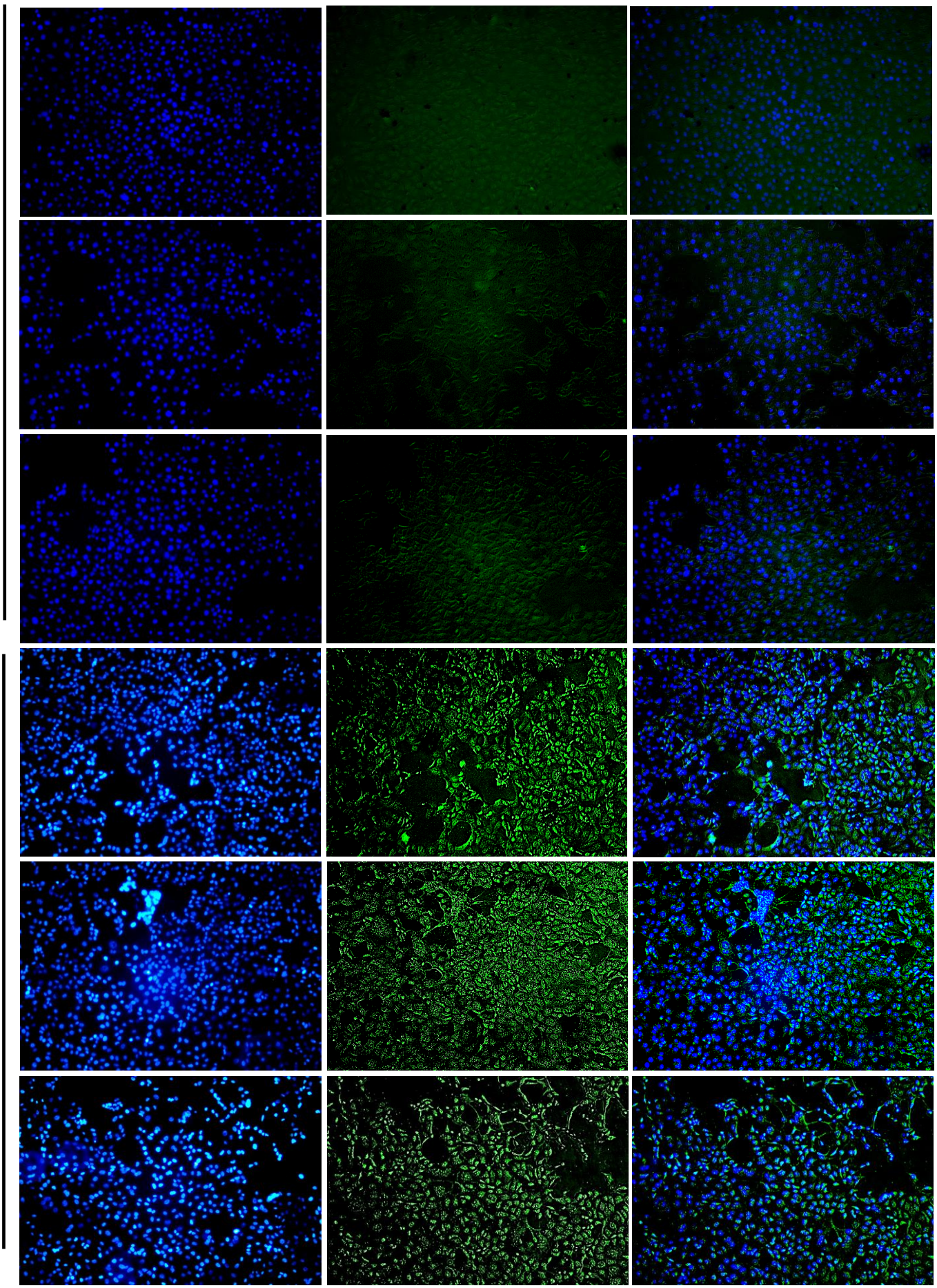
Figure 1

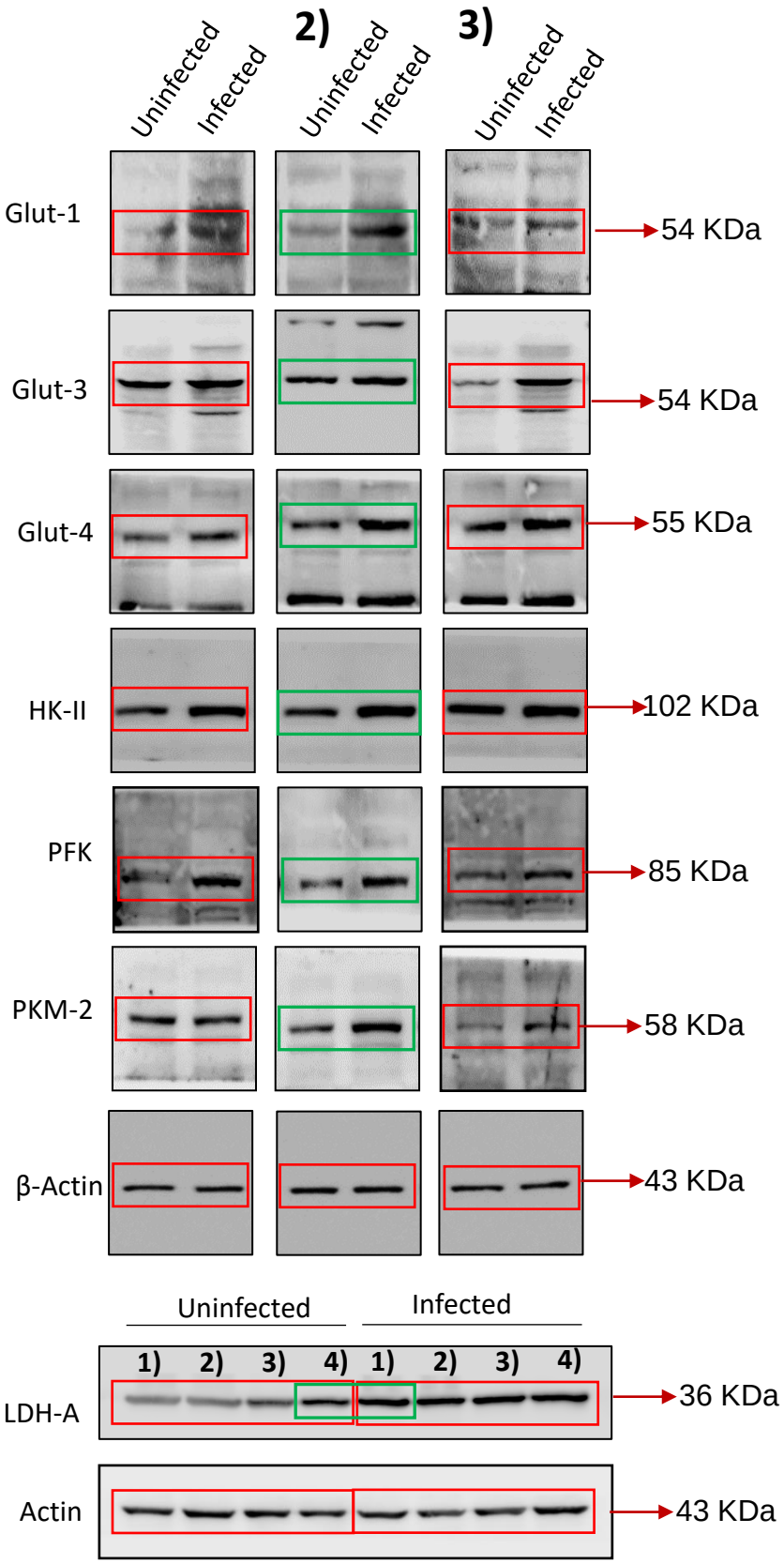
A



Supplementary Figure 1. 2-NBDG uptake analysis of uninfected and infected Vero E6 cells:

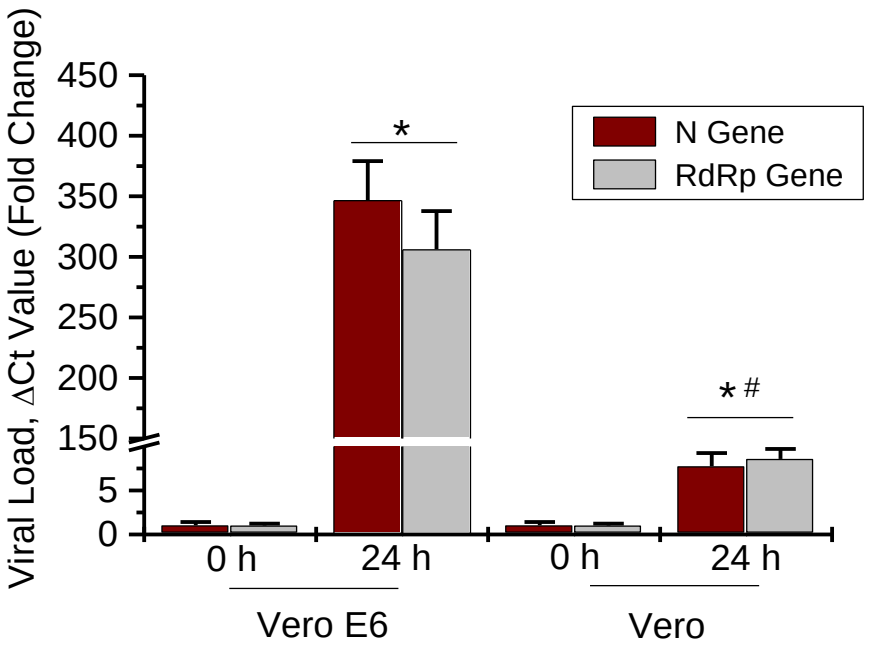
Three panel of photomicrographs are provided for the better appreciation of 2-NBDG uptake analysis in the uninfected and SARS-CoV-2 infected groups. Photomicrographs in the left panel shows the nuclear staining (Hoechst-3342), 2-NBDG (200µM) staining in the middle panel and right panel indicating the merge images of both staining presented at 48 h post-infection captured under 10×10 X magnification.

Figure 2


2)
3)
Uninfected
Infected
Uninfected
Infected
Uninfected
Infected
Glut-1
54 KDa
Glut-3
54 KDa
Glut-4
55 KDa
HK-II
102 KDa
PFK
85 KDa
PKM-2
58 KDa
β-Actin
43 KDa
Uninfected
Infected
1) 2) 3) 4) 1) 2) 3) 4)
LDH-A
36 KDa
Actin
43 KDa

Supplementary Figure 2. Immunoblotting of glycolytic proteins in Vero E6 cells: Three blot panels of indicated glycolytic proteins presented with 3 independent sets of uninfected and infected samples at 48 h post-infection. Green outline blot image of all the glycolytic proteins is presented in the main figure (Fig.1D) of the manuscript.

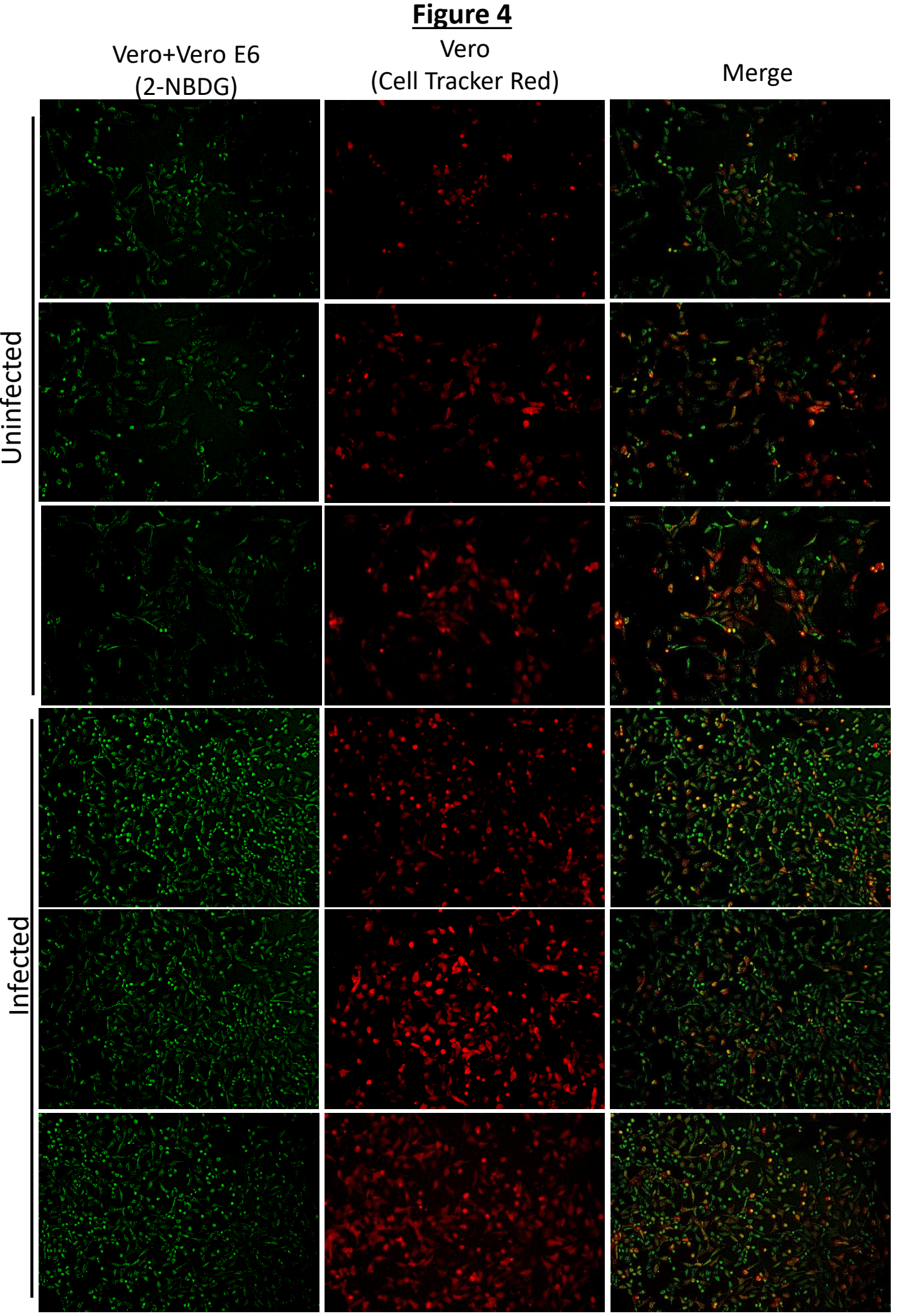
Figure 3



Supplementary figure 3 Comparative analysis of SARS-CoV-2 infection and multiplication:

RT-PCR of viral N and RdRP genes were performed at 0 and 24 h post infection in the Vero E6 and Vero cells. The growth kinetics graph shows change in viral load (ΔCt-Y-axis) presented as relative fold change (RFC) of control viral load at 0 hrs. *$p < 0.05$ compared to 0 h of respective cell line and $^{\#}p < 0.05$ compared to Vero E6 cells at 24 h (student's *t*-tests paired analysis). Nearly 50 fold significantly increased viral replication was observed in Vero E6 cells compared to Vero at 24 hrs. post infection.

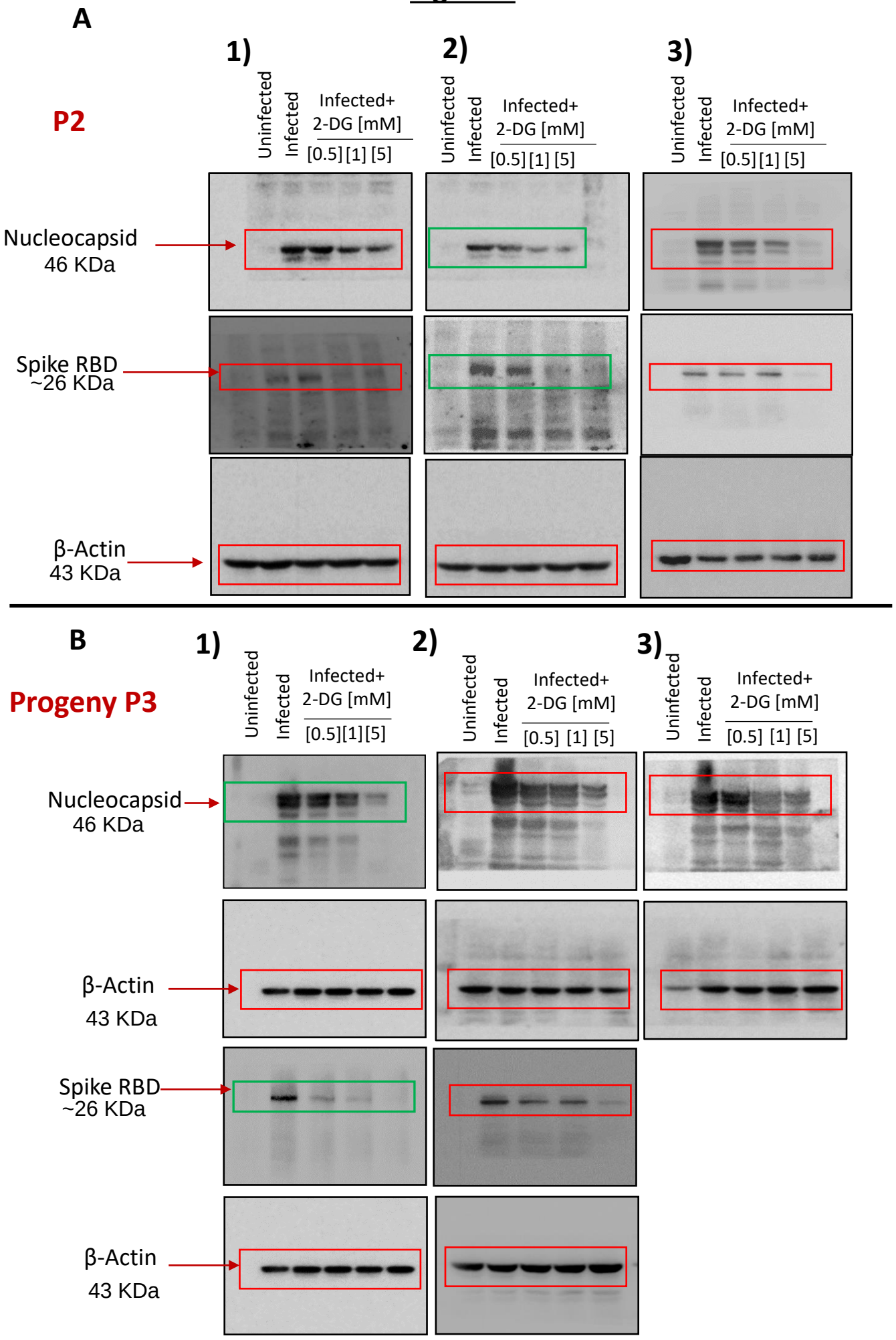
Figure 4


Vero+Vero E6
(2-NBDG)
Vero
(Cell Tracker Red)
Merge
Uninfected
Infected

Supplementary Figure 4. 2-NBDG uptake analysis in Co-culture of Vero and Vero E6 cells:

Three panel of photomicrographs are provided, showing the 2-NBDG uptake in Vero (cell tracker red stained population) and unstained Vero E6 cells presented at 48 h post-infection captured under 10×10 X magnification. Photomicrographs in the left panel (captured under green emission channel) shows the 2NBDG staining in both Vero and Vero E6 cells, whereas middle panel shows the cell tracker red staining only in Vero cells (captured under red emission channel), the right panel micrographs are the merged representation of the left and right panel for the better appreciation of differential 2-NBDG accumulation in both the cell lines. Quantitative analysis of these images was performed using the measurement of pixel intensity of each cell (total $\geq$1000 cell objects) employing algorithms from CELLSEGM and Image Processing toolbox in Matlab 2020a (Mathworks).

Figure 5


A
1)
2)
3)
P2
Uninfected
Infected
Infected+ 2-DG [mM]
[0.5] [1] [5]
Nucleocapsid 46 KDa
Spike RBD ~26 KDa
β-Actin 43 KDa
B
Progeny P3
Uninfected
Infected
Infected+ 2-DG [mM]
[0.5] [1] [5]
Nucleocapsid 46 KDa
β-Actin 43 KDa
Spike RBD ~26 KDa
β-Actin 43 KDa

Supplementary Figure 5. Immunoblotting of SARS-CoV-2 Nucleocapsid (N) and Spike (S) proteins:
Indicated blot panels of nucleocapsid and spike proteins presented with independent sets of uninfected, infected and 2-DG treated (0.5, 1 and 5mM) samples at 24 h post-infection in P2 cell lysate and 12 h post infection in progeny cell lysate. Green outline blot image of N and S proteins is presented in the main figure (Fig.4 E;P2 and Fig.7D;P3) of the manuscript.

Figure 6

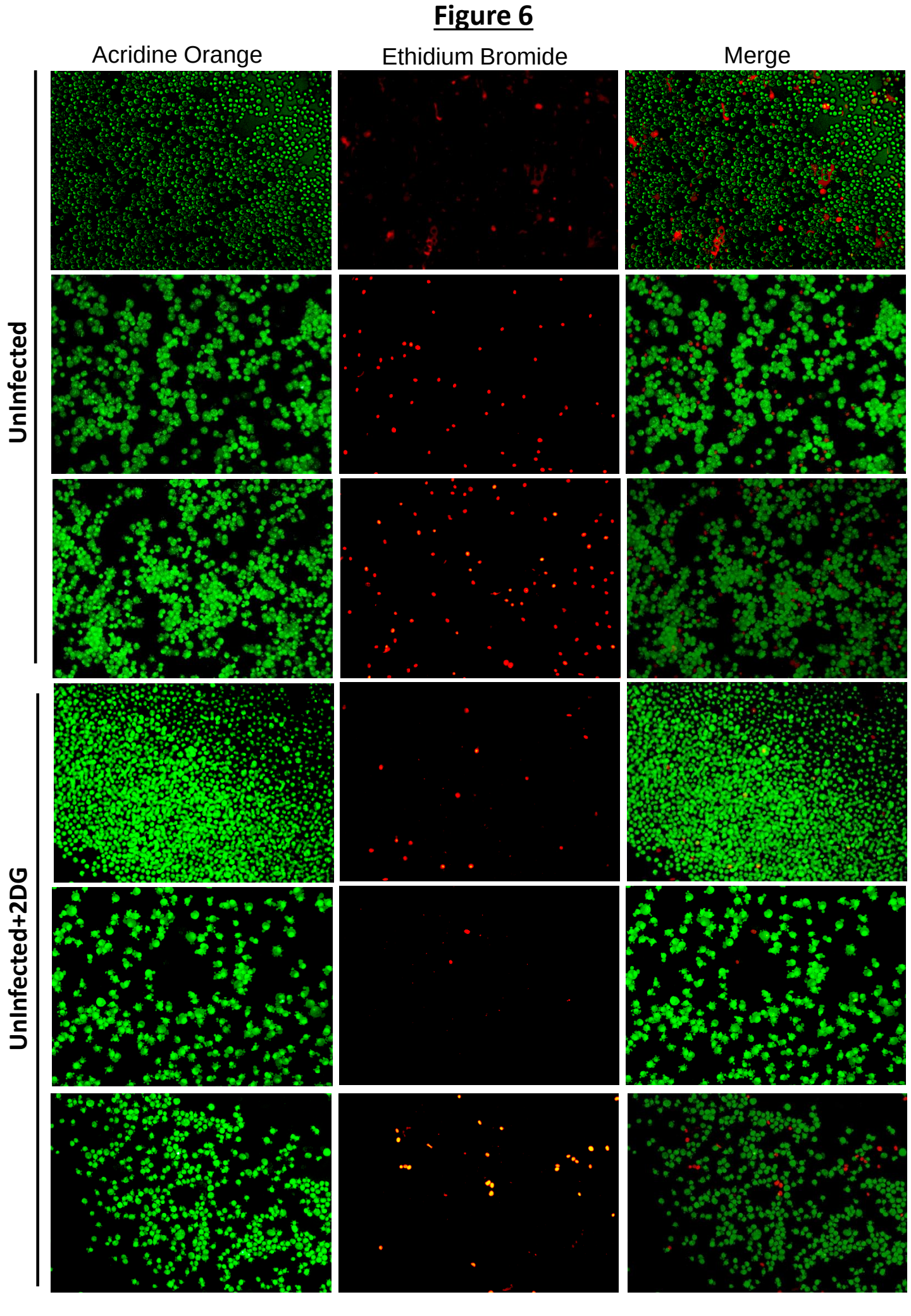
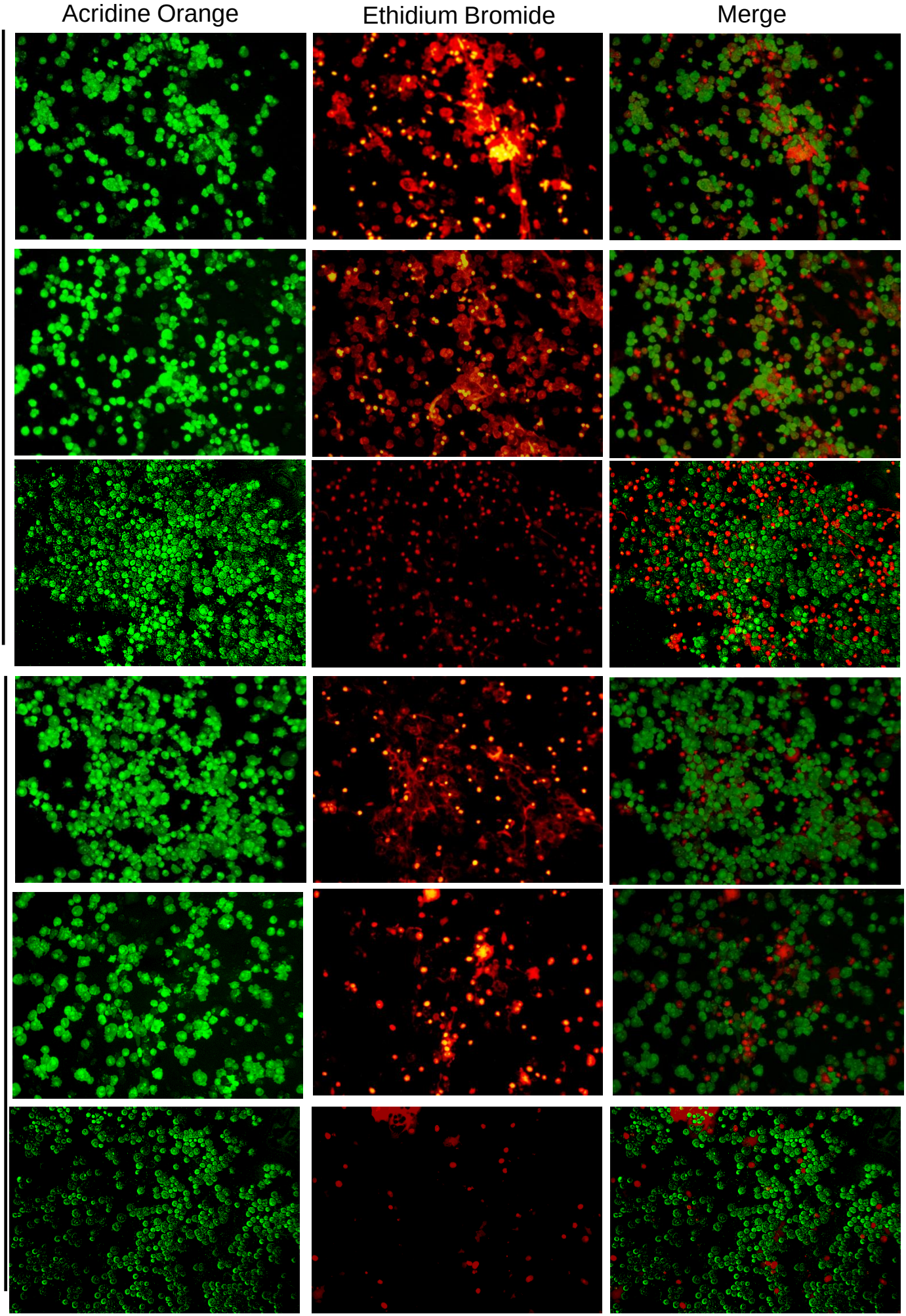
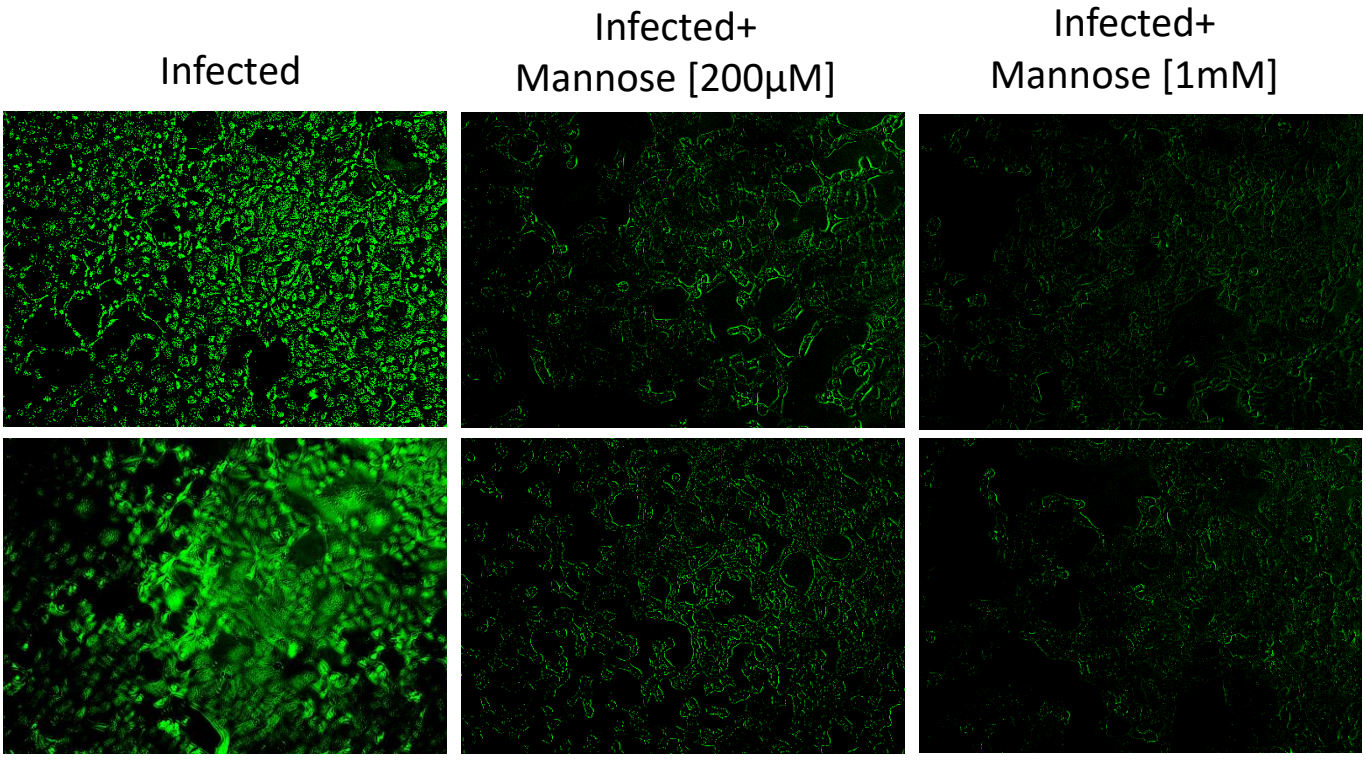

Acridine Orange
Ethidium Bromide
Merge
UnInfected
UnInfected+2DG

Figure 6 Continued



Supplementary Figure 6. Ethidium bromide (EB) and Acridine orange (AO) based cell death analysis in Vero E6 cells:
Three panels of micrographs in each treatment groups including 1) uninfected, 2) uninfected+2-DG, 3)infected and 4)infected+2-DG, shows the AO stained cell population in left panel, EB stained population in middle panel and EB-AO merge cell population in the right panel at 48 h post infection in Vero E6 cells captured under 10×10 X magnification. Quantitative estimation of images was performed using the acquired green and red area measurement for each cell (total cell objects >500) employing algorithms from CELLSEGM and Image Processing toolbox in Matlab 2020a (Mathworks).

Figure 7

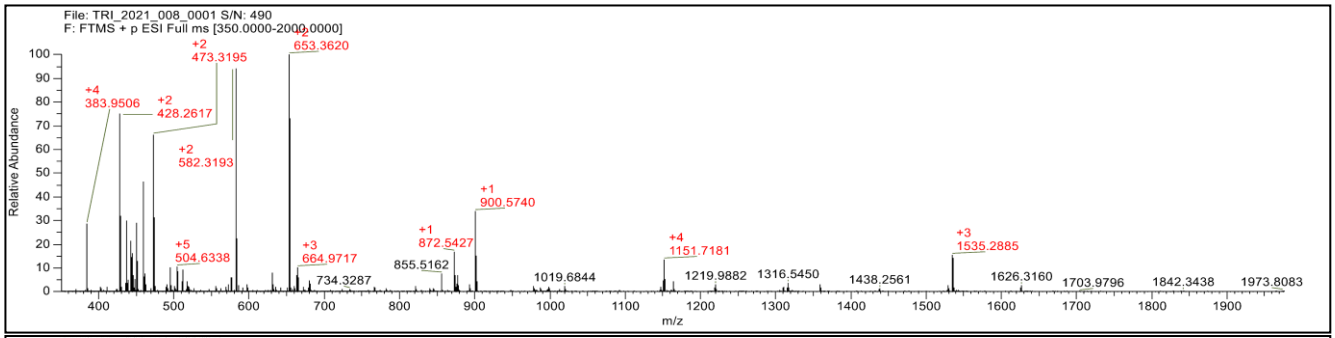


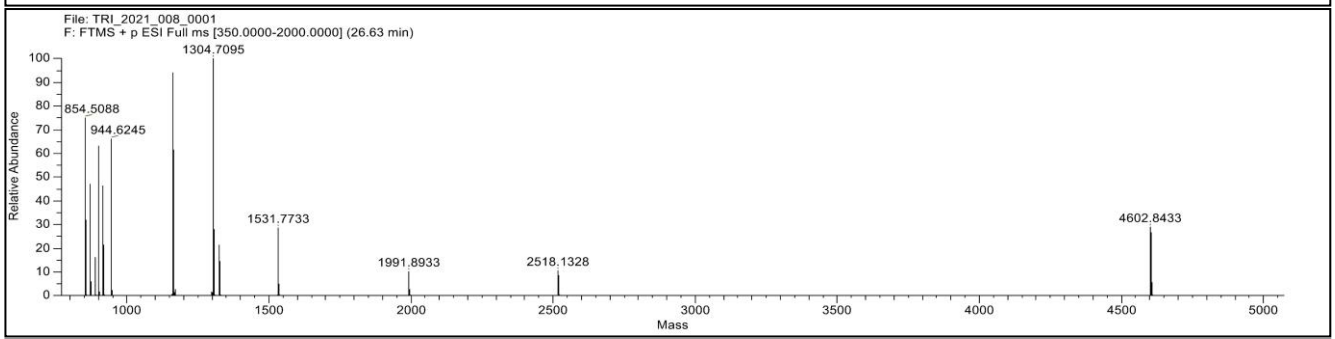
Supplementary Figure 7. 2-NBDG uptake analysis of infected and Infected+ Mannose treated Vero E6 cells:

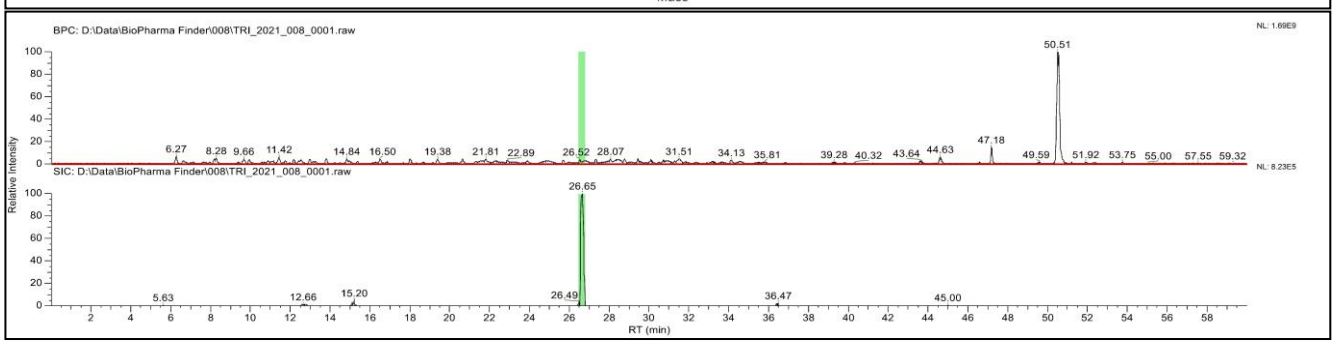
Two panel of micrographs showing the differential 2-NBDG uptake in infected, infected+mannose(200µM) and, infected+mannose(1mM) in Vero E6 cells presented at 48 h post-infection captured under 10×10 X magnification.

Figure 8

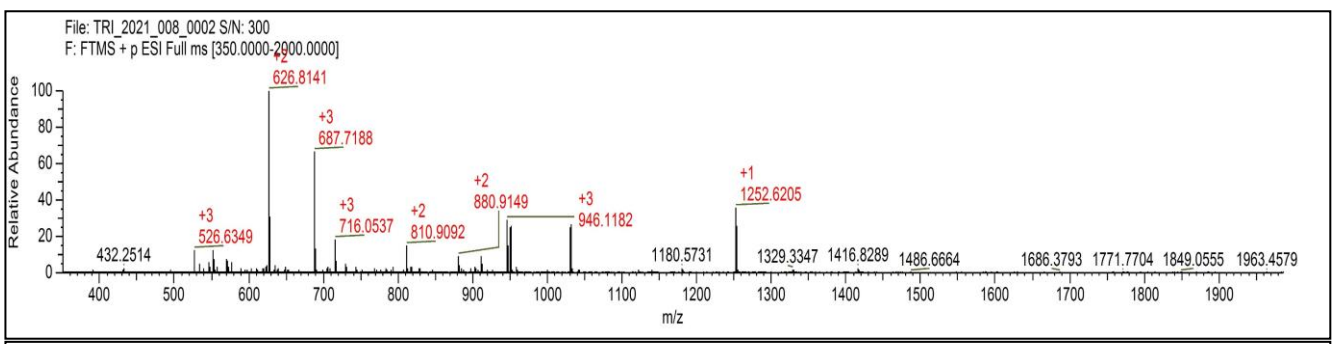
Infected

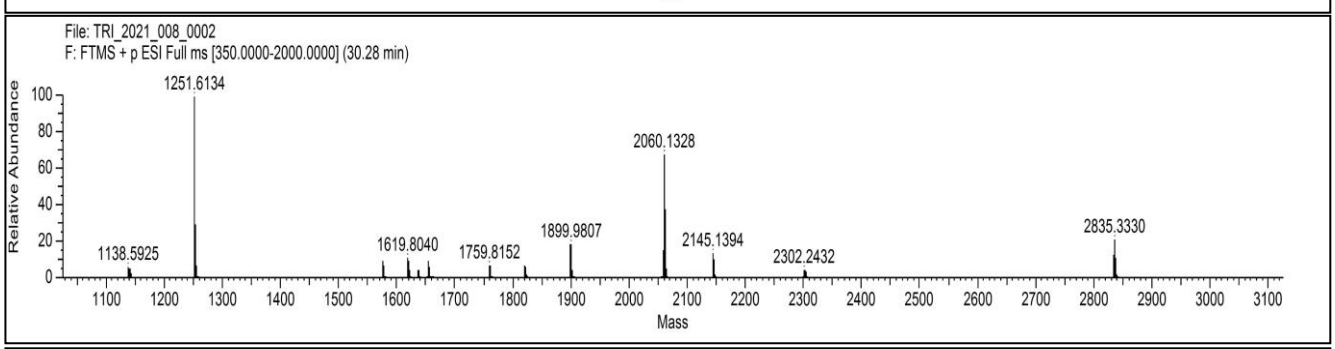






P3 virions Infected + 2DG [1mM]





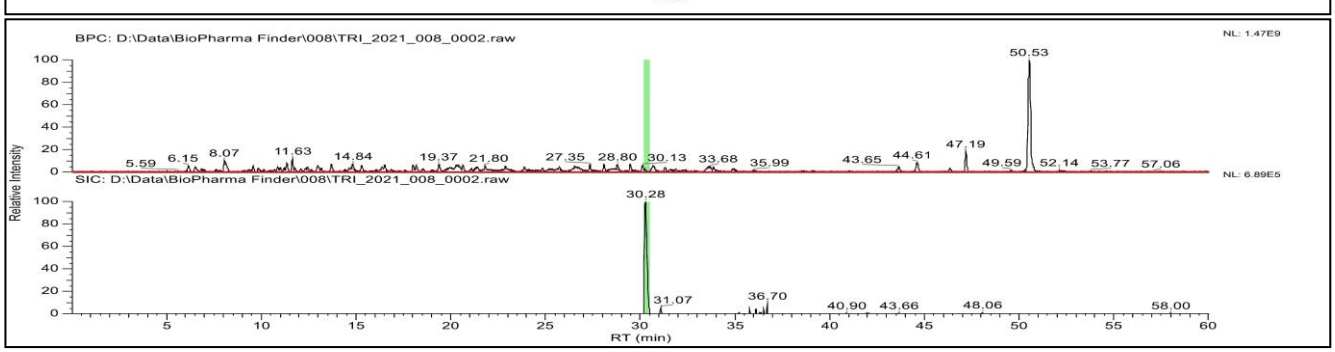
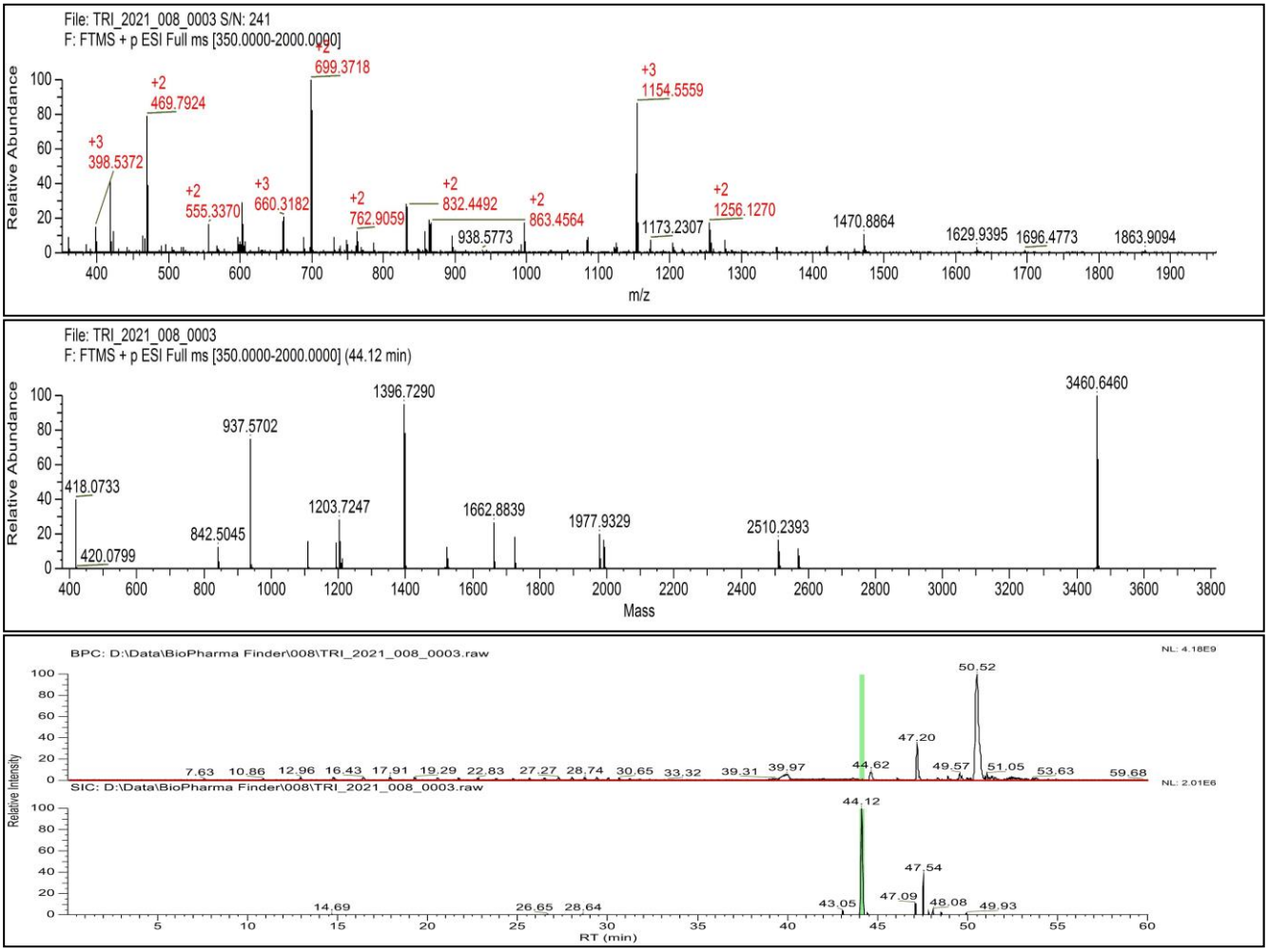


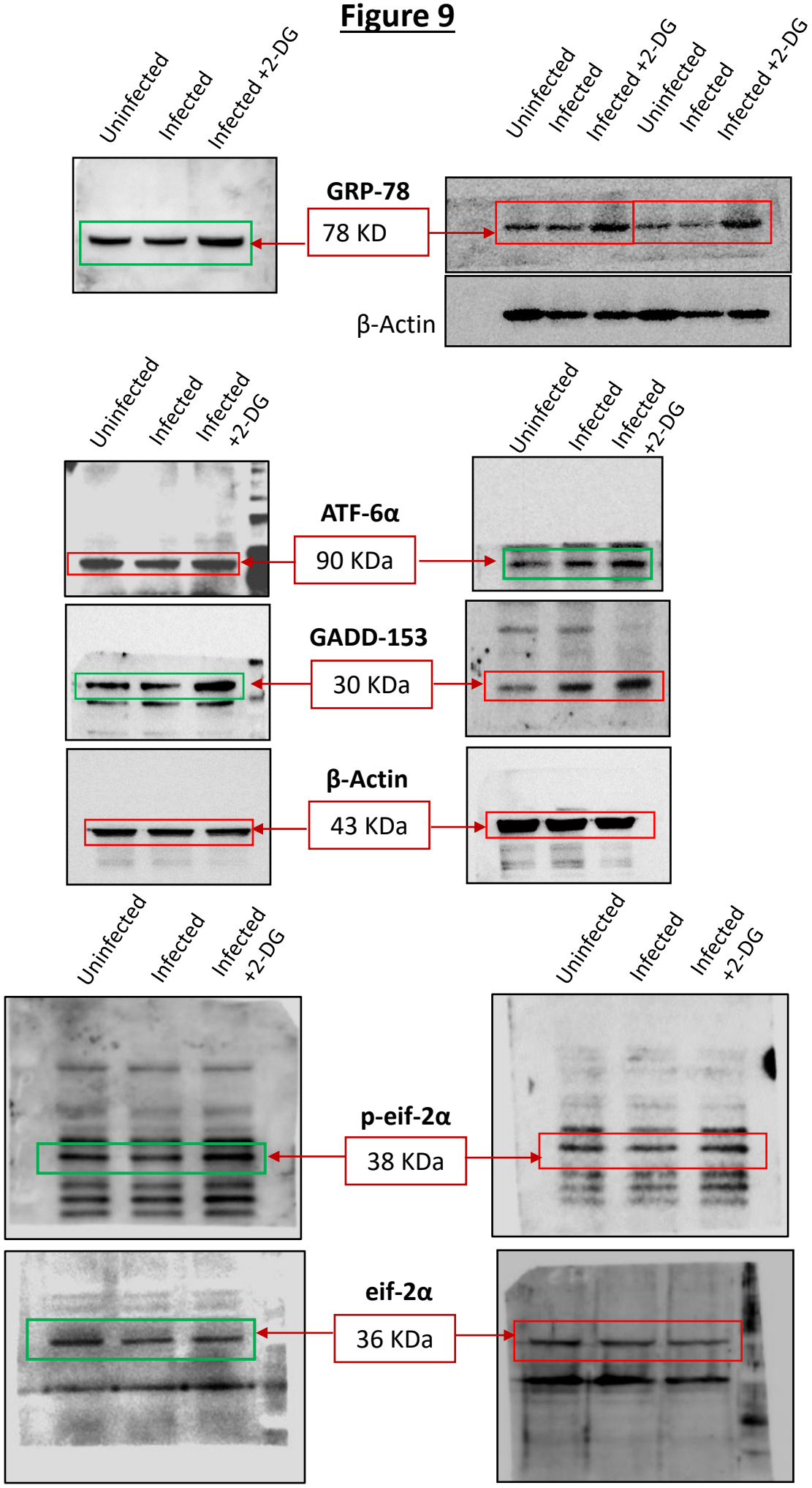
Figure 8 continued



Supplementary Figure 8 Total ion chromatogram from the SARS-CoV-2 proteins produced in Vero E6 cells:

MS/MS fragment ion spectrum obtained from the SARS-CoV-2 proteins produced in Vero E6 cells infected with the progeny virions of 1) Infected (ID:TRI/2021/008/0001), 2) Infected+2-DG[1mM];(TRI/2021/008/0002) and, 3) and Infected+2-DG [5mM];(ID:TRI/2021/008/0003) samples.

Figure 9


Uninfected
Infected
Infected +2-DG
Uninfected
Infected
Infected +2-DG
Uninfected
Infected
Infected +2-DG
GRP-78
78 KD
β-Actin
Uninfected
Infected
Infected +2-DG
Uninfected
Infected
Infected +2-DG
ATF-6α
90 KDa
GADD-153
30 KDa
β-Actin
43 KDa
Uninfected
Infected
Infected +2-DG
Uninfected
Infected
Infected +2-DG
p-eif-2α
38 KDa
eif-2α
36 KDa

Supplementary Figure 9. Immunoblotting of ER stress marker proteins:
Indicated blot panels of GRP-78, ATF-6α, GADD-153, p-eif-2α, and eif-2α presented with independent sets of uninfected, infected and 2-DG [5mM] treated P2 cell lysate at 48 h post-infection. Green outline blot image is presented in the main figure (Fig.8D) of the manuscript.