.

The 32nt Krona Trace system is used for elucidating the ratio of different taxa within a sample. As Specific BLAST analysis confirmed the significant presence of Human and Primate derived Genetic material--The most basal group of primates detected in all Coronavirus-positive samples belong to Catarrhini—or Humans, Apes and Old-World Monkeys. Therefore, Trace classification results that can be classified into sister nodes of Catarrhini should be considered as Contamination by Primate-derived material.

Since Catarrhini is under Simiiformes; Haplorrhini; Primates; Euarchonta; Euarchontoglires and Manis is under Pholidota; Laurasiatheria, If a read is TRACEd down to Catarrhini, it can not be from a Pangolin, and it will have to be from a Primate-derived source—Contamination by material from the lab.

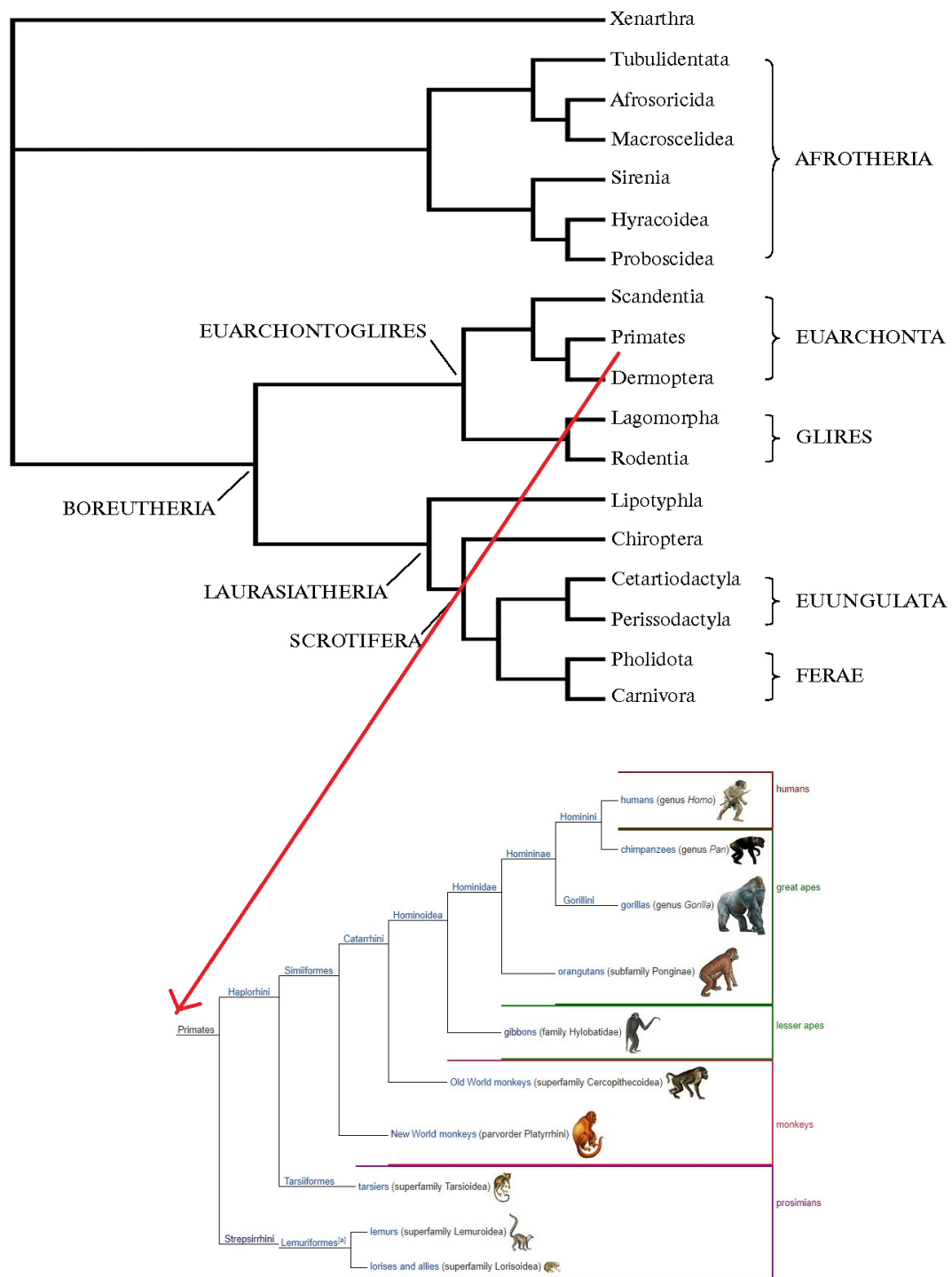


Fig. 12 Family tree of mammals, Including the position and classification of Primates in the lineage of Mammalia.

Table 3a Ratios of Hominid-traced reads to Pangolin-traced reads in the SRA datasets that contained reads of the GD- Pangolin-CoV sequence, and had Hominid reads.

| Accession and date | Primate classification and total traced Kbps | Total traced Kbps to Manis Javanica (Pangolin) | Ratio of Primate to Pangolin | Virus classification and amount of reads by Kbps |
|---|--|--|------------------------------|---|
| SRX7756769 18-Feb-2020 | Homo sapiens 5457929 | 15401134 | 0.35 | Bat SARS-like coronavirus 2Kbp Wuhan seafood market pneumonia virus 2Kbp |
| SRX6893139 20-Sep-2019 | Homo sapiens 491120 | 5301351 | 0.0926 | Pangolin coronavirus 2Kbp |
| SRX6893157 20-Sep-2019 | Catarrhini 644546 | 1889448 | 0.34 | N/D*** |
| SRX6893156 20-Sep-2019 | Homo sapiens 81948 | 4765461 | 0.01719 | Pangolin coronavirus 2Kbp |
| SRX6893155 20-Sep-2019 | Homininae 3534150 | 525801 | 6.7214 | Pangolin coronavirus 5Kbp |
| SRX6893154 20-Sep-2019 | Hominoidea 356003 | 2232008 | 0.159 | Pangolin coronavirus 154Kbp |
| SRX6893153 20-Sep-2019 | Homo sapiens 162180 | 3110158 | 0.05214 | Pangolin coronavirus 41Kbp |

***: No trace result on Coronaviruses, despite claimed reads from [3]

Table 3b Ratios of Primate-traced reads to Coronavirus-traced reads in the SRA datasets that contained reads claimed to be traced to of the GD- Pangolin-CoV sequence, and lacked Hominid reads.

| Accession and date | Primate classification and reads (in Kbp) | Virus classification and reads | Ratio of virus reads to Primate reads |
|---|--|---|---------------------------------------|
| SRX7756766 18-Feb-2020 | Cercopithecidae 3116; BLAST to Macaca Mulatta | Betacoronavirus 2Kbp ** | 0.000642 |
| SRX7756762 18-Feb-2020 | Catarrhini 2831; BLAST to Chlorocebus sabaeus | Nidovirales 0Kbp Claimed 10x150bp reads | 0.000530 |
| SRX7756765 22-Apr-2020 | Cercopithecinae 11339 BLAST to Chlorocebus Aethiops | N/D*** | N/A |
| SRX7732094 15-Feb-2020 | N/A* | Pangolin coronavirus | N/A* |

*: No non-coronavirus reads available in the dataset with a total of 2,633 reads, making analysis impossible.

**: No claimed reads from [2]

***: Claimed 8 reads from [10]

DISCUSSIONS

The extent of contamination in the pangolin sequencing datasets

As the samples were supposed to be pangolin lung tissue, which will neither contact with nor be contaminated by non-pangolin derived mammalian tissues when still inside the animal, any non-pangolin mammalian reads within such a dataset can only be introduced to the sequencing process after the sample itself have been taken and brought into a lab.

As the classification Catarrhini itself is phylogenetically very deep down the Primate line which is itself distinguished from the Pangolin line at a very basal node (Boreoeutheria), and since we have already confirmed that the Primate line in PRJNA573298 traces mostly to humans by using Specific BLAST analysis, ([SRX6893157](#), the only one of the claimed coronavirus read dataset that gives a classification just down to Catarrhini, contained 213 full length 100% matches to the Human Mitochondrial reference genome alone, which is only 16569 bp in length. All other datasets gives definitive TRACE mapping to Homo Sapiens and contained distinct 100% matched reads to even very small parts of the Human genome.), We can deduce the extent of contamination of the PRJNA573298 dataset by Primate-related materials as from a minimum of 1.6% to as high as 87% by sample mass—using the ratio of Primate reads to Pangolin reads on TRACE. Such high level of contamination with Primate-derived material is unacceptable for a sample that was supposed to be Lung tissue. And therefore, the virome data of such samples in PRJNA573298 no longer reflects the original virome of the animal, and an potential “novel” reads from these contaminated samples may have been from in-lab contamination instead.

Deducing the dynamic of contamination in PRJNA607174

Of all 7 PRJNA607174 datasets, only [SRX7756769](#) and [SRX7756762](#) is claimed by Xiao et. Al to contain SARS-CoV-2-like reads. However, TRACE results revealed low level of contamination by Cercopithecidae (Old World Monkey) reads across all the samples. In particular, the [SRX7756762](#) dataset contained definitive mappings to *Chlorocebus sabaeus*, or African Green Monkey, while [SRX7756766](#) which contained 2Kbp unclaimed reads of Betacoronaviruses on TRACE, contained 100% full-length definitive mappings to *Macaca Mulatta* that may also be mapped to *Homo Sapiens*.

[SRX7756769](#) genetically resembles other samples in PRJNA573298, in both the kind of contamination and the extent of contamination. It contained an large excess of homo sapiens reads in levels similar to the contaminated samples in PRJNA573298.

From the method section of Lam et.al, we knew that they have performed Virus isolation using VERO E6 cells—Species *Chlorocebus Sabaeus* on one of the samples that have a positive PCR test for coronaviruses. The low level of contamination by Cercopithecidae-related reads in all the samples in PRJNA607174 except for [SRX7756769](#) itself support the possibility that [SRX7756769](#) is the first sample to be sequenced, and it happens before the lab begun using VERO E6 cells in the experiment. They then isolated the virus from the contaminated [SRX7756769](#) in VERO E6 cells, characterized it but did not sequence it, and this cell culture material then contaminated [SRX7756762](#) and possibly [SRX7756766](#), resulting the 10 reads in [SRX7756762](#) and the 2Kb batacoronavirus reads in [SRX7756766](#).

The exact nature of [SRX7732094](#) needs to be further scrutinized.

The P2S dataset, [SRX7732094](#), displays very unusual property when compared to other Datasets under the same BioProject. It is the only dataset with all Non-coronavirus reads being filtered out, and contained too little spots for it to be an ILLUMINA NextSeq 550 run. Furthermore, it was the only dataset that did not contain metadata with either an isolation source or a Library prep procedure, other than “This dataset contains coronavirus-like sequence reads, based on BLAST search.”

Such a strange designation and the fact of the dataset being heavily filtered, Raises problems on whether such a dataset is an actual BioSample at all. If this sample is really as claimed by Lam et. Al, Why the dataset have to be put through such heavy filtering when the other sequencing runs was clearly not filtered as severely as this dataset? Why there was no BioSample metadata on either Biomaterial provider, Source Tissue or Collector when all other Sequencing runs clearly provided such metadata information?

Unless the complete, unfiltered sequencing reads are made available on [SRX7732094](#), and the rest of [PRJNA696875](#), this Dataset can not be considered to be a real, reliable sample, and it must be excluded as “evidence” of a SARS-CoV-2-like virus infecting

pangolins in GuangDong, 2019.

Table 4 Sequencing runs in PRJNA696875, Accession number, BioSample, Content and designation

| Accession number and date | Size | Non-Coronavirus reads? | Source Tissue Provider and Collected by | Virus Designation: GD or GX? | Design |
|---------------------------|---------|------------------------|--|------------------------------|--|
| SRX7732094 15-Feb-2020 | 2,633 | No | N/A | GD | This dataset contains coronavirus-like sequence reads, based on BLAST search. |
| SRX7732093 15-Feb-2020 | 470,344 | Yes | Intestine Yanling Hu Wuchun Cao | GX | NEBNext Ultra II DNA Library Prep Kit, paired sequencing data has been integrated. |
| SRX7732092 15-Feb-2020 | 340,661 | Yes | Lung Yanling Hu Wuchun Cao | GX | NEBNext Ultra II DNA Library Prep Kit, paired sequencing data has been integrated. |
| SRX7732091 15-Feb-2020 | 416,659 | Yes | Intestine Yanling Hu Wuchun Cao | GX | NEBNext Ultra II DNA Library Prep Kit, paired sequencing data has been integrated. |
| SRX7732090 15-Feb-2020 | 520,254 | Yes | Lung Yanling Hu Wuchun Cao | GX | NEBNext Ultra II DNA Library Prep Kit, paired sequencing data has been |

| | | | | | |
|---------------------------|------------|-----|--|----|-----------------------------|
| | | | | | integrated. |
| SRX7732089 15-Feb-2020 | 19,607,536 | Yes | Blood Yanling Hu Wuchun Cao | GX | Ion Total RNA-Seq Kit v2 |
| SRX7732088 15-Feb-2020 | 4,550,437 | Yes | lung and intestine Yanling Hu Wuchun Cao | GX | Ion Total RNA-Seq Kit v2 |

By closely examining the P2V dataset, SRX7732088, which claimed to be a culture sample in VERO E6 cells, Chlorocebus Sabaeus, the exact viral load in-culture when compared to Cellular mRNA can be deduced by dividing the total identifiable coronavirus signal to the total identifiable Primate signal within the dataset, 6943Kbp/451932Kbp, which correspond to 0.01536:1 Viral RNA to Cellular RNA.

This places the viral loads on the other datasets with Coronavirus-like reads from GD well within the threshold expected from cell culture contamination of the sequencing samples—including the samples in PRJNA607174.

Potential breach of data availability statement by Xiao et al.[2]

Sequence data that support the findings of this study have been deposited in GISAID with the accession numbers EPI_ISL_410721. Raw data of RNAseq are available from the NCBI SRA under the study accession number PRJNA607174.

Fig 13. The Data Availability Statement of Xiao et al.

In the Data availability statement, the “Raw data of RNAseq” are clearly stated to be deposited under PRJNA607174. However, only 2 of the “Extended Data Table S3” datasets actually matches the datasets deposited on PRJNA607174. The other 7 datasets were completely unavailable. And the actual deposited datasets on PRJNA607174 does not match what have been claimed by Extended Data Table S3. As the RNA-seq Raw data was stated to be available within PRJNA607174, the failure to publish all the claimed data constitute a breach of the Data Availability statement on the article. Unless such datasets are published and independently examined, All such claimed reads from the strangely unpublished datasets can not be trusted as evidence of a SARS-CoV-2-like virus infecting pangolins in GuangDong, 2019.

Identifying the Etiological agent of the GuangDong 2019 incident.

By using an approach of both SRA TRACE analysis and specific BLAST Analysis, We have uncovered the fact that all samples that does not Contain confirmed Human-derived material, also lacked Claimed reads of a SARS-CoV-2 like virus that can be confirmed using NCBI Trace. All samples with claimed or traced reads of Coronaviruses in general, contained confirmed primate reads with the lowest common phylogenetic node Catarrhini. Samples that does not give a TRACE result on primate-derived material all lacked identifiable or claimed coronavirus reads.

This strongly imply that the Coronavirus-like reads are associated with human/Primate-sourced contamination material.

Most importantly, of all dead pangolins being sampled in the studies, only 9 out of a total of 29 Analyzable samples/datasets contained TRACEd or Claimed Coronavirus reads—despite all dead pangolins displayed similar symptoms in captivity. This imply that the alleged pangolin coronavirus is not the Etiological agent of the death of the pangolins being sampled in the studies. This is further supported by the fact that 4 out of 10 lung samples in PRJNA573298 and 4 out of 7 lung samples in PRJNA607174 lacked any claimed or TRACEd coronavirus reads—despite the same symptoms displayed and similar date of death.

In order to establish the Etiological agent of the dead pangolins in the single GuangDone Accident that leads to the sampling and studies. A full virome TRACE analysis is conducted on the available samples for the determining of the exact etiological agent.

Extended Data Table S1

Full virome TRACE results of all Analyzable datasets of the GD pangolin incident

| | Mammarenavirus | Nairoviridae | Murine respirovirus | Flaviviridae | Nidovirales | Rubulavirus | Nonanavirus | Peribunyavi | Amigovirus | Siphoviridae | Siphoviridae | Paheviridae |
|------------|----------------|--------------|---------------------|--------------|-------------|-------------|-------------|-------------|------------|--------------|--------------|-------------|
| SRX6893158 | Yes | Yes | No | No | No | No | Yes | No | Yes | Yes | No | No |
| SRX6893157 | Yes | Yes | No | No | Claimed | No | No | Yes | No | No | No | No |
| SRX6893156 | No | No | Yes | Yes | Yes | No | No | No | Yes | No | No | Yes |
| SRX6893155 | No | No | Yes | No | Yes | No | No | No | No | No | No | No |
| SRX6893154 | No | No | Yes | No | Yes | No | No | No | No | No | No | No |
| SRX6893153 | No | No | Yes | Yes | Yes | No | No | No | Yes | No | No | No |
| SRX6893152 | Yes | Yes | Yes | Yes | No | No | No | Yes | No | No | No | No |
| SRX6893151 | Yes | Yes | No | Yes | No | No | No | Yes | Yes | No | No | No |
| SRX6893150 | Yes | Yes | Yes | No | No | No | No | Yes | Yes | No | No | No |
| SRX6893149 | Yes | Yes | No | No | No | No | No | No | No | No | Yes | No |
| SRX6893148 | Yes | Yes | Yes | No | No | No | No | No | Yes | No | No | No |
| SRX6893147 | Yes | Yes | "Respirovirus" | Yes | No | No | Yes | No | Yes | No | No | No |
| SRX6893146 | Yes | Yes | Yes | No | No | No | No | No | No | No | No | No |
| SRX6893145 | Yes | Yes | No | No | No | No | No | No | No | No | No | No |
| SRX6893144 | Yes | Yes | Yes | Yes | No | No | No | No | No | No | No | No |
| SRX6893143 | Yes | Yes | No | No | No | No | No | No | No | No | No | No |
| SRX6893142 | Yes | Yes | No | No | No | No | No | Yes | Yes | No | No | No |
| SRX6893141 | Yes | Yes | No | Yes | No | No | No | No | No | No | No | No |
| SRX6893140 | Yes | Yes | Yes | No | No | No | No | Yes | No | No | No | No |
| SRX6893139 | No | No | Yes | No | Yes | No | No | No | No | No | No | No |
| SRX6893138 | Yes | Yes | Yes | Yes | No | No | Yes | Yes | Yes | No | No | No |
| SRX7756766 | No | No | Yes | Yes | Yes | Yes | No | No | No | No | No | No |
| SRX7756765 | No | No | Yes | No | No | Yes | No | No | No | No | No | No |
| SRX7756764 | No | No | Yes | No | No | Yes | No | No | No | No | No | No |
| SRX7756763 | No | No | Yes | No | No | Yes | No | No | No | No | No | No |
| SRX7756762 | No | No | Yes | No | Claimed | Yes | No | No | No | No | No | No |
| SRX7756761 | No | No | Yes | No | No | Yes | No | No | No | No | No | No |
| SRX7756769 | No | No | Yes | Yes | Yes | No | No | No | No | No | No | No |

A full Virome TRACE result suggest all the dead pangolins were infected by either Mammarenaviruses or Murine Respirovirus, or both. Including both samples that contained Claimed Or TRACEd Coronavirus reads and the samples that didn't.

Murine Respirovirus and Mammarenaviruses co-infect 7 out of 29 Available Analyzable datasets, while None of the 29 datasets lacked both—indicating that both viruses were prevalent in the location where the pangolins were captive at The Guangdong Wildlife Rescue Center.

Symptoms of Murine Respirovirus in animals resembles that of SARS-CoV-2 in humans—It forms massive Syncytiums in Eukaryotic cells, suppresses the immune system and causes secondary bacterial infections. The virus causes necrosis of Lung tissue in 5 days, with similar inflammation and immunopathological effects in the lung tissues of infected animals [5]—creating the histopathological effect as reported by Xiao et al.

It should be worth pointing out that the only examined lung tissues were examined by Xiao et al. And all Lung tissue samples examined by Xiao et.al contained Reads from the Murine Respirovirus.

Similarly, Mammarenaviruses are also known to cause multi organ, lethal[7] infections, characterized by endothelial pathology and swelling of internal organs. [6] All of which were Symptoms reported in the incident. As these samples were not examined Histopathologically by

either the authors of [4] nor by any of the authors of any other article who have used the datasets/samples, leaving the only mean of elucidating the cause of death being the observed symptoms and the coarse examination of the organs during sampling. Mammarenavirus infection therefore remains the most likely cause of death of the Murine Respirovirus Negative samples in the available datasets.

Is the “GD pangolin CoV” really a virus of the pangolin?

The only examination of the binding affinity of the GD pangolin CoV RBD to different animal receptors was done by Xiao et al [2], which performed molecular dynamic simulation of the RBD docking to the Human ACE2 receptor, The Civet ACE2 receptor and the pangolin ACE2 receptor. If the RBD of GD pangolin CoV in deed evolved in pangolins, we should expect the binding affinity of the RBD toward the pangolin ACE2 receptor to be the highest binding affinity returned from the examination.

However, neither the GD pangolin CoV RBD, nor the RBD of SARS-CoV-2 which is highly similar, produced a higher binding affinity to the pangolin ACE2 receptor than to the human ACE2 receptor, and both binds the Human ACE2 receptor with the highest affinity across all 3 animal species (Human, Civet, Pangolin) examined.

This fact argues strongly against the RBD residues of the GD pangolin CoV being evolved in pangolins, and instead favoring the RBD and the virus being the result of a passage experiment of a possible virus of pangolin origin (The GX/P2V virus was isolated and passaged in VERO E6 cells during it’s collection in 2017) in Primate-derived cell lines.

There are only 2 locations of Biological sample storage in GuangDong, the Guangdong Institute of Applied Biological Resources and the China National GeneBank.

As all Credible (Non-filtered and contained analyzable Non-Coronavirus reads) samples were collected in a single incident from the Guangdong Wildlife Rescue Center[1][4][2], which the initial sample collection and storage was carried out by the Guangdong Institute of Applied Biological Resources[4], this experimental culture likely contaminated the GD pangolin samples during their initial collection or Storage, Either by the lab worker doing the initial sampling, or during their storage in the facility.

Epidemiology analysis of SARS-CoV-2 and related viruses argues strongly against the existence of a Coronavirus with the claimed RBD residues and sequence similarity in or near the Guangdong Wildlife Rescue Center at the time and date of the incident and the collection of the samples.

The earliest collection date of the GD pangolin CoV available, MP789, GenBank MT084071.1, is displayed at 29 March 2019.

Since the original location of the animals and samples in question was inside the Guangdong Wildlife Rescue Center which is neither a certified Biosafety Laboratory nor possessed adequate

PPE when handling the animals, from the Simulation results by Xiao et al[2] and the observed high human transmissibility of SARS-CoV-2 which had a very similar RBD, Should the GD pangolin CoV genuinely exists at that date and within the unprotected GuangDong Wildlife Rescue Center, It would almost certainly infect one to multiple On-site workers (Rescue workers which lacked either the Biosafety training or the adequate PPEs required to handle tissues or animals infected with a virus as characterized by the GD pangolin CoV papers) in the GuangDong Wildlife Rescue Center, and caused a SARS-level epidemic in GuangDong 2013 beginning in or around April 2019. However, no such epidemic was recorded, nor there have been any virus that genetically resembled the GD pangolin CoV sequence (which is only 90% similar to SARS-CoV-2) being isolated in humans anywhere in the world even till today.

Nor there is a possibility that the current SARS-CoV-2 pandemic may have stemmed from the 29 March incident with the GD pangolin CoV, since the estimated time of divergence between the current SARS-CoV-2 genome to the GD pangolin CoV Genome was estimated to be at least 100 years ago , ranging from 1851 [1730,1958] to 1877 [1746,1986] [8], for a genome that is only 90% similar to SARS-CoV-2 and possessed significant difference in the sequence and composition of the viral proteins they encodes.

As the Earliest time of discovery and the incident on the GD pangolin CoV is no earlier than the beginning of Year 2019, The time between the incident and the first isolate of SARS-CoV-2 is far too short for GD pangolin CoV incident to be involved in the formation of the current SARS-CoV-2 pandemic, since even the neutral sites on the RBD itself would have taken more than 19.8 years to drift/evolve into what we seen today on the actual SARS-CoV-2 genome. [9]

Conclusions

The Extreme lack of transparency and the sheer level of contamination from the original samples, the lack of epidemiological evidence of it's existence at the location of it's collection, and the receptor binding affinity of the Viral RBD itself indicating it as not being evolved nor adapted in pangolins, all strongly argue against the existence of a SARS-CoV-2 like virus infecting pangolins captive in GuangDong at 2019.

Moreover, it suggests that the GD pangolin CoV exists only as a culture in Primate-derived cells within the lab/facility used for the initial collection and/or storage of the samples of the pangolins in question, raising important issues on the serial passage Gain-Of-Function research of viral pathogens.

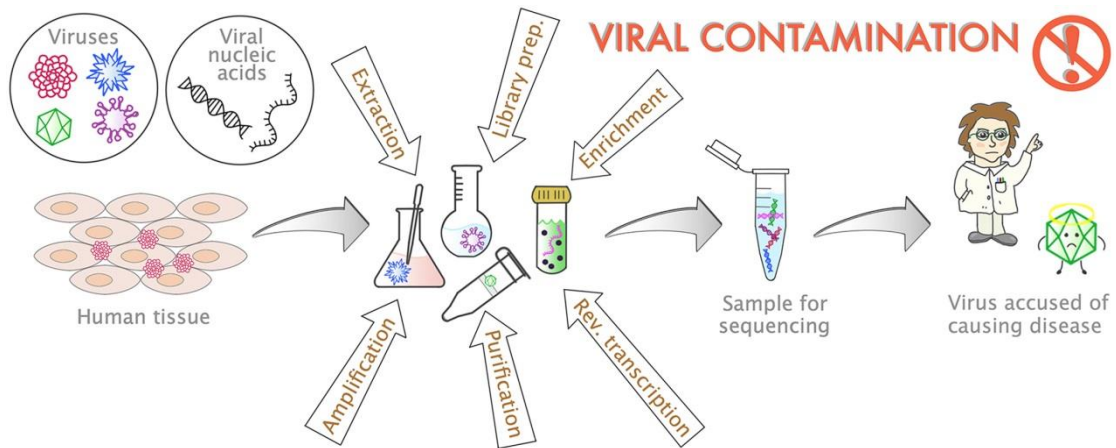


Figure 14. A cartoon diagram of contamination in sequencing experiment leading to false results and false “discoveries”.

Note as in 2020/7/23

A recent Dataset, seemingly unrelated to the Xiao et.al Nature dataset, [SRX8582289](#), appeared under [PRJNA607174](#). This dataset seems to be newly sequenced, and it was not referred in [2].

| Accession number and registration date | Primary Mammalian Trace results and percentage | Primate-related results in Krona and read size by Kbp | Identification of “Coronaviridae” as by Trace and total read size |
|---|--|---|---|
| SRX8582289 22-Jun-2020 | Manis javanica: 43.52% | Catarrhini 98913 | Pangolin coronavirus 792 |

Table S2: TRACE analysis result of the [SRX8582289](#) dataset.

Nevertheless, in-depth analysis revealed significant amount of contamination from the Human genome, with ratio of Virus to cell=0.8%.

Description: Homo sapiens BAC clone RP11-460N20 from 7, complete seq ...

Molecule type: nucleic acid

Query Length: 203396

Other reports: [Distance tree of results](#) [MSA viewer](#)

Percent Identity: to

E value: to

Query Coverage: to

[Filter](#) [Reset](#)

Descriptions | Graphic Summary | Alignments

Sequences producing significant alignments | Download | Manage Columns | Show: 100

select all | 100 sequences selected

| Description | Max Score | Total Score | Query Cover | E value | Per Ident | Accession |
|--|-----------|-------------|-------------|---------|-----------|--|
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 278 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.88444297.1 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 402 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.83916175.2 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 388 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.83916175.1 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 278 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.82221130.1 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 278 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.71234261.2 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 278 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.71234261.1 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 5169 | 2% | 8e-69 | 100.00% | SRA_SRR12053850.51889132.2 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 7268 | 3% | 8e-69 | 100.00% | SRA_SRR12053850.26027930.2 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 5671 | 2% | 8e-69 | 100.00% | SRA_SRR12053850.21554419.1 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 278 | 0% | 8e-69 | 100.00% | SRA_SRR12053850.13271287.2 |
| <input checked="" type="checkbox"/> SRX8582289 | 278 | 4760 | 1% | 8e-69 | 100.00% | SRA_SRR12053850.62042.2 |
| <input checked="" type="checkbox"/> SRX8582289 | 276 | 276 | 0% | 3e-68 | 100.00% | SRA_SRR12053850.82221130.2 |

Figure S1A: Some BLAST hits out of a human Somatic BAC clone.

Job Title **2 sequences (gnl|SRA|SRR12053850.88444297.1...**

RID [HJSZ72932014](#) Search expires on 07-24 18:18 pm [Download All](#) ▼

Results for ▼

Program **BLASTN** [Citation](#) ▼

Database **nt** [See details](#) ▼

Query ID **lc|Query_748**

Description **gnl|SRA|SRR12053850.88444297.1 88444297 (Biological)**

Molecule type **dna**

Query Length **150**

Other reports [Distance tree of results](#) ?

Filter Results

Organism *only top 20 will appear* exclude

[+ Add organism](#)

Percent Identity to

E value to

Query Coverage to

[Filter](#) [Reset](#)

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download Manage Columns Show 100 ?

select all 98 sequences selected

[GenBank](#) [Graphics](#) [Distance tree of results](#)

| | Description | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession |
|-------------------------------------|--|-----------|-------------|-------------|---------|------------|--------------------------------|
| <input checked="" type="checkbox"/> | Homo sapiens BAC clone RP11-460N20 from 7 . complete sequence | 278 | 278 | 100% | 7e-71 | 100.00% | AC073210.8 |
| <input checked="" type="checkbox"/> | Pan troglodytes BAC clone CH251-623C19 from chromosome 7 . complete sequence | 267 | 267 | 100% | 1e-67 | 98.67% | AC184799.2 |
| <input checked="" type="checkbox"/> | Pan troglodytes BAC clone CH251-2015 from chromosome 7 . complete sequence | 267 | 267 | 100% | 1e-67 | 98.67% | AC174000.3 |
| <input checked="" type="checkbox"/> | Pan troglodytes BAC clone CH251-565C10 from chromosome 7 . complete sequence | 267 | 267 | 100% | 1e-67 | 98.67% | AC148313.3 |
| <input checked="" type="checkbox"/> | PREDICTED: Pan paniscus uncharacterized LOC117981001 (LOC117981001) . transcript variant X4 . mRNA | 261 | 261 | 100% | 7e-66 | 98.00% | XM_034964262.1 |
| <input checked="" type="checkbox"/> | PREDICTED: Pan paniscus uncharacterized LOC117981001 (LOC117981001) . transcript variant X3 . mRNA | 261 | 261 | 100% | 7e-66 | 98.00% | XM_034964260.1 |
| <input checked="" type="checkbox"/> | PREDICTED: Pan paniscus uncharacterized LOC117981001 (LOC117981001) . transcript variant X2 . mRNA | 261 | 261 | 100% | 7e-66 | 98.00% | XM_034964259.1 |

Fig. S1B: BLAST results returned only Homo Sapiens as 100% match. This indicate that the listed Catarrhini reads come from Homo Sapiens. The significance of this particular dataset is yet unknown.

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