

There and back again: characterising SARS-CoV-2 wildlife spillover and spillback

(Pre-Print: [10.1101/2022.02.22.481551v3](https://doi.org/10.1101/2022.02.22.481551v3))

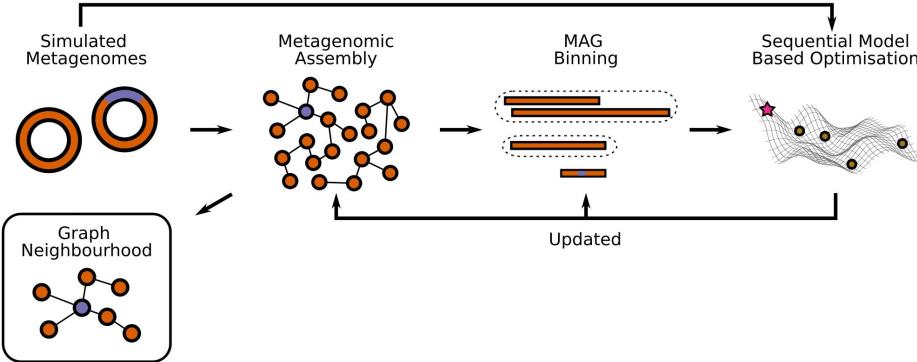


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Maguire Lab: 2022-

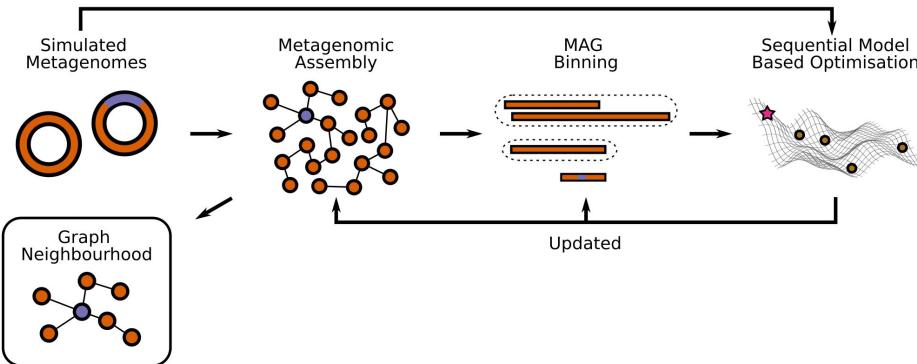
Genomic Epidemiology of Infectious Diseases



- **SARS-CoV-2**
 - CIHR PG: genotype to phenotype
 - NSERC CANMOD: creating genomic SIR models
- **Antimicrobial resistance**
 - NSERC DG: LGT via metagenomic graphs
 - PHA4GE: Emerging threats & public health bioinformatics

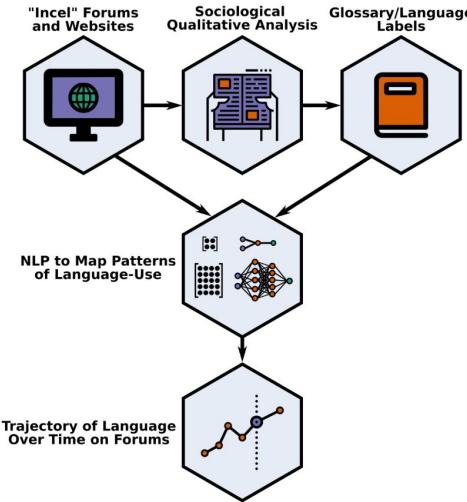
Maguire Lab: 2022-

Genomic Epidemiology of Infectious Diseases



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Collaborative Health Data Science



- **Social disconnection**
 - SSHRC IDG: online “Incel” radicalisation
- **Health inequality**
 - SSHRC IDG: modelling interplay of “luck” + frailty/resilience on health outcomes

“WILD-CoV”



National Centre for Foreign Animal Disease

- Bradley Pickering (Iowa State/Manitoba)
- Oliver Lung (Manitoba)
- Peter Kruczkievicz
- Melissa Goolia, Matthew Suderman, Mathieu Pinette, Greg Smith, Daniel Sullivan, Josip Rudar, Michelle Nebroski, Oksana Vernygora



Computer Science / Epidemiology

- Finlay Maguire



- Jennifer Guthrie (Western)
- Alex Marchand-Austin



Sunnybrook Research Institute

- Samira Mubareka (Toronto)
- Jonathan Kotwa
- Bryan Griffin
- Kuganya Nirmalarajah, Juliette Blais-Savoie, Hsien-Yao Chee, Emily Chien, Winfield Yim, Andra Banete, Lily Yip

Shared Hospital Laboratory

- Patryk Aftanas



Ministry of Northern
Development, Mines, Natural
Resources and Forestry

- Jeff Bowman (Trent)
- Tore Buchanan
- Larissa Nituch
- Elizabeth Adey



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- Marceline Côté
- Geneviève Laroche
- Ardesir Ariana, Brett Vahkal



- Alison McGeer (Toronto)



Guillaume Goyette, Andrés Finzi, Claire Jardine, Ariane Massé Heather McClinchey



Canadian Institutes of Health Research Institut de recherche en santé du Canada



CoVaRR+Net

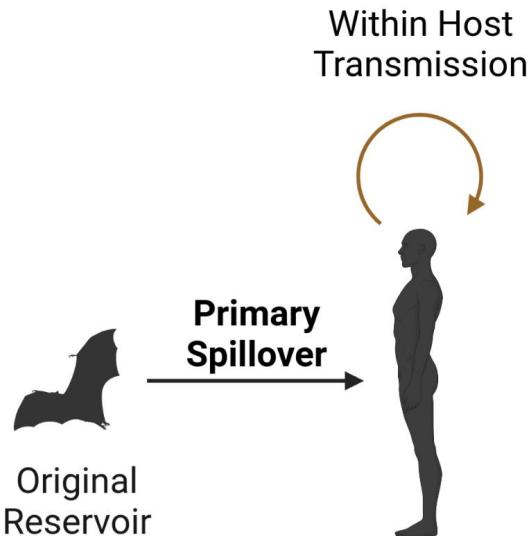


CanCOGeN

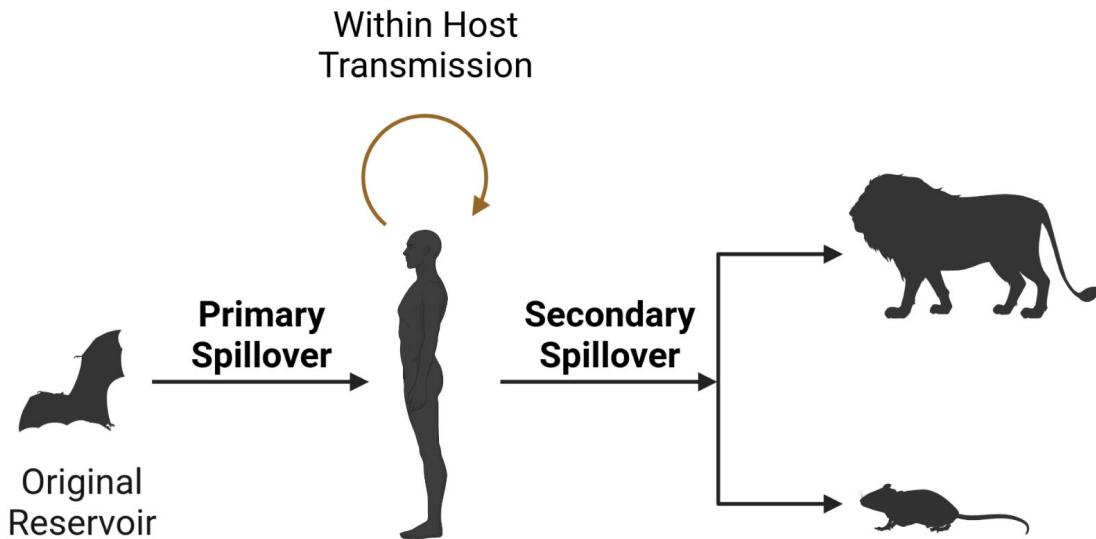


Why monitor non-human mammals?

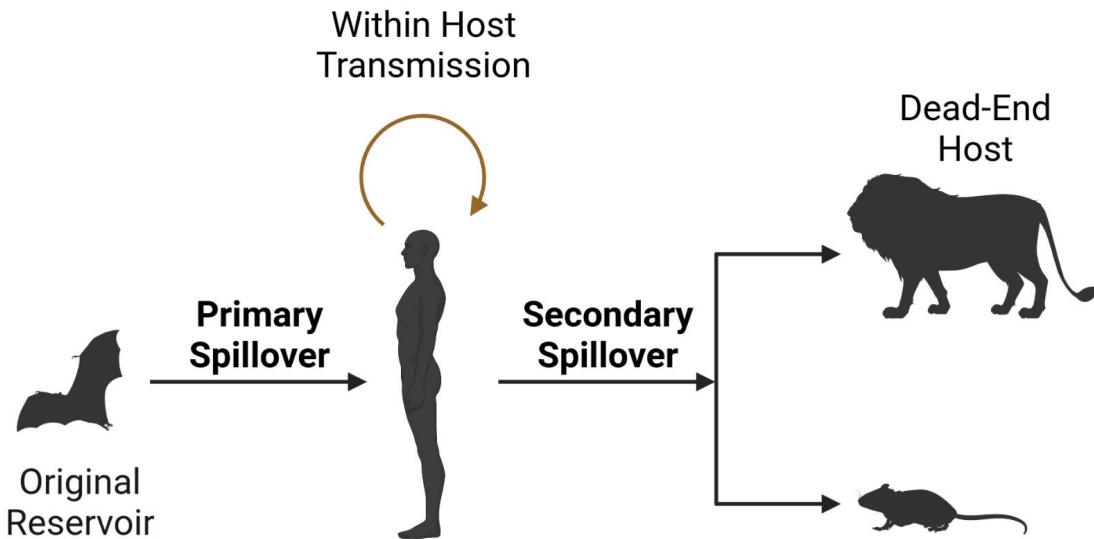
Animal infections can impact evolution of SARS-CoV-2



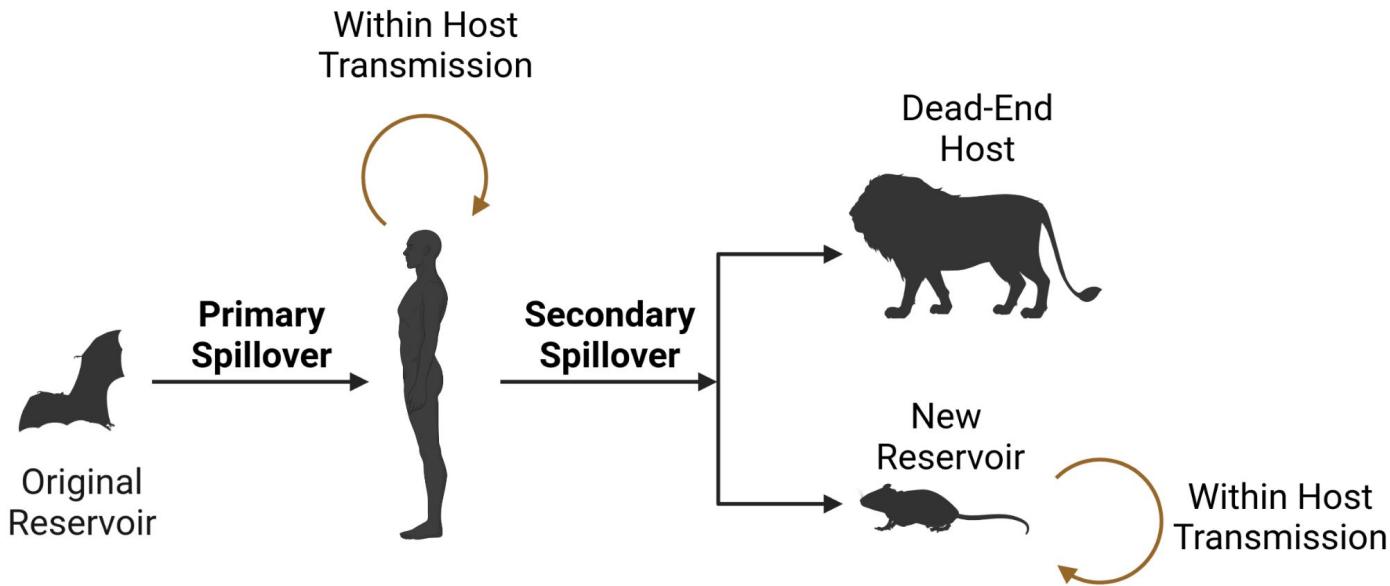
Animal infections can impact evolution of SARS-CoV-2



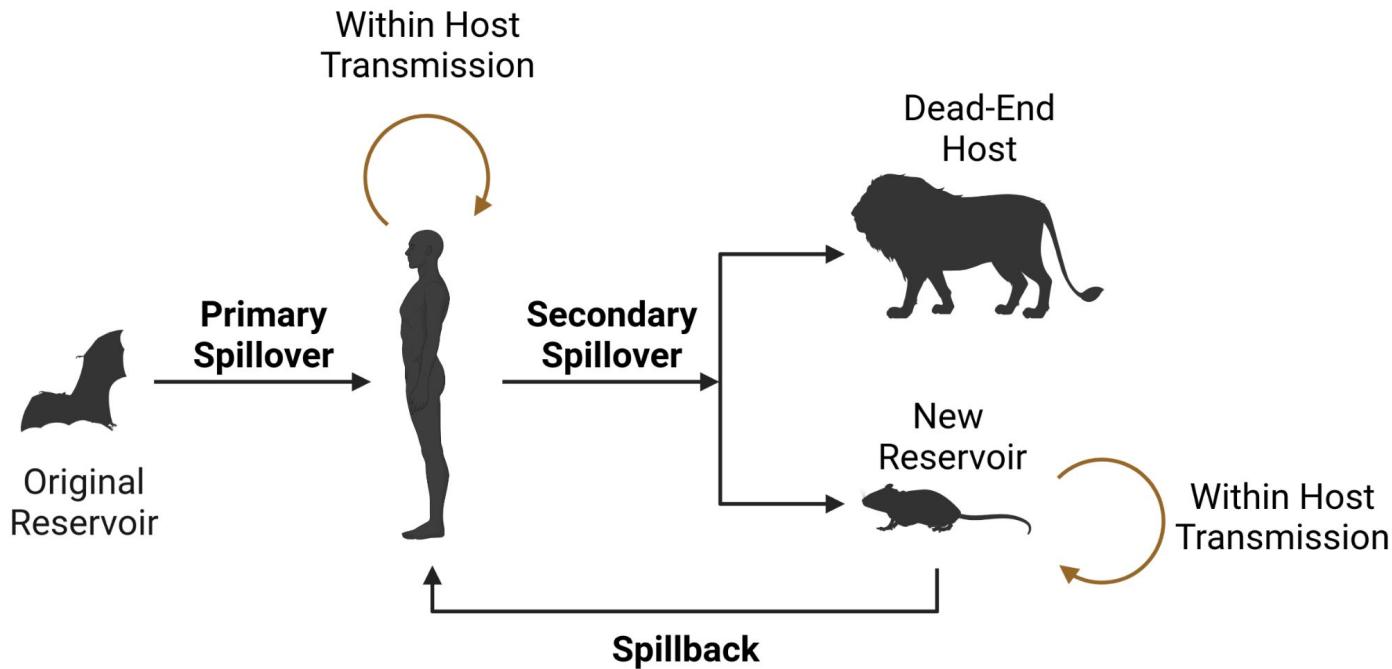
Animal infections can impact evolution of SARS-CoV-2



Animal infections can impact evolution of SARS-CoV-2



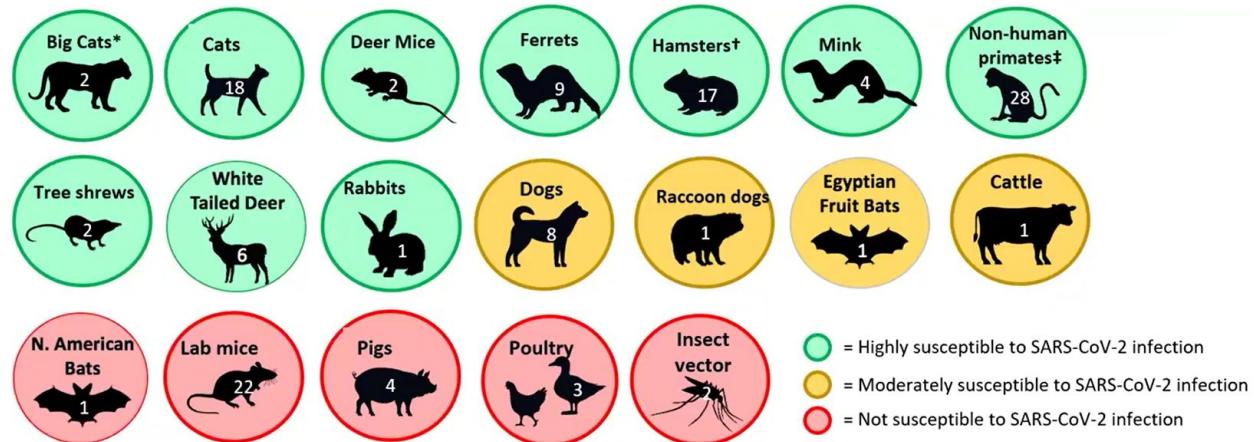
Animal infections can impact evolution of SARS-CoV-2



Are secondary animal reservoirs a problem in
SARS-CoV-2?

SARS-CoV-2 can infect ~50 non-human mammals

Published or pre-print articles –
SARS-CoV-2 experimental or natural infection in animals



*Big cats include: lions, tigers and puma

†Hamster species include: Chinese hamsters and golden Syrian hamsters

‡Non-human primate species include: African green monkeys, baboons, common marmosets, cynomolgus macaques, pigtail macaques, rhesus macaques, and savanna monkeys



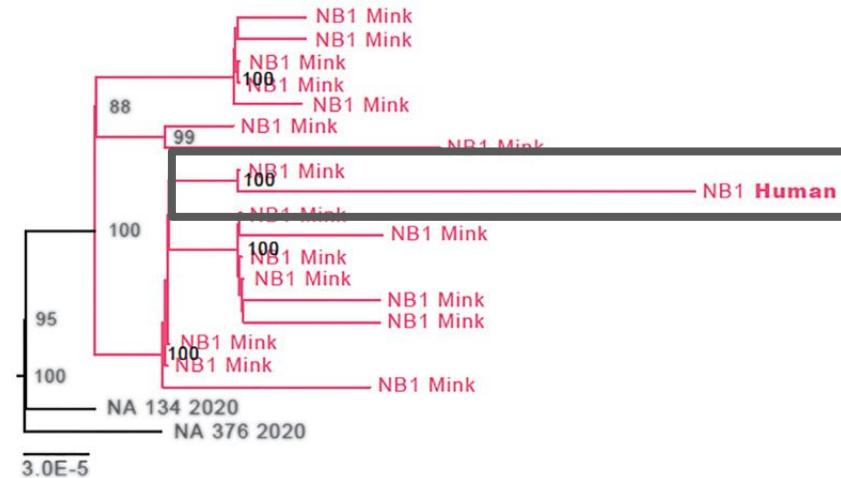
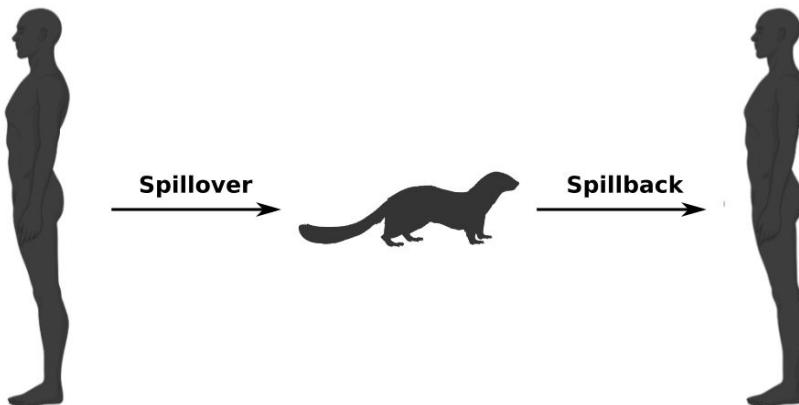
Secondary Spillback into humans has been observed

Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans

BAS B. OUDE MUNNINK, REINA S. SIKKEMA, DAVID F. NIEUWENHUIJSE, ROBERT JAN MOLENAAR, EMMANUELLE MUNGER, RICHARD MOLENKAMP, ARCO VAN DER SPEK, PAULIEN TOLMSA, ARIENE RIETVELD, LIMARION P. G. KOOPMANS, +13 authors

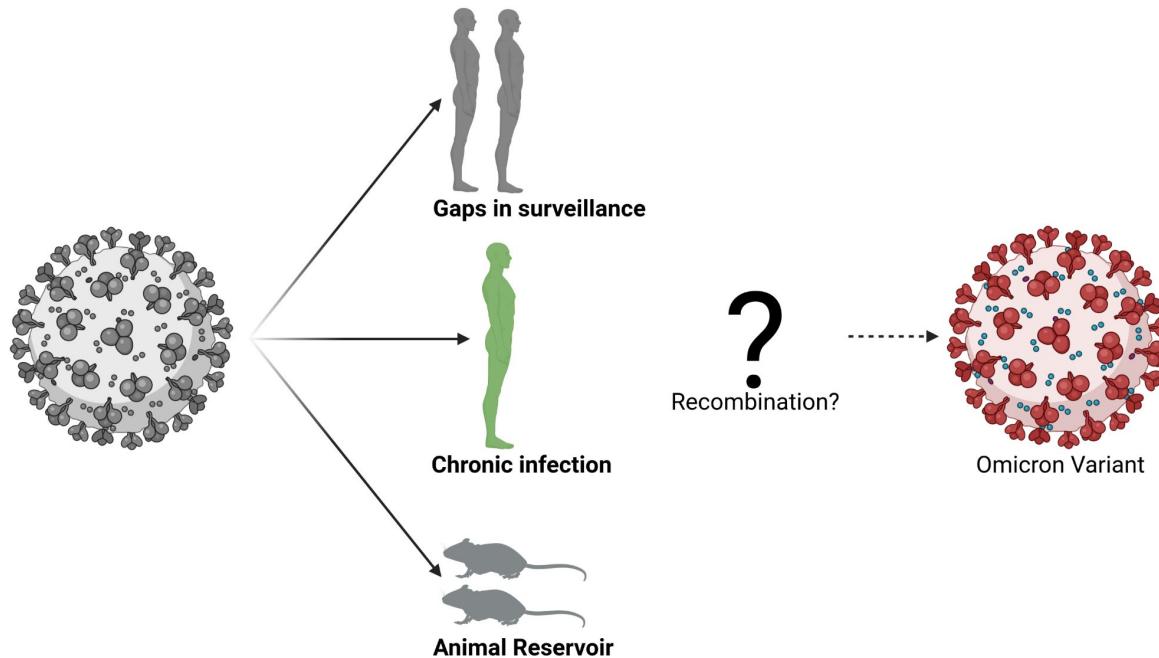
Authors Info & Affiliations

SCIENCE • 10 Nov 2020 • Vol 371, Issue 6525 • pp. 172-177 • DOI: 10.1126/science.abe5901



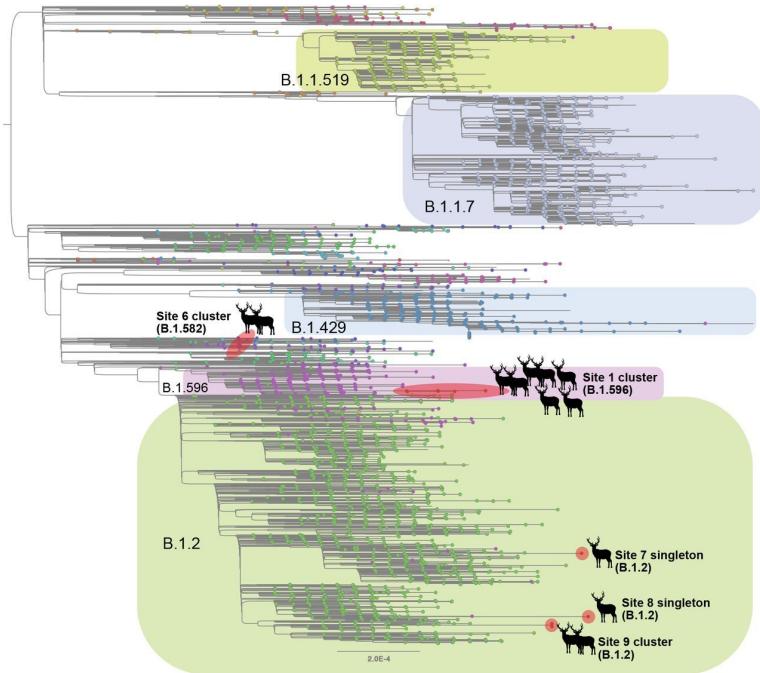
10.1126/science.abe5901

Omicron may have originated in animal reservoirs

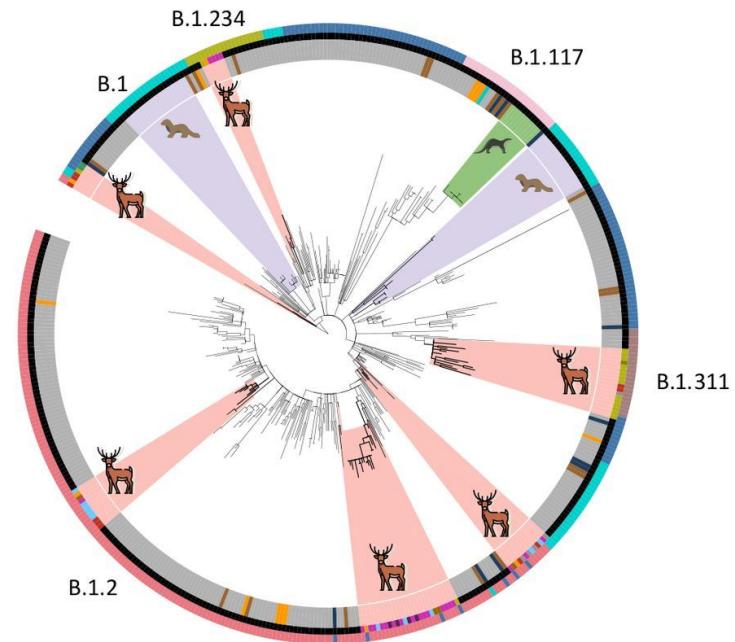


Why are White-Tailed Deer a priority?

White-Tailed Deer are susceptible

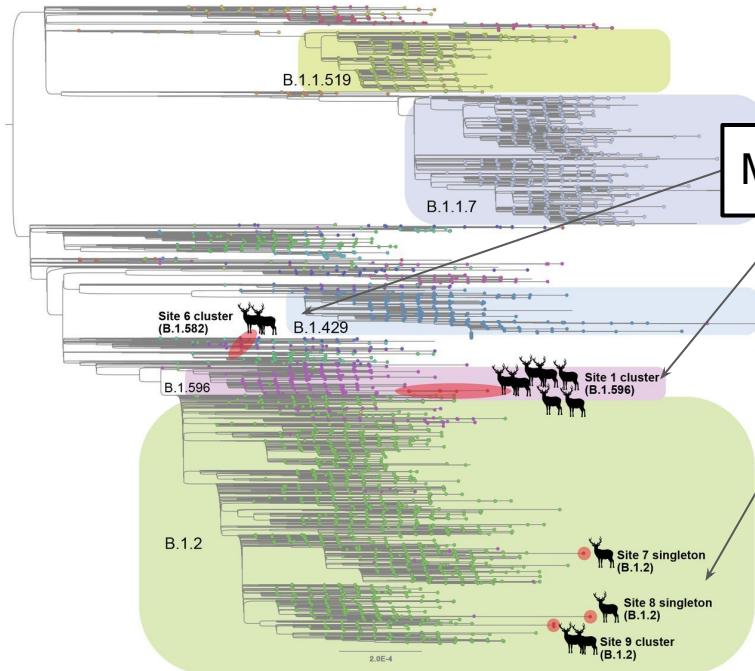


(Hale, 2021) 10.1101/2021.11.04.467308

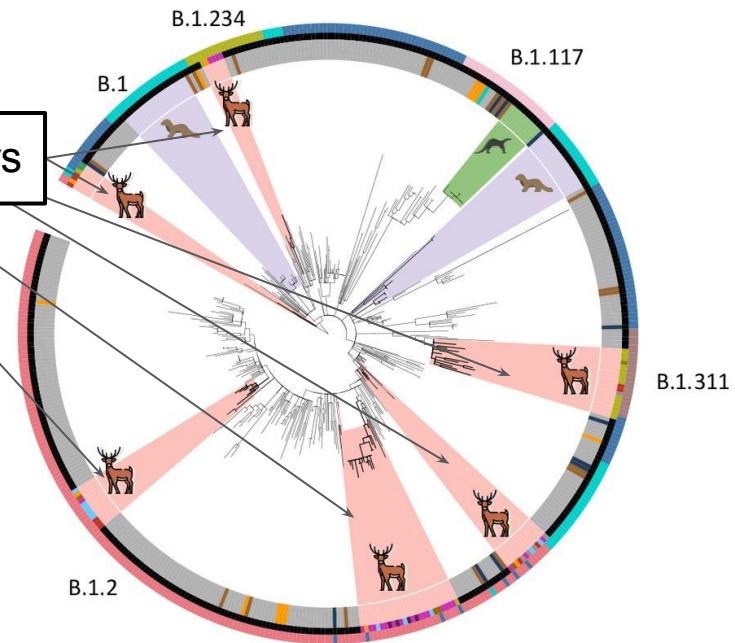


(Kuchipudi, 2021) 10.1101/2021.10.31.466677

White-Tailed Deer are susceptible

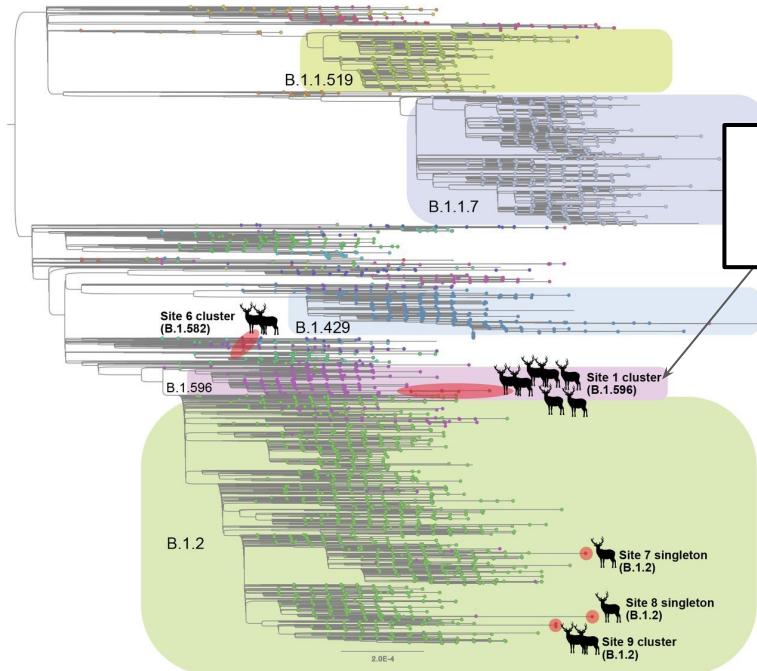


(Hale, 2021) 10.1101/2021.11.04.467308

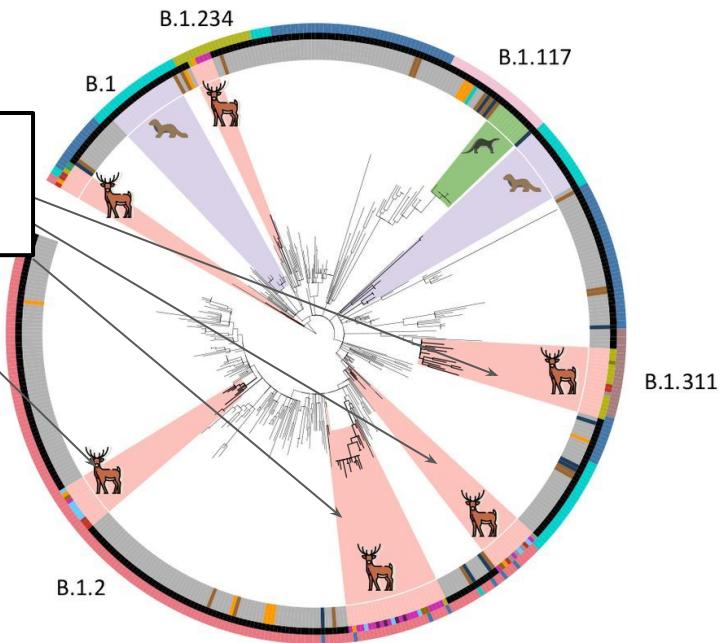


(Kuchipudi, 2021) 10.1101/2021.10.31.466677

White-Tailed Deer are susceptible



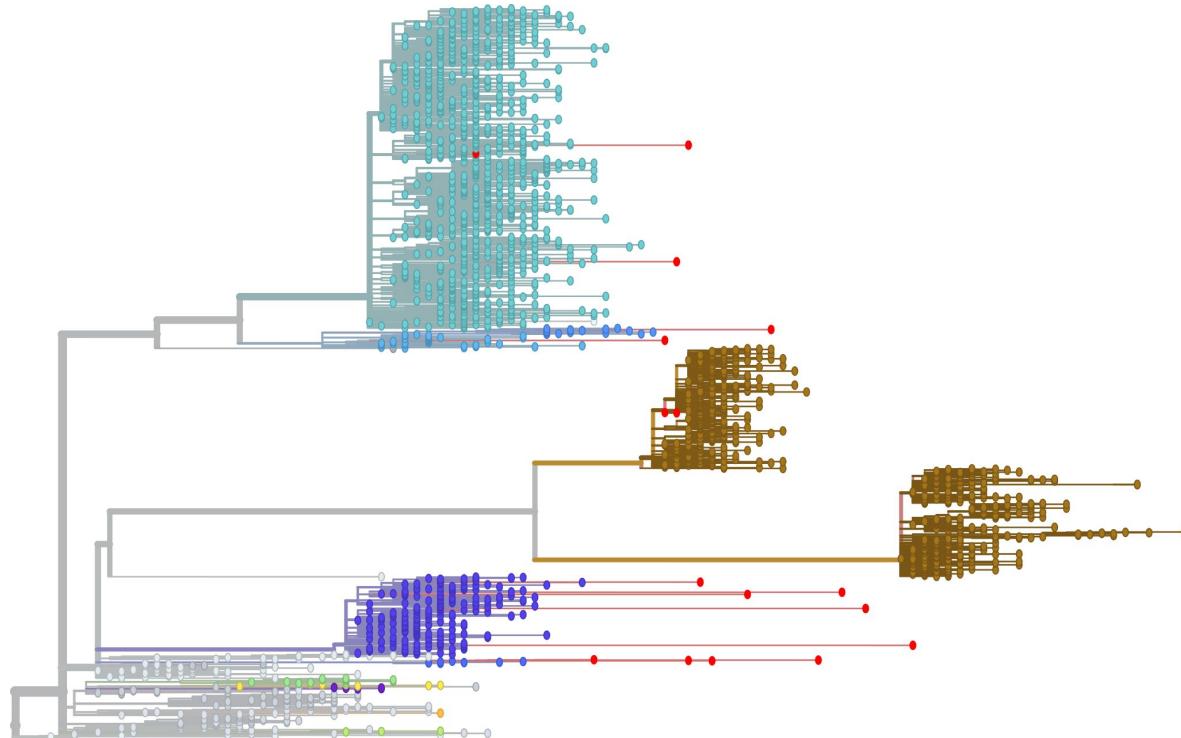
Deer to Deer
Transmission



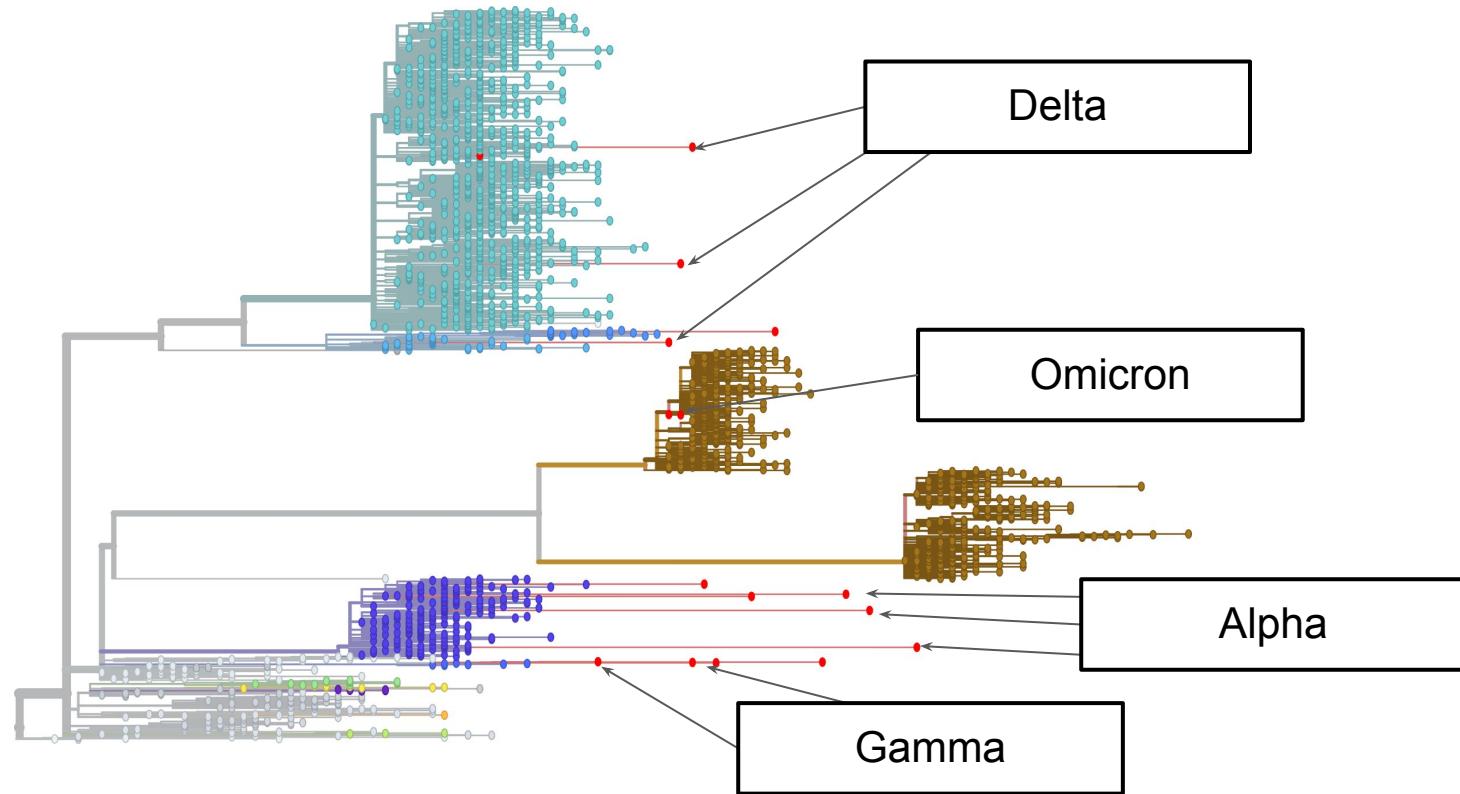
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(Kuchipudi, 2021) 10.1101/2021.10.31.466677

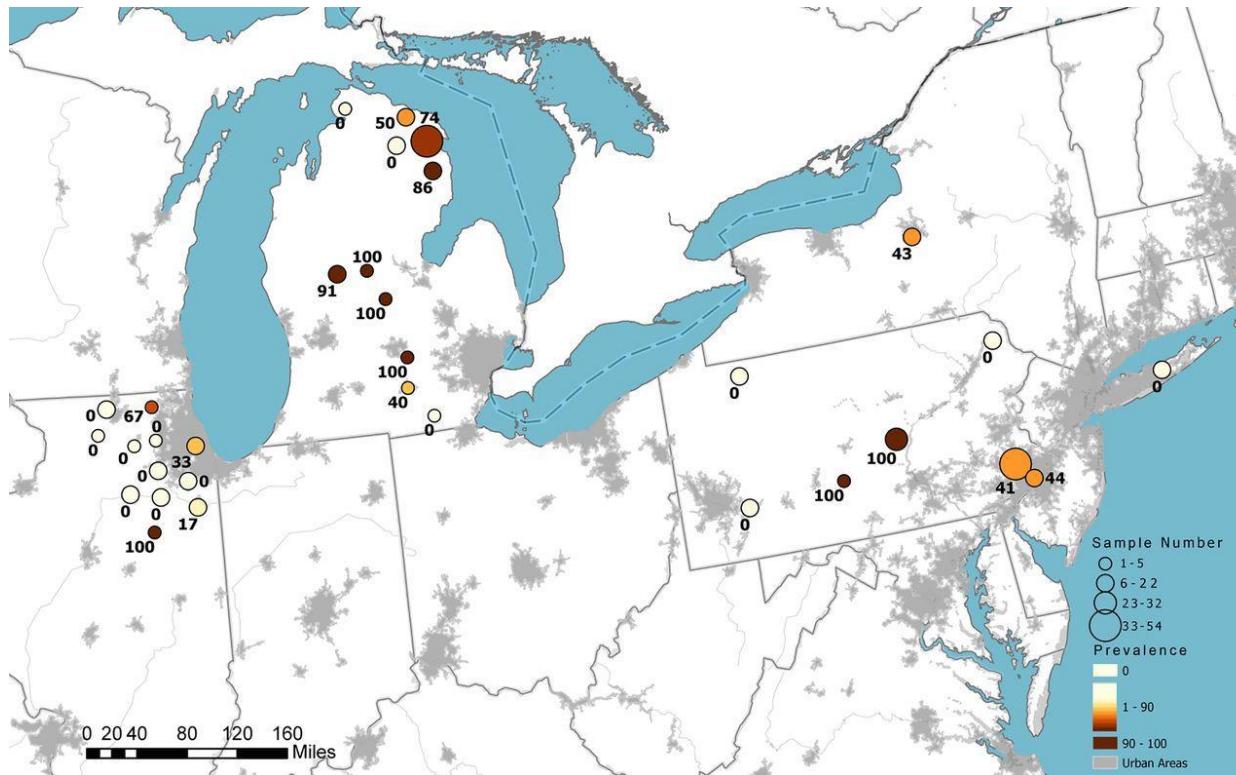
Spillover into White-Tailed Deer includes VOCs



Spillover into White-Tailed Deer includes VOCs

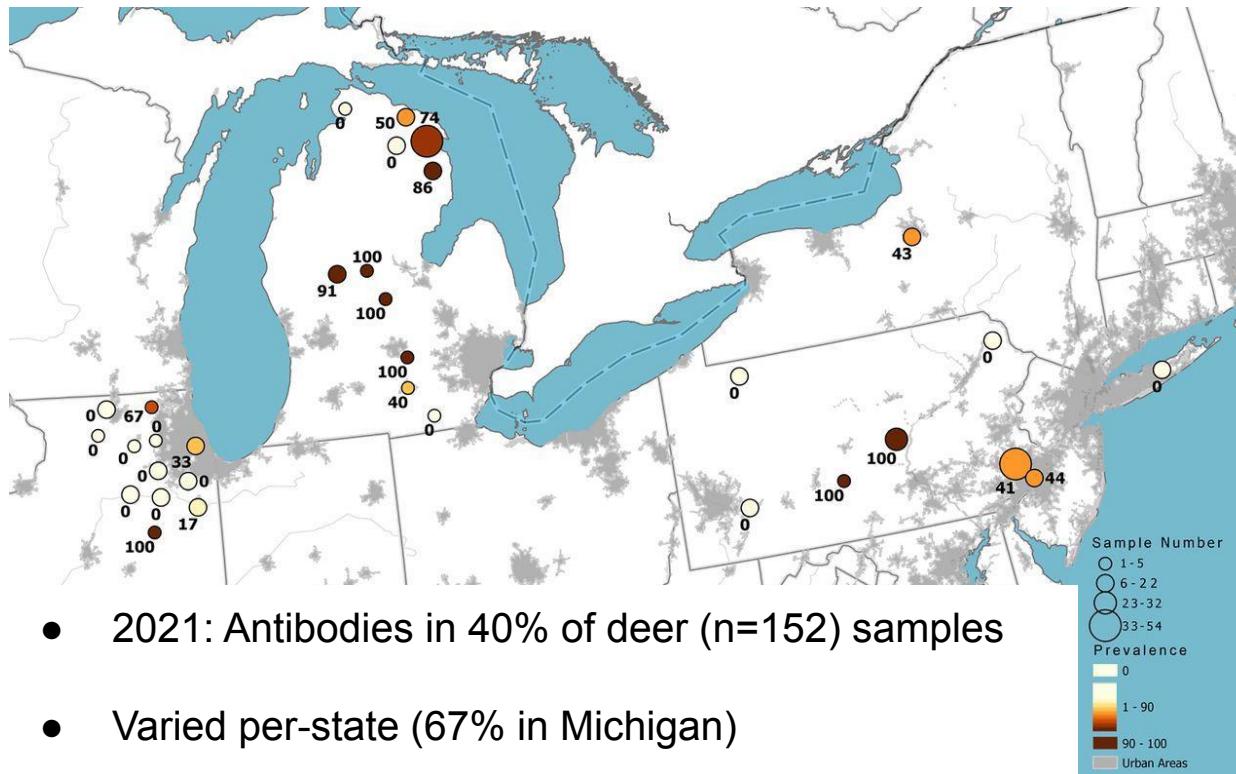


Serology indicates prevalent exposure



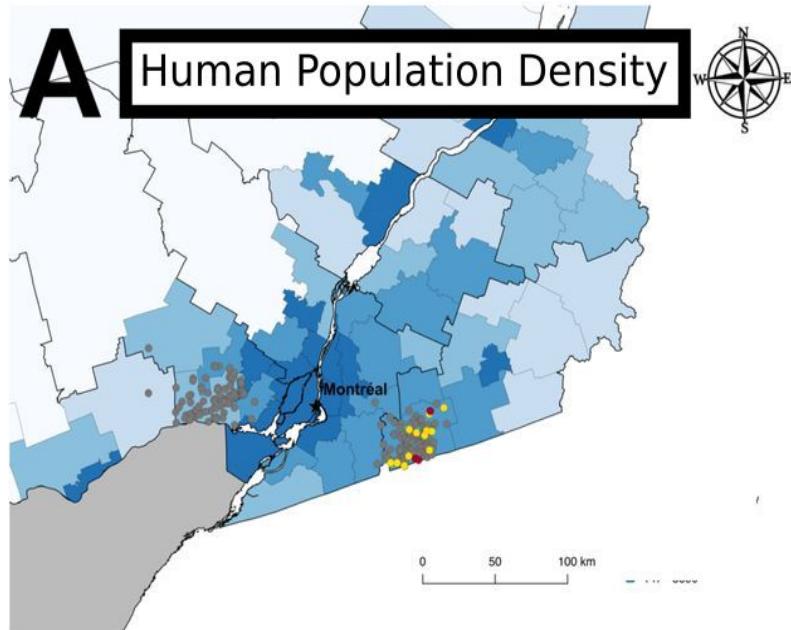
(Chandler, 2021) 10.1073/pnas.2114828118

Serology indicates prevalent exposure



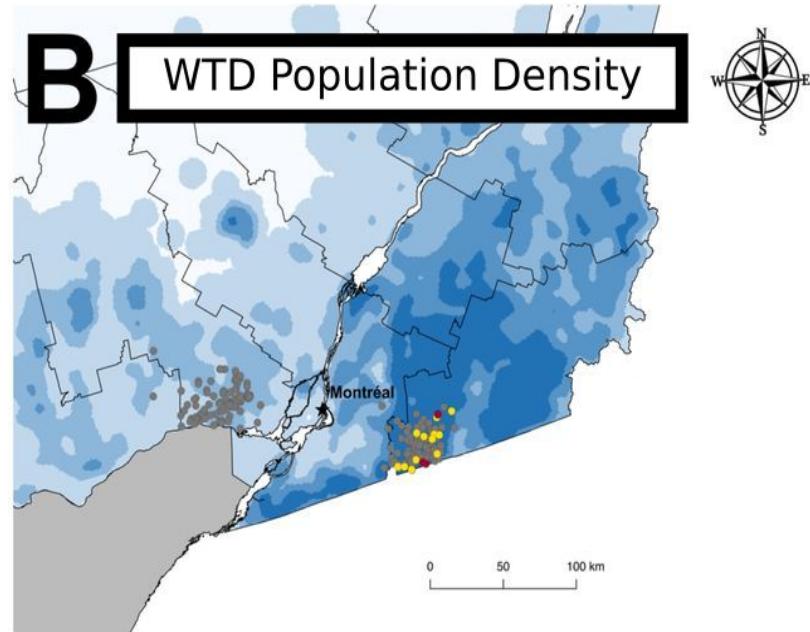
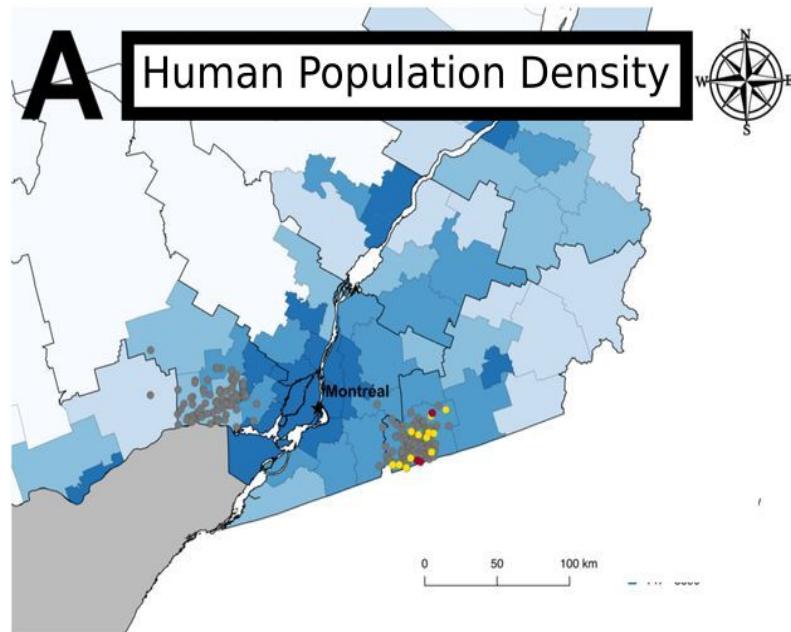
(Chandler, 2021) 10.1073/pnas.2114828118

White-Tailed Deer: large/mobile populations near humans



(Kotwa, 2022) 10.1101/2022.01.20.476458

White-Tailed Deer: large/mobile populations near humans



How can we monitor SARS-CoV-2 evolution
in White-Tailed Deer?

Use pre-existing surveillance programs for WTD

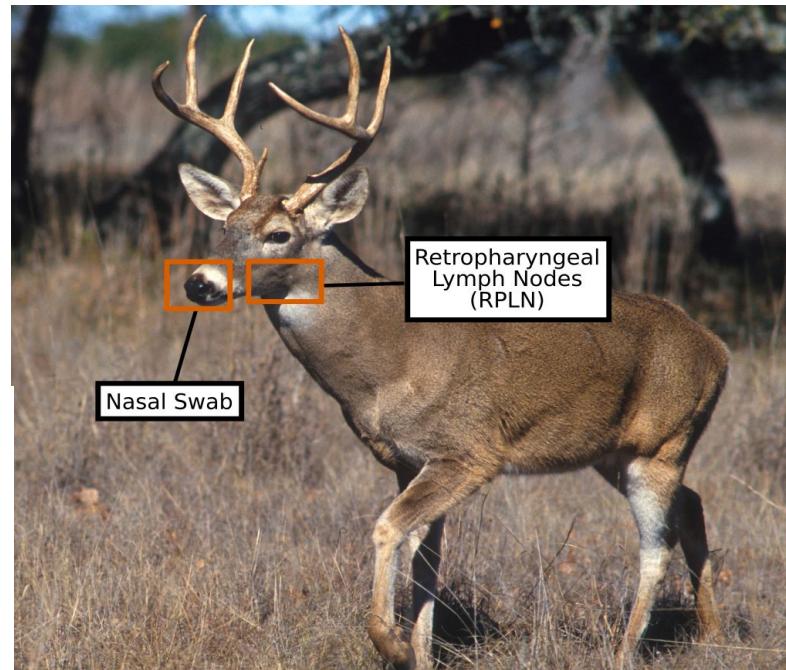
- SARS-CoV-2 sampling added to Chronic Wasting Disease surveillance program (Nov 1st - Dec 31st 2021)



USDA photo by Scott Bauer - Image Number: K5437-3

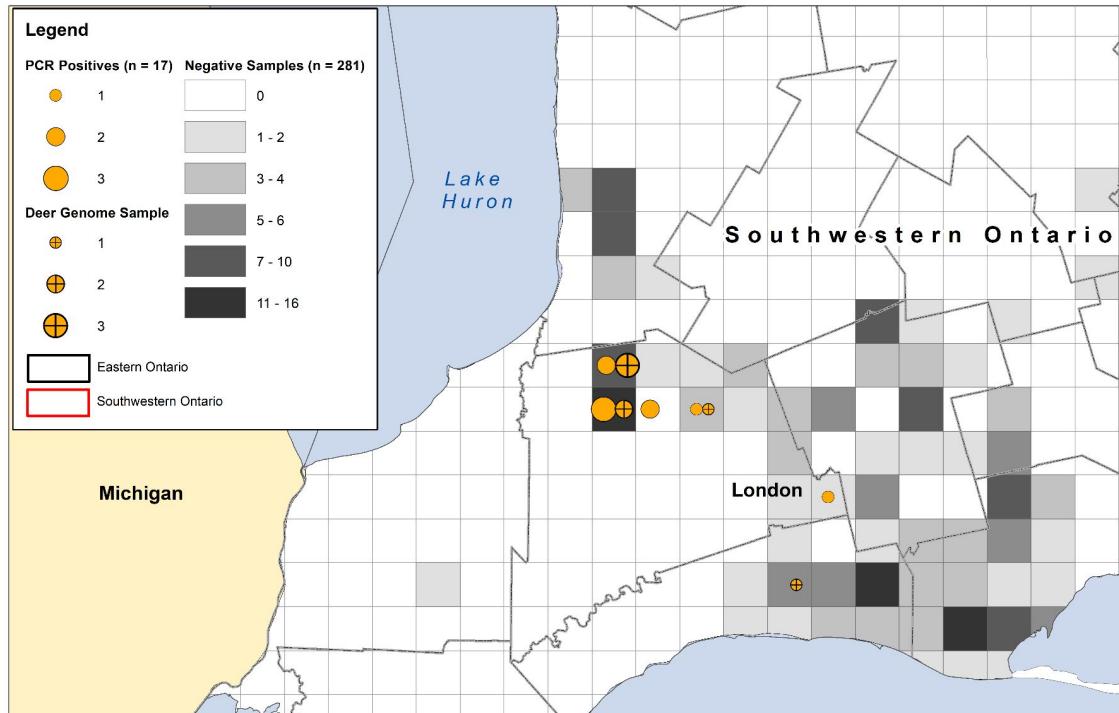
Use pre-existing surveillance programs for WTD

- SARS-CoV-2 sampling added to Chronic Wasting Disease surveillance program (Nov 1st - Dec 31st 2021)
- Nasal swabs and RPLN samples from hunter-harvested carcasses



USDA photo by Scott Bauer - Image Number: K5437-3

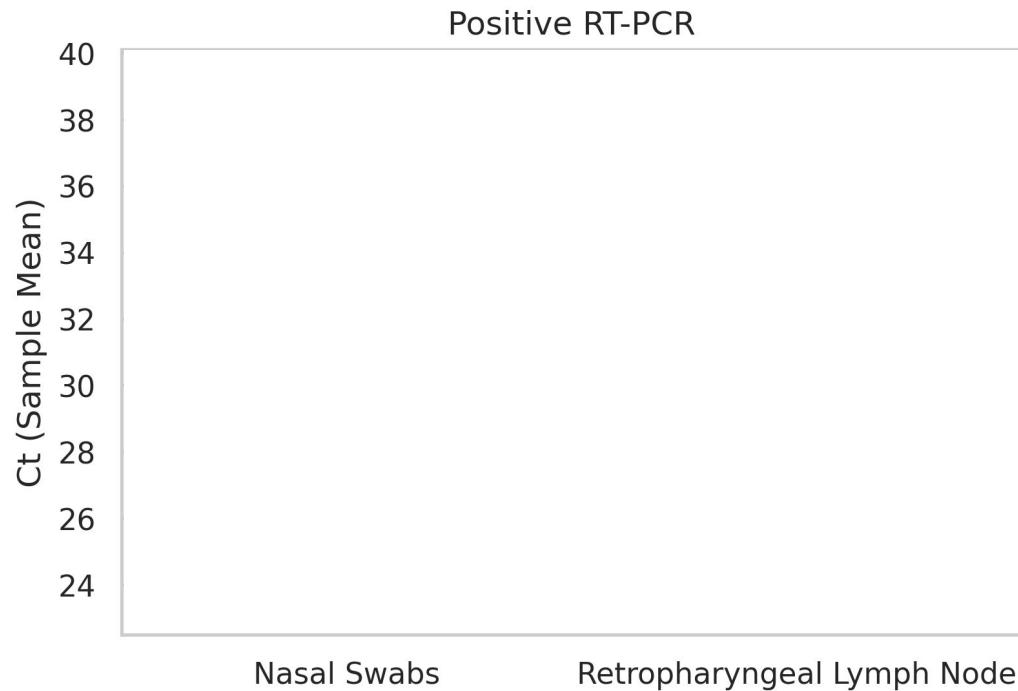
17/298 White-Tailed Deer were positive for SARS-CoV-2



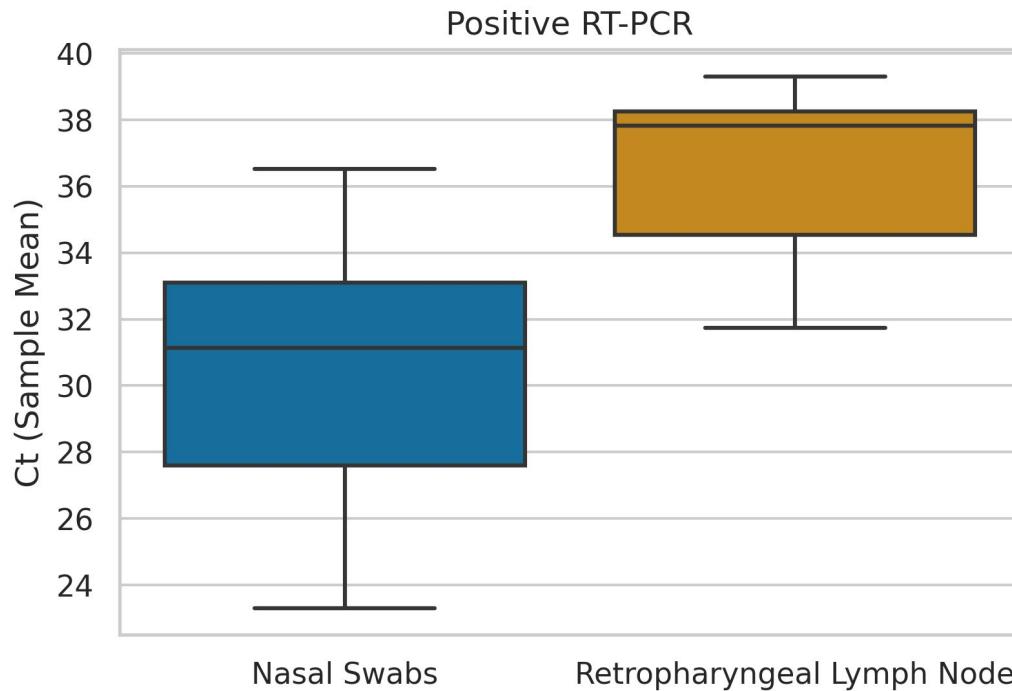
- Independent extraction qRT-PCR (UTR+E, N+E) at separate institutes.
- Viral sequencing attempted for confirmed positive samples.

Can we sequence genomes from these positive samples?

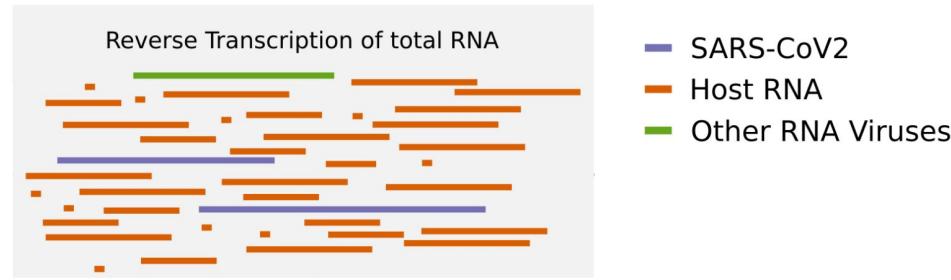
Sequencing challenging due to apparent low viral titre



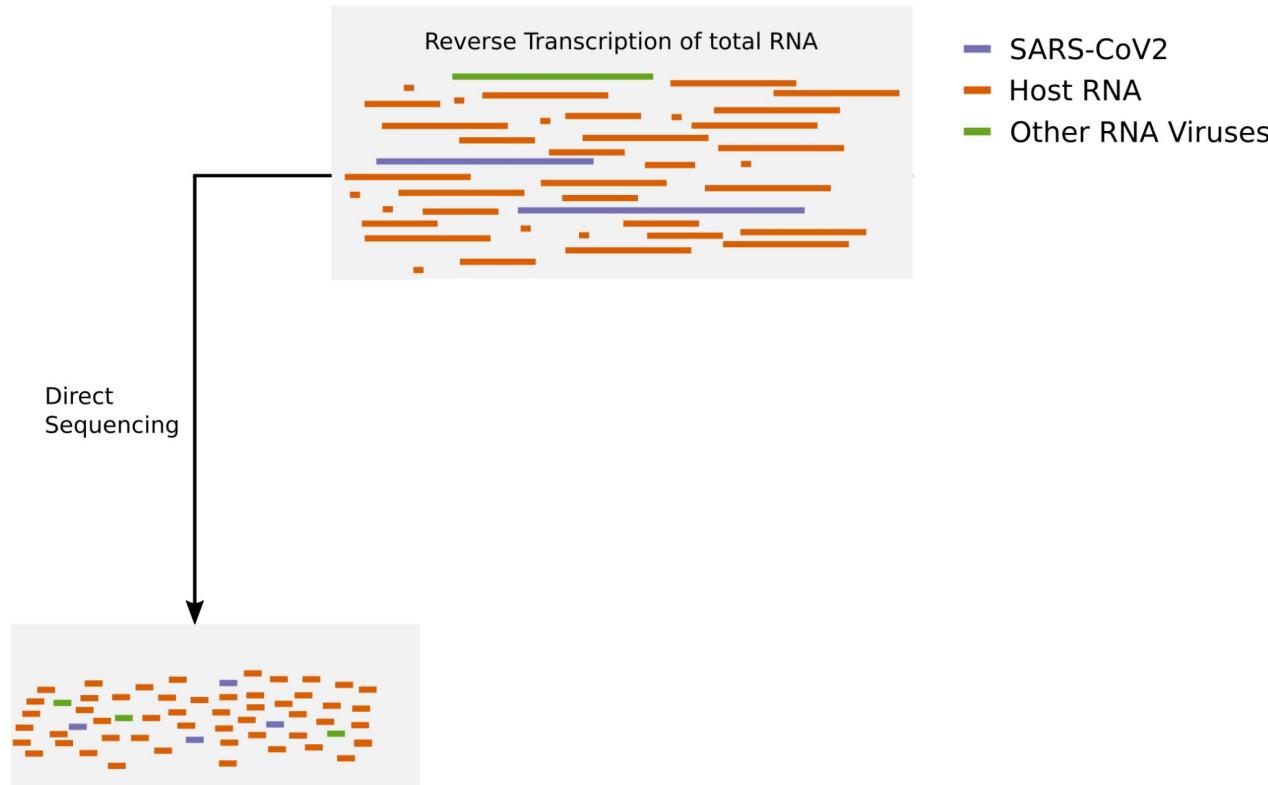
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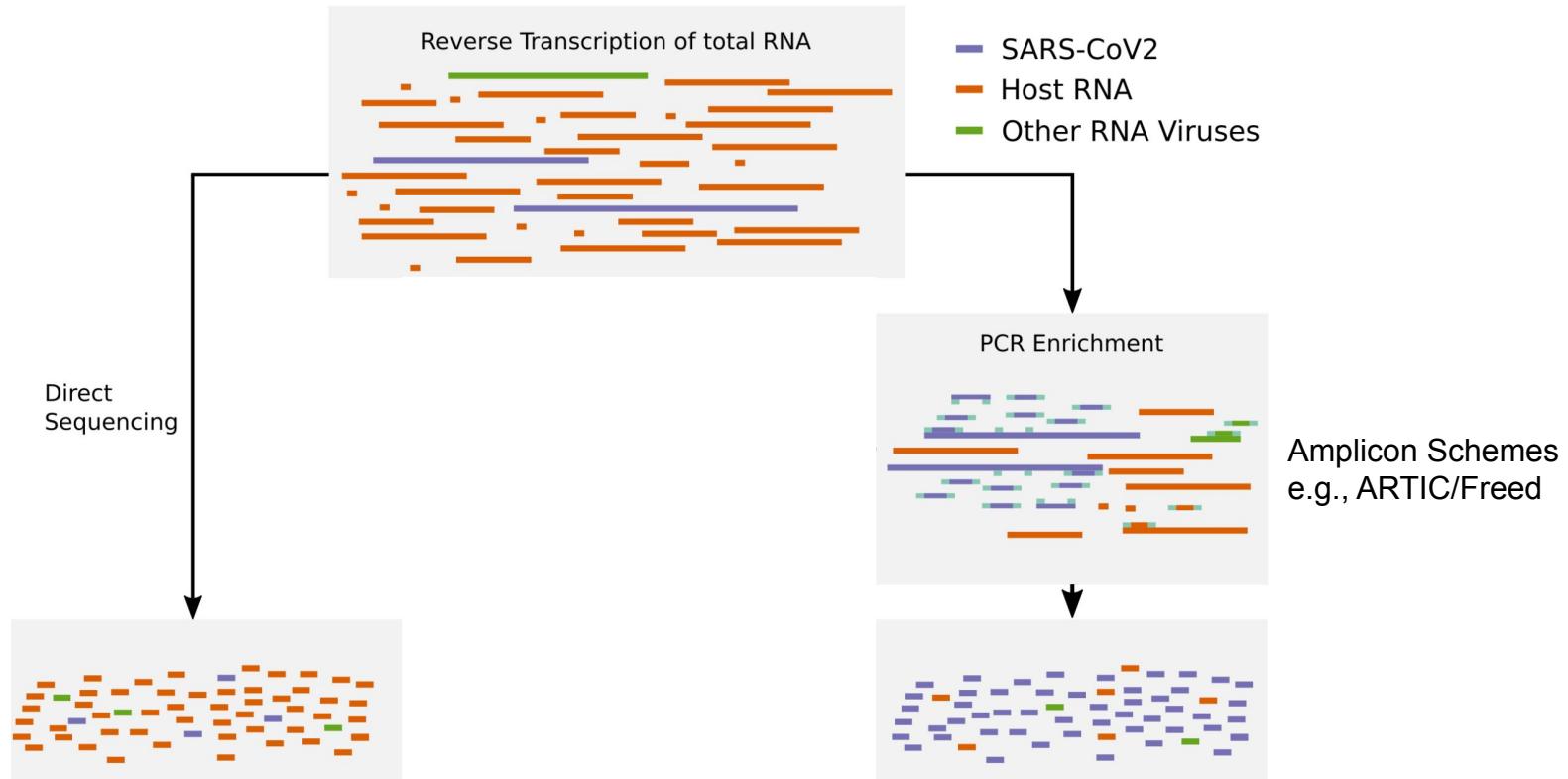
SARS-CoV-2 sequencing requires enrichment



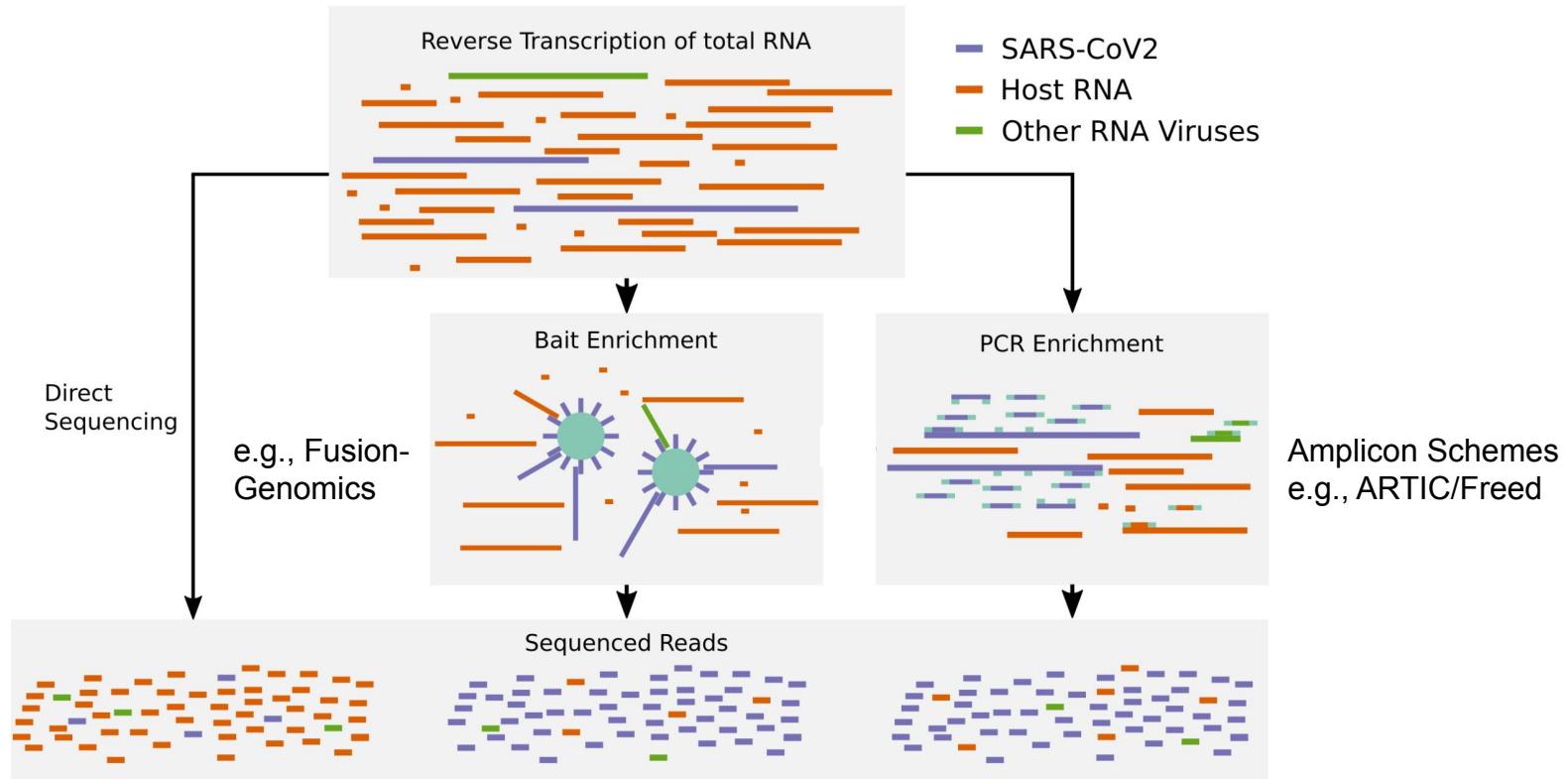
SARS-CoV-2 sequencing requires enrichment



SARS-CoV-2 sequencing requires enrichment



SARS-CoV-2 sequencing requires enrichment



Combining enrichment methods to maximise coverage

ARTICv4 – Illumina (SRI)

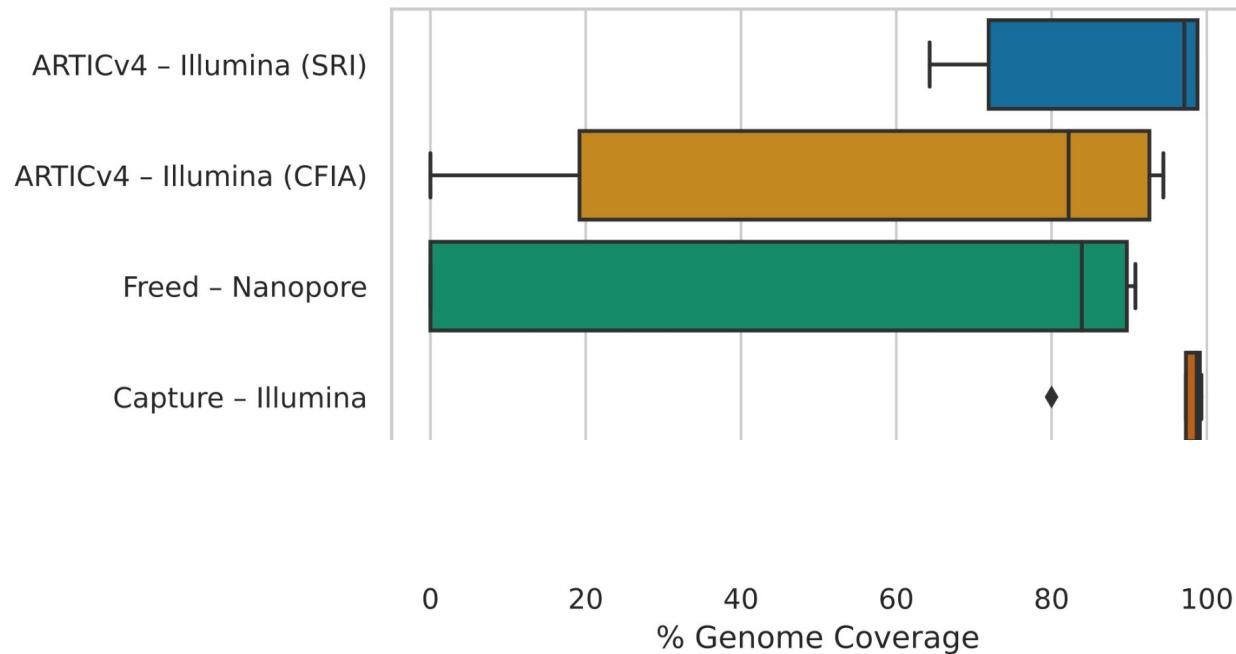
ARTICv4 – Illumina (CFIA)

Freed – Nanopore

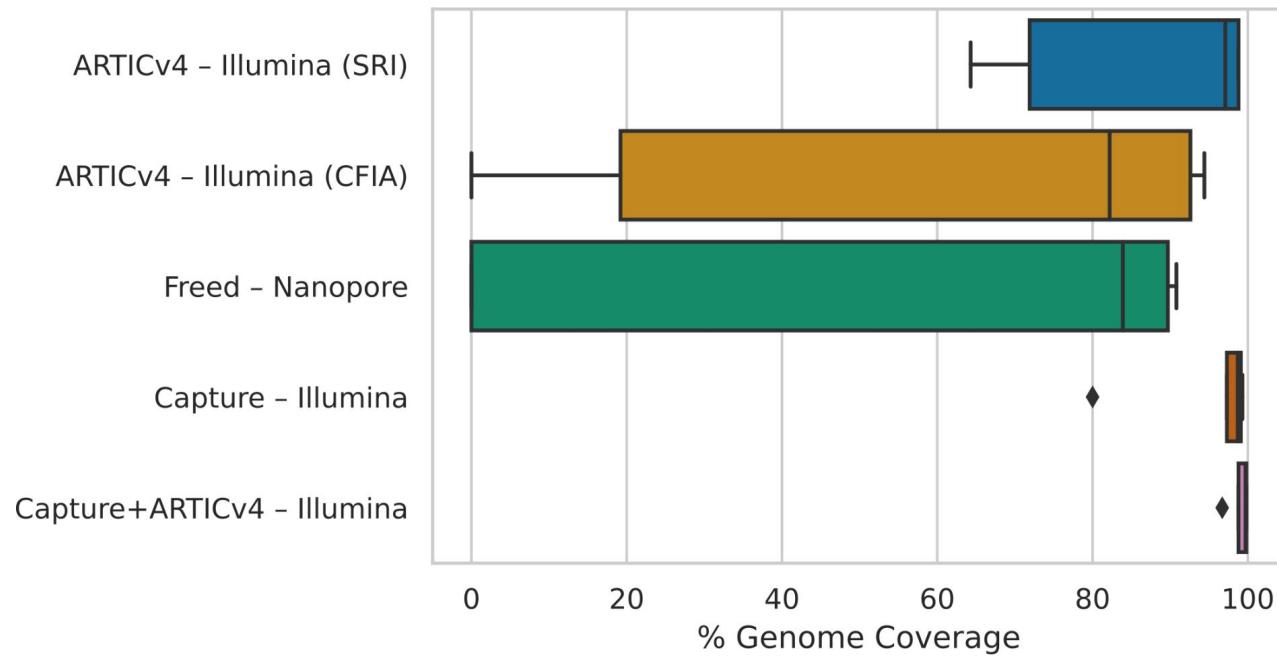
Capture – Illumina



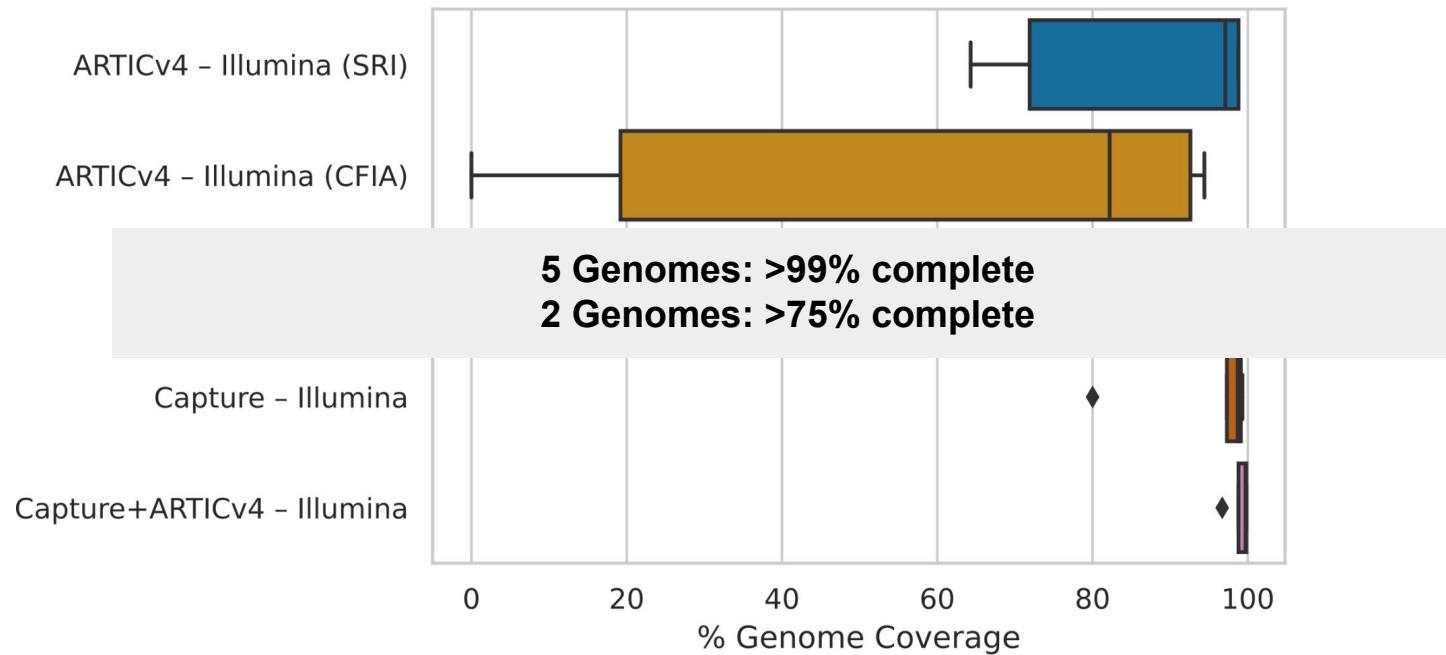
Combining enrichment methods to maximise coverage



Combining enrichment methods to maximise coverage



Combining enrichment methods to maximise coverage



Are these viruses actually from deer or just
human contamination?

Ruling out contamination from human SARS-CoV-2

- Independent RNA extractions + qRT-PCR
- Independent sequencing efforts

Ruling out contamination from human SARS-CoV-2

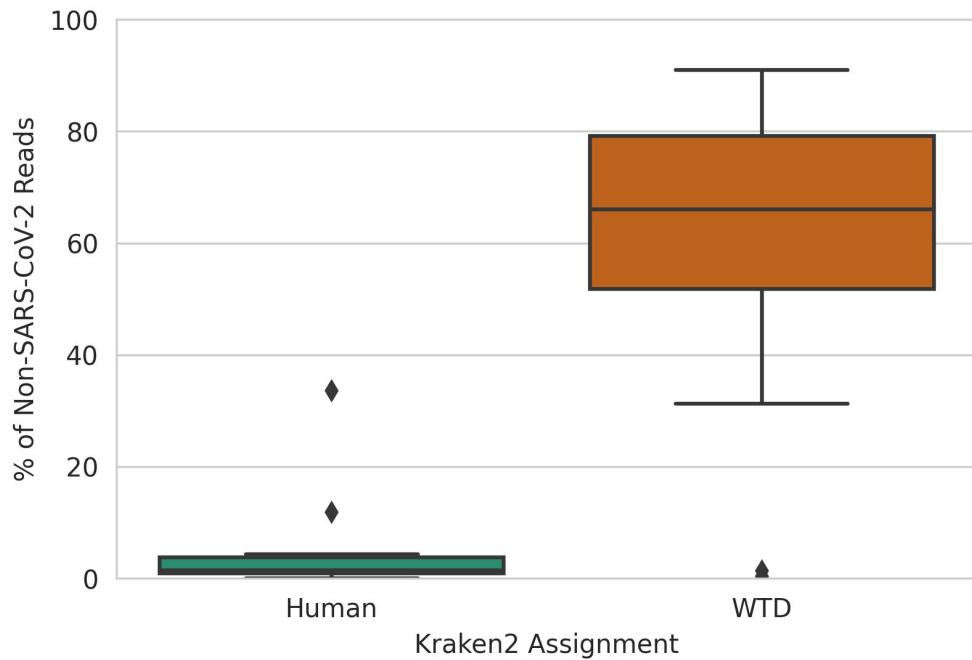
- Independent RNA extractions + qRT-PCR
- Independent sequencing efforts
- Two sample sites: RPLN and Nasal swabs

Ruling out contamination from human SARS-CoV-2

- Independent RNA extractions + qRT-PCR
- Independent sequencing efforts
- Two sample sites: RPLN and Nasal swabs
- Negative Human RNAase PCR

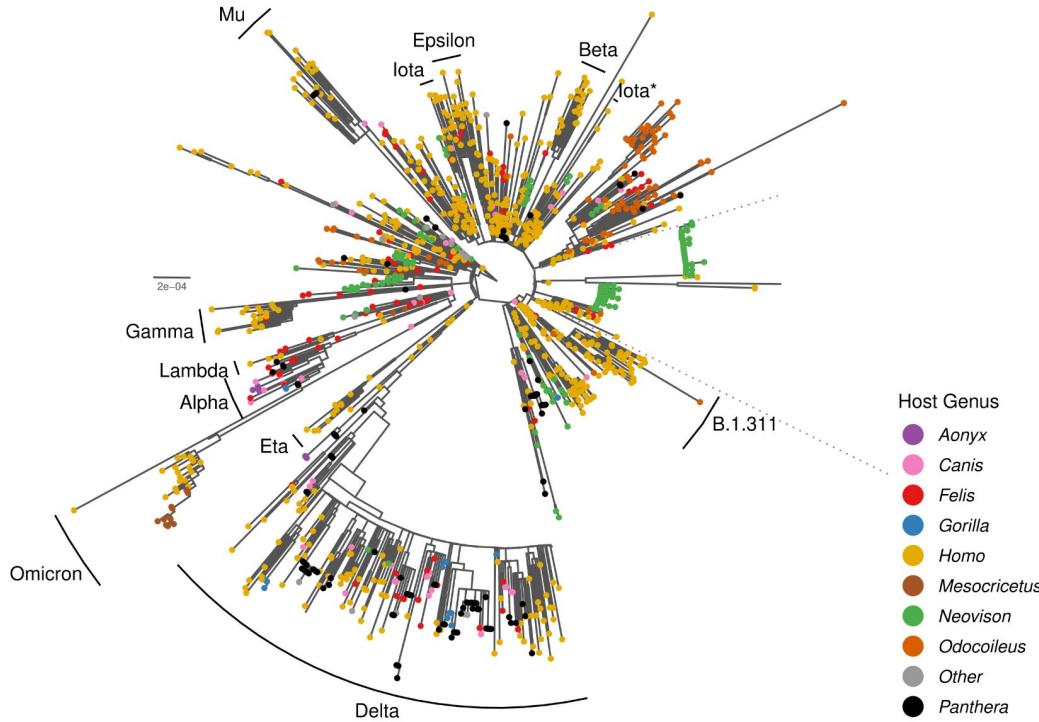
Ruling out contamination from human SARS-CoV-2

- Independent RNA extractions + qRT-PCR
- Independent sequencing efforts
- Two sample sites: RPLN and Nasal swabs
- Negative Human RNAase PCR
- Taxonomic read profiling

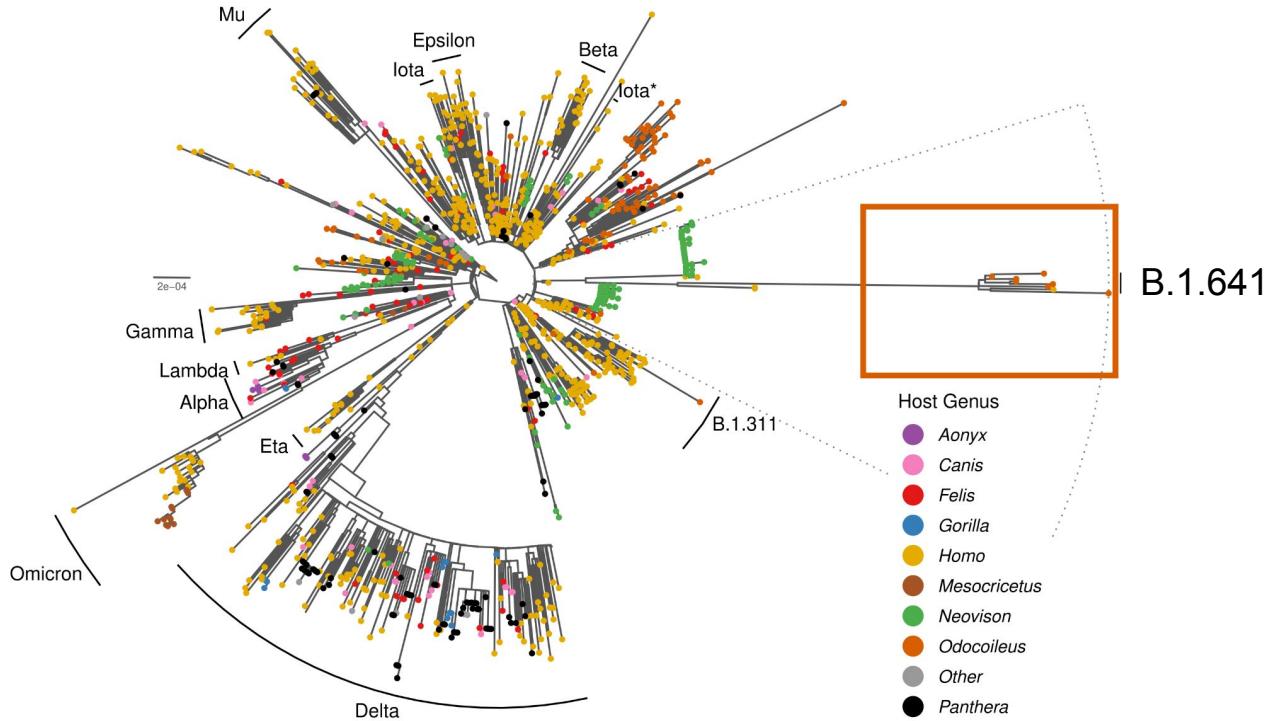


Another recent spillover from local human infections?

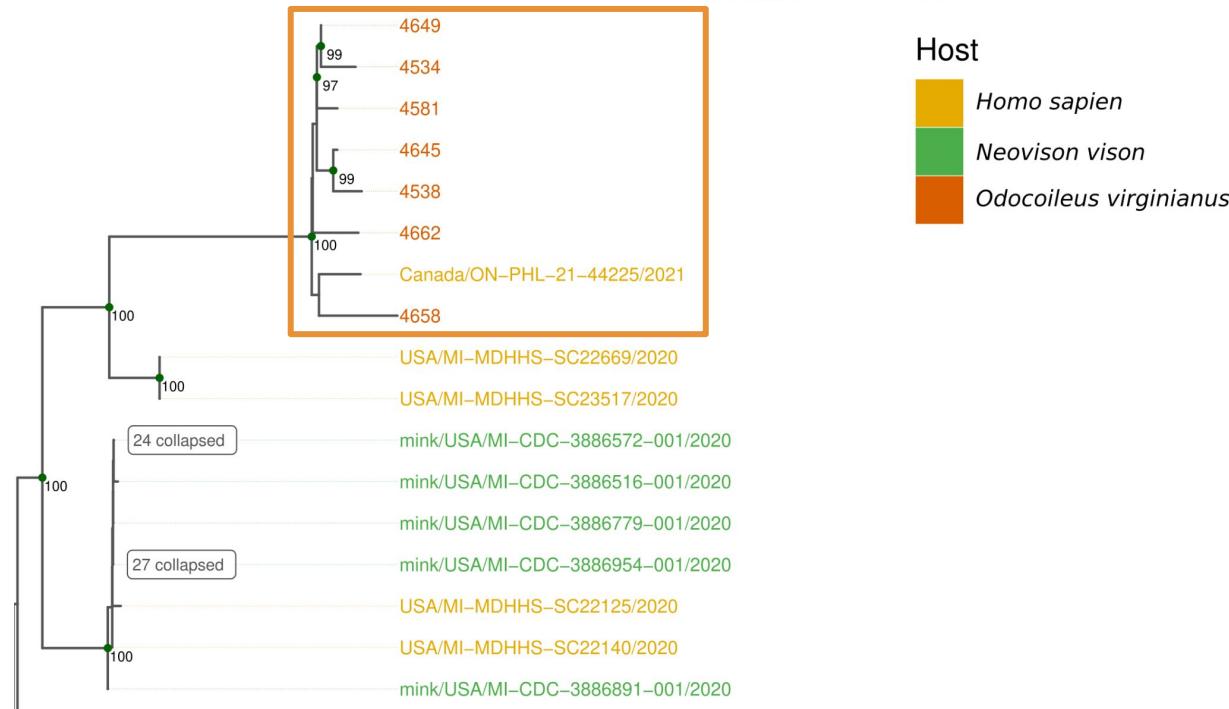
Highly Divergent B.1 Lineage



Highly Divergent B.1 Lineage

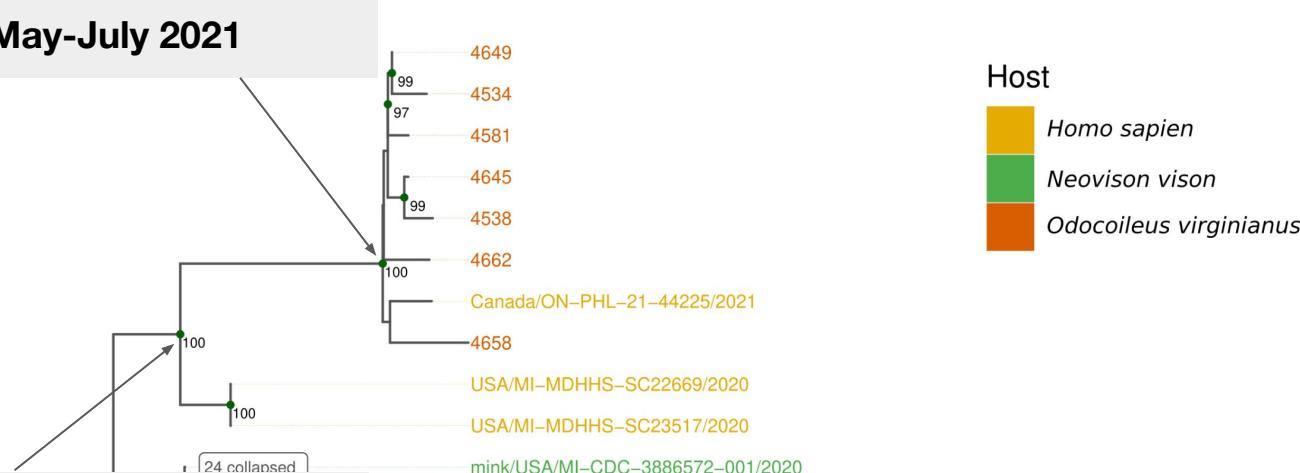


Related to 2020 Michigan Human & Minkk



Node dates indicate considerable cryptic transmission

May-July 2021



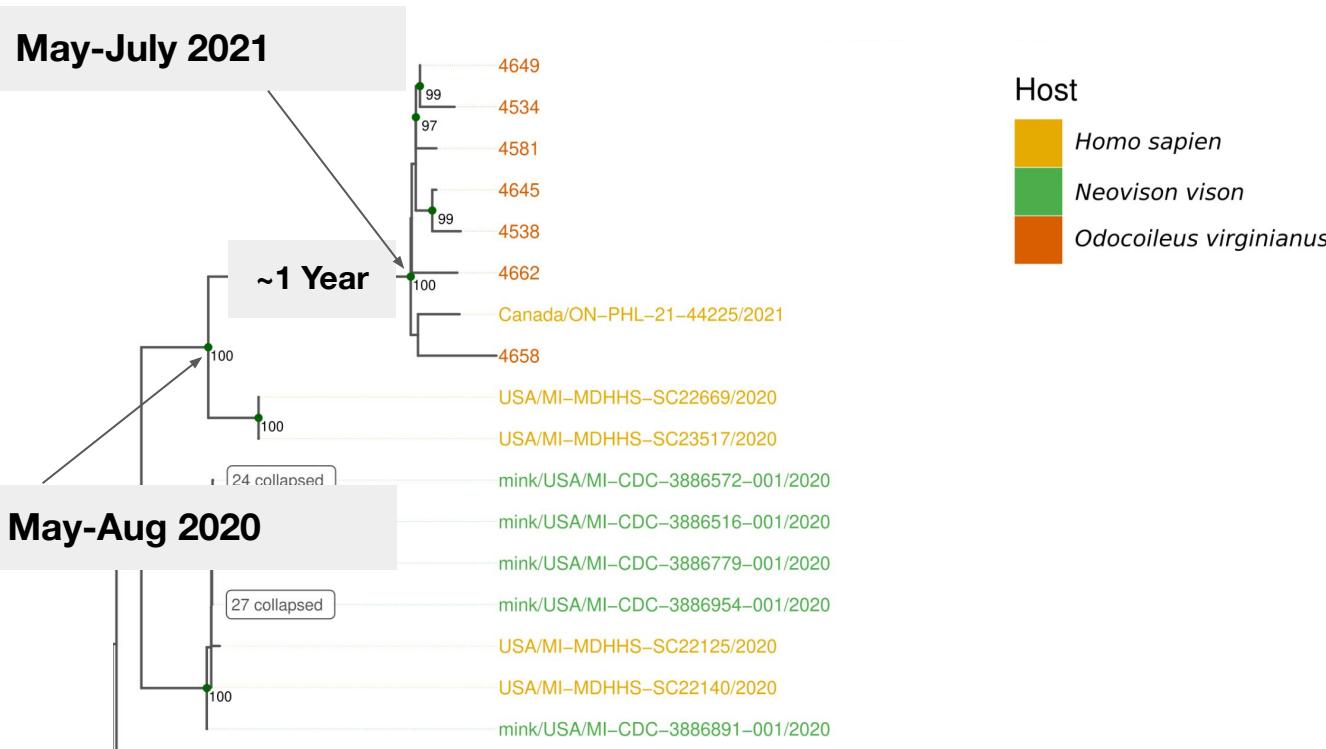
Host

- Homo sapien*
- Neovison vison*
- Odocoileus virginianus*

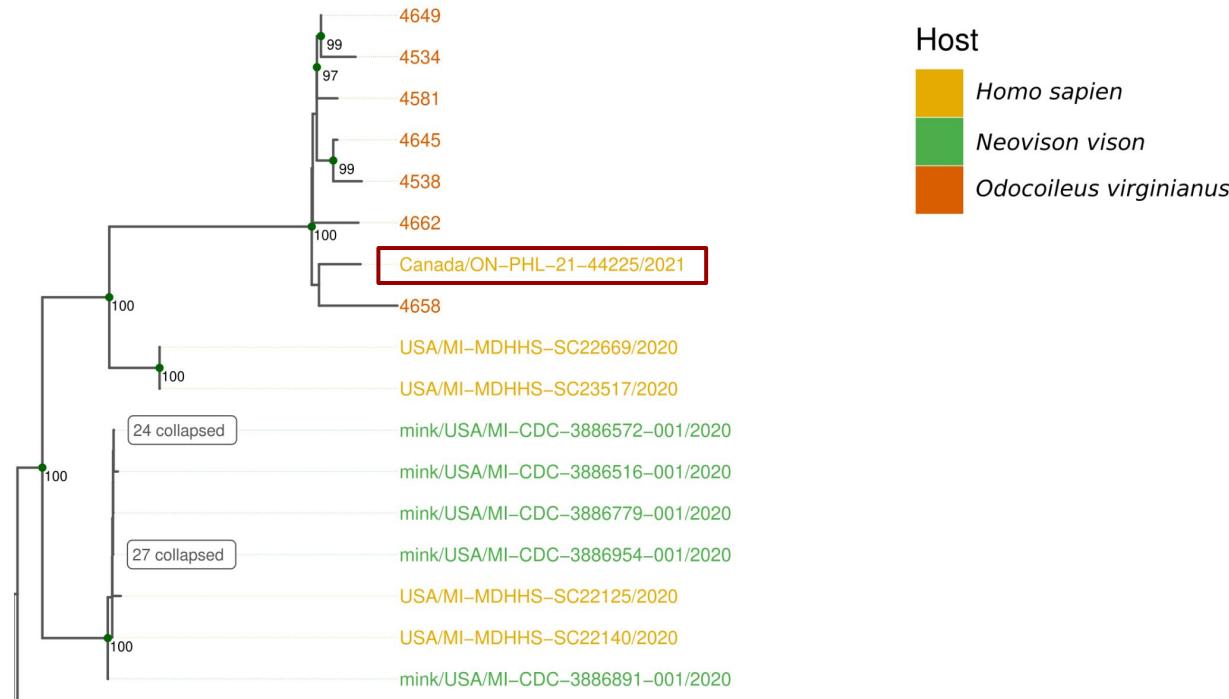
May-Aug 2020



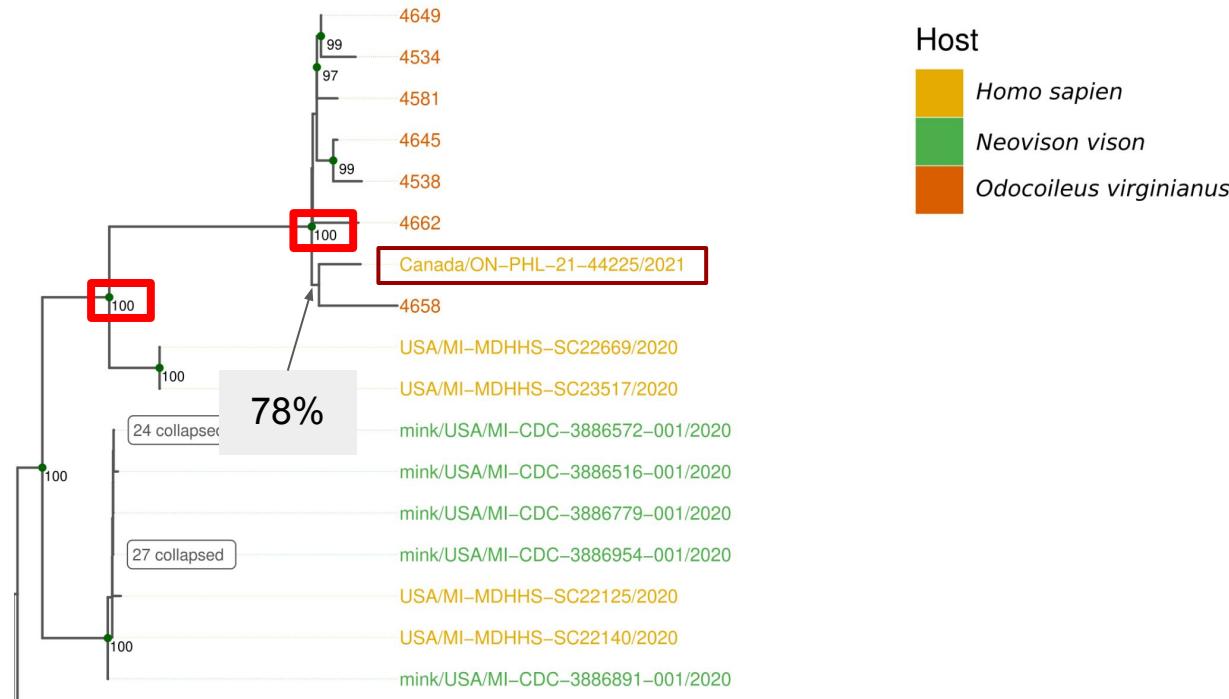
Node dates indicate considerable cryptic transmission



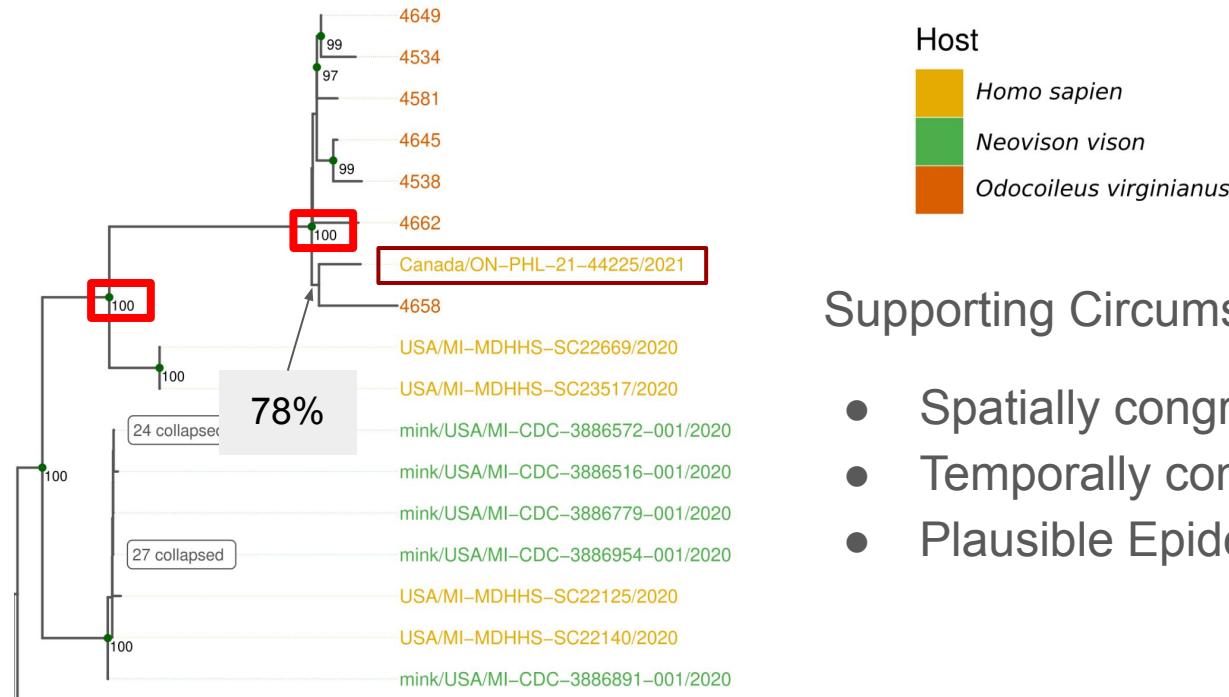
Possible Deer-to-Human transmission



Possible Deer-to-Human transmission



Possible Deer-to-Human transmission



Supporting Circumstantial Evidence:

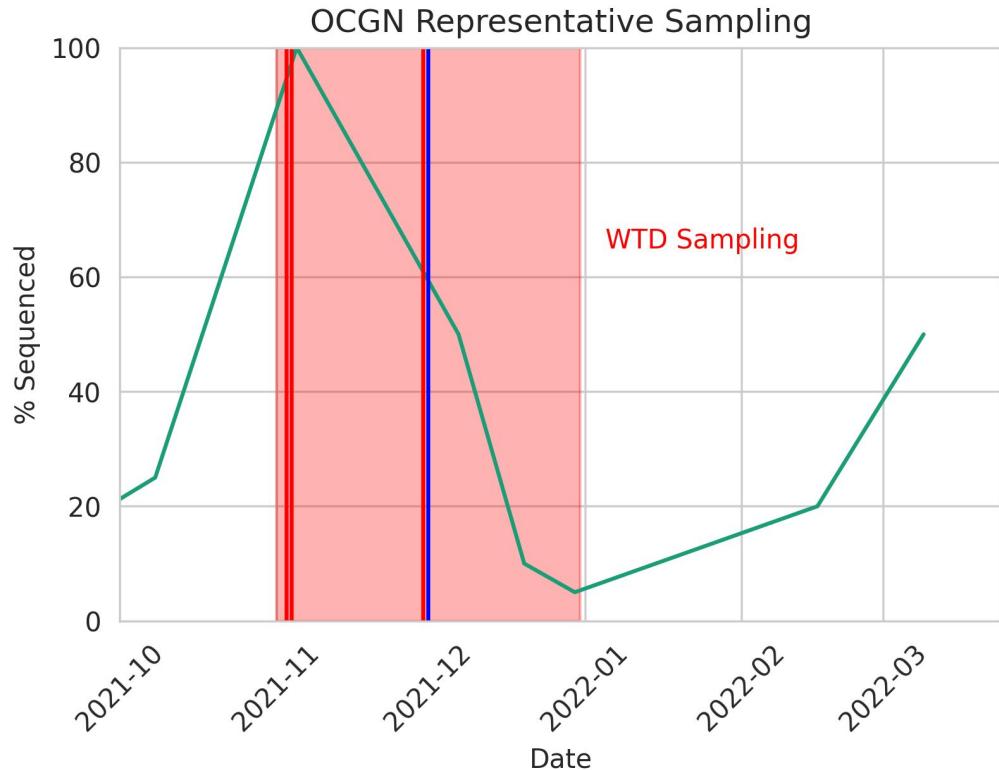
- Spatially congruent
- Temporally congruent
- Plausible Epidemiological Link

No sign of additional human cases

No sign of additional human cases

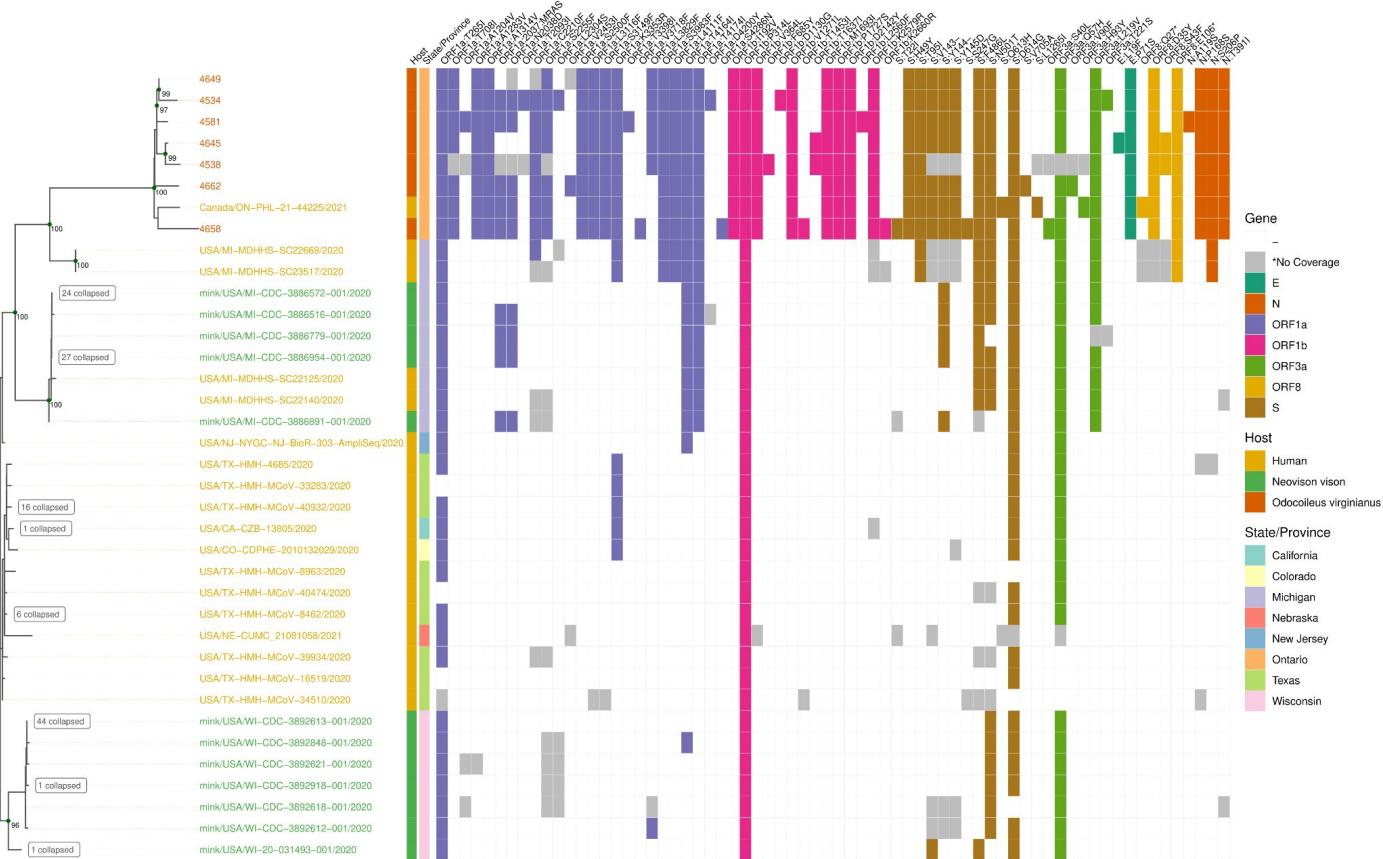
Caveats:

- Omicron induced drop in human surveillance levels
- End of deer hunting season/deer sampling

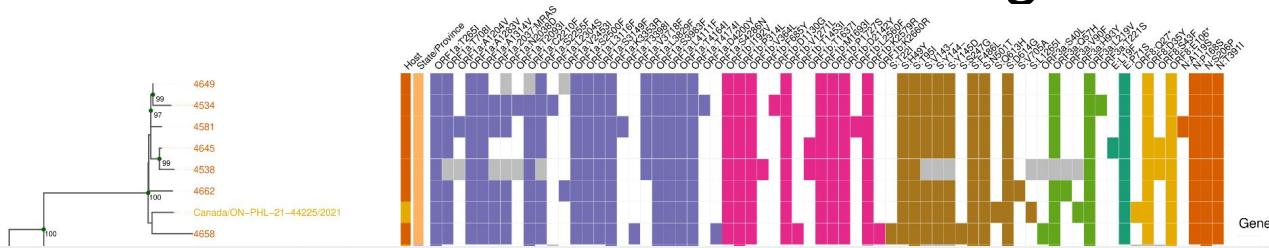


What mutations did we see?

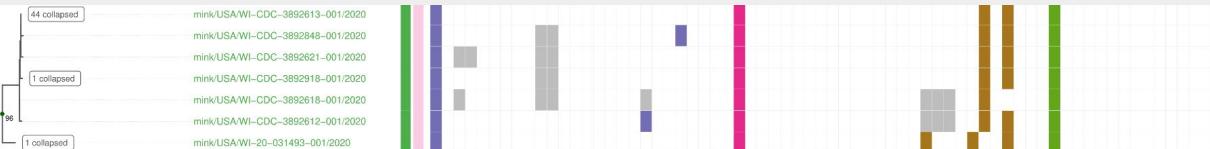
76 Mutations: 49 since MRCA with Michigan Human



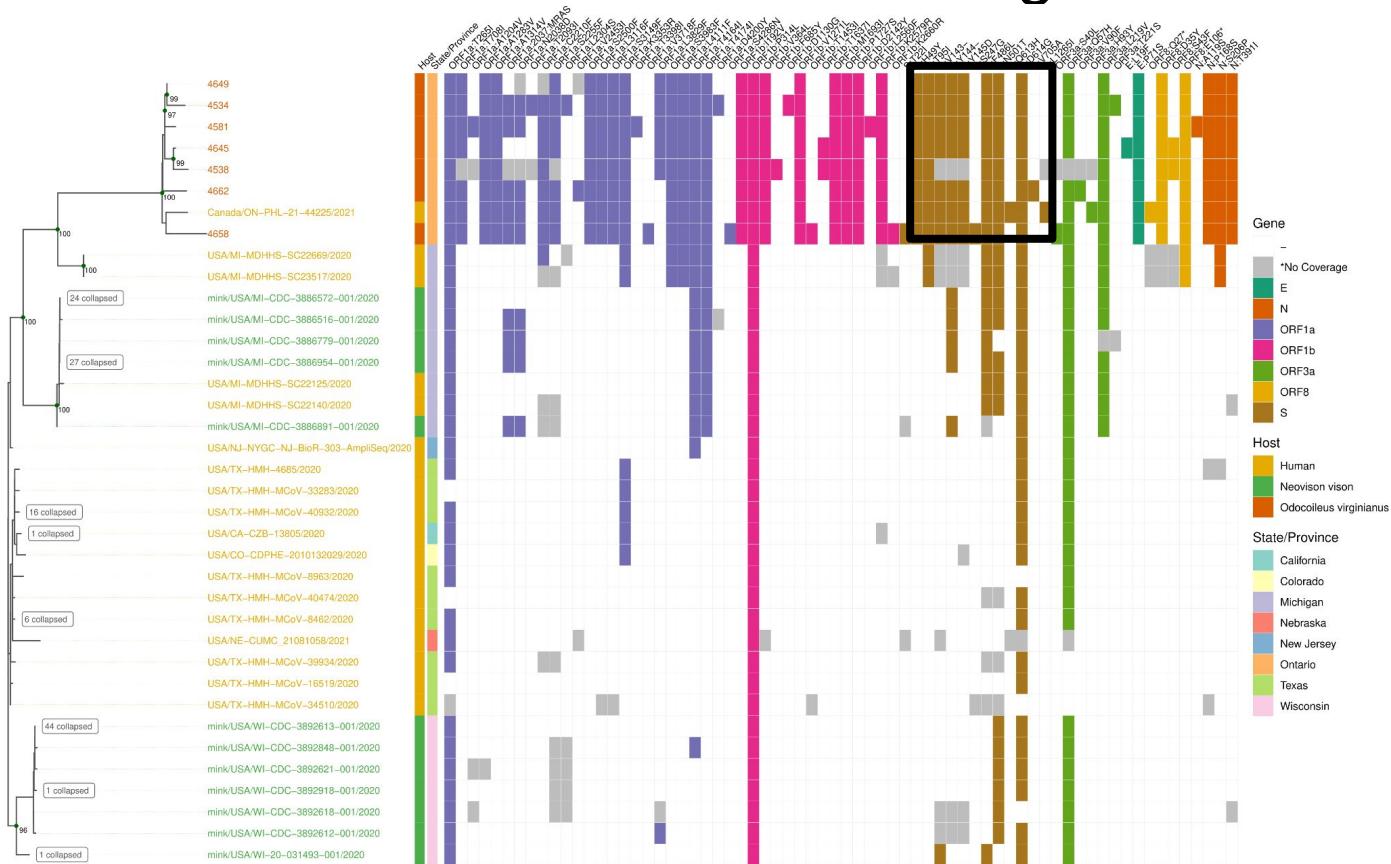
76 Mutations: 49 since MRCA with Michigan Human



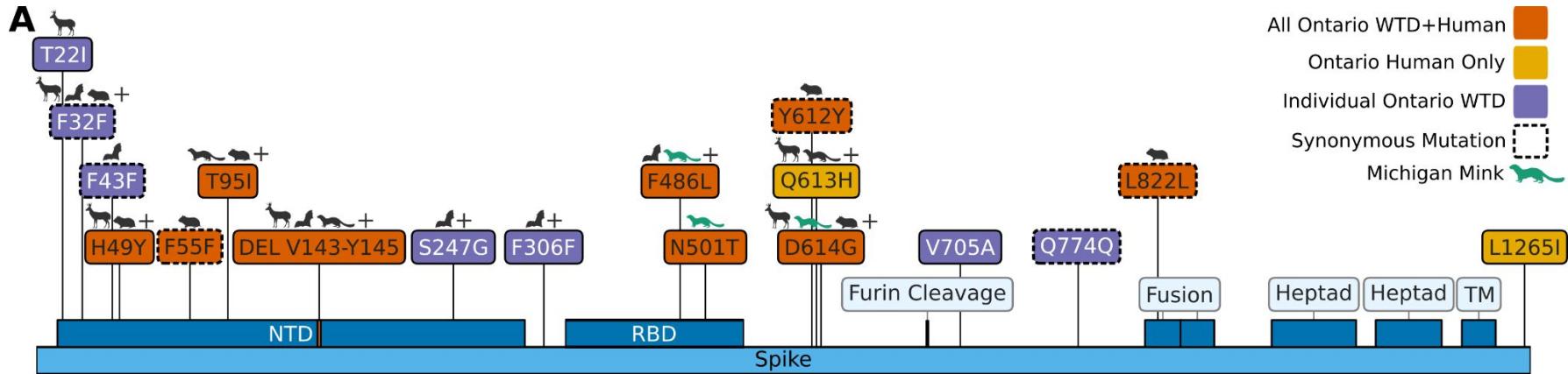
- 38 Synonymous Mutations : 38 Non-synonymous Mutations
- Several rare mutations:
 - ORF1a:insertion2038N/MRASD (n=32, including 31 mink from Michigan, USA)
 - ORF1b:V373L (n=425, all human sequences)
 - S:F486L (n=439)
 - ORF3a:L219V (n=805)
 - ORF10:L37F (n=0)



76 Mutations: 49 since MRCA with Michigan Human



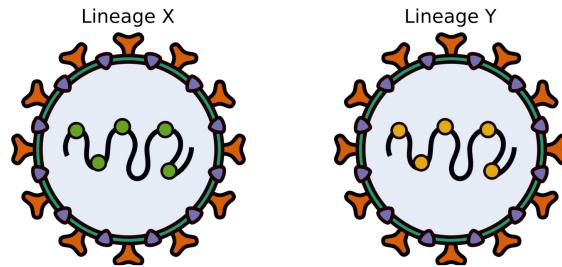
Mutations previously associated with animals



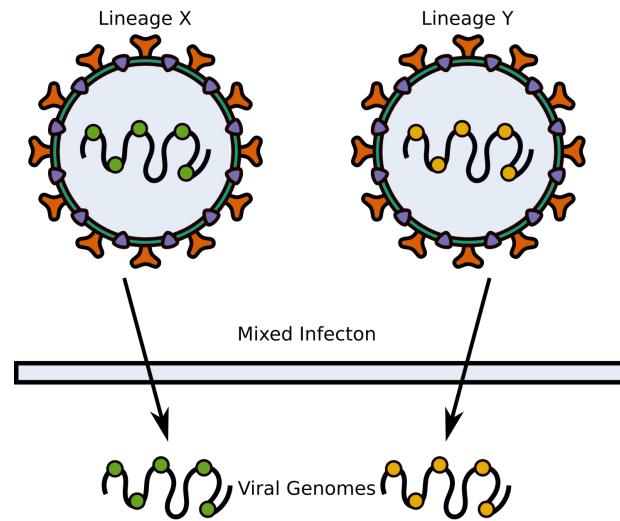
- 37/49 previously associated with non-human animal hosts
- 23 new to WTD

How did all this diversity evolve?

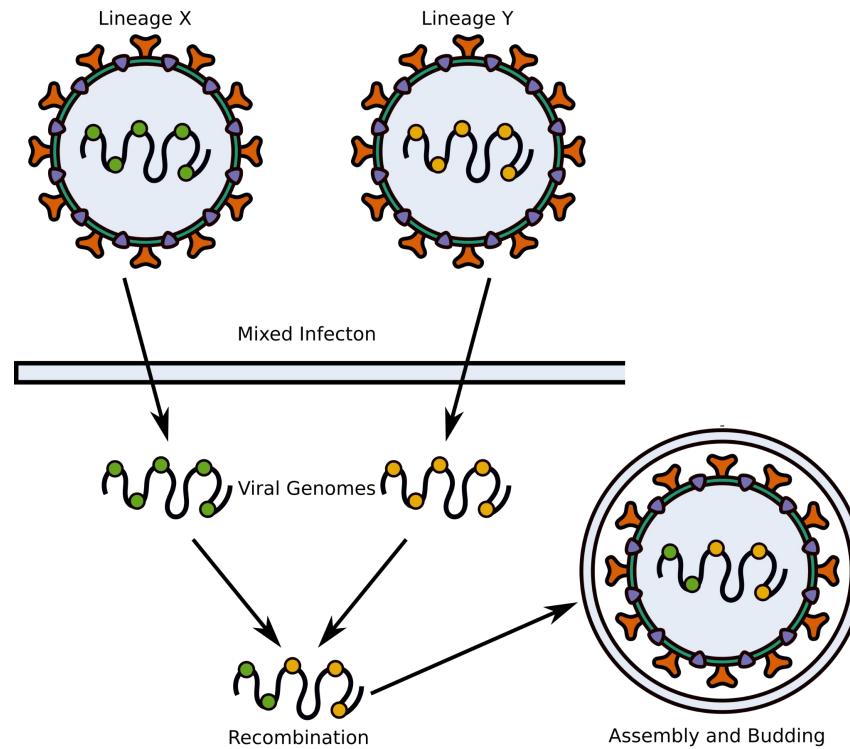
Recombination can lead to sudden novel diversity



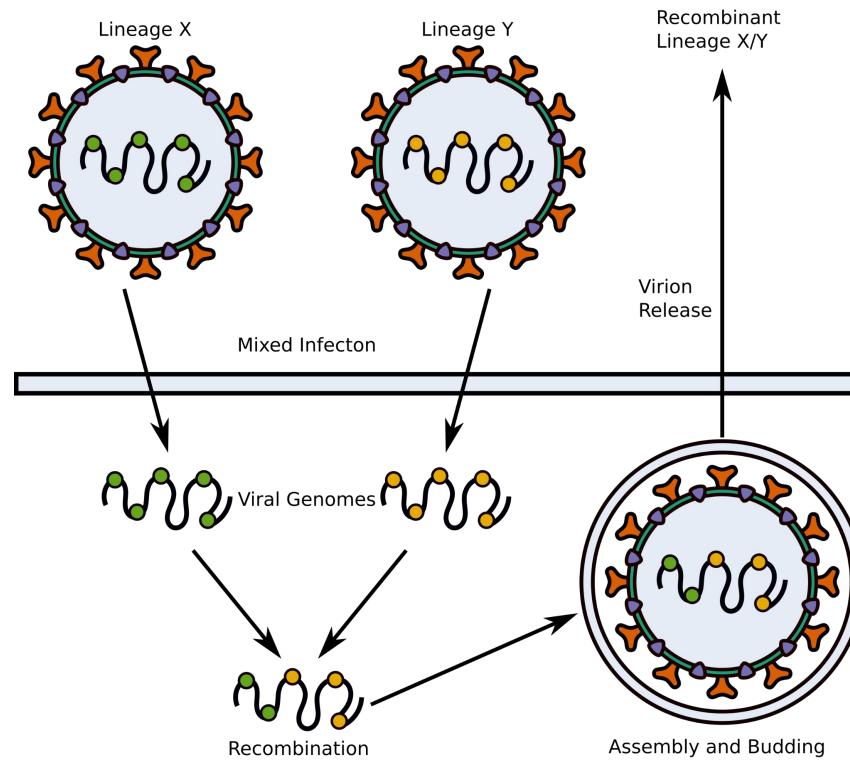
Recombination can lead to sudden novel diversity



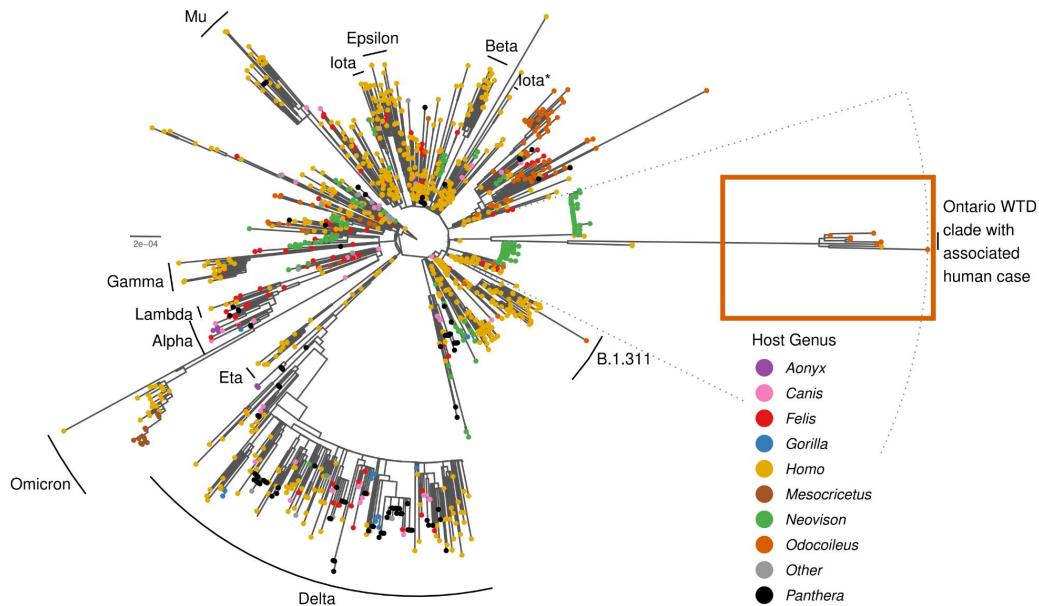
Recombination can lead to sudden novel diversity



Recombination can lead to sudden novel diversity



No indication of recombination



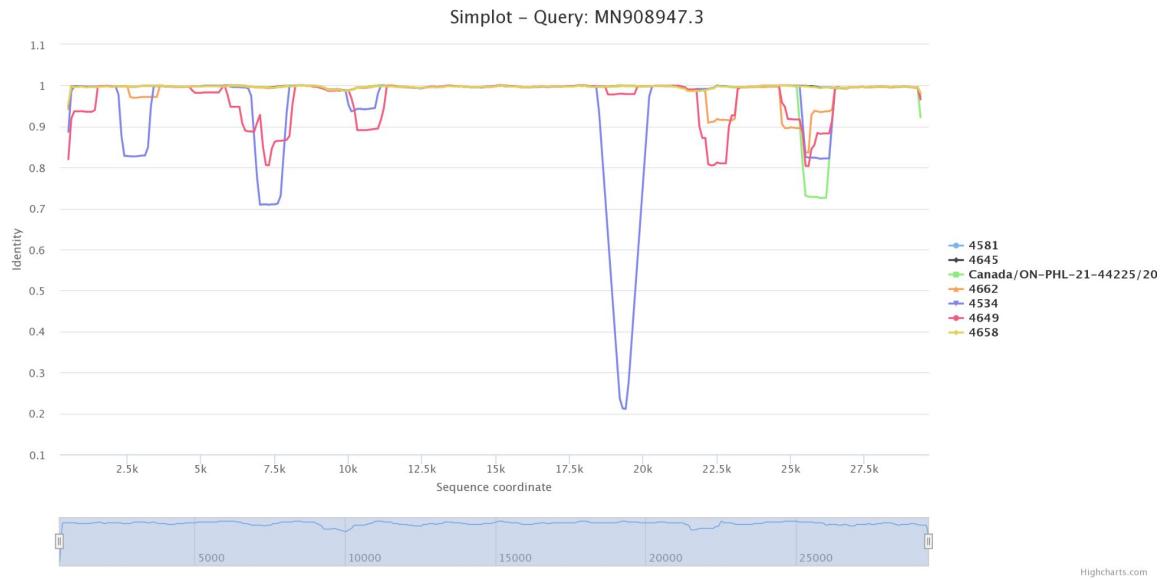
- SNP tables (**sc2rf**)

No indication of recombination



- SNP tables (**sc2rf**)
- Mosaicism (**3Seq**)

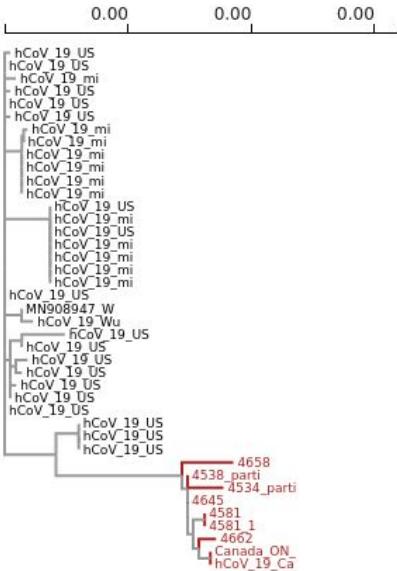
No indication of recombination



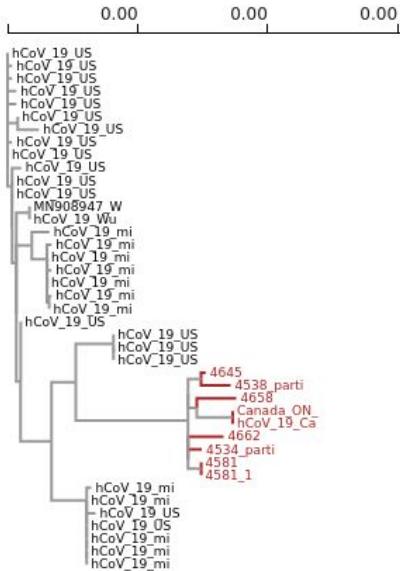
- SNP tables (**sc2rf**)
- Mosaicism (**3Seq**)

No indication of recombination

Tree 1, coordinate range 1-12731



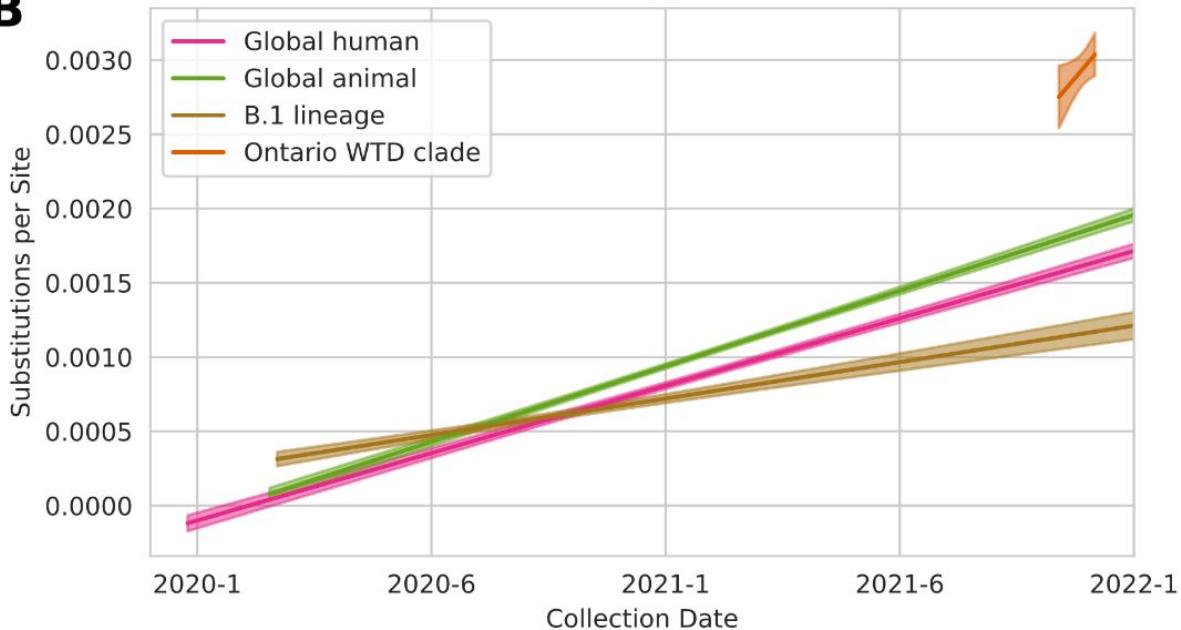
Tree 2, coordinate range 12732-29903



- SNP tables (**sc2rf**)
- Mosaicism (**3Seq**)
- Phylogenetic incongruence (**Hyphy-GARD**)

Possibly elevated mutation rate

B



Global human: 0.9×10^{-3} to 1.0×10^{-3}

Global animal: 1.0×10^{-3} to 1.1×10^{-3}

B.1 lineage: 0.4×10^{-3} to 0.6×10^{-3}

Ontario WTD: 0 to 8×10^{-3}

Possibly elevated mutation rate

Evolutionary rate of SARS-CoV-2 increases during zoonotic infection of farmed mink

SARS-CoV-2 coronavirus | SARS-CoV-2 Molecular Evolution

A ash.porter

3d

Evolutionary rate of SARS-CoV-2 increases during zoonotic infection of farmed mink

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Affiliations:

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2. Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne at The Peter Doherty Institute for Infection and Immunity, Melbourne, VIC, Australia.

*Corresponding author. Email: ashleigh.porter@unimelb.edu.au, sebastian.duchene@unimelb.edu.au

Global human: 0.9×10^{-3} to 1.0×10^{-3}

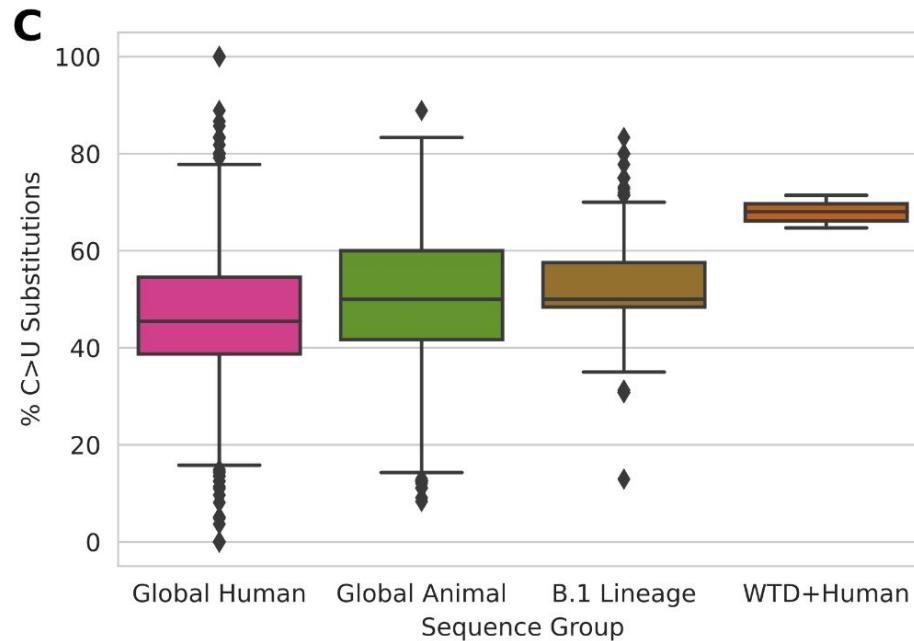
Global animal: 1.0×10^{-3} to 1.1×10^{-3}

B.1 lineage: 0.4×10^{-3} to 0.6×10^{-3}

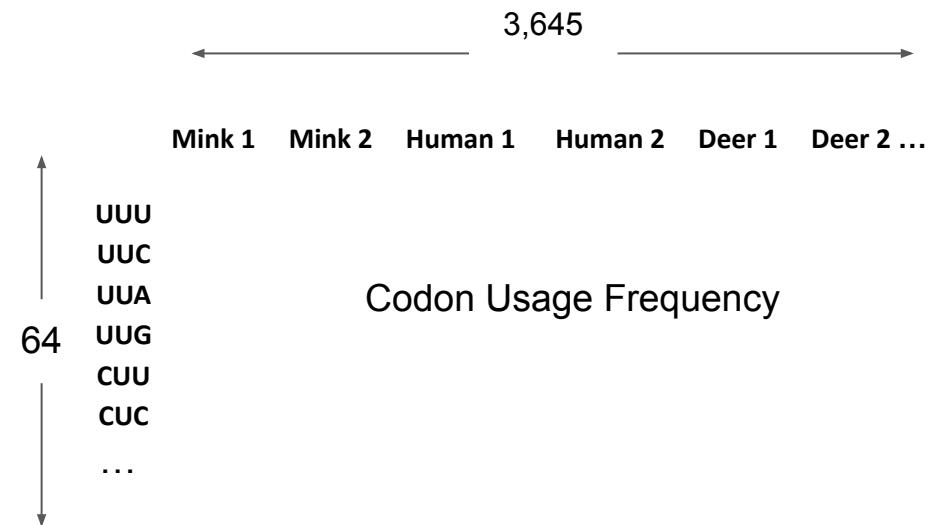
Ontario WTD: 0 to 8×10^{-3}

Mink: 3.18×10^{-3} to 10.6×10^{-3}

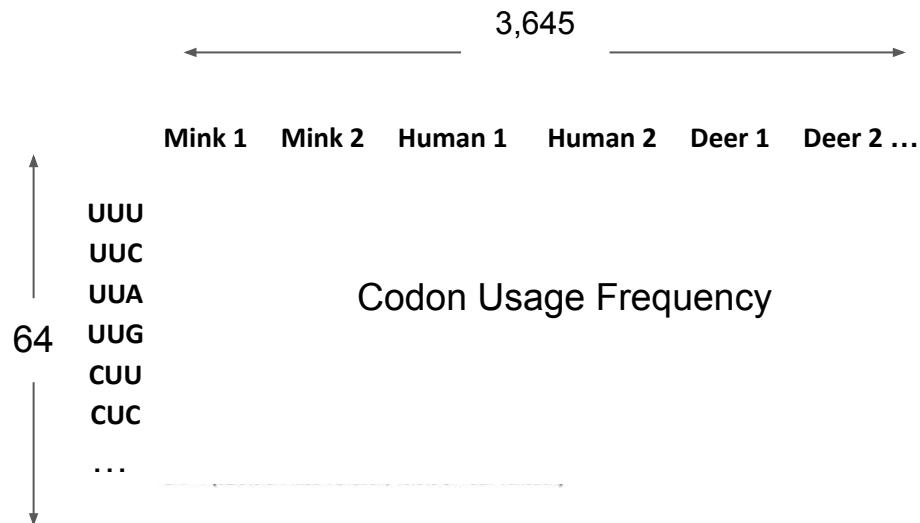
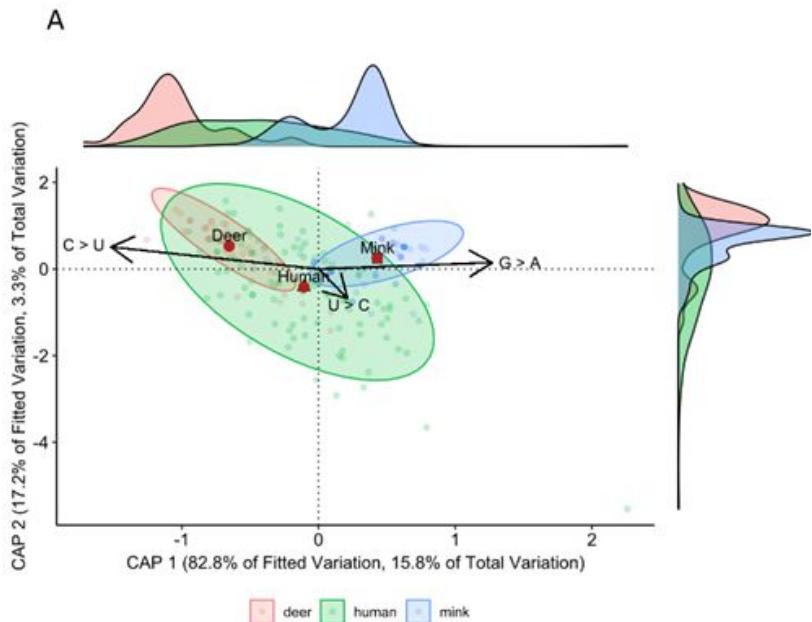
Elevated C>U indicative of host adaptation



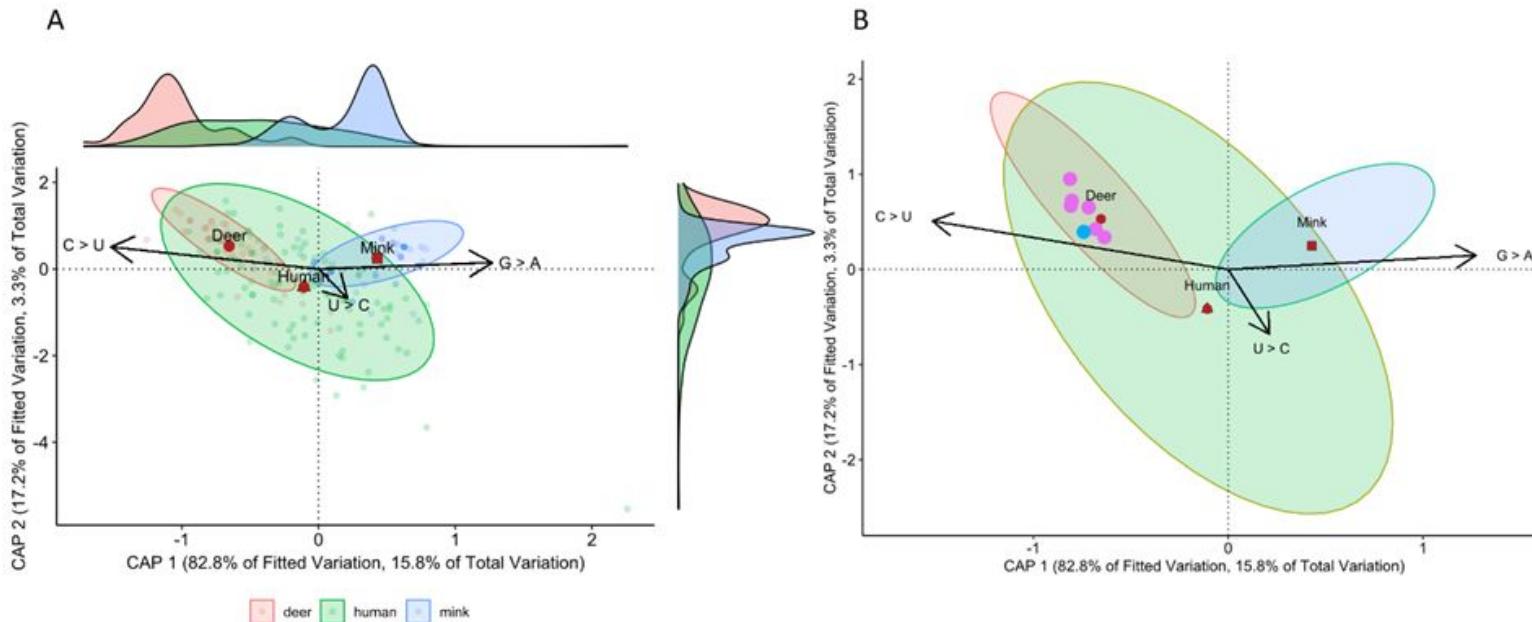
Codon usage patterns also support host adaptation



Codon usage patterns also support host adaptation



Codon usage patterns also support host adaptation



But, no sign of diversifying selection!

dN/dS:

- >1 positive/diversifying selection
- ~1 neutral evolution
- <1 negative/purifying selection

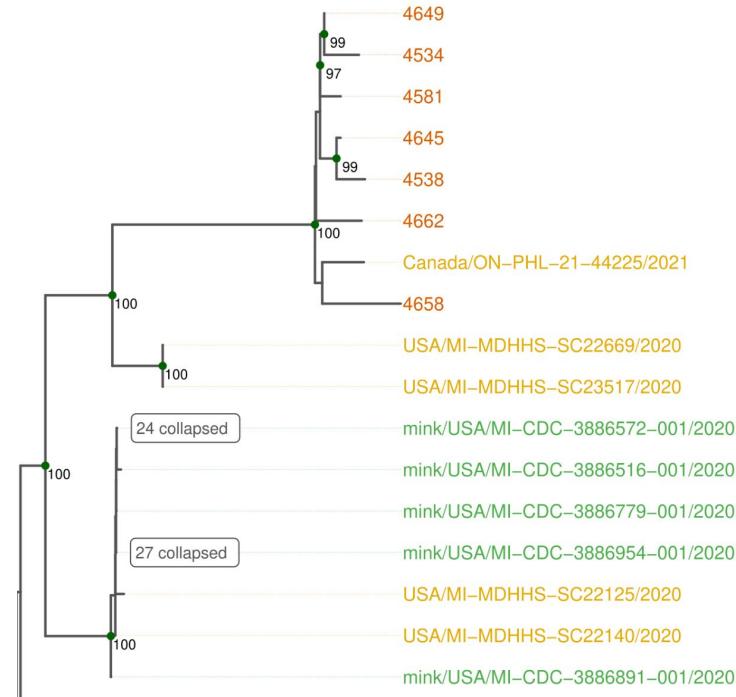
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Challenge:

- Mutation rates vary over time/branches



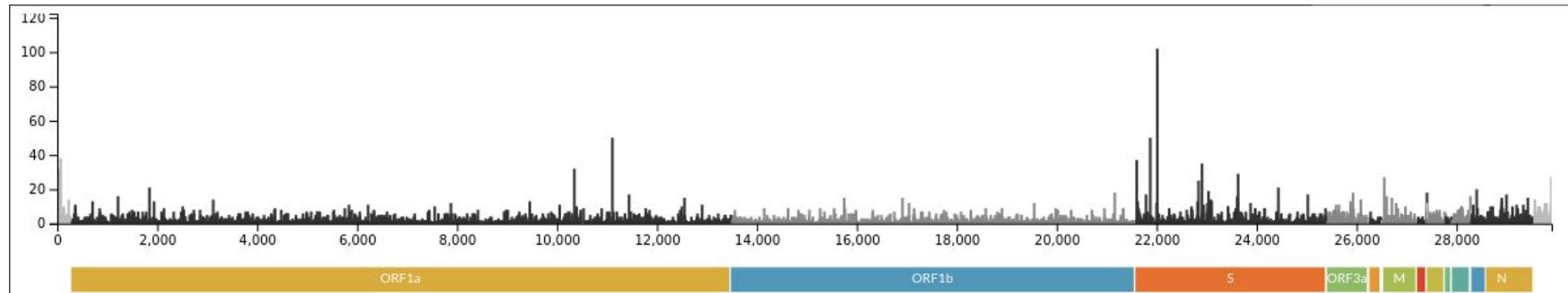
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Codon-alignment gene-based phylogenies

Hyphy:

- **abSREL**: positive selection in proportion of branches
- **BUSTED**: gene-wide positive selection
- **RELAX**: selection changing in set of branches

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No significant positive selection or intensification of selection detected

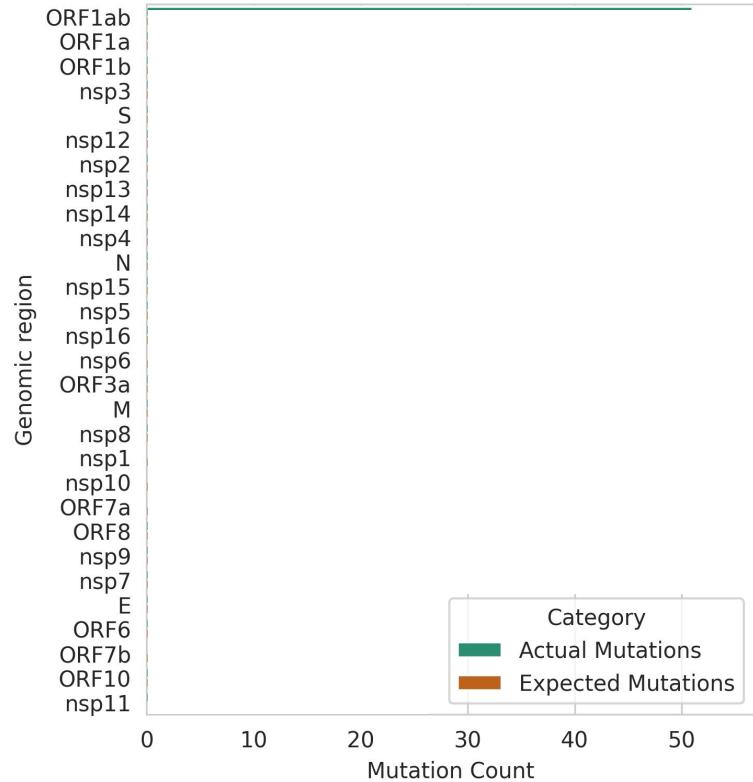
Relaxation of selection on ORF1ab amongst WTD clade p=0.0032)

But, no sign of diversifying selection!

76 total consensus mutations in WTD

ORF1ab (71% of genome):
Expected mutations: **54.1**
Actual mutations: ?

S (12.7% of genome):
Expected mutations: **9.7**
Actual mutations: ?

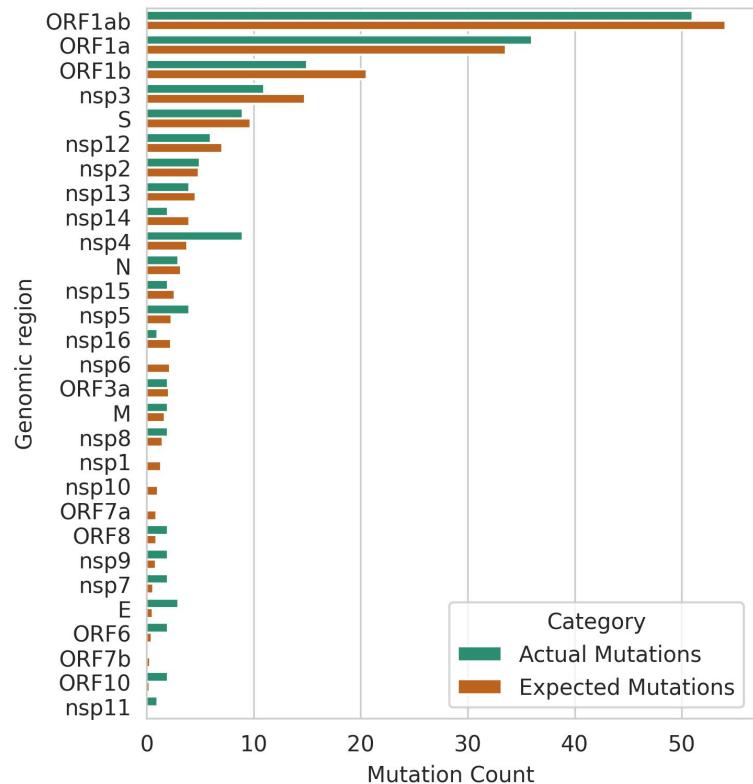


But, no sign of diversifying selection!

76 total consensus mutations in WTD

ORF1ab (71% of genome):
Expected mutations: **54.1**
Actual mutations: **51**

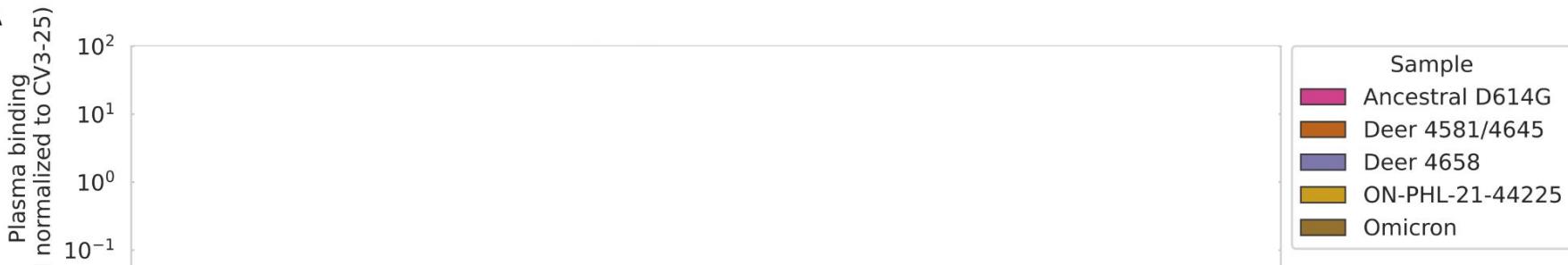
S (12.7% of genome):
Expected mutations: **9.7**
Actual mutations: **9**



So, what does all this mean in terms of phenotype?

No change of spike antigenicity

A

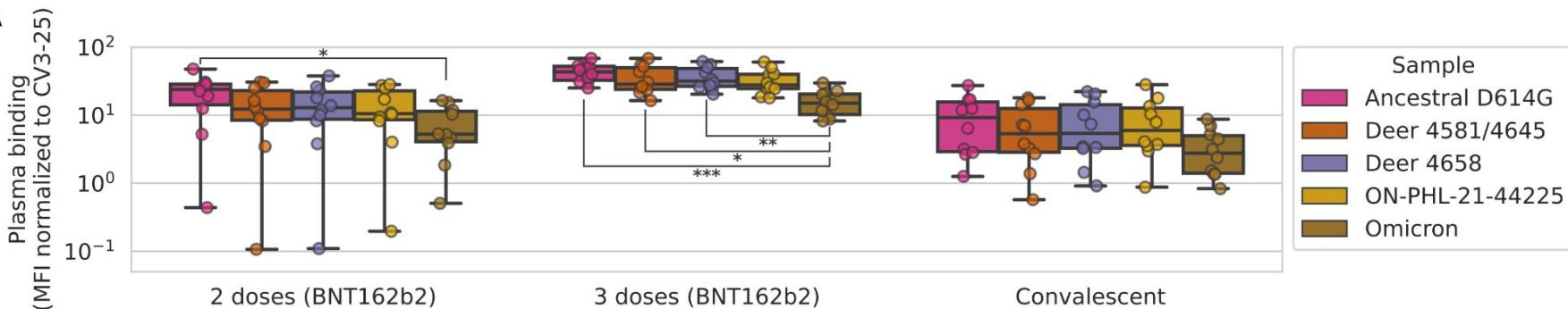


B



No change of spike antigenicity

A

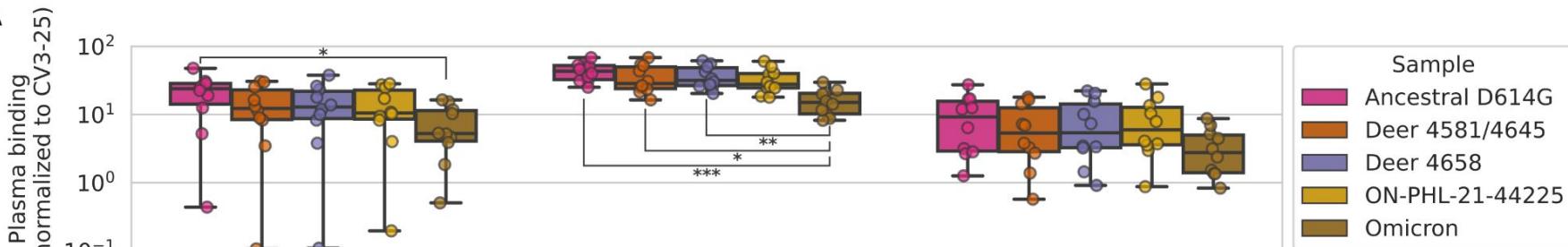


B

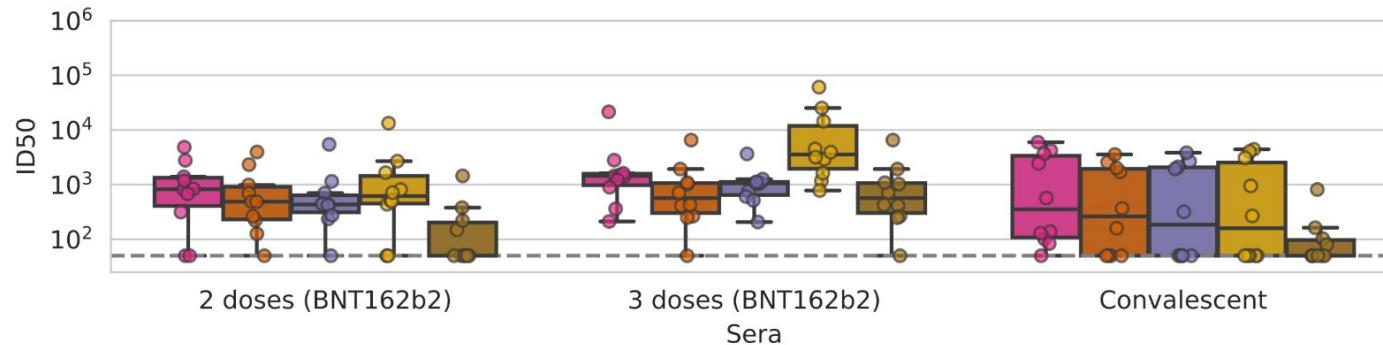


No change of spike antigenicity

A

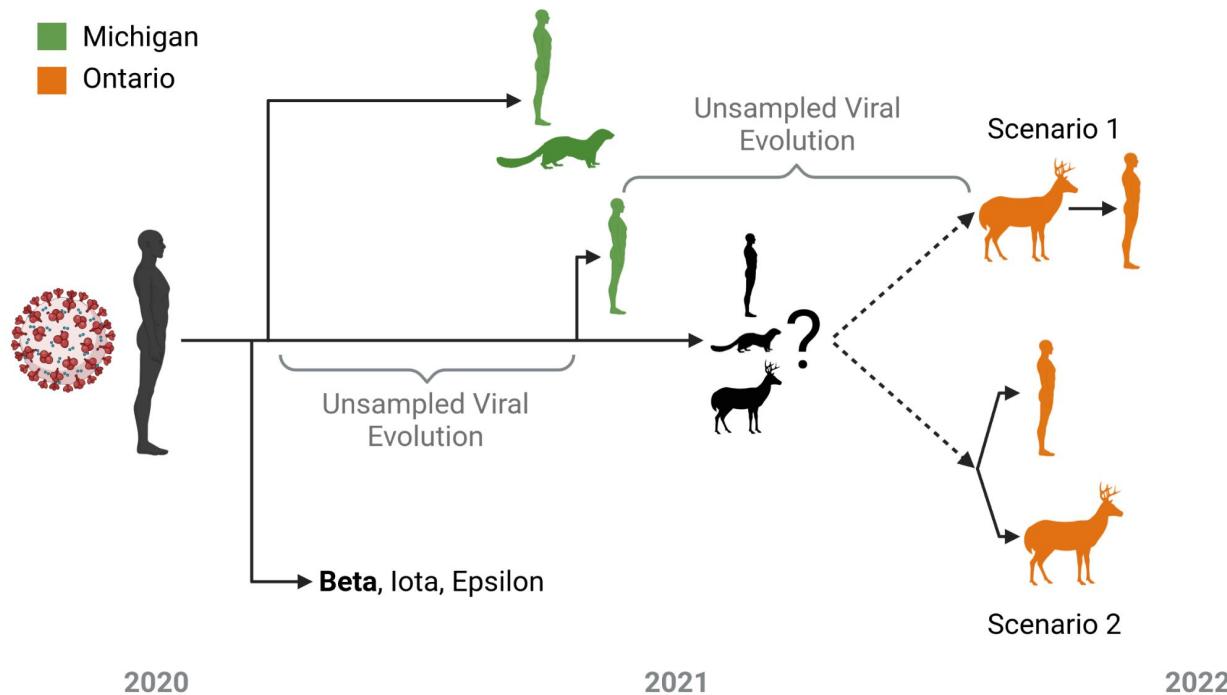


B



So, are WTD a secondary reservoir?

Limited “One Health” surveillance means lots of uncertainty



Take-aways

- Highly divergent SARS-CoV-2 in WTD with likely deer-to-human transmission
- Signs of genomic adaptation to animal host (animal-associated mutations, C>U, codon usage, elevated mutation rate)
- No indication of strong selection or change of antigenicity (*c.f.* Omicron)

Take-aways

- Highly divergent SARS-CoV-2 in WTD with likely deer-to-human transmission
 - Signs of genomic adaptation to animal host (animal-associated mutations, C>U, codon usage, elevated mutation rate)
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-
- Need to better understand the interplay of virus, disease, and immune selection in non-human animals (and impact on pathogen evolution)
 - Similar scenarios could generate future variants of concern
 - Therefore, clear need for broader “One-Health” surveillance

“WILD-CoV”



National Centre for Foreign Animal Disease

- Bradley Pickering (Iowa State/Manitoba)
- Oliver Lung (Manitoba)
- Peter Kruczkievicz
- Melissa Goolia, Matthew Suderman, Mathieu Pinette, Greg Smith, Daniel Sullivan, Josip Rudar, Michelle Nebroski, Oksana Vernygora



Computer Science / Epidemiology

- Finlay Maguire



- Jennifer Guthrie (Western)
- Alex Marchand-Austin



Sunnybrook Research Institute

- Samira Mubareka (Toronto)
- Jonathan Kotwa
- Bryan Griffin
- Kuganya Nirmalarajah, Juliette Blais-Savoie, Hsien-Yao Chee, Emily Chien, Winfield Yim, Andra Banete, Lily Yip

Shared Hospital Laboratory

- Patryk Aftanas



Ministry of Northern
Development, Mines, Natural
Resources and Forestry

- Jeff Bowman (Trent)
- Tore Buchanan
- Larissa Nituch
- Elizabeth Adey



- Marceline Côté
- Geneviève Laroche
- Ardesir Ariana, Brett Vahkal



- Alison McGeer (Toronto)



Guillaume Goyette, Andrés Finzi, Claire Jardine, Ariane Massé Heather McClinchey



Canadian Institutes of Health Research Institut de recherche en santé du Canada



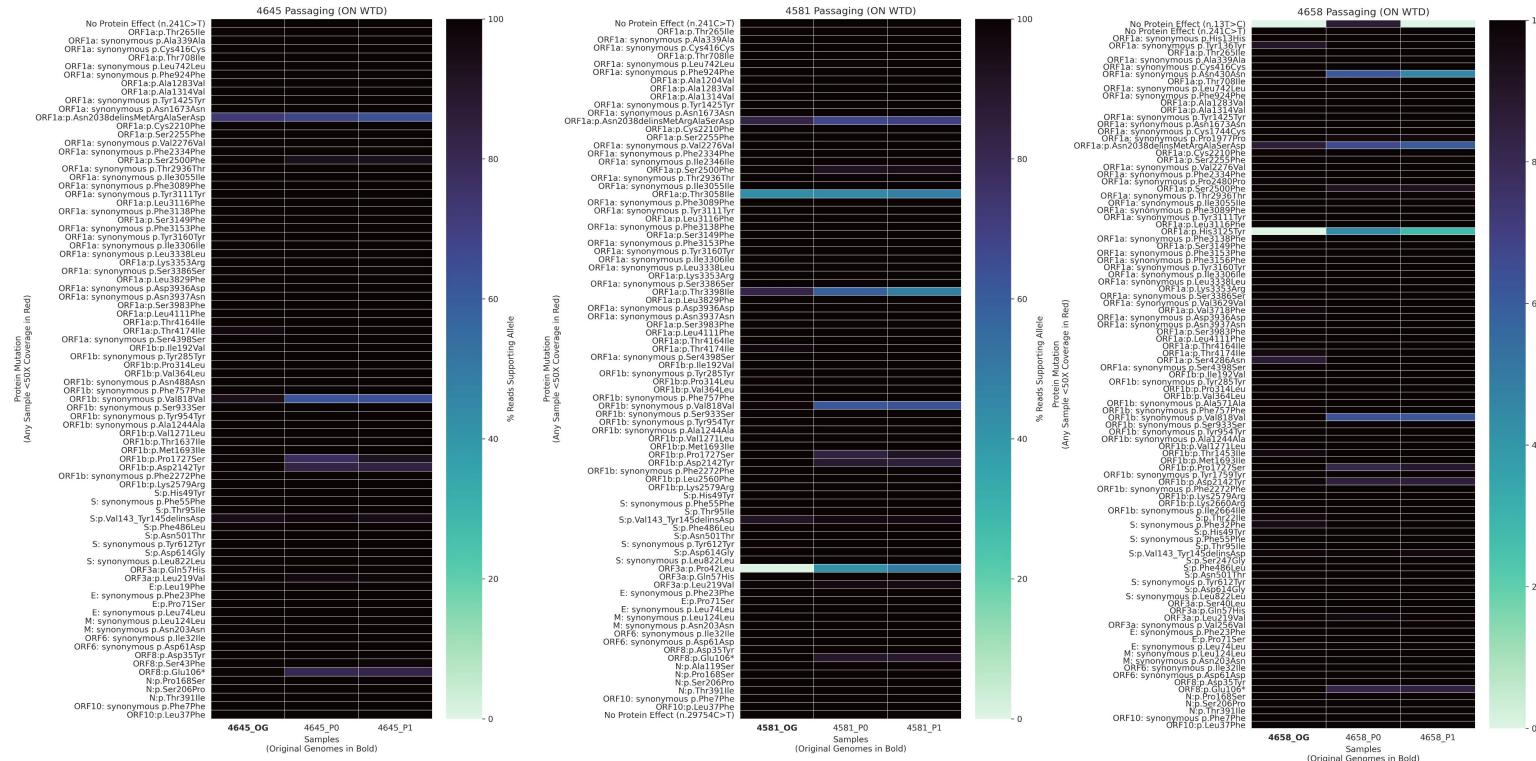
CoVaRR+Net



CanCOGeN



Viral cultures



Viral cultures

