SARS-CoV-2 causes brain inflammation and induces Lewy body formation in macaques

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Abstract:

SARS-CoV-2 may cause acute respiratory disease, but the infection can also initiate neurological symptoms. Here we show that SARS-CoV-2 infection causes brain inflammation in the macaque model. An increased metabolic activity in the pituitary gland of two macaques was observed by longitudinal positron emission tomography-computed tomography (PET-CT). Post-mortem analysis demonstrated infiltration of T-cells and activated microglia in the brain, and viral RNA was detected in brain tissues from one animal. We observed Lewy bodies in brains of all rhesus macaques. These data emphasize the virus' capability to induce neuropathology in this nonhuman primate model for SARS-CoV-2 infection. As in humans Lewy body formation is an indication for the development of Parkinson's disease, this data represents a warning for potential long-term neurological effects after SARS-CoV-2 infection.

One-Sentence Summar:

SARS-CoV-2 causes brain inflammation and Lewy bodies, a hallmark for Parkinson, after an asymptomatic infection in macaques.

Report

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes a multi-system inflammatory disease syndrome, COVID-19 (*1*). Although SARS-CoV-2 predominantly affects the respiratory organs, over 30% of the hospitalized COVID-19 patients also suffer from neurological manifestations, including loss of smell or taste, delirium, diminished consciousness, epilepsy, and psychosis (*2-5*). Besides these general neurological symptoms, some patients additionally endure Parkinsonism (*6-8*). The mechanisms behind this process are poorly understood. Neurological symptoms may be triggered by infection of the brain tissue, or indirectly, via virus-induced immune cell activation (*9*). In humans a direct link between brain inflammation and the presence of SARS-CoV-2 RNA has not yet been established (*10*), and thus, formal proof that central nervous system (CNS)-related symptoms of COVID-19 are directly caused by the infection, or indirectly due to overactivation of the immune system, is lacking. Additionally, the long-term effects on the CNS after a mild to moderate SARS-CoV-2 infection, likely the vast majority of human cases, are unknown, and post-mortem brain samples from these individuals are not expected to become available for research in the near future. Controlled infection studies in a standardized experimental setting are crucial to investigate SARS-CoV-2-induced brain pathology (*11*). To address this issue, a study was performed in two macaques species, rhesus macaques (*Macaca mulatta*) and cynomolgus macaques (*Macaca fascicularis)* (Table 1), both well-accepted animal models for COVID-19 (*12*). Four male rhesus and four male cynomolgus macaques were inoculated with 10^6 TCID$_{50}$ of SARS-CoV-2 strain BetaCoV/BavPat1/2020 via a combined intratracheal and intranasal route (*13, 14*). Following infection, SARS-CoV-2 genomic material was detected in tracheal and nasal swabs up to ten days, and based on clinical signs and thorax CTs, all animals showed mild to moderate disease symptoms (*13, 15*). We initiated weekly ^{18}F-FDG

PET-CTs of the animals' brains of all macaques when the virus became undetectable in nasal and

tracheal swabs. The uptake of tracer renders a marker for metabolic activity. Two of four

cynomolgus macaques (C1 and C2), displayed an increased uptake of ^{18}F-FDG in the pituitary gland

at multiple time points. In animal C1, an increased uptake of ^{18}F-FDG in the pituitary gland was

seen at days 30 and 36 post-infection (Fig. 1). In animal C2, increased metabolic activity was

already visible at day 8 and continued through day 35 when the final scan was obtained (Table S1).

In humans and macaques, the volume of the pituitary gland is small, and under physiological

conditions its metabolic activity is comparable to the background level of the entire brain (*16, 17*).

The ^{18}F-FDG uptake of the pituitary gland may even be underestimated due to the partial-volume-

effects that affect the emission signal recovery (*16*). Because pituitary gland tissue expresses

angiotensin-converting enzyme 2 (ACE2)(*18*), the increased ^{18}F-FDG uptake may be a direct effect

of the infection or an indirect effect due to either a (reversible) hypophysitis, or transient

hypothalamic-pituitary dysfunction. Yet, hypocortisolism has never been documented in patients

with active COVID-19 (*19*).

To further investigate the consequences of SARS-CoV-2-infection on macaque brain tissue, the

animals were euthanized 5-6 weeks after experimental infection. Sections of the whole brain were

systematically collected for further examination. As several regions of the brain express the SARS-

CoV-2 receptor ACE2, and inflammation was found in the human brain (*10, 20, 21*), we used

various immunological markers for innate and adaptive immune activation to investigate for signs

of immune activation, and also explored the localization of virus particles (Fig. 2 and Table 2).

Viral RNA was detected by real-time quantitative polymerase chain reaction (RT-qPCR) in

multiple brain areas of the right hemisphere of cynomolgus macaque C3 (Fig. 2). More precisely,

cerebellum (1.48×10^5 RNA genome equivalents (GE)/gram), medial motor cortex (2.09×10^5

GE/gram), sensory cortex (2.07×10^5 GE/gram) and frontal basal cortex (8.29×10^4 GE/gram), as well

as hippocampus (1.24×10^5 GE/gram), hypothalamus (1.05×10^6 GE/gram), and globus pallidus

(5.45×10^4 GE/gram) all tested positive in the RT-qPCR. No viral RNA was detected in samples

collected from the pituitary gland or olfactory bulb, substantia nigra, medulla oblongata, pons,

nucleus caudatus, and putamen. Subgenomic viral RNA analysis did not show evidence for active

virus replication in the brains at the time-point of euthanasia. Additionally, SARS-CoV-2 antigen

was not detectable by immunohistochemistry the brains of all macaques.

The brains of all SARS-CoV-2-infected macaques showed evidence of inflammation. Presence of

T-cells was visualized by CD3 staining in intraparenchymal brain tissue, suggesting the infiltration

of T-cells that passed the blood-brain barrier after SARS-CoV-2 infection (Fig.3A, top panel).

Additionally, activation of microglia cells in different areas of the brain, including the olfactory

bulb and pituitary gland, was confirmed by Mamu-DR staining (upregulation of MHC class II

expression) (Fig. 3A, middle panel). However, nodule formation, which is a measure for severity

of activation, was rarely present (Table 2). No B-lymphocytic infiltration was found as evidenced

by lack of CD20 staining (not shown). Hematoxylin and eosin (HE) staining did not show any

abnormalities in the brain tissue of the virus-exposed macaques, including the absence of

ischemic/necrotic lesions. For comparison, post-mortem brain tissues from two healthy, age-

matched macaques of each species were used as controls (Table 1), none of the four control animals

displayed obvious signs of immune activation (T-cells and microglia) were observed.

Brain tissues were screened for α-synuclein deposits, known as Lewy bodies, by

immunohistochemistry. In humans, Lewy body formation is linked to the development of

Parkinson's disease or Lewy body dementia (*22, 23*). It has been hypothesized that certain

neurotropic viruses, including MERS and SARS coronaviruses, can trigger formation of Lewy

bodies and cause Parkinsonism (*24-29*).

The formation of intracellular Lewy bodies was clearly shown in the midbrain region of the caudate

nucleus of all infected rhesus macaques (Table 2, Fig. 3B), and in one aged cynomolgus macaque

(C4), while Lewy bodies were absent in the brains of all four control animals. The data provide

evidence for SARS-CoV-2-driven inflammation in the brain of macaques. In humans,

neuropathology has been described in moribund COVID-19 patients, but we report of SARS-CoV-

2-related brain involvement in macaques without displaying overt clinical signs. In general,

macaque models for SARS-CoV-2 infection typically represent mild to moderate COVID-19

symptoms on the CT scan, as compared to humans (*12, 14, 30*). Detection of viral RNA in the brain

of an animal demonstrates the virus' neuroinvasive capability. This matches a recent study

describing neuroinvasion in mouse brains and in human brain organoids (*31*).

How exactly SARS-CoV-2 caused widespread brain inflammation and induced Lewy body

formation remains unknown. Viruses can enter the brain via different pathways. In this study,

infiltration of T-cells was found perivascular and in the brain parenchyma, which indicates that the

blood-brain barrier integrity may have been disturbed, offering the virus the opportunity to enter

the brain. Alternatively, we hypothesize that SARS-CoV-2 gained access to the brain via neuronal

pathways, such as the retrograde and anterograde neuronal transport through infected motor or

sensory neurons (*32*), and can have entered the pituitary gland via binding to the ACE2 receptor

protein expressed on its cell surfaces (*18, 33*). Such neural connection also exists between the

olfactory bulb and the nasal mucosa (*34*), and the loss of taste and smell, a characteristic of COVID-

19, can thus be explained by nasal infection and subsequent inflammation in the olfactory bulb.

Such a scenario is in line with the finding that in all the SARS-CoV-2-exposed macaques, immune

system activation in the olfactory bulb was evidenced by the presence of T-cells and/or activated

microglia.

Neuronal transport can also explain why some COVID-19 patients develop Parkinson's disease-

like symptoms. Viruses can also, via retrograde transport in parasympathic motor neurons of the

nervus vagus to the medulla, pons, and midbrain, reach the substantia nigra in the midbrain (*26,*

35). Notably, the α-synuclein inclusions were found in the ventral midbrain region of the animals.

In humans, these inclusions of accumulated misfolded proteins are associated with Parkinson's

disease or Lewy body dementia (*36*).

There is a growing concern that symptomatic COVID-19 patients may suffer from long-term

consequences (*9, 37*). In this light the finding of Lewy bodies in brains of infected macaques

without overt clinical signs is intriguing. They are considered a hallmark for the development of

Parkinson's disease, or Lewy body dementia. More confirmation is required, but the observations

in the translational macaque models for COVID-19 (*12-14, 38, 39*) can be regarded as a serious

warning as they may be predictive for COVID-19-related dementia cases in humans in the future,

even after an asymptomatic infection or mild disease process.

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The authors declare that they have no competing interests.

Data and materials availability:

All data are available in the main text or the supplementary materials. Correspondence and request

for materials should be addressed to IHCHMP (philippens@bprc.nl).

Table 1: Animals featuring in this study

Macaque species	Monkey ID	Infected Y/N	Age (Year)	Body weight[#] (kg)	Sex M/F
Rhesus	R1	Y	6	8.2	M
Rhesus	R2	Y	5	7.9	M
Rhesus	R3	Y	5	7.8	M
Rhesus	R4	Y	5	8.7	M
Rhesus	control R5	N	5	8.5	M
Rhesus	control R6	N	6	5.1	F
Cynomolgus	C1	Y	4	5.7	M
Cynomolgus	C2	Y	4	3.3	M
Cynomolgus	C3	Y	4	4.9	M
Cynomolgus	C4	Y	16	9.7	M
Cynomolgus	control C5	N	5	5.3	M
Cynomolgus	control C6	N	7	5.1	M

364 [#]at start of study

Fig. 1. ¹⁸F-FDG PET-CT image of a SARS-CoV-2 infected cynomolgus macaque (C1).

Representative images of cynomolgus macaque C1 (A) on day 29, and a healthy control animal

(B) are shown. The pituitary gland is indicated by the cross-hairs in all three directions and is boxed

(right pictures). Similar window-level settings are applied for all sections. The pituitary gland-brain

ratio of animal C1 was calculated with both the mean and peak standard uptake value (SUV); for

the SUV_{mean} this ratio was 1.9, and for the SUV_{peak} 1.3. The average values calculated from a group of

non-infected control animals (n=6) were 1.1 (std 0.3) for the SUV_{mean}, and 0.6 (std 0.1) for the SUV_{peak}

ratio. The uptake values of the brain, defined as background, were similar with SUV_{mean} values of

2.2 and 1.9 for the SARS-CoV-2-infected animals and the non-infected controls, respectively. After

the relevant corrections for attenuation, scatter and decay, our results are indeed indicative for

pituitary hypermetabolism after SARS-CoV-2 infection in animals C1 and C2.

1.	pituitary gland
2.	olfactory bulb
3.	substantia nigra
4.	medulla oblongata
5.	pons
6.	cerebellum
7.	motor cortex
8.	sensory cortex
9.	frontal basal cortex
10.	hippocampus
11.	caudate nucleus
12.	hypothalamus
13.	globus pallidus
14.	putamen
15.	thalamus

Fig. 2. Overview of CNS effects by SARS-CoV-2 exposure in a macaque brain. Presence of viral RNA was investigated in multiple regions of the brain as indicated by the numbers. Viral RNA-positive regions in cynomolgus macaque C3 are indicated by a yellow background. The analysed brain regions are indicated with a number. Brain areas with T-cells (CD3+) and activated microglia (Mamu-DR+) are shown in light blue (mild expression) and dark blue (moderate expression), respectively. Brain areas with Lewy bodies (α-synuclein+) are shown in orange.

Fig. 3. SARS-CoV-2 causes brain inflammation and Lewy body formationin brains of macaques. Immunohistochemical stainings of macaque brain tissues. **A, t**op panel: T-cells (CD3+) in the pituitary gland (left), perivascular (middle) and in the brain parenchyma (right) from a rhesus macaque (20x). **A,** middle panel: activated microglia (Mamu-DR+) in the pituitary gland (left), olfactory bulb (middle) and in the brain parenchyma (right) from a cynomolgus macaque (20x). **B,** bottom panel: Lewy bodies (α-synuclein +) were found next to the hippocampus next to the caudate nucleus indicated with a circle (left) in the coronal section of one hemisphere (anterior-posterior 0), presence of Lewy bodies in a SARS-CoV-2-infected rhesus macaque (20x) (middle), a magnified image (40x) of the square in the left image (right).

397 **Table 2**: **Histological findings.**

Marker		Brain area	Rhesus				Cynomolgus				Controls			
			R1	R2	R3	R4	C1	C2	C3	C4	R5	R6	C5	C6
T-cells (CD3+)	intra-parenchymal	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
	perivasculair	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
	nodules	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
	meninges	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
Activated microglia (Mamu-DR+)	presence	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
	morphology: ramified/ amoeboid	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
	nodules	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
	meninges	pituitary gland olfactory bulb front brain dorsal ventral cerebellum												
Lewy bodies (α-synuclein+)	inclusions	ventral midbrain												

400 Table 2 outlines the presence of 1) T-cells (CD3+ cells) in the brain tissue (intraparenchymal),

401 around blood vessels (perivascular), in group formation (nodules), or in the meninges, 2) activated

microglia (Mamu-DR+ cells) in different parts of the brain, the morphology as a measure for the

severity of activation (ramified or amoeboid), in group formation (nodules) or in the meninges, 3)

α-synuclein/Lewy bodies (α-synuclein + cells with inclusions) in the ventral midbrain region of

the caudate nucleus. The last column shows the absence of most of these markers in the control

animals. Light grey: mild observation; dark grey: moderate observation (including amoeboid

microglia cells); black: moderate to severe observation of these markers.

Supplementary Materials for

SARS-CoV-2 causes brain inflammation and induces Lewy body formation in macaques

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459 **This file includes: Materials and Methods, Table S1**

MATERIALS AND METHODS

Animals and SARS-CoV-2 exposure

Four cynomolgus macaques (*Macaca fascicularis*) and four Indian-origin rhesus macaques (*Macaca mulatta*) (Table 1) were selected for this study. All macaques were mature, outbred animals, purpose-bred and socially housed at the BPRC. The animals were in good physical health with normal baseline biochemical and hematological values. All were pair-housed with a socially compatible cage-mate. The animals were offered a daily diet consisting of monkey food pellets (Ssniff, Soest, Germany) supplemented with vegetables and fruit. Enrichment was provided daily in the form of pieces of wood, mirrors, food puzzles, and a variety of other homemade or commercially available enrichment products. Drinking water was available *ad libitum* via an automatic system. Animal Care staff provided daily visual health checks before infection, and twice-daily after infection. The animals were monitored for appetite, general behavior, and stool consistency. All possible precautions were taken to ensure the welfare and to avoid any discomfort to the animals. All experimental interventions (intratracheal and intranasal infection, swabs, blood samplings, and PET-CTs) were performed under anesthesia. The research protocol was approved by an independent animal ethics committee (DEC), as well as BPRC's institutional animal welfare body (IvD).

On day 0, all animals were exposed to a dose of 10^5 TCID$_{50}$ of SARS-CoV-2 (strain BetaCOV/BavPat1/2020), diluted in 5 ml phosphate-buffered saline (PBS). The virus was inoculated via a combination of the intratracheal route (4.5 ml) and intranasal route (0.25 ml per nostril). For the histological examination brains from naive control macaques from the same age were obtained from the BPRC biobank, two cynomolgus, and two rhesus macaques.

Positron Emission Tomography – Computed Tomography

Positron Emission Tomography (PET)-computed tomography (CT) data were acquired on multiple

time points post-infection using a MultiScan Large Field of View Extreme Resolution Research

Imager (LFER) 150 PET-CT (Mediso Medical Imaging Systems Ltd., Budapest, Hungary) as

described before(*40*). Animals were fasted overnight (glucose level > 8.5 mmol/l). The animals

were sedated with ketamine (10 mg/kg ketamine hydrochloride (Alfasan Nederland BV, Woerden,

The Netherlands)) combined with medetomidine hydrochloride (0.05 mg/kg (Sedastart; AST

Farma B.V., Oudewater, The Netherlands)) to induce sedation and muscle relaxation, both applied

intramuscularly (IM). The animals were positioned head first supine (HFS) with the arms up. The

scans were acquired under mechanical ventilation in combination with a forced breathing pattern.

For anesthetic maintenance, a minimum alveolar concentration of isoflurane (iso-MAC) of around

0,80%-1.00% was used. The body temperature of the animal was maintained by using the Bair

Hugger (3M™, St Paul, MN, USA) supplied with 43°C airflow. Typically, around 100 MBq of ^{18}F-

FDG was applied intravenously (GE Healthcare, Leiderdorp, NL). Thirty minutes after injection

the plateau in tracer activity uptake is reached, subsequently a PET of 15 minutes was acquired.

After the scan, upon return to their home cage, atipamezole hydrochloride (Sedastop, ASTFarma

B.V., Oudewater, NL, 5 mg/ml, 0.25 mg/kg) was administrated IM to antagonize medetomidine.

Afterward the emission data was iteratively reconstructed (OSEM3D, 8 iterations, and 9 subsets)

into a single frame PET image normalized and corrected for attenuation, scatter, and random

coincidences using a reference CT and corrected for radioactive decay. The analysis was performed

in VivoQuant 4.5 (Invicro, Boston, USA). Based on repeatability parameters for correct

interpretation of the results, a standardized uptake value (SUV) ratio was used for robustness(*17,*

40). An increased uptake, and pituitary gland hypermetabolism is defined as a SUV_{mean} ratio above

1.5 for the pituitary gland over the surrounding brain in combination with a SUV_{peak} ratio above

background levels (>1.0). A group of non-infected control rhesus macaques (n=6) were used to

calculate average background uptake of ^{18}F-FDG.

Brain tissue collection

Five weeks after virus exposure the macaques were euthanized and the brains were collected for

further examination. The right hemisphere was used for RT-qPCR analysis and the left hemisphere

was fixed in formalin for histology. Fifteen different regions were collected from the right

hemisphere for RT-qPCR analysis: 1) part of the pituitary gland, 2) the olfactory bulb, 3) substantia

nigra, 4) medulla oblongata, 5) pons, 6) anterior part of the cerebellum, 7) motor cortex medial, 8)

sensory cortex, 9) frontal basal cortex, 10) hippocampus, 11) caudate nucleus, 12) hypothalamus,

13) globus pallidus, 14) putamen, and 15) thalamus. For the preparation of paraffin-embedded

sections of the formalin-fixed left hemisphere, the cerebrum and cerebellum were dissected in 3-4

mm parts on the anterior-posterior axis. Pituitary gland and olfactory bulb were also embedded.

From each part, sections (4 μm) were prepared for different staining methods.

Immunohistochemistry stains were used for T-cells (CD3), B-cells (CD20), activated microglia

(Mamu-DR), Lewy bodies (α-synuclein ab), and for SARS-CoV-2. Hematoxyline-eosine (HE)

staining was used for general morphology.

Viral RNA detection in brain tissue

Brain tissue samples were weighed and placed in gentleMACS M tubes (30 mg in 100 μl PBS) and

treated using a gentleMACS Tissue Dissociator (protein01 program)(Miltenyi Biotec B.V., Leiden,

The Netherlands). Next, the homogenized tissue was centrifuged, and 100 μl supernatant was used

for RNA isolation. Viral RNA was isolated from using a QIAamp Viral RNA Mini kit (Qiagen

Benelux BV, Venlo, The Netherlands) following the manufacturer's instructions. Viral RNA was

reverse-transcribed to cDNA using a Transcriptor First Strand cDNA Synthesis kit (Roche

Diagnostics BV, Almere, The Netherlands). Viral RNA was quantified by RT-qPCR specific for

RdRp gene of SARS-CoV-2, as described by Corman *et al.*(*41*). The lower detection limit of the

RT-qPCR was 3.6 viral RNA copies per reaction. Viral sub-genomic RNA was detected essentially

as described by Wölfel *et al.*(*42*). For both assays, RNA standard curves were generated by *in vitro*

transcription of the target regions.

Tissue preparation for histology

The left hemisphere of the brains, part of the pituitary gland, and one olfactory bulb were fixed in

formalin for 24 hours and thereafter stored in buffered PBS. Preserved brains were cryoprotected

in 30% w/v sucrose in PBS. The cerebrum was dissected in 12 different parts cut anterior-posterior

axis at +10, +8, +5, +1, -3, -6, -8, -11, -14, -18, -22 from Bregma(*43*), the cerebellum and pons

were cut in 4 parts. These part were embedded in paraffin. From the eight brain parts in which viral

RNA was detected by RT-qPCR, strips of brain sections were sliced into 12-series of 4 μm sections

for different stains. These parts included the frontal cortex, midbrain parts, cerebellum, pituitary

gland, and olfactory bulb. Sections were stained with virus antibody staining for virus detection

and immunohistochemistry for immune reaction such as T-cell staining (CD3), B-cell staining

(CD20), MHC-II cell staining (HLA-DR). Mirror sections were analyzed with a HE staining for

brain morphology.

Immunohistochemistry

The optimal concentration was determined for each antibody: CD3 (polyclonal rabbit – anti-human

CD3 IgG, cat. no. A045201-2, Agilent Technologies), 1:60; CD20 (monoclonal mouse – anti-

human CD20 IgG2a, clone L26, cat. no. M075501-2, Agilent Technologies), 1:800; Mamu-DR

(monoclonal mouse – anti-human HLA-DR/DQ- IgG1, clone CR3/43, cat. no. M077501-2, Agilent

Technologies), 1:150. For antigen retrieval, a steamer was used. Antigen Retrieval solution: IHC-

TEK epitope retrieval solution, ready to use (catno IW-1100, IHC world). All incubation steps

were at room temperature unless mentioned otherwise. Additionally, hematoxylin was used as a

counterstaining in all protocols. After a dehydration sequence, the slides were mounted in Malinol.

The counting of cells was performed in a blind matter.

CD3 and CD20 staining

The slides were deparaffinized by putting the slides sequentially in xylene, 100% ethanol, 96%

ethanol, 70% ethanol, and PBS. Subsequently, an epitope antigen retrieval was executed in a

steamer for 1h. After cooling down, the slides were placed in cuvettes (Sequenza cover plate system

productnr 36107 Ted Pella inc.). Endogenous peroxidase (PO) activity was blocked by the PO

blocking solution from DAKO (S2023) for 15 minutes. After a washing step (PBS with 0.05%

Tween) Avidin was added from the DAKO kit (X0590) for 10 minutes. Thereafter, another

washing step and biotin was added from the same DAKO kit (10 min) for blocking endogenous

biotine. After washing a blocking step was executed for 20 minutes (PBS with 0.1% BSA and 1%

normal human serum, NHS). The primary antibody was added (diluted in 0.1% BSA in PBS) and

the slices were left overnight at 4◦C. After washing a secondary antibody (Rabbit-anti-mouse IgG

biotinylated (E0354), Agilent Technologies; 1:200 diluted in PBS + 1% BSA + 1% NHS) was

added and, after washing, the slides were incubated with Vectastain ABC-peroxidase (ABC-PO,

from Vector Laboratories; PK-4000; diluted 1:100 in PBS) for 30 minutes. After washing, 3,3'-

diaminobenzidine (DAB) with 0.02% H_2O_2 was added to visualize the antigen-antibody binding (20

min).

Mamu-DR staining

The EnVision™ staining kit (G|2 Double-stain System, Rabbit/Mouse, DAB+/Permanent RED

code K5361; Agilent technologies, Dako DK) was used for the immunohistochemical stain of

Mamu-DR. The slides were deparaffinized by putting them sequentially in xylene, 100% ethanol,

96% ethanol, 70% ethanol, and PBS?. Subsequently, an epitope antigen retrieval was executed and

the slides were put in a steamer for 1h. The cooled down slides were placed in cuvettes and the

endogenous peroxidase activity was blocked by the envision kit. The slides were washed and

thereafter a blocking step was used consisting of 1% NHS + 1% BSA + 0.2% triton x100 in PBS

for 10 minutes. Subsequently, the primary antibody was added (diluted in 0.1% BSA/PBS) for 30

minutes. Thereafter a washing step was implemented and the EnVision™ polymer/HRP (secondary

antibody) was added for 10 minutes. Polymer HRP was added for 10 minutes followed by a

washing step. Thereafter DAB+ was added for 15 minutes to visualize the antigen-antibody

binding.

α-Synuclein staining

The slides were deparaffinized by immersing them sequentially in xylene, 100% ethanol, 96%

ethanol, 70% ethanol, and PBS. Subsequently, an epitope antigen retrieval was executed by putting

the slides for 15 minutes in Formic acid (100%) diluted 1:10 in demineralized water. After 2

washing steps in PBS with 0,05% Tween, the slides were placed in cuvettes (Sequenza cover plate

system product no. 36107 Ted Pella inc.). Endogenous PO activity was blocked by the PO blocking

solution from DAKO (S2023) for 20 minutes. After washing (PBS with 0.05% Tween), avidin was

added from the DAKO kit (X0590) for 10 minutes. Then, after another washing step, biotin was

added from the same DAKO kit (10 min) for blocking of endogenous biotine. After washing, a

blocking step was executed for 30 minutes (PBS with 0.1% BSA and 1% NHS and 0.02% Triton-

X100). The primary antibody, α-synuclein clone 4D6 (Biolegend SIG-39720), was added (diluted

in 0.1% BSA in PBS) and the slides were left overnight at 4°C. After washing, a secondary antibody

(rabbit anti-mouse IgG Biotinylated (E0354), Agilent Technologies; 1:200 diluted in PBS + 1%

BSA) was added for 30 minutes and the slides were incubated with Vectastain ABC-PO kit from

Vector Laboratories (PK-4000; diluted 1:100 in PBS) for 30 minutes. After a final washing step,

DAB with 0.02% H_2O_2 was added to visualize the Antigen-antibody binding (20 min).

SARS-CoV-2 staining

The Roche Optiview DAB IHC kit was used in a Ventana Benchmark Ultra (Roche, Basel

Switzerland) immunostainer to immunohistochemically stain SARS-CoV-2. Two monoclonal

antibodies of ThermoFisher raised to SARS-CoV-2 Nucleocapsid (clone B46F, catno MA1-7404,

and E16C, catno. MA1-7403) were validated on formaldehyde-fixed and paraffin-embedded

SARS-CoV-2 and mock-infected Vero E6 cells(*10*), as well as lung tissue sections of human

SARS-CoV-2 patients. The clone E16C was superior to B46F and was further used in this study.

Antigen retrieval took place with cell conditioning 1 (CC1 , Ventana Medical Systems) (pH 8,5)

for 24 minutes at 100°C, 1/5.000 diluted. Thereafter, incubation took place with the primary

antibody for 48 minutes at 36°C followed by standard Optiview detection/visualization with DAB

and Copper. After immunohistochemical staining, the sections were dehydrated with grades of

 ethanol and cleared with xylene. All sections were mounted with TissueTek® coverslipping film

 (Sakura Finetek Europe B.V., Alphen aan den Rijn, The Netherlands).

628 Table S1: Quantitative PET-CT analysis of the macaque brains

The standardized uptake values (SUVs) of animals C1 and C2 are represented together with the

SUVs of six non-infected control rhesus macaques. Of these animals the average and peak uptake

are determined for the pituitary gland, and the brain minus the pituitary gland. By dividing these

the pituitary gland/brain ratio is calculated. For the SUVmean values above 1.0 are defined as

slightly increased (light grey) and increased (dark grey) when equal or above 1.5. For the SUVpeak

values above 1.0 are demarcated as slightly increased and above 1.2 as increased.

C1	**SUVmean**					**SUVpeak**				
Tissue/day	*D8/10*	*D16/17*	*D22/23*	*D28/29*	*D35/36*	*D8/10*	*D16/17*	*D22/23*	*D28/29*	*D35/36*
Pituitary gland	3.1	2.5	2.5	3.5	3.9	5.3	3.9	4.1	6.1	6.4
Brain	2.2	1.9	2.4	1.9	2.6	5.0	4.6	4.7	4.6	4.6
Ratio	1.4	1.3	1.0	1.9	1.5	1.1	0.8	0.9	1.3	1.4
C2	**SUVmean**					**SUVpeak**				
Tissue/day	*D8/10*	*D16/17*	*D22/23*	*D28/29*	*D35/36*	*D8/10*	*D16/17*	*D22/23*	*D28/29*	*D35/36*
Pituitary gland	3.1	2.6	2.7	3.8	3.2	7.1	6.3	4.5	6.5	6.1
Brain	2.0	1.8	2.1	2.2	2.1	5.1	3.6	3.8	5.0	3.8
Ratio	1.5	1.5	1.3	1.7	1.5	1.4	1.8	1.2	1.3	1.6

Controls	SUVmean						SUVpeak					
Tissue/ animal	*NHP1*	*NHP2*	*NHP3*	*NHP4*	*NHP5*	*NHP6*	*NHP1*	*NHP2*	*NHP3*	*NHP4*	*NHP5*	*NHP6*
Pituitary gland	2.3	2.6	2.1	2.7	1.3	1.3	3.3	3.7	2.9	3.9	1.9	1.6
Brain	2.3	2.0	1.9	1.9	1.5	1.8	5.6	6.1	4.9	3.9	3.7	3.5
Ratio	1.0	1.3	1.1	1.4	0.9	0.7	0.6	0.6	0.6	1.0	0.5	0.5

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