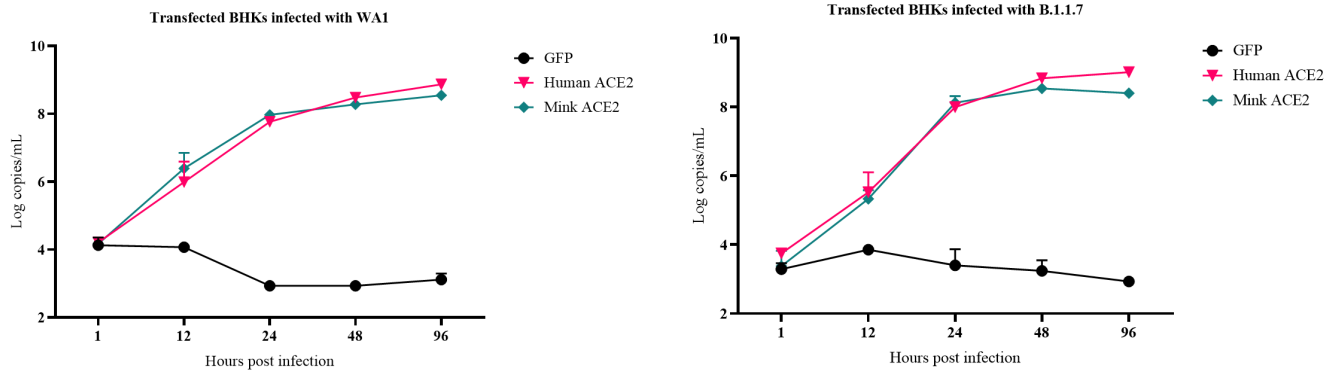
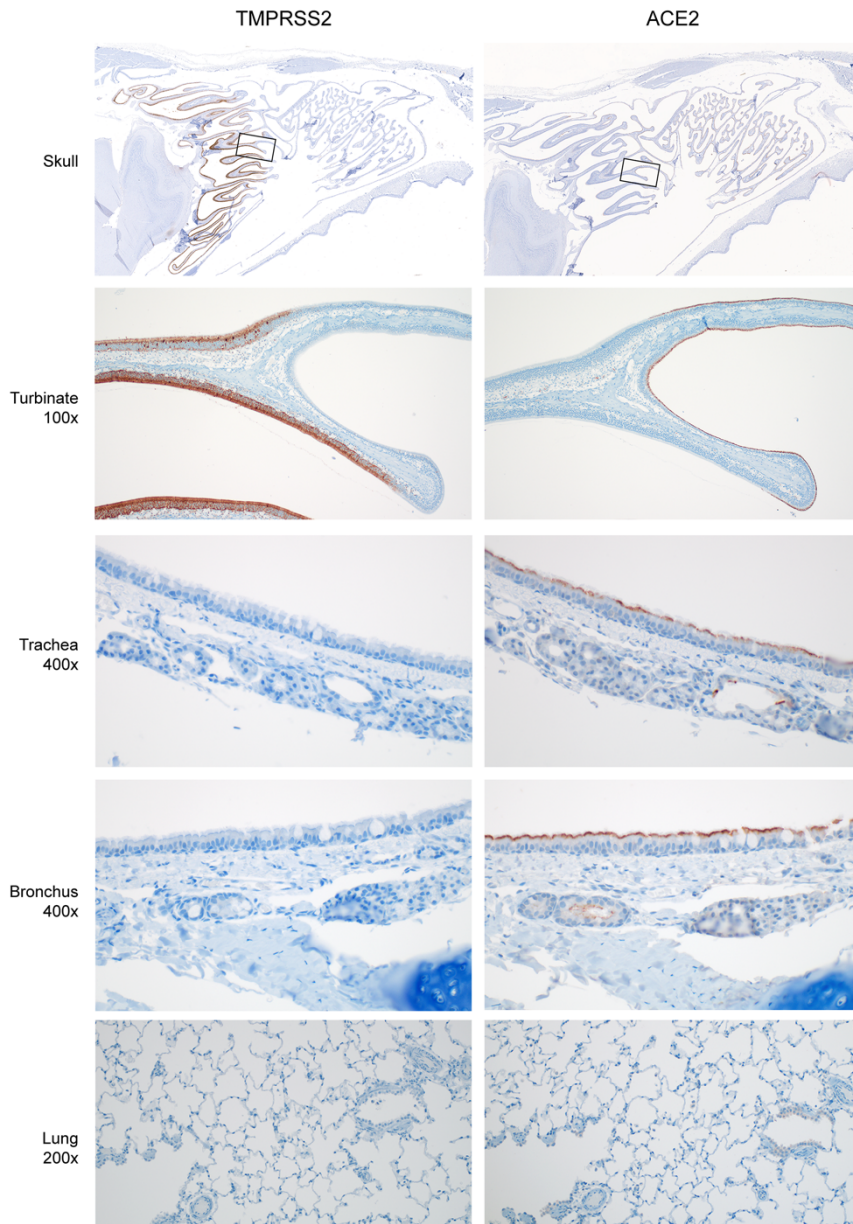


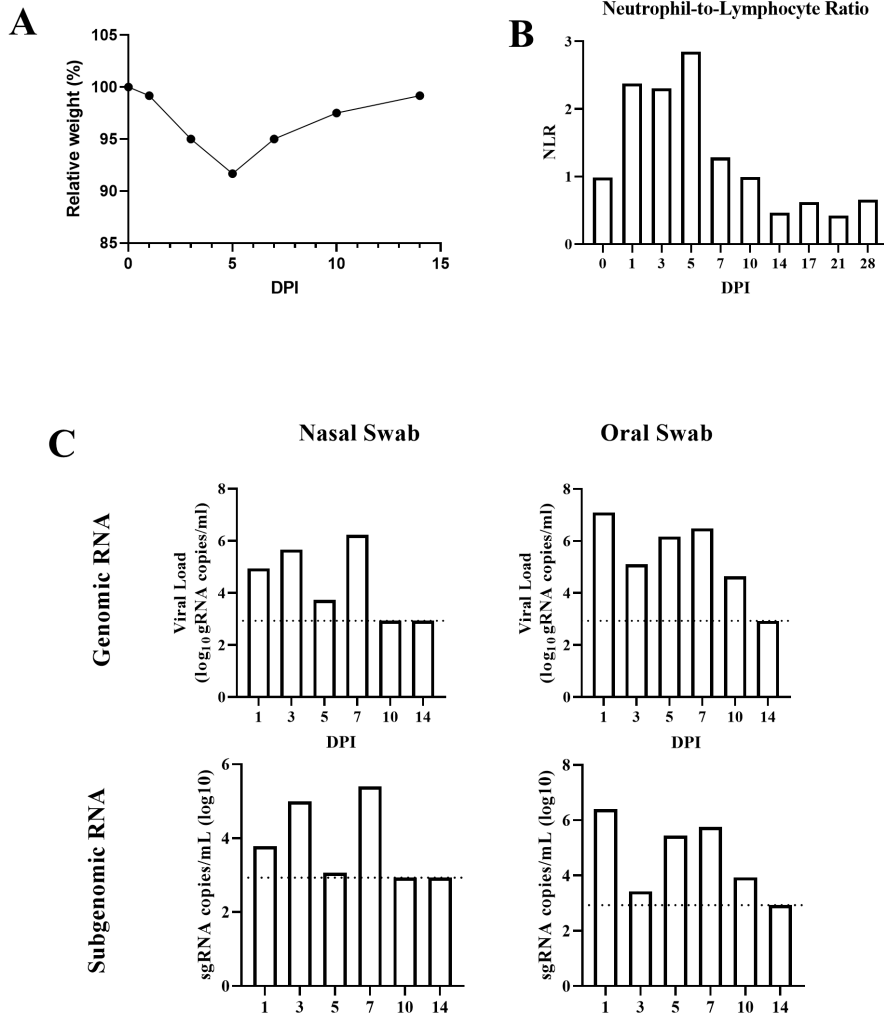
Supplementary Materials



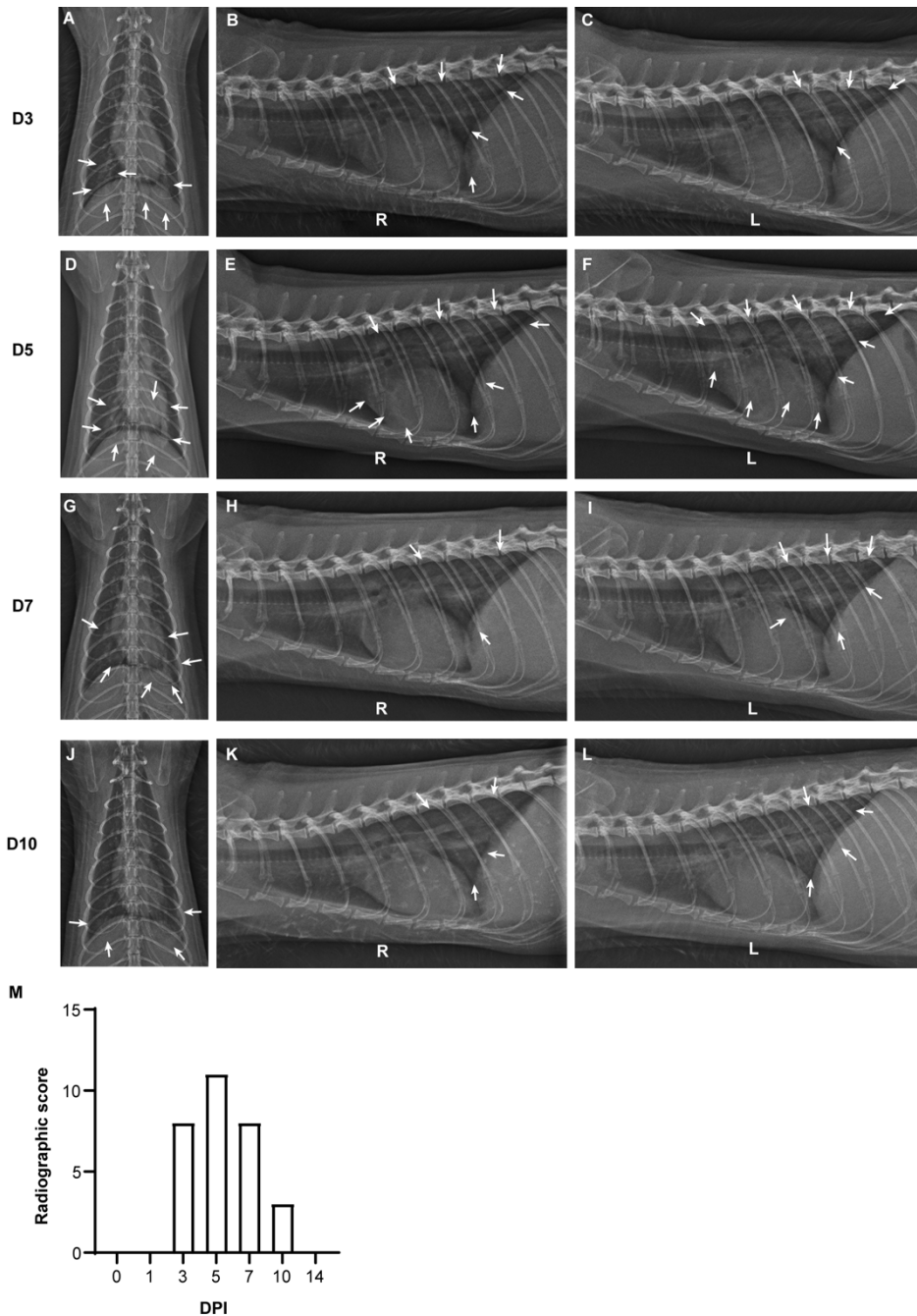
Supplemental Figure 1. Viral growth curves. Supernatant was collected from human and mink ACE2 and GFP transfected BHKs infected with either lineage A or B.1.1.7 SARS-CoV-2 variants at 1-, 12-, 24, 48-, and 96- hours post-infection in triplicate. Data are mean and standard error of the mean genomic RNA represented as log copies/mL



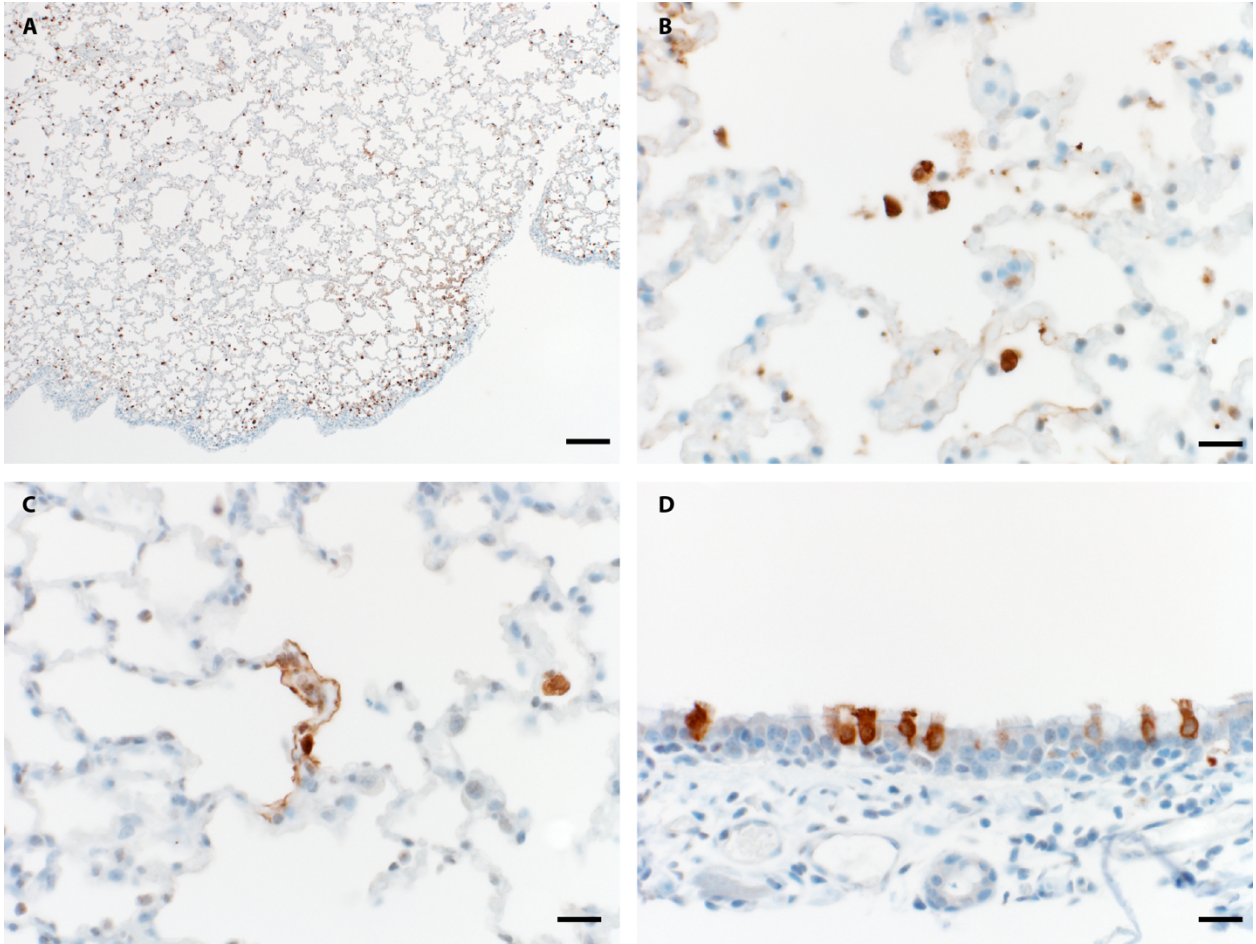
Supplemental Figure 2. Nasal turbinate olfactory and respiratory epithelial TMPRSS2 and ACE2 immunohistochemistry. Sagittal section of mink skull, TMPRSS2 (left column) and ACE2 (right column). Note the TMPRSS2 immunoreactivity of the caudal (olfactory epithelial) region of the turbinates. Higher magnification of the turbinate reveals TMPRSS2 immunoreactivity of the olfactory epithelium sharply demarcated from the ACE2 immunoreactivity of the respiratory epithelium lining the more rostral portion of the turbinate. The tracheal and bronchial epithelium are not immunoreactive for TMPRSS2 but are for ACE2; whereas the lung is immunoreactive for neither.



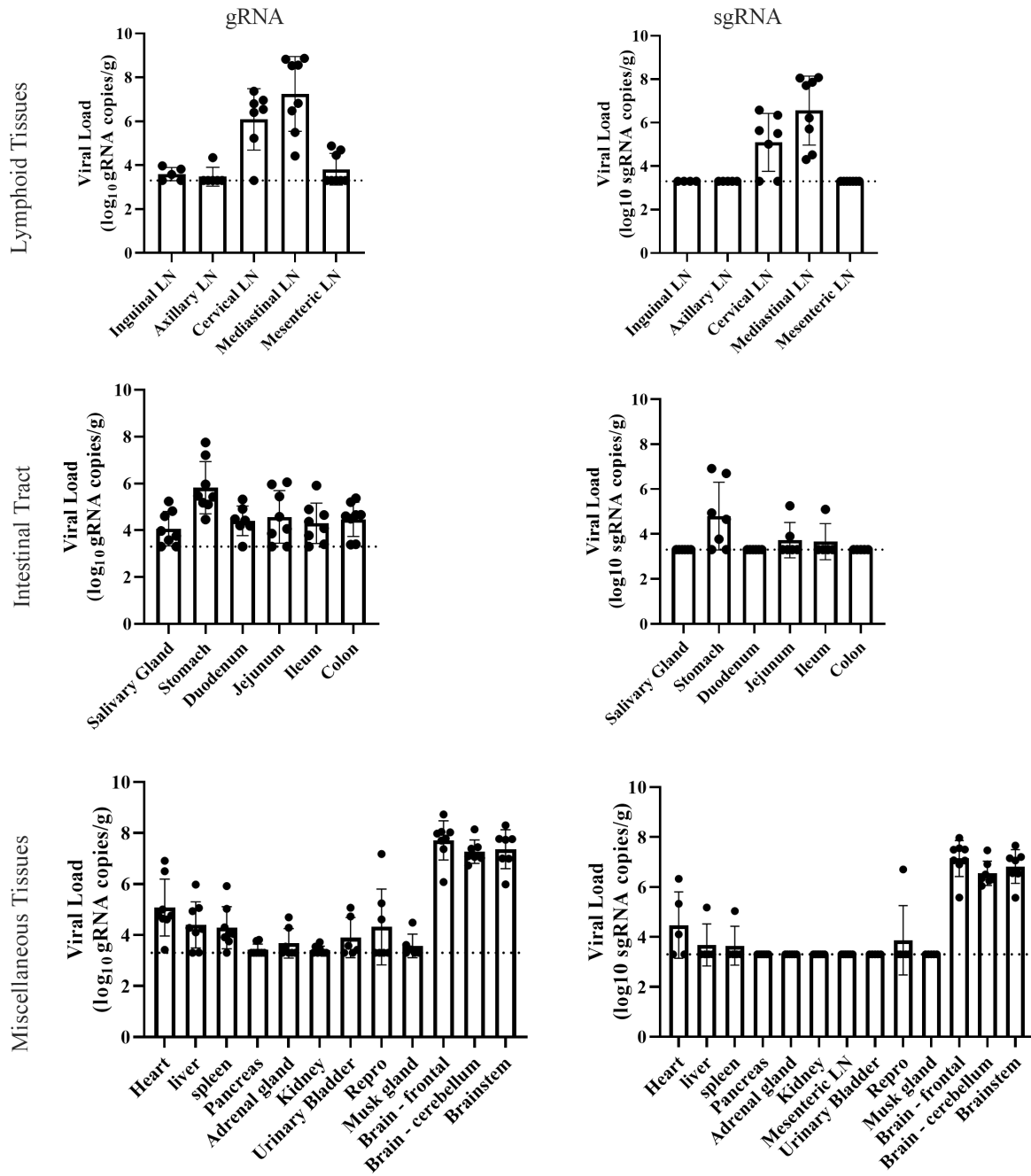
Supplemental Figure 3. Resolution of clinical disease in the surviving animal. The surviving animal was monitored for change in relative weight (A). Weight loss was most severe on 5 DPI, after which the animal began recovery. Neutrophil-to-lymphocyte ratio was monitored over time (B), with the most severe change appreciated on 5 DPI. Nasal and oral swabs were evaluated for resolution of viral shedding through genomic and subgenomic RT-PCR (C). All swabs on 14 DPI were below the limit of detectable virus.



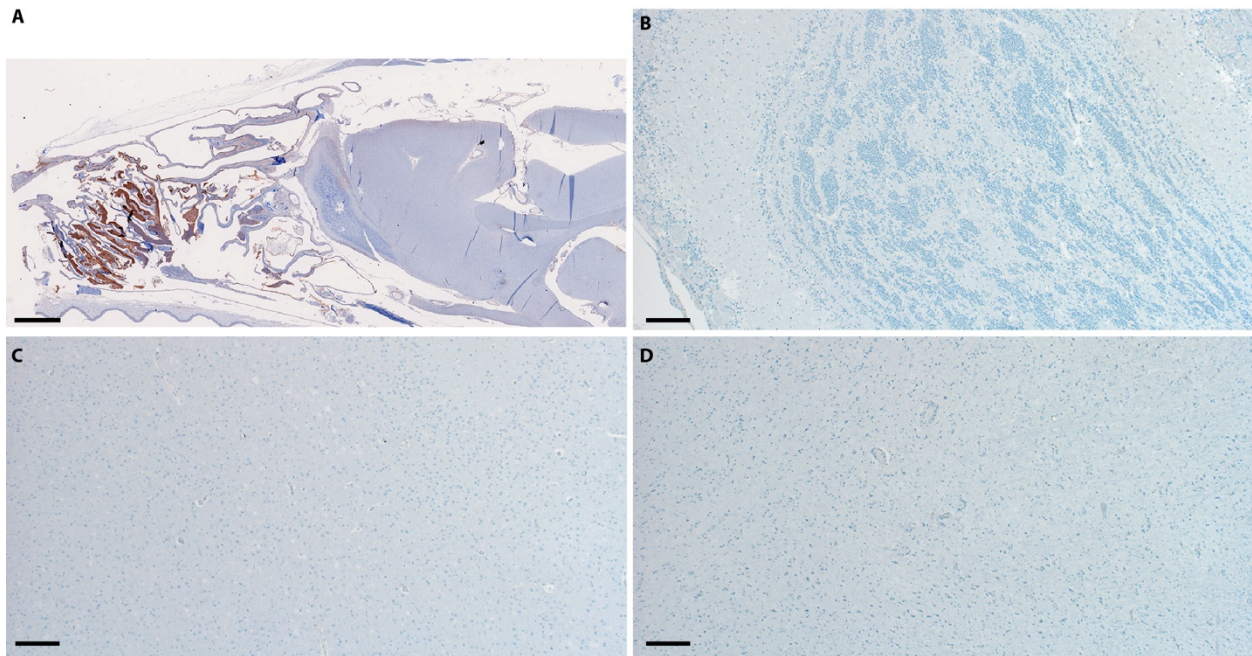
Supplemental Figure 4. Resolution of radiological disease in the surviving animal. (A-L) Dorsoventral, right lateral, and left lateral radiographs from surviving animal on 3, 5, 7, and 10 DPI. Arrows indicate pulmonary infiltrates, first visible in the left and right caudal lung lobes at 3 DPI (A-C) with additional involvement in the caudal subsegment of the left cranial lung lobe on 5 DPI (D-F). There is mild improvement in the alveolar pattern in the left and right caudal lung lobes on 7 DPI, with resolution in the caudal subsegment of the left cranial lung lobe (G-I). The pulmonary changes continued to improve by 10 DPI, with grade 2 pulmonary disease in the right caudal lung lobe with grade 1 pulmonary disease in the left caudal lung lobe consistent with improving viral pneumonia and pneumonitis (J-L). (M) Radiographic scores for surviving animal.



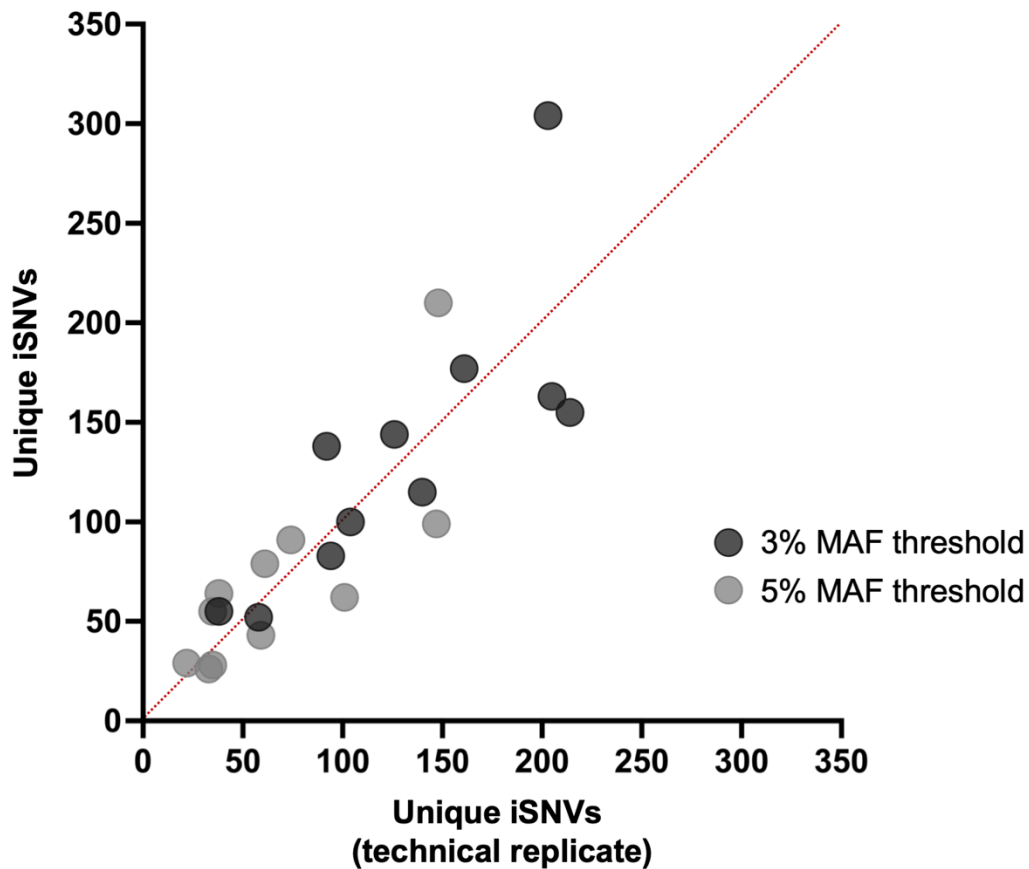
Supplemental Figure 5. SARS-CoV-2 Pulmonary immunohistochemistry. (A) Lung: Bar=200um (B) Alveolar macrophage immunoreactivity (C) Type I & II pneumocyte immunoreactivity (D) Bronchiolar epithelium immunoreactivity (brown=immunoreactive cells) C-E Bar=20um



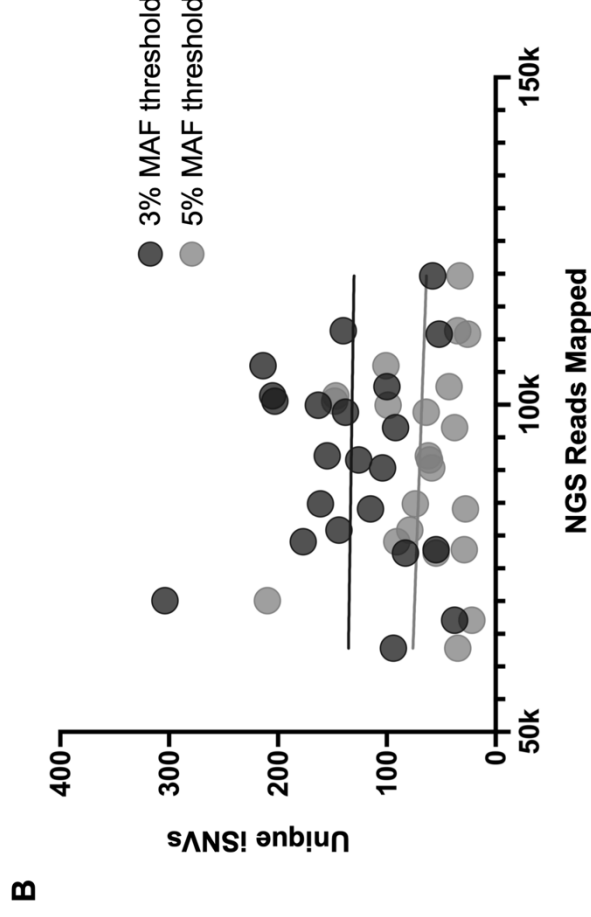
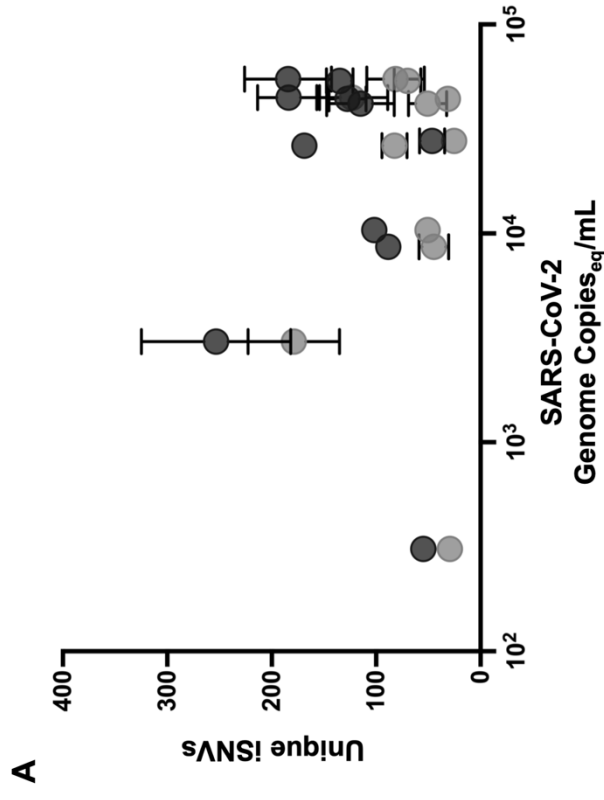
Supplemental Figure 6. Viral burden in non-respiratory tissues. Lymphoid (A), intestinal (B), and miscellaneous (C) tissues from animals euthanized on 3 DPI were evaluated for genomic and sub-genomic RNA. Graphs depict the mean and standard deviation.



Supplemental Figure 7. Nasal turbinate and brain SARS-CoV-2 immunohistochemistry. (A) Sagittal section of skull: Abundant nasal turbinate epithelium and exudate immunoreactivity (brown); bar = 3mm (B) Olfactory bulb: no immunoreactivity (C) Cerebral cortex: no immunoreactivity (D) Brainstem: no immunoreactivity. B-D bar = 200 μ m



Supplemental Figure 8. Comparison of intrahost single nucleotide variants (iSNVs) detected between technical replicates at minor allele frequencies (MAFs) of 3% and 5%. Dots along the red line indicate perfect concordance between replicates, whereas dots farther from the red line indicate less concordance between replicates.



Supplemental Figure 9 (A) Unique intrahost single nucleotide variants (iSNVs) relative to SARS-CoV-2 genome copy number or (B) number of sequenced reads mapped for each sample. Data shown for all samples with minor allele frequency thresholds of 3% and 5%.

Name	Days Post Inoculation	Sample Type	NSP5 (Ct)	SARS-CoV-2	Reads Mapped	Reads Mapped (Technical Rep)
				genome copies (eq)/mL		
mink01	1	oral swab	25.2	1.82E+05	82,994	
	3	lung tissue	24.8	2.34E+05	96,688	
mink02	3	oral swab	25.4	1.59E+05	73,964	
	1	oral swab	23.5	5.48E+05	94,620	
	2	lung tissue	20.5	3.53E+06	83,812	
mink03	2	oral swab	27.1	5.48E+04	92,177	105,980
	1	oral swab	27.1	5.37E+04	80,835	91,544
	3	lung tissue	20.5	3.72E+06	68,368	
mink04	3	oral swab	25	2.08E+05	87,343	
	1	oral swab	23.9	4.16E+05	89,083	
	3	lung tissue	17.9	1.90E+07	120,414	
mink05	3	oral swab	24.1	3.72E+05	90,275	
	1	oral swab	27.5	4.18E+04	98,844	96,509
	3	lung tissue	17.6	2.28E+07	95,960	
mink06	3	oral swab	25.1	1.91E+05	82,691	
	1	oral swab	24.9	2.12E+05	82,531	
	3	lung tissue	16.9	3.59E+07	83,560	
mink07	3	oral swab	31.6	3.04E+03	70,069	100,539
	1	oral swab	23.1	6.73E+05	82,750	
	2	lung tissue	25.2	1.84E+05	83,869	
mink08	2	oral swab	29.7	1.04E+04	102,762	90,328
	1	oral swab	25.8	1.24E+05	96,249	
	3	lung tissue	16.6	4.44E+07	91,707	
mink09	1	oral swab	26	1.10E+05	105,882	
	3	lung tissue	16.1	5.93E+07	70,836	
	3	oral swab	27.4	4.47E+04	99,943	101,347
mink10	1	oral swab	27.8	3.32E+04	77,189	13 (excluded)
	3	lung tissue	28.1	2.77E+04	77,862	67,088
	3	oral swab	27.4	4.41E+04	84,064	111,319
mink11 (survivor)	1	oral swab	24.9	2.14E+05	66,375	
	3	oral swab	28.2	2.63E+04	79,066	84,833
	5	oral swab	35.2	3.09E+02	110,791	119,696
Group 1	7	oral swab	30	8.64E+03	77,324	62,811
Group 1	0	inoculum	24.7	2.50E+05	75,081	
Group 2	0	inoculum	24.2	3.34E+05	91,597	

Supplemental Table 1. Samples from mink experimentally challenged with SARS-CoV-2 that were deep sequenced for within-host evolutionary analyses.

Supplementary Table 3: Long range PCR primers for amplification of ACE2.

Primer	Sequence (5' - 3')
Amplicon 1-F	CCCAACCCAAGTTCAAAGGCTGATGAGAGAGAA
Amplicon 1-R	CTTCATGTTTAGCTATTTGACAAAGGGCTTCTT
Amplicon 2-F	GGACACATCCAGTATGACATGGCATATG
Amplicon 2-R	TGGGGGAGTACAAGATTTAAGAGATTGGGAA