Dysregulated neuroimmune interactions and sustained type I interferon signaling after human immunodeficiency virus type 1 infection of human iPSC derived microglia and cerebral organoids

Andrew J. Boreland[1,2], Alessandro C. Stillitano[1], Hsin-Ching Lin[1], Yara Abbo[1], Ronald P. Hart[3], Peng Jiang[3], Zhiping P. Pang[1,2*], Arnold B. Rabson[1,4*]

[1] Child Health Institute of New Jersey, Rutgers Robert Wood Johnson Medical School, New Brunswick, NJ

[2] Department of Neuroscience, Rutgers Robert Wood Johnson Medical School, New Brunswick, NJ

[3] Department of Cell Biology and Neuroscience, Rutgers University, Piscataway, NJ

[4] Departments of Pharmacology, Pathology & Laboratory Medicine, and Pediatrics, Rutgers Robert Wood Johnson Medical School, New Brunswick, NJ

*Correspondence: zhiping.pang@rutgers.edu and rabsonab@rwjms.rutgers.edu

Highlights of the work:

• HIV-1 productively infects iPSC-derived microglia and triggers inflammatory activation.

• HIV-1 infection of microglia results in sustained type I interferon signaling.

• Microglia infected by HIV-1 incorporate into sliced neocortical organoids with persistent

type I interferon signaling and disease risk gene expression.

ABSTRACT

Human immunodeficiency virus type-1 (HIV-1) associated neurocognitive disorder (HAND)

affects up to half of HIV-1 positive patients with long term neurological consequences, including

dementia. There are no effective therapeutics for HAND because the pathophysiology of HIV-1

induced glial and neuronal functional deficits in humans remains enigmatic. To bridge this

knowledge gap, we established a model simulating HIV-1 infection in the central nervous

system using human induced pluripotent stem cell (iPSC) derived microglia combined with

sliced neocortical organoids. Upon incubation with two replication-competent macrophage-tropic

HIV-1 strains (JRFL and YU2), we observed that microglia not only became productively

infected but also exhibited inflammatory activation. RNA sequencing revealed a significant and

sustained activation of type I interferon signaling pathways. Incorporating microglia into sliced

neocortical organoids extended the effects of aberrant type I interferon signaling in a human

neural context. Collectively, our results illuminate the role of persistent type I interferon signaling

in HIV-1 infected microglial in a human neural model, suggesting its potential significance in the

pathogenesis of HAND.

INTRODUCTION

The global burden of human immunodeficiency virus-1 (HIV-1) infection remains profound, with neurocognitive complications manifesting in a significant proportion of infected individuals despite the remarkable success of combined antiretroviral therapy (cART) in reducing morbidity and mortality. Up to 55% of HIV-1 positive people experience neurological complications that may develop into HIV associated neurocognitive disorder (HAND) (Simioni et al. 2010; Sacktor et al. 2016; Eggers et al. 2017; Sacktor 2018). This debilitating disorder manifests across a spectrum of cognitive, motor, affective, and behavioral impairments, which can severely impact the quality of life for affected individuals, emphasizing an urgent need for a better understanding of its underlying mechanisms (Lew et al. 2018; Israel et al. 2019). The etiology and neuropathogenesis of HAND remain enigmatic, as there has been no evidence of neuronal HIV-1 infection. Decades of research suggest that HAND development is caused by a combination of both direct and indirect effects involving viral proteins, inflammatory cytokines and chemokines, and dysregulated neuroimmune interactions (Koenig et al. 1986; Gendelman et al. 1994; Rappaport et al. 1999; González-Scarano and Martín-García 2005; Kraft-Terry, Buch, Fox, and Gendelman 2009; Lindl, Marks, Kolson, and Jordan-Sciutto 2010; Burdo, Lackner, and Williams 2013; Alvarez-Carbonell et al. 2020). Interestingly, clinical symptoms of HAND correlate more closely with cytokine production, neuronal pathology, decreased synaptic density, and increased microglia than with central nervous system (CNS) viral load (Kaul, Garden, and Lipton 2001; Kaul et al. 2005). Currently there is a lack of mechanistic understanding due to a need for better experimental models that can address these questions, especially regarding neuroimmune interactions.

A pivotal component of neuroimmune interactions is the innate immune response, including the production and signaling of interferons, which have recently been implicated in the neuropathology of various neurological diseases [Reviewed in (Hofer and Campbell 2013; McGlasson, Jury, Jackson, and Hunt 2015)]. Interferons and their downstream signaling through

interferon stimulated genes (ISGs) are primarily an innate immune response to viral infection

[reviewed in (Platanias 2005)]. However, recent literature suggests a role for dysregulated type I

interferon signaling in neurological diseases such as Alzheimer's disease (Roy et al. 2020; Roy

et al. 2022), COVID-19 related brain fog (Lee and Shin 2020; Phetsouphanh et al. 2022), aging

associated dementia (Baruch et al. 2014), and HIV associated dementia (Rho et al. 1995;

Krivine et al. 1999; Perrella et al. 2001; Anderson et al. 2017; Solomon et al. 2020). Clinically,

type I interferons have been shown to be a driver of cognitive impairment both in diseased

states and when administered exogenously (Merimsky, Reider-Groswasser, Inbar, and

Chaitchik 1990). Indeed, many studies using interferon treatment for various severe cancers

and chronic viral hepatitis C have reported that patients receiving interferon-alpha displayed

cognitive, mood, and behavioral deficits that arose and worsened with prolonged, multiweek

treatment regimens (Christina, Randall, and Arthur 1991; Pavol et al. 1995; Capuron, Ravaud,

and Dantzer 2001; Capuron et al. 2002; Wichers et al. 2005; Raison, Demetrashvili, Capuron,

and Miller 2005). Taken together, these studies indicate a role for aberrant type I interferon

signaling in compromising neuronal and glial function, leading to cognitive deficits and

degeneration.

Microglia, as the resident immune cells of the CNS and the primary CNS target and

reservoir of HIV-1 infection (Tang et al. 2023), contribute significantly to the pathophysiology of

HAND, largely through their secretory and functional dysregulation. Under homeostatic

conditions, microglia play important roles in synaptic pruning, phagocytic functions, immune

surveillance, and extracellular matrix remodeling (Paolicelli et al. 2011; Casano and Peri 2015).

When challenged, microglial activation can be either neurotoxic, producing proinflammatory

cytokines and chemokines, or neurotrophic, producing anti-inflammatory cytokines (Durafourt et

al. 2012). Microglia exhibit a heterogeneous spectrum of activation and disease-associated

states with unique properties and consequences on neuronal functions (Gosselin et al. 2017;

Song and Colonna 2018; Hammond et al. 2019).

Since HIV-1 specifically infects humans, the ability of traditional animal model organisms

to replicate the complex disease processes of HAND is inherently limited. HIV-1-Simian

immunodeficiency virus chimeras (SHIVs) have been studied in monkey models. However,

these models are limited in their availability and utility for molecular analyses [reviewed in

(Byrnes et al. 2022; Moretti et al. 2021)]. Recent advances in stem cell technologies have

opened up new possibilities for modeling and studying HAND, particularly the development of

human iPSC derived neurons, astrocytes, and microglia capable of mimicking complex in vivo

neuroimmune interactions when grown in three dimensional cerebral organoid cultures (Abud et

al. 2017; Ormel et al. 2018; Xu et al. 2021). Cerebral organoids offer a powerful and

physiologically relevant platform to study complex neuroimmune interactions, but traditional

organoid differentiation protocols do not produce microglia [reviewed in(Dos Reis, Sant, and

Ayyavoo 2023; Swingler et al. 2023; Wei et al. 2023)]. Recent studies have demonstrated the

feasibility of infecting iPSC-derived macrophages (Vaughan-Jackson et al. 2021) and microglia

(Rai et al. 2020) with HIV-1. Moreover, these infected microglia have been effectively cocultured

in various model systems, including human stem cell derived neural tricultures (Alvarez-

Carbonell et al. 2020; Ryan et al. 2020), primary neuron progenitor cell derived organoids (dos

Reis et al. 2020), iPSC-derived cerebral organoids (Gumbs et al. 2022), and a humanized

mouse model (Min et al. 2023).

In this study, we hypothesized that by infecting iPSC-derived microglia with replication

competent HIV-1 and integrating them into sliced neocortical organoids, we could recapitulate

neuroimmune dysregulation related to HAND pathology. We demonstrate that HIV-1 infection of

iPSC-derived microglia leads to persistent activation of type I interferon signaling and microglial

activation in both microglial monocultures and in the context of cerebral organoids.

RESULTS

Human microglia are efficiently generated from iPSCs

To induce microglial differentiation, we used three iPSC lines and employed previous protocols (Haenseler et al. 2017; Xu et al. 2021). To mimic in vivo microglial development from the yolk sac, iPSC embryoid bodies were patterned toward a mesodermal yolk sac lineage that generates primitive macrophage precursors (PMPs) after 3 weeks of culture (**Figure 1A**). The identity of the PMPs was confirmed by immunocytochemistry against CD235, a marker for yolk sac (Claes, Van den Daele, and Verfaillie 2018), and CD43, a marker for hematopoietic progenitor like cells (Vodyanik, Thomson, and Slukvin 2006) (**Figure 1B**). Upon further maturation under the influence of a colony stimulating factor 1 receptor (CSF1R) antagonist, interleukin 34 (IL-34), and granulocyte maturation factor (GM-CSF), PMPs exhibit a more pronounced microglial phenotype. This was evidenced by a significant increase in mRNA expression of the microglial markers ionized calcium binding molecule 1 (IBA1) and purinergic receptor P2Y12 across all three cell lines (**Figure 1C,** biological replicates of each cell line shown in **Figure S1**). Supporting these gene expression results, we noted robust immunocytochemical staining of the microglial markers IBA1, P2Y12, CX3CR1, transmembrane protein 119 (TMEM119), and transcription factor PU.1 in maturing microglia from these same lines (**Figure 1D**). Upon coculture of microglia with iPSC-derived neurons (Xu et al. 2021), we found that microglia display a more elaborate morphology (**Figure 1E**). Furthermore, costaining with the neuronal dendritic marker microtubule-associated protein 2 (MAP2) and the presynaptic marker synapsin 1 (SYN1) revealed that microglial processes interact with dendrites and colocalize with synaptic puncta, indicating putative microglia-synapse interactions (**Figure 1F**).

Given the tropism of HIV-1 for CD4 receptor expressing cells and the requirement of CCR5 coreceptor expression for infection of monocyte/macrophage related cell lineages, we assessed the gene expression of *CD4* and *CCR5* in iPSC-derived microglia. Results showed significantly increased mRNA expression of *CD4* and *CCR5* in microglia differentiated from all

three iPSC lines (**Figure 1G,** biological replicates of each cell line shown in **Figure S1**). These

results demonstrate that microglia can be successfully and reproducibly generated from iPSCs.

Crucially, these cells express appropriate markers for microglial identity and infection by HIV-1.

iPSC derived microglia are productively infected by HIV-1 and exhibit inflammatory

activation

Having confirmed the generation and maturation of iPSC-derived microglia, we next determined

whether these cells could sustain a productive infection by replication competent, macrophage

tropic HIV-1. To this end, we incubated male 03SF iPSC-derived microglia with JRFL HIV (2

ng/ml), an R5 tropic HIV-1 strain isolated from the cerebral spinal fluid (CSF) of a patient with

severe HAND (Koyanagi et al. 1987; Merrill et al. 1992). Compared to uninfected controls, HIV-

1-infected microglia robustly expressed HIV-1 *gag/pol* RNA within 6-9 days after infection (Yu et

al. 1996) (**Figure 2A**). As a key indicator of productive HIV-1 infection, the production of

secreted p24 was measured (Chargelegue and O'Toole 1992; Marodon, Warren, Filomio, and

Posnett 1999). Using ELISA to detect secreted p24 in the culture supernatant, we observed

increased protein production starting 1 week post infection, peaking around day 16, and then

maintaining consistent levels for more than 2 weeks (**Figure 2B**). Finally, we found that after

just 4 days post infection, circular polymerase chain reaction (PCR) products from both long

terminal repeats (LTR) were detected in HIV-1 incubated cultures indicating the presence of

active viral replication (Butler, Hansen, and Bushman 2001) (**Figure S2**).

After establishing the infectability of iPSC microglia with HIV-1 JRFL, we then asked

whether HIV-1 infection elicits differential expression of inflammatory and canonical microglial

mRNAs using reverse transcription□quantitative PCR (RT-qPCR). In this second experiment

found we found HIV-1 infection augmented the expression of the inflammation-associated

genes interleukin 1ß (IL1ß, on day 16) and tumor necrosis factor alpha (TNFα), while the

expression of interleukin 6 (IL6) displayed no change (**Figure 2C**). We then examined the

mRNA expression of the chemokines CCL2 (monocyte chemoattractant protein 1, MCP-1),

CCL3 (macrophage inflammatory protein 1 alpha, MIP-1), and CCL5 (RANTES). These three

chemokines play important roles in immune cell recruitment and migration to sites of

inflammation and infection and have been found to be elevated in cognitively impaired

individuals with HIV-1 (Letendre, Lanier, and McCutchan 1999). A significant elevation in the

mRNA expression of CCL2 and CCL3 was observed by day 16 post-infection, whereas the

expression of CCL5 remained unchanged (**Figure 2D**). To assess whether microglial identity

was altered by HIV-1 infection, we assessed the mRNA expression of the canonical microglial

genes IBA1 and P2Y12. While IBA1 remained stable, P2Y12 exhibited significantly increased

expression by day 23 post infection (**Figure 2E**). Next, we asked how HIV-1 infection might alter

microglial chemokine and cytokine production. Although the levels of most cytokines were below

the detection threshold (**Table S1**), we noted a significant surge in the secretion of chemokines

M-CSF and interferon inducible protein 10 (IP-10/CXCL10) following HIV-1 infection in the same

supernatant used in figure 2B (**Figure 2F**). Finally, to visualize HIV-1 infected cells, we detected

HIV-1 p24 protein using a biotin-streptavidin amplification protocol (Eugenin and Berman 2016).

On day 13 post infection with JRFL, p24 positive microglia were found (**Figure 2G**). Collectively,

our findings suggest that iPSC-derived microglia can sustain an R5 tropic HIV-1 infection and

exhibit an inflammatory activation profile consistent with previous studies.

To confirm that HIV-1 JRFL infection of human iPSC-derived microglia resulted in

productive infection and inflammatory activation, we chose a female iPSC line, CD06, and

infected it with the JRFL strain as well as a second R5 tropic HIV-1 strain, YU2 (Li et al. 1991),

isolated from the CSF of a different patient with severe HAND. We confirmed infection by RT-

qPCR of viral *gag-pol* RNA, which exhibited significantly increased expression for both strains

by day 16 post-infection, with a subsequent decrease (**Figure 3A**). Using ELISA to detect

secreted p24 revealed productive infection for both viral strains (**Figure 3B**). We then assessed

the expression of key inflammatory markers and microglial core mRNAs by qPCR. Both JRFL

and YU2 infections led to a significant increase in IL1β expression compared to uninfected

microglia (**Figure 3C**). Similarly, TNFα was significantly upregulated in the first two weeks of

infection but decreased as the productive infection waned (**Figure 3C**). We also observed

increased expression of the chemokines CCL2 and CCL3 by days 16 and 23 post infection with

both strains (**Figure 3D**). This upregulation then decreased by day 27, correlating with the

reduction of productive infection as indicated by the p24 ELISA (**Figure 3A**). In comparison to

the unaltered IBA1 expression we found previously, HIV-1 led to a significant reduction in IBA1

expression in CD06 infected microglia (**Figure 3E**). Similar to 03SF infected microglia, CD06

had significant increased expression of P2RY12 (**Figure 3E**). Together, these results

demonstrate infectability of human iPSC-derived microglia with multiple, macrophage tropic

HIV-1 strains and their ability to elicit an inflammatory response.

Type I interferon stimulated gene expression and sustained activation following HIV-1

infection

To investigate the transcriptional landscape of HIV-1 infected microglia, we performed bulk RNA

sequencing on male 03SF iPSC-derived microglia infected by HIV-1 JRFL day 16 post infection.

Principal component analysis (PCA) revealed clear separation of the infected vs mock infected

samples (**Figure S2**). Differential gene analysis revealed differentially expressed genes (DEGs)

including several classic ISGs, such as IFIT3, MX2, ISG15, RSAD2 and others (**Figure 4A**)

(**Table S2**). Gene set enrichment analysis (GSEA) confirmed a significant enrichment of genes

related to the interferon alpha response (**Table S3**) (**Figure 4B**). Gene ontology analysis

identified activation of innate immune responses and several related terms in the biological

process component (**Figure 4C, D** and **Figure S3**). The upregulated DEG GO set includes

pathways falling into the overall signaling clusters related to interferon signaling and positive

regulation of antiviral biotic, interferon alpha/beta, defense against virus, cytokine mediated and

interferon mediated pathways, and negative regulation of viral processes. Among the

downregulated DEG GO clusters are pathways related to positive regulation of antigen

processing, extracellular organization, granulocyte/leukocyte migration, chemokine-mediated

signaling, and spindle assembly checkpoints. Importantly, HIV-1 infection was found to lead to

significant induction of many ISGs, including ISG15, IRF7, MX1, OAS1, OAS2, OAS3, STAT1,

CXCL10, and IFITM3 (**Figure 4A, E**). **Figure 4F** shows the expression of various genes

encoding SIGLEC proteins that are responsible for regulating microglial cell☐cell interactions

[Reviewed in (Crocker, Paulson, and Varki 2007)]. Consistent with previous studies, we found

that HIV-1 infection causes significant upregulation of SIGLEC1, which has been implicated in

the direct cell☐cell transmission of HIV (Izquierdo-Useros et al. 2012; Zou et al. 2011).

However, we found that SIGLEC11 and SIGLEC16 were significantly downregulated after

infection.

We then validated the expression of a subset of the ISGs identified in the sequencing

dataset by RT-qPCR of JRFL infected 03SF iPSC-derived microglia. We found significant

upregulation of CXCL10, RSAD2, ISG15, and IDO1 (**Figure 4G**). Elevated expression of these

genes persisted over an additional week of infection on day 23 (**Figure 4G**). Additionally, we

performed RT-qPCR on CD06 iPSC-derived microglia infected with either JRFL or YU2 HIV

strains. We also found increased expression of CXCL10 and RSAD2 in these HIV-infected cells;

however, only the day 16 YU2 condition reached significance (**Figure 4H**). Comparison of

Figure 4G and 4H indicates potential differences with infecting different cell lines. Together,

these data support the conclusion that HIV-1 infection induces sustained type I interferon

signaling in iPSC-derived microglia and alters the gene regulation of many microglial biological

processes including interferon signaling.

HIV-1 infected microglia incorporate into cerebral organoids

After characterizing the response of isolated human iPSC-derived microglia to HIV-1 infection

we then investigated whether HIV-1 infected microglia could incorporate into iPSC-derived

cerebral organoids and whether interferon signaling was similarly upregulated in microglia and

potentially other neural cell types. Cerebral organoids were grown using modified, published

protocols (Lancaster and Knoblich 2014; Paşca et al. 2015; Sloan et al. 2018; Yoon et al. 2019;

Qian et al. 2020; Xu et al. 2021). To create microglia-containing organoids, we cocultured

human microglia with sliced neocortical organoids (SNO), prepared as described previously

(Qian et al. 2020). SNOs exhibit enhanced neurogenesis and laminar expansion (Qian et al.

2020). We found that microglia exhibit the ability to incorporate with organoid slices to form

human microglia containing sliced neocortical organoids (mSNOs). **Figure 5A** shows mSNO

containing neurons (MAP2$^+$), astrocytes (GFAP$^+$), and microglia (IBA1$^+$). These neuroimmune

organoids provide a model system for studying the impact of HIV-1 infection on the physiology,

localization, and interactions of these three cell types.

To create an HIV-1 infected human cerebral organoid, we infected 03SF iPSC-derived

microglia with JRFL HIV. Following 2 weeks in culture, infected or noninfected microglia were

added to 400 µM organoid slices and cultured for 2 additional weeks. On day 14 post coculture

with microglia, mSNOs were fixed for immunohistochemistry or total RNA was extracted for RT-

qPCR analysis. HIV-1-infected microglia (p24$^+$, IBA1$^+$) were detected in a mSNO (**Figure**

5B&C). Interestingly, neurons (MAP2$^+$) appeared to be sparser in regions of HIV-1-infected

microglia (**Figure 5B** "arrows"). These regions had scattered MAP2$^+$ processes (**Figure 5B1**)

compared with the denser MAP2 staining throughout the bulk of the organoid. HIV-1 *gag/pol*

RNA exhibited significant expression in mSNOs containing HIV-1 infected microglia (**Figure**

5D). To provide evidence of productive infection in mSNOs, we identified secreted p24 only in

the media of organoid cultures that had received HIV-1 infected microglia (**Figure 5E**).

Because we observed significant and sustained interferon signaling in microglial

monocultures, we evaluated mRNA expression of a panel of ISGs (ISG15, RSAD2, IFITM3,

MX1, IFI44, IFI27). We found that ISG15 mRNA was significantly upregulated and RSAD2 also

showed an increasing trend of expression in mSNOs containing HIV-1 infected microglia

(**Figure 5F**). IFITM3 has been touted as a marker for interferon-responsive microglia and has

been shown to play a newly discovered role in amyloid precursor protein processing to amyloid

beta (Hur et al. 2020). Interestingly, we found significant upregulation of IFITM3 mRNA in

mSNOs containing HIV-1 infected microglia (**Figure 5F**). We also evaluated the expression of

MX1, IFI27, and IFI44, which, along with ISG15 and RSAD2, were among the top 10

persistently upregulated genes in a recent study on two cohorts of 22 HIV-1 seroconverts from

Uganda and 22 from South Africa (Mackelprang et al. 2023). Expression of MX1, IFI27, and

IFI44 appeared to be increased but failed to reach significance. Especially considering the small

fraction of HIV-1 infected microglia in the cultured mSNO (**Figure 5B**), these increases suggest

that HIV-1 infected microglia are associated with increased interferon signaling in the organoids

and may have indirect consequences for neuronal viability and inflammatory responses in other

cell types.

DISCUSSION:

In this study, we used iPSC-derived human microglia and microglia containing cortical

organoids to model HIV-1 related neuroimmune dysregulation and pathology. In this model,

iPSC-derived microglia were shown to be infected with two strains of replication competent HIV-

1, JRFL and YU2, and exhibited inflammatory activation, as shown by gene expression changes

and cytokine/chemokine secretion (**Figures 2 & 3**). Importantly, we found persistent activation

of type I interferon response pathways and downstream interferon stimulated genes (ISGs),

which may have important implications for understanding the pathogenesis of HAND.

In comparison to the recently developed primary human neural progenitor cell-derived

organoid HIV-1 model (dos Reis et al. 2020) and the 2D neuron, astrocyte, and microglia

"triculture" HIV-1 model (Ryan et al. 2020), an iPSC-derived human microglia containing sliced

neocortical organoid model has distinct advantages. Organoids recapitulate 3D cell-cell and

cell-matrix interactions more faithfully than 2D cultures and develop complex tissue architecture

(Lancaster et al. 2013; Paşca et al. 2015; Birey et al. 2017; Quadrato et al. 2017; Velasco et al.

2019); thus, organoids are well suited to studying aspects of altered brain anatomy and

physiology seen in individuals with *HAND* (Di Sclafani et al. 1997; Clifford et al. 2017; Israel et

al. 2019). While others have also generated microglia containing organoids using a protocol in

which microglia innately develop within organoids, this system is associated with a high degree

of heterogeneous cell types (Gumbs et al. 2022), which could make dissection of the relative

contributions and effects on specific cell types more complex. In our method, we have greater

freedom to manipulate the timing, proportion, and infection stage of microglia addition in sliced

neocortical organoids. While some previous studies used pseudotyped virus (dos Reis et al.

2020), our study examined infection using two macrophage tropic, replication competent strains

of HIV-1. Our findings, showing induction of inflammatory gene expression associated with

active viral expression align with recent studies on brain samples from HIV-1^{+} patients from the

National NeuroAIDS Tissue Consortium (NNTC). In that study, HIV-1 RNA load was found to

correlate with increased interferon signaling and inflammatory gene sets while inversely

correlating with neuronal and synaptic gene sets, suggesting neuronal pathology (Sanna et al.

2021).

Microglia secrete diverse cytokines and chemokines implicated in HIV-1 neuropathology

(Hanisch 2002; Ramesh, MacLean, and Philipp 2013; Chen et al. 2017). Cytokine/chemokine

analysis of the supernatant of HIV-1 infected microglia identified the secretion of M-CSF and IP-

10/CXCL10 (**Figure 2F**). M-CSF overexpression has been linked to microglial proliferation,

increased phagocytosis, cytokine secretion, and inflammatory responses in both Alzheimer's

disease (AD) and HAND, as well as increased microglial susceptibility to HIV-1 infection and

increased virus replication (Gallo et al. 1990; Kalter et al. 1991; Kutza et al. 2000; Mitrasinovic

et al. 2001; Kutza, Fields, Grimm, and Clouse 2002; Smith et al. 2013). IP-10/CXCL10 is a

chemotactic chemokine that recruits leukocytes, T cells, and monocytes while also being neurotoxic and strongly correlated with HIV-1 related disease progression (van Marle et al. 2004; Jiao et al. 2012; Lei, Yin, Shang, and Jiang 2019). Clinical studies have shown elevated IP-10/CXCL10 levels (~200-1000 pg/ml) in the cerebral spinal fluid of HIV-1^{+} individuals (Kolb et al. 1999; Peluso et al. 2017); these levels are strikingly similar to our observations (**Figure 2F**). CXCL10/IP-10 has been shown to be induced by HIV-1 proteins gp120, Nef, and Tat (Kutsch, Oh, Nath, and Benveniste 2000; Asensio et al. 2001; van Marle et al. 2004; Lei, Yin, Shang, and Jiang 2019). Importantly, IP-10/CXCL10 and RANTES (CCL5) were the strongest predictors of neurocognitive impairment in a screen of 139 HIV-1^{+} individuals (Ruhanya et al. 2021), similar to findings from earlier studies (Valverde-Villegas et al. 2018; Burlacu et al. 2020). HIV-1 brain infection leads to an abnormal inflammatory state and dysregulated cytokine/chemokine production (Kaul, Garden, and Lipton 2001; González-Scarano and Martín-García 2005; Burdo, Lackner, and Williams 2013). Despite this knowledge, there remains a large gap in our understanding of how CXCL10 and other cytokines/chemokines associated with CNS HIV-1 infection alter aspects of neuronal excitability, synaptic transmission, and inward and outward currents vital to healthy neuronal physiology.

A striking finding in our study was the persistent activation of interferon response genes. Induction of these pathways is known to be a hallmark of HIV-1 infection in monocytes and macrophages, much more prominently than in T cells (Berg et al. 2014; Aso, Ito, Koyanagi, and Sato 2019; Elsner et al. 2020; Jeremiah et al. 2023). Thus, it is not surprising to have seen this strong response in microglia, which share many physiologic properties with macrophages [reviewed in (Li and Barres 2018)]. Most studies suggest that the interferon response is relatively transient; thus, the persistent expression of at least a subset of ISGs may be a relatively unique feature of microglial HIV-1 infection that may have important pathophysiologic consequences. Increasing evidence suggests a role for type I interferons in cognitive-related deficits seen in patients with various neurodegenerative diseases. Using single-cell sequencing,

researchers have dissected a unique sub-population of interferon-responsive microglia that may

potentiate dysregulated immune interactions in the form of aberrant pruning of synapses,

altered phagocytic function, and dysregulated cytokine/chemokine production (Jin et al. 2022).

Constitutive overexpression of type I interferons seen in the "interferonopathies" can be

associated with profound CNS disease [reviewed in (Goldmann, Blank, and Prinz 2016), and

(Blank and Prinz 2017)](Wiley, Steinman, and Wang 2023). Patients receiving type I interferons

therapeutically may experience cognitive impairment and neurological symptoms (Christina,

Randall, and Arthur 1991; Pavol et al. 1995; Capuron, Ravaud, and Dantzer 2001; Capuron et

al. 2002; Wichers et al. 2005; Raison, Demetrashvili, Capuron, and Miller 2005).

Whether interferon induction inhibits or enhances HIV infection and latency in microglia

remains to be understood. Recent studies have highlighted that interferon can inhibit HIV

infection of primary microglia but less so of iPSC-derived microglia, as well as macrophages

(Nasr et al. 2017; Woodburn et al. 2022). Interestingly, interferon may promote latency in

macrophages (Dickey, Martins, Planelles, and Hanley 2022). An important feature of HIV

infection of microglia identified in previous in vitro studies has been the rapid induction of viral

latency (Alvarez-Carbonell et al. 2019; Sreeram et al. 2022). Our cerebral organoid model will

provide an interesting system to examine the induction of HIV latency, its reactivation, and its

effects on both adjacent and more distant neural cells.

An important future direction, facilitated by the development of this model system, will be

experiments aimed at understanding the functional consequences that HIV infection,

dysregulated interferon signaling, inflammatory activity, and changes in other important genes

expressed in the CNS, may have on neuronal synaptic transmission. A number of ISGs have

predicted downstream effects that could trigger or enhance neurodegeneration. For example,

indoleamine 2,3-dioxygenase 1 (IDO) is a key enzyme in tryptophan catabolism, leading to the

formation of kynurenic acid, an antagonist of NMDA receptors (Schwarcz and Stone 2017). This

pathway and its products, such as the neurotoxin and NMDAR antagonist quinolinic acid, have

been previously implicated in neurodegenerative diseases, including Huntington's, Alzheimer's

and Parkinson's disease (Malpass 2011; Maddison and Giorgini 2015).

Overall, the HIV-1 mSNO model presents an effective in vitro platform for investigating

the underlying molecular and cellular mechanisms associated with HIV-1 and human neural cell

interactions. **Our results predict that interferon stimulated genes likely play a role in**

altering neuronal function and contributing to HAND.

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AUTHOR CONTRIBUTIONS

AJB, ZPP, PJ, RPH, and ABR conceived the study. AJB designed the experiments and

interpreted the data. AJB performed most of the experiments with technical assistance from

ACS, HL, and YA. ACS and AJB performed qPCR. HL and AJB performed ELISA. AJB

performed immunocytochemistry, immunohistochemistry, and confocal imaging. AJB and HS

performed viral infections. RPH and AJB performed computational analysis of RNA-seq data.

AJB prepared the figures and wrote the manuscript with input from all coauthors.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

METHODS

Human induced pluripotent stem cell maintenance

Three human iPSC lines were used in this study (male 03SF iPSC line; female CD06 iPSC line;

male CD52 iPSC line). Human iPSCs were cultured in stem cell medium consisting of MACs

iPS-Brew XF complete media. The culture medium was changed daily. Human iPSCs were

passaged one to two times per week onto new plates coated with Matrigel. Human iPSCs were

detached with Accutase treatment for 5 min and centrifuged at 120 rcf for 5 min. The pellet was

resuspended in stem cell medium plus Y-27632 (10 µM). The iPSCs used in this study were

below passage 50. All studies were performed with protocols approved by Rutgers University.

Generation of microglia

Primitive microglia precursors (PMPs) were generated from 3 iPSC cell lines using a previously

established protocol (Haenseler et al. 2017). iPSCs were detached with Accutase, plated at

20,000 cells per well in a 96-well low-adherence plate in yolk sac induction medium plus the

rock inhibitor Y-27632 (10 µM), and centrifuged at 1000 rpm for 3 min to aggregate the cells for

embryoid body formation. Yolk-sac induction medium consisted of MAC iPS-Brew XF complete

media plus bone morphogenetic protein 4 (BMP4, 50 ng/ml), vascular endothelial growth factor

(VEGF, 50 ng/ml), stem cell factor (SCF, 20 ng/ml), and ß-mercaptoethanol. Yolk-sac induction

media was given for the first 5 days of culture. On day 6, YS-EBs were plated in 100 mm cell

culture plates in factory media consisting of XVIVO15 supplemented with 0.5% NEAA, ß-

mercaptoethanol, macrophage colony stimulating factor (M-CSF, 100 ng/ml) and interleukin-3

(25 ng/ml). At 2-4 weeks after plating, human PMPs egress from the yolk sac lumen into the

surrounding media and are continuously produced for more than 3 months.

To mature PMPs into microglia, PMPs were transitioned to maturation media composed

of XVIVO15 supplemented with N2, Glutamax, 0.5% NEAA, interleukin-34 (IL-34, 100 ng/ml),

granulocyte macrophage colony stimulating factor (GM-CSF, 10 ng/ml, and M-CSF (25 ng/ml)

for 1-2 weeks. The medium was changed every 4 days. Cells were then detached with 20 min

Accutase treatment and used for experiments.

Generation of iPSC-derived Cerebral Organoids

Cerebral organoids were generated from 1 iPSC line using adapted previously published

protocols (Qian et al. 2020). In this study, 9,000 iPSCs were cultured in low-adherence 96-well

plates to form uniform embryoid bodies. On day 1, the medium was changed to neural induction

medium composed of DMEM/F12 supplemented with 1X N2, 2 μM A83-01, and 2 μM

dorsomorphin. On days 5 and 6, half of the medium was replaced with DMEM/F12

supplemented with 1X N2, 10 μM SB431542, and 1 μM CHIR99021. On day 7, EBs were

embedded in a Growth-Factor-Reduced Matrigel 'cookie' as previously described (Qian et al.

2020). Half of the medium was changed every two days until day 14. On day 14, organoids

were dissociated from the Matrigel cookie and placed in low-adherence 6-well plates on an

orbital shaker at 85 rpm. On day 16, organoids were fed 1:1 DMEF12: Neurobasal, 1X N2, 1X

B27-RA, 0.5% NEAA, and 200 μM L-AA. Media was replenished every 2-3 days until day 30.

On day 30, the medium was changed to 1:1 DMEF12: Neurobasal, 1X N2, 1X B27, 0.5% NEAA,

200 μM L-AA, and.25% GFR-Matrigel. Half of the media was changed every 3-4 days.

Organoid Slicing

To create sliced neocortical organoid cultures, cerebral organoids were sectioned with a

vibratome and transferred back into in vitro cell culture. Briefly, a fresh stock of 3% low-melting

temperature agarose in PBS was prepared and kept at 39°C to remain liquid. Artificial cerebral

spinal fluid (ACSF) for sectioning contained (in mM): NaCl 125, KCl 2.5, $NaH_2PO_4 \cdot H_2O$ 1.25,

$NaHCO_3$ 25, $MgCl_2$ 1.2, $CaCl_2$ 2.5, glucose ($C_6H_{12}O_6$) 2.5, and sucrose ($C_{12}H_{22}O_{11}$) 22.5. The

ACSF was then bubbled with 5% CO_2/95% O_2 for 10 minutes before bivalent cations (in mM):

MgCl$_2$ 1.2, CaCl$_2$ 0.625. The solution was then filtered through a 0.2-micron PES filter and

returned to bubbling on ice. Cerebral organoids were then transferred to 37°C DMEF12, 200 μM

L-AA, and 55 μM beta-mercaptoethanol before being embedded in 3% low-melting temperature

agarose. The agarose block containing organoids was then sectioned at 400 μM thickness.

Slices were then subjected to two washing processes in Primocin-treated media to reduce the

chance of contamination.

HIV-1 Stock Preparation

HIV-1 JRFL virus (ARP-395) and HIV-1 YU2 proviral DNA (ARP-1350) were obtained through

the NIH HIV Reagent Program, Division of AIDS, NIAID. HIV-1 JRFL was propagated in

phytohemagglutinin (PHA, 5 μg/ml)-stimulated human peripheral blood mononuclear cells.

Viruses were harvested on days 7-10 post infection. HIV-1 YU2 stocks were generated by

transfection of 293T cells with HIV-1 YU2 proviral DNA. The transfected cells were cocultivated

with PHA-PBMCs 48 h after transfection, and cell supernatants were harvested 7 days after

coculture. The YU2 HIV stocks were further propagated in PHA-PBMCs as described. The

amount of viral p24 was determined using the HIV-1 Gag p24 DuoSet ELISA (R &D System,

DY7360-05).

HIV-1 infection

PMPs were matured for 1-2 weeks in microglia maturation medium. Matured PMPs were then

incubated with 2 ng/ml p24 of either JRFL strain or YU2 strain HIV-1 (NIH AIDS Repository) for

24 hours at 300,000 cells per 100 μl of media. After 24 hours, DMEF12 was added, and the

cells were centrifuged for 3 min at 120 rcf. The cells were then resuspended in microglia

maturation media minus M-CSF and plated. Half of the media was changed every 3-6 days.

HIV-1 2-LTR circles PCR

For detection of HIV 2LTR circles, total DNA (including small nongenomic DNA) was isolated

with a DNeasy Blood and Tissue kit (Qiagen 69504). End point PCR analysis (Taq 2X Master

Mix, NEB) was performed using 300 ng DNA template and 2-LTR circle primers: forward,

MH535: 5′-AACTAGGGAACCCACTGCTTAAG-3′; reverse, MH536: 5′-

TCCACAGATCAAGGATATCTTGTC-3′ (Butler, Hansen, and Bushman 2001).

Tissue preparation

Organoids were fixed in 4% PFA overnight at 4°C. Organoids were then transferred to 15%

sucrose and 0.05% sodium azide in PBS for 24 hours, followed by another 24 hours in 30%

sucrose and 0.05% sodium azide in PBS. Organoids were then embedded in OCT freezing

medium and snap frozen on an ethanol dry ice slurry. Frozen embedded organoids were given

at least 3 hours to warm to -20°C before cryosectioning on a Leica cryostat at thicknesses

between 10-30 µM. Sections were mounted on charged microscope slides (VWR) and placed

on a slide warmer at 37°C for 30 min. Slides were then stored in a slide box at -20°C until used

for staining.

Immunofluorescence

For immunocytochemistry, half of the medium was left in each well with an equal amount of 4%

PFA and then added at a final concentration of 2% PFA overnight at 4°C. The next day, PFA

was removed, and the cells were washed with PBS plus 0.3 M glycine for 30 min. The cells

were then permeabilized with 0.2% Triton X-100 in PBS for 7 min. The cells were then blocked

for 1 hour in blocking buffer consisting of 5% normal goat serum (NGS), 4% bovine serum

albumin (BSA), 0.05% Triton X-100, 0.05% sodium azide, and PBS.

For immunohistochemistry, cryosectioned organoid slides were warmed to 37°C for 5

min. A hydrophobic barrier was then drawn around the specimens and allowed to dry for 5 min.

PBS plus 0.3 M glycine was then added in a liquid dome over the specimens to rehydrate for 10

min. Sections were permeabilized with 0.5% Triton X-100, 0.3 M glycine, and PBS for 1 hr. After

permeabilization, the sections were blocked with blocking solution consisting of 5% normal goat

serum, 4% BSA, 0.05% Triton X-100, 0.05% sodium azide, and PBS for 1 hr. Primary

antibodies were diluted in blocking solution and applied to the sections overnight at 4°C. The

primary antibodies and their dilutions are summarized in the Key Resources Table. After

washing with 0.05% Triton X-100 and PBS (PBST) 5 times, secondary antibodies diluted in

blocking buffer were added for 1 hr at RT. Finally, the sections were washed five times with

PBST before a final wash in deionized water and mounting with DAPI Fluroshield (Fisher).

Secondary antibodies were Alexa Fluor 488-, 546-, 633- or 647-conjugated goat antibodies

(Invitrogen) used at a 1:500 dilution. Images were taken on a Zeiss LSM700 confocal

microscope.

RNA isolation

Total RNA was prepared with an RNeasy Plus kit (Qiagen) with preprocessing through

Qiashredder (Qiagen) and frozen at -80°C.

RT-qPCR

cDNA was generated using SuperScript VILO Master mix. RNA expression was measured

using SYBR green on a QuantStudio 3 (Agilent). Probes were generated using NCBI primer

blast and are listed in Table X. Two technical replicates were performed per sample. When a

high standard deviation between replicates occurred, replicates were rerun in triplicate. All

expression levels were normalized to GAPDH expression and represented as $2^{-(\Delta\Delta CT)}$. For null

result values where a ct was not achieved, a max ct value of 40 was used for statistical analysis.

Bulk RNA sequencing and analysis

We performed bulk RNA-sequencing analysis of iPSC-derived microglia. Total RNA was

prepared using an RNeasy kit (QIAGEN). Library construction and sequencing were performed

by Novogene. The libraries were subjected to 75 bp paired read sequencing using a

NextSeq500 Illumina sequencer. Approximately 30–36 million paired reads were generated for

each sample. Bc12Fastq software, version 1.8.4, was used to generate Fastq files. The genome

sequence was then indexed using the rsem-prepare-reference command.

Each fastq file was trimmed and checked for quality with fastp (v. 0.12.2) and then

aligned to the UCSC hg38 human genome using HISAT2 (v.2.1.0)[71,72]. Transcript counts were

extracted using the featureCounts function of the Rsubread package.

Statistics and reproducibility. All data represent the mean ± s.e.m. When only two

independent groups were compared, significance was determined by a two-tailed unpaired t test

with Welch's correction. A p value <0.05 was considered significant. The analyses were

performed in GraphPad Prism v.9. All experiments were independently performed at least three

times with similar results.

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FIGURE LEGENDS

Figure 1: Human microglia are efficiently generated from induced pluripotent stem cells

(A) Representative brightfield images showing the induction of iPSCs to mesodermal yolk sac embryoid

bodies (EB) and then to primitive microglia progenitor cells (PMPs) and microglia.

(B) Representative confocal images of PMPs expressing the yolk sac marker CD235 and the

hematopoietic progenitor cell marker CD43 in the 03SF cell line.

(C) RT-qPCR analysis of *IBA1* and *P2RY12* mRNA expression in iPSCs and iPSC-derived microglia;

n=3 cell lines (03SF, CD06, CD52); t test; data are presented as the mean ± SEM.

(D) Representative confocal images of microglia stained for the microglial markers IBA1, P2Y12,

CX3CR1, TMEM119, and PU1 and costained with DAPI; n = 3 cell lines (03SF, CD06, CD52).

(E) Representative confocal image of a microglial cell displaying ramified morphology after 4 weeks of

coculture with neurons.

(F) Representative confocal images of a 03SF cell line iPSC-derived microglial neuronal coculture

stained for neurons (MAP2), synapses (SYN1), and microglia (IBA1). (F1 and F2) Orthogonal view of

microglial (IBA1+) processes colocalized with neuronal dendrites (MAP2) and synapses (SYN1).

(G) RT-qPCR analysis of *CD4* and *CCR5* mRNA from iPSCs and microglia; n=3 cell lines (03SF,

CD06, CD52); t test; data are presented as the mean ± SEM.

Figure 2: HIV-1-infected microglia exhibit productive infection, activation, and dysregulated

cytokine/chemokine production

(A) RT-qPCR analysis of viral *gag/pol* mRNA after infection with HIV-1 JRFL in microglia monocultures;

n=3 independent infections of 03SF line iPSC-derived microglia.

(B) ELISA analysis of secreted p24 in the culture supernatant of microglia infected with HIV-1 JR-FL

reveals productive infection; n=3 independent infections of 03SF iPSC-derived microglia.

(C) RT-qPCR analysis of *IL1β, TNFα*, and *IL-6* mRNA at days 16 and 23 post infection with HIV-1

JRFL; n=3 independent infections of 03SF iPSC-derived microglia, t test; data are presented as the

mean ± SEM.

(D) RT-qPCR analysis of *CCL2, CCL3*, and *CCL5* mRNA at days 16 and 23 post infection with HIV-1

JRFL; n=3 independent infections of 03SF iPSC-derived microglia.

(E) RT-qPCR analysis of *IBA1* and *P2RY12* mRNA at days 16 and 23 post infection with HIV-1 JRFL;

n=3 independent infections of 03SF iPSC-derived microglia.

(F) Luminex cytokine/chemokine analysis of secreted M-CSF and IP-10/CXCL10 culture supernatant

from HIV-1 JRFL-infected microglia; n=3 independent infections of 03SF microglia, two-way ANOVA;

data are presented as the mean ± SEM.

(G) Representative confocal images of nucleocapsid protein p24 staining in HIV-1 JRFL-infected 03SF-

derived microglia (IBA1^{+}).

Figure 3: HIV-1-infected microglia exhibit productive infection, activation, and dysregulated

cytokine/chemokine production

(A) RT-qPCR analysis of viral *gag/pol* mRNA at days 9, 16, 23, and 30 post infection with HIV-1 JRFL

and HIV-1 YU2; n=3 independent infections of CD06 iPSC-derived microglia. t test

(B) ELISA analysis of secreted p24 in the culture supernatant of microglia infected with HIV-1 JRFL and

HIV-1 YU2 at days 9, 15, 21, and 27 reveals productive infection; n=3 independent infections of CD06

iPSC-derived microglia.

(C) RT-qPCR analysis of *IL1β* and *TNFα* mRNA at days 9, 16, 23, and 30 post infection with HIV-1

JRFL and HIV-1 YU2; n=3 independent infections of CD06 iPSC-derived microglia.

(D) RT-qPCR analysis of *CCL2* and *CCL3* mRNA at days 9, 16, 23, and 30 post infection with HIV-1

JRFL and HIV-1 YU2; n=3 independent infections of CD06 iPSC-derived microglia.

(E) RT-qPCR analysis of *IBA1* and *P2RY12* mRNA at days 9, 16, 23, and 30 post infection with HIV-1

JRFL and HIV-1 YU2; n=3 independent infections of CD06 iPSC-derived microglia.

Figure 4: HIV-1 causes enrichment of type I interferon signaling pathways and sustained

interferon activation

(A) A volcano plot illustrating differentially expressed genes (DEGs) in HIV-1 JRFL-infected vs mock-

infected microglia on day 16 post infection; n=3 independent infections of 03SF line iPSC-derived

microglia.

(B) GSEA plot showing enrichment of IFNα-responsive genes in HIV-1 JRFL-infected vs mock-infected

microglia on day 16 post infection (NES, normalized enrichment score; FDR, false discovery rate).

(C) Gene Ontology (GO) analysis of upregulated DEGs in HIV-1 JRFL vs mock-infected microglia on

day 16 post infection; n=3 independent infections of 03SF microglia.

(D) Gene Ontology (GO) analysis of downregulated DEGs in HIV-1 JRFL vs mock-infected microglia on

day 16 post infection; n=3 independent infections of 03SF microglia.

(E) A heatmap illustrating significant upregulation of interferon-stimulated genes in HIV-1-infected vs

mock-infected microglia on day 16 post infection; n=3 independent infections of 03SF microglia.

(F) A heatmap illustrating SIGLEC gene expression in HIV-1-infected vs mock-infected microglia on day

16 post infection; n=3 independent infections of 03SF microglia.

(G) RT-qPCR analysis of *CXCL10*, *RSAD2*, *ISG15*, and *IDO1* mRNA from HIV-1 JRFL-infected vs

mock-infected microglia at days 16 and 23 post infection; n = 3 independent infections of 03SF iPSC-

derived microglia, t test; *p < 0.05, **p < 0.01, ***p < 0.001; data are presented as the mean ± SEM.

(H) RT-qPCR analysis of *CXCL10* and *RSAD2* mRNA from HIV-1 JRFL- and HIV-1 YU2-infected and

mock-infected microglia at days 16 and 23 post infection; n = 4 independent infections of CD06 iPSC-

derived microglia, t test; *p < 0.05, **p < 0.01, ***p < 0.001; data are presented as the mean ± SEM.

Figure 5: HIV-1-infected microglia incorporate into sliced cerebral organoids

(A) Representative confocal images of a day 144 organoid with neurons (MAP2$^+$), astrocytes (GFAP$^+$),

and microglia (IBA1$^+$).

(B) Representative confocal images of day 144 organoids 14 days after the addition of HIV-1 JRFL-

infected or mock-infected microglia; (B1) shows a high-magnification image of HIV-1-infected microglia

from (B).

(C) High-magnification image of a single HIV-1-infected microglial cell within a sliced organoid.

(D) RT-qPCR of *gag/pol* mRNA from HIV-1 JRFL-infected or mock-infected microglia organoids on day

14; n=3 independent infections of 03SF microglia; one-tailed t test; ****$P<0.001$; error bars represent

SEM.

(E) ELISA analysis of secreted p24 in culture supernatant from HIV-1 JRFL-infected or mock-infected

microglia organoid day 14; n=3 independent infections of 03SF microglia; one-tailed t test; **$p<0.01$;

data are presented as the mean ± SEM.

(F) RT-qPCR analysis of *ISG15*, *RSAD2*, *IFITM3*, *MX1*, *IFI44*, and *IFI27* mRNA from HIV-1 JRFL-

infected or mock-infected microglia organoids on day 14; n=3 independent infections of 03SF microglia;

one-tailed t test; *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$; data are presented as the mean ± SEM.

Figure S1: Microglial RT-qPCR analysis

(A) RT-qPCR analysis of *IBA1* and *P2RY12* mRNA expression in iPSCs and iPSC-derived microglia;

n=3 cell lines (03SF, CD06, CD52) and 3 biological replicates/line; t test; data are presented as the

mean ± SEM.

(B) RT-qPCR analysis of *CD4* and *CCR5* mRNA expression in iPSCs and iPSC-derived microglia; n=3

cell lines (03SF, CD06, CD52) and 3 biological replicates/line; t test; data are presented as the mean ±

SEM.

Figure S2: PCR analysis of 2-LTR circles

(A) A schematic representation of HIV-1 structure.

(B) A schematic representation of an HIV-1 2-LTR circle.

(C) PCR analysis of 2-LTR circles on day 4 post HIV-1 JRFL infection and mock infection.

Figure S3: RNA-seq analysis of HIV-1 JRFL- vs mock-infected 03SF microglia

(A) A PCA plot of RNA-seq data collected from HIV-1 JRFL-infected microglia vs mock-infected

microglia on day 16; n=3 independent infections of 03SF microglia.

(B) A REVIGO treemap indicating major dysregulated pathways from gene ontology (GO) analysis of

HIV-1 JRFL-infected microglia vs mock-infected microglia on day 16; n=3 independent infections of

03SF microglia.

Figure 1

Figure 2

Figure 3

Figure 4

Figure 5

Supplemental Figure 1

Supplemental Figure 2

Supplemental Figure 3