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(54) METHOD FOR DETECTION AND QUANTITATIVE MONITORING OF INFECTIONS WITH HERPESVIRUSES

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(73) Assignee: **The Trustees of Princeton University**, Princeton, NJ (US)

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(52) **U.S. Cl.**
CPC ... ***G01N 33/56994*** (2013.01); *G01N 2800/26* (2013.01); *G01N 2800/52* (2013.01)

(57) **ABSTRACT**

Described are systems and assays that monitor presence and/or quantity of herpesviruses viral proteins. Embodiments offer accurate detection and quantification of viral proteins from all temporal classes of viral replication. Three exemplary assays provide specific detection of: herpes simplex vims type 1 (HSV1), human cytomegalovirus (HCMV), and Kaposi's sarcoma-associated herpesvirus (KSHV). These assays can be utilized in combination with drug treatments, genetic modifications, or other perturbations to assess the impact of the intervention on viral protein production. Also provided are kits for use with such assays, peptides useful in the describes assays (including labeled peptides and collections of a plurality of different peptides), nucleic acids and other genetic constructs encoding such peptides, systems for carrying out the described assays (including computer-based or computer-assisted systems), and methods for using the assays for instance in drug development and analysis, vaccine development and analysis, genetic analysis, environmental analysis, etc.

Specification includes a Sequence Listing.

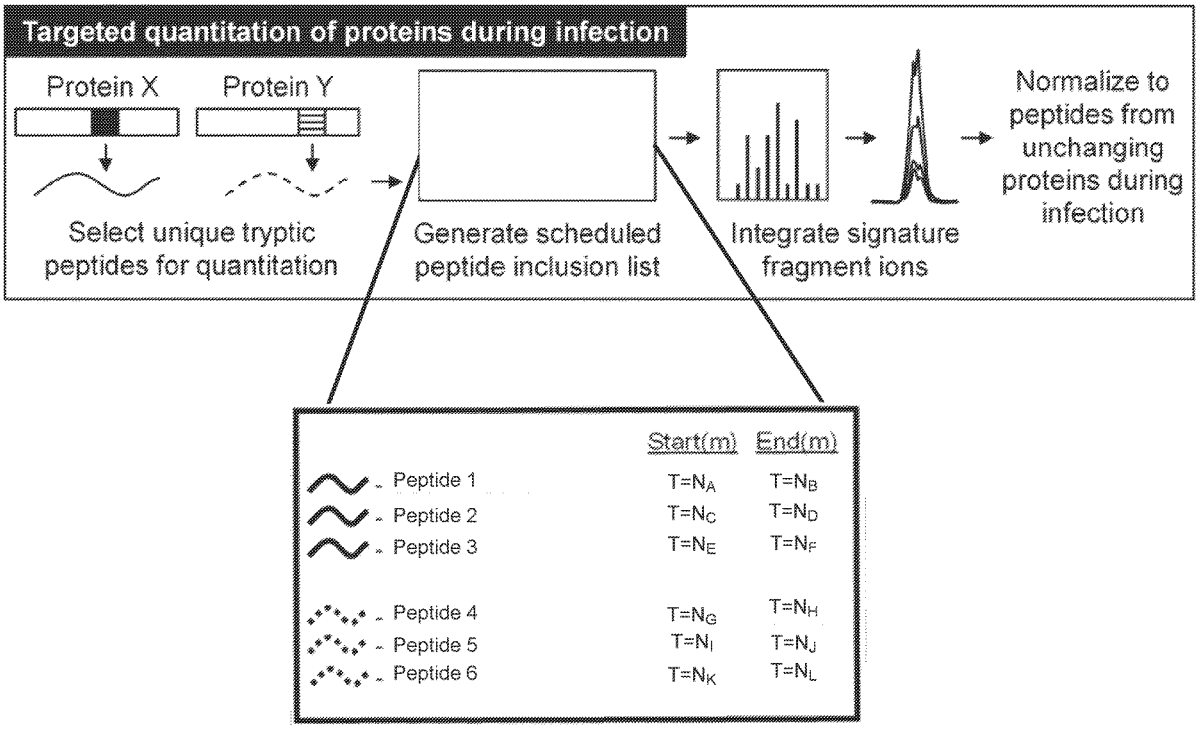
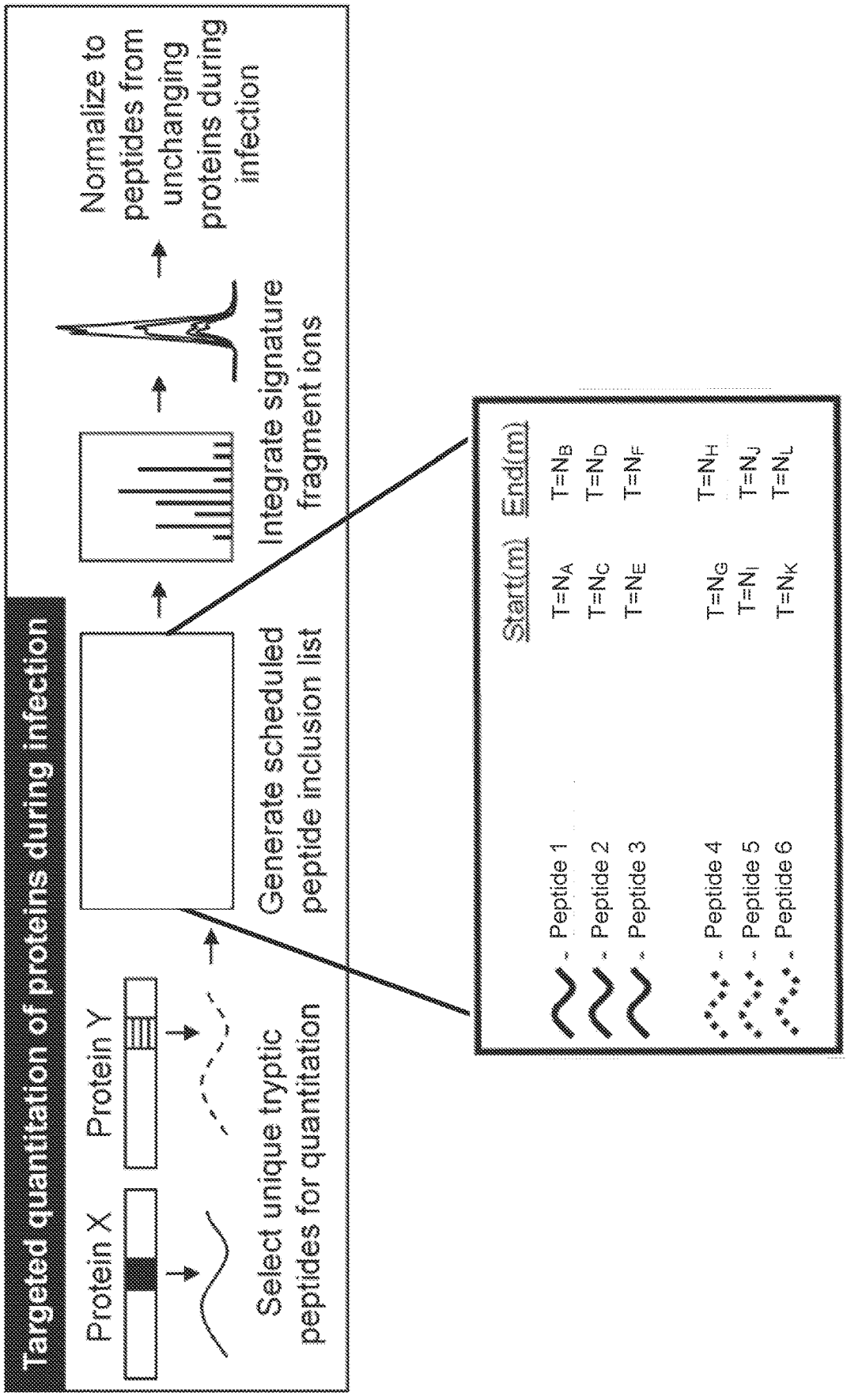


FIG. 1


Targeted quantitation of proteins during infection
Protein X
Protein Y
Select unique tryptic peptides for quantitation
Generate scheduled peptide inclusion list
Integrate signature fragment ions
Normalize to peptides from unchanging proteins during infection
Start(m)
End(m)
Peptide 1
T=NA
T=NB
Peptide 2
T=NC
T=ND
Peptide 3
T=NE
T=NF
Peptide 4
T=NG
T=NH
Peptide 5
T=NI
T=NJ
Peptide 6
T=NK
T=NL

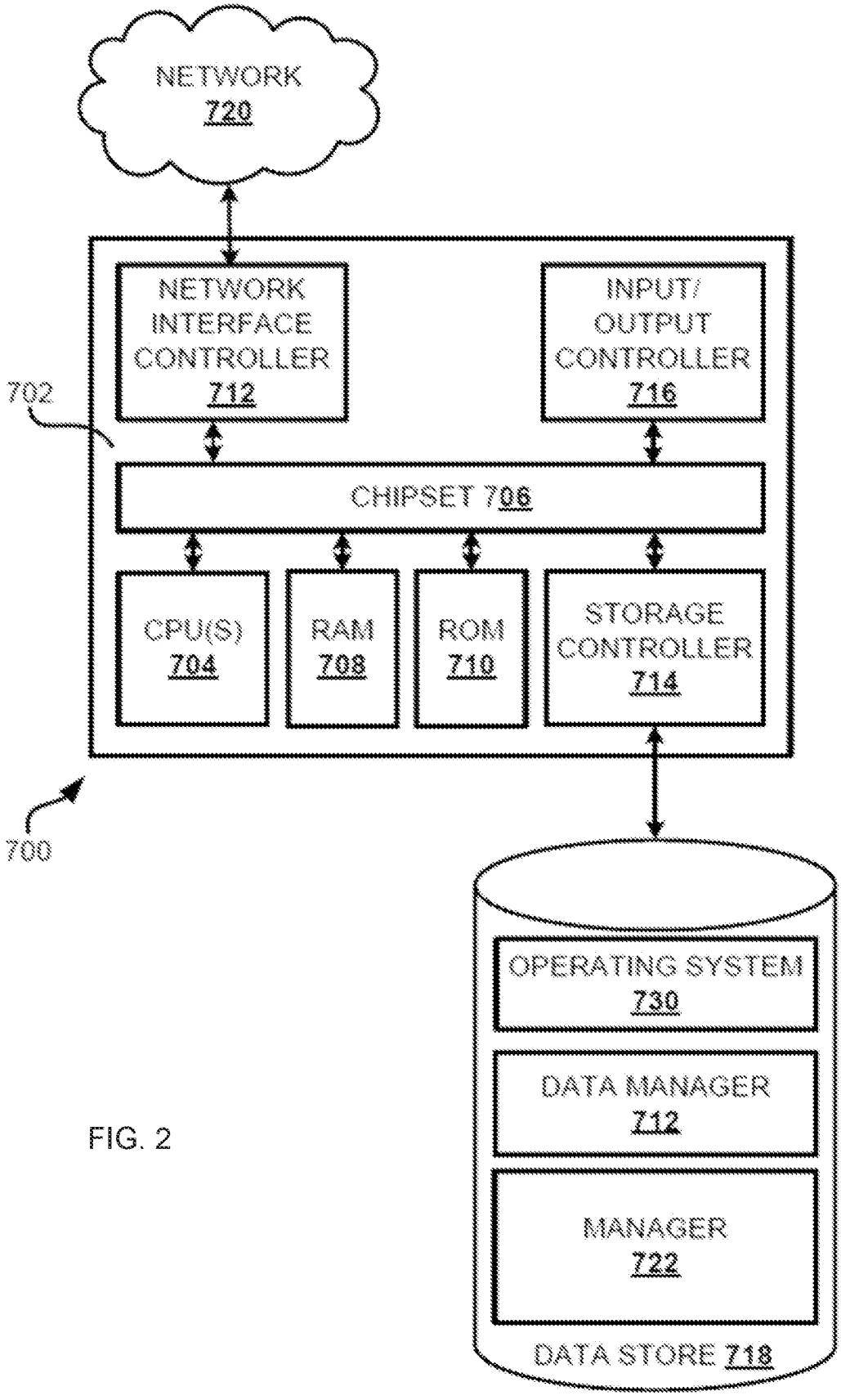

NETWORK
720
NETWORK INTERFACE CONTROLLER
712
INPUT/ OUTPUT CONTROLLER
716
702
CHIPSET 706
CPU(S)
704
RAM
708
ROM
710
STORAGE CONTROLLER
714
700
OPERATING SYSTEM
730
DATA MANAGER
712
MANAGER
722
DATA STORE 718

FIG. 2

FIG. 3A

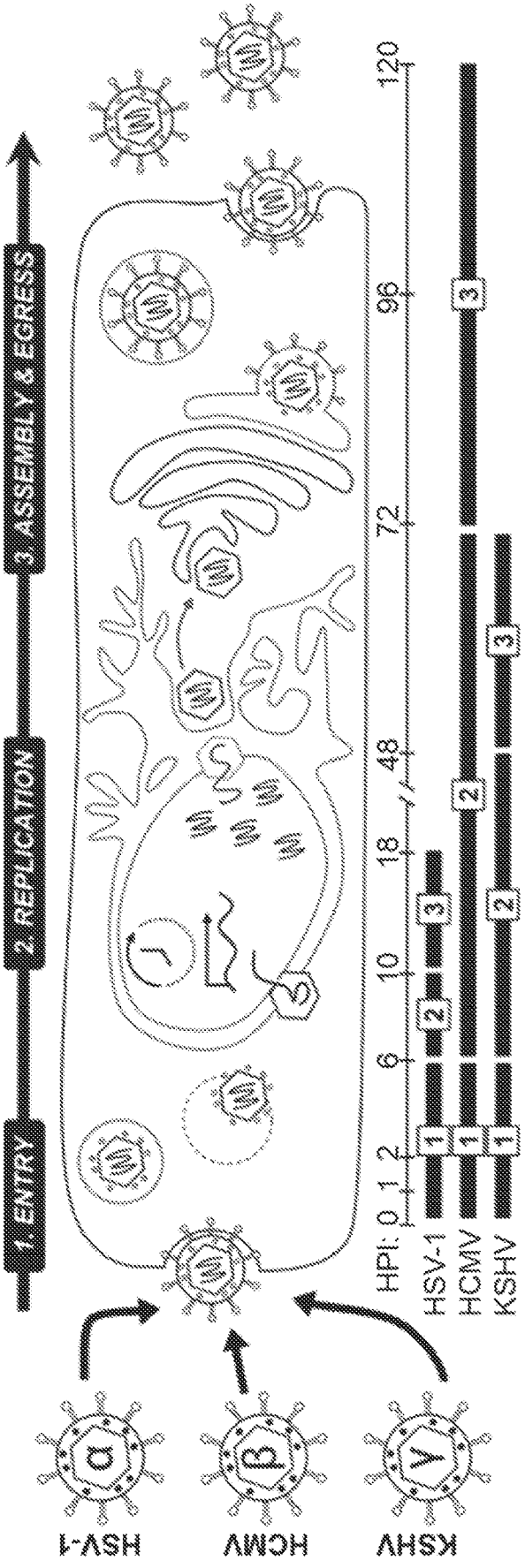

1. ENTRY
2. REPLICATION
3. ASSEMBLY & EGRESS
HPI: 0 1 2 6 10 18 48 72 96 120
HSV-1
HCMV
KSHV
HSV-1
HCMV
KSHV

FIG. 3B

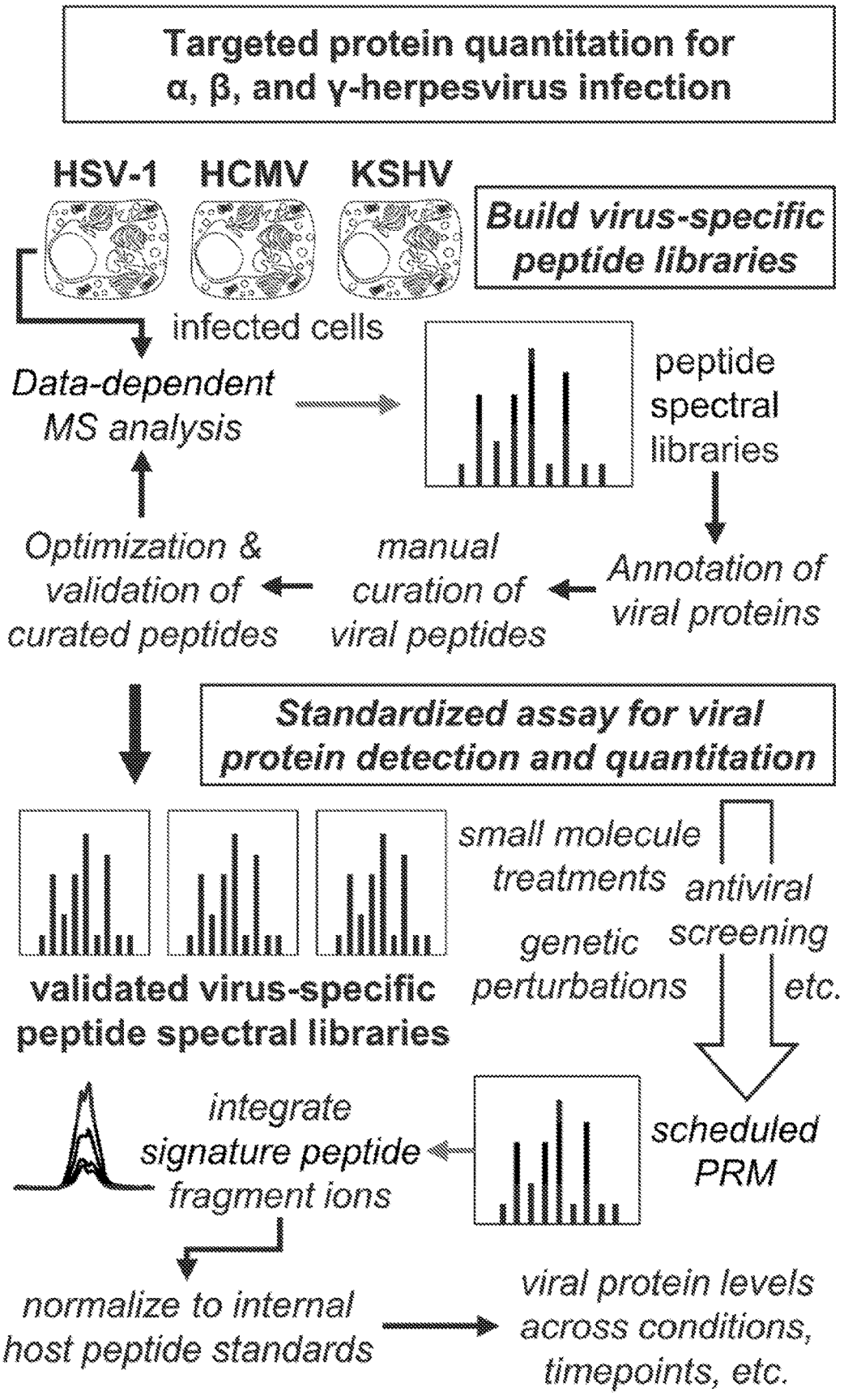

Targeted protein quantitation for α, β, and γ-herpesvirus infection
HSV-1
HCMV
KSHV
Build virus-specific peptide libraries
infected cells
Data-dependent MS analysis
peptide spectral libraries
Optimization & validation of curated peptides
manual curation of viral peptides
Annotation of viral proteins
Standardized assay for viral protein detection and quantitation
small molecule treatments
antiviral screening
genetic perturbations
etc.
validated virus-specific peptide spectral libraries
scheduled PRM
integrate signature peptide fragment ions
normalize to internal host peptide standards
viral protein levels across conditions, timepoints, etc.

FIG. 3C

	HSV-1	HCMV	KSHV
# viral proteins targeted	60	90	62
# peptides targeted	87	230	156
% of reported proteins	82%	47%	71%
# proteins targeted per temporal class	IE (5), E (17), L (38)	IE (7), DE (41), LL (15), L (27)	IE (6), DE (27), L (29)
# proteins targeted per virion component	capsid (8), envelope (12), tegument (21), non-structural (19)	capsid (7), envelope (11), tegument (34), non-structural (38)	capsid (7), envelope (8), tegument (23), non-structural (24)

FIG. 3D

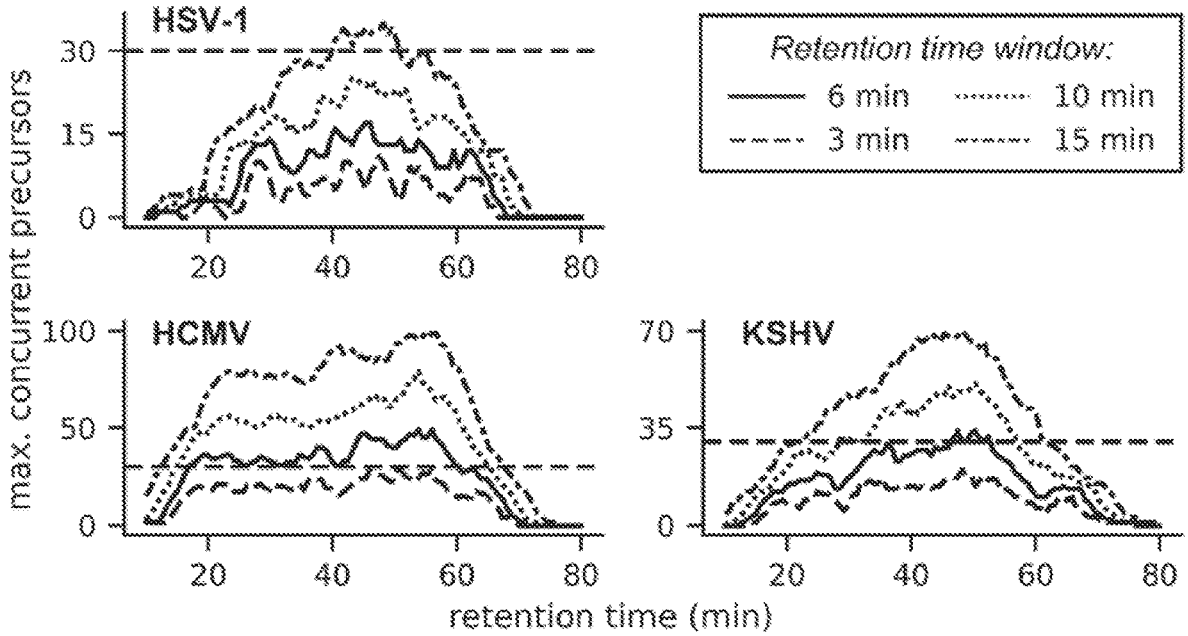


FIG. 3E

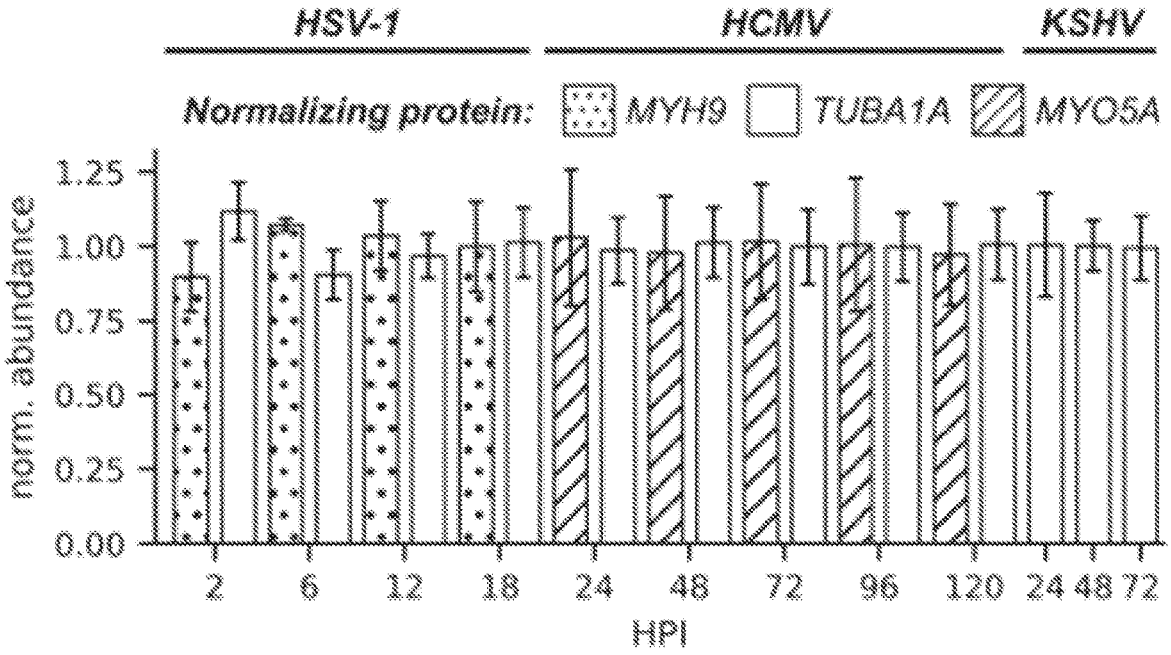

HSV-1
HCMV
KSHV
Normalizing protein:
MYH9
TUBA1A
MYO5A
norm. abundance
1.25
1.00
0.75
0.50
0.25
0.00
2
6
12
18
24
48
72
96
120
24
48
72
HPI

FIG. 3F

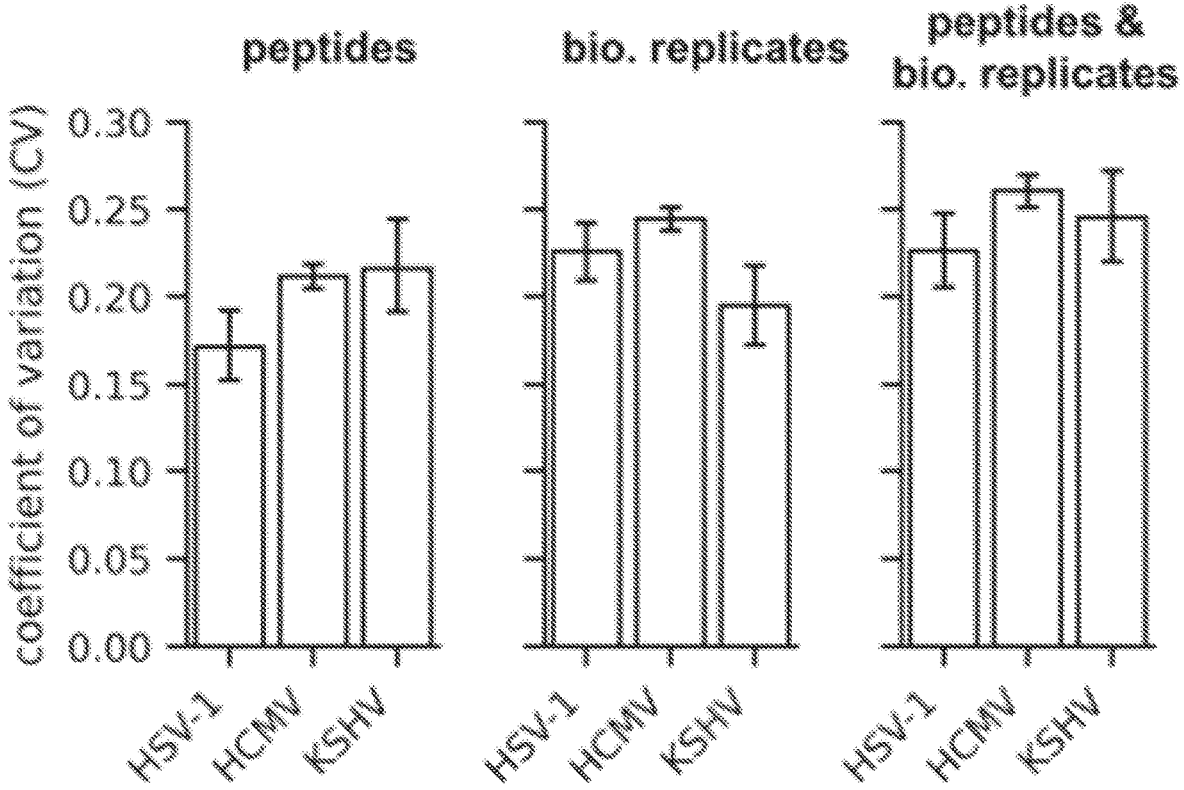

peptides
bio. replicates
peptides & bio. replicates
coefficient of variation (CV)
0.30
0.25
0.20
0.15
0.10
0.05
0.00
HSV-1
HCMV
KSHV

FIG. 4A

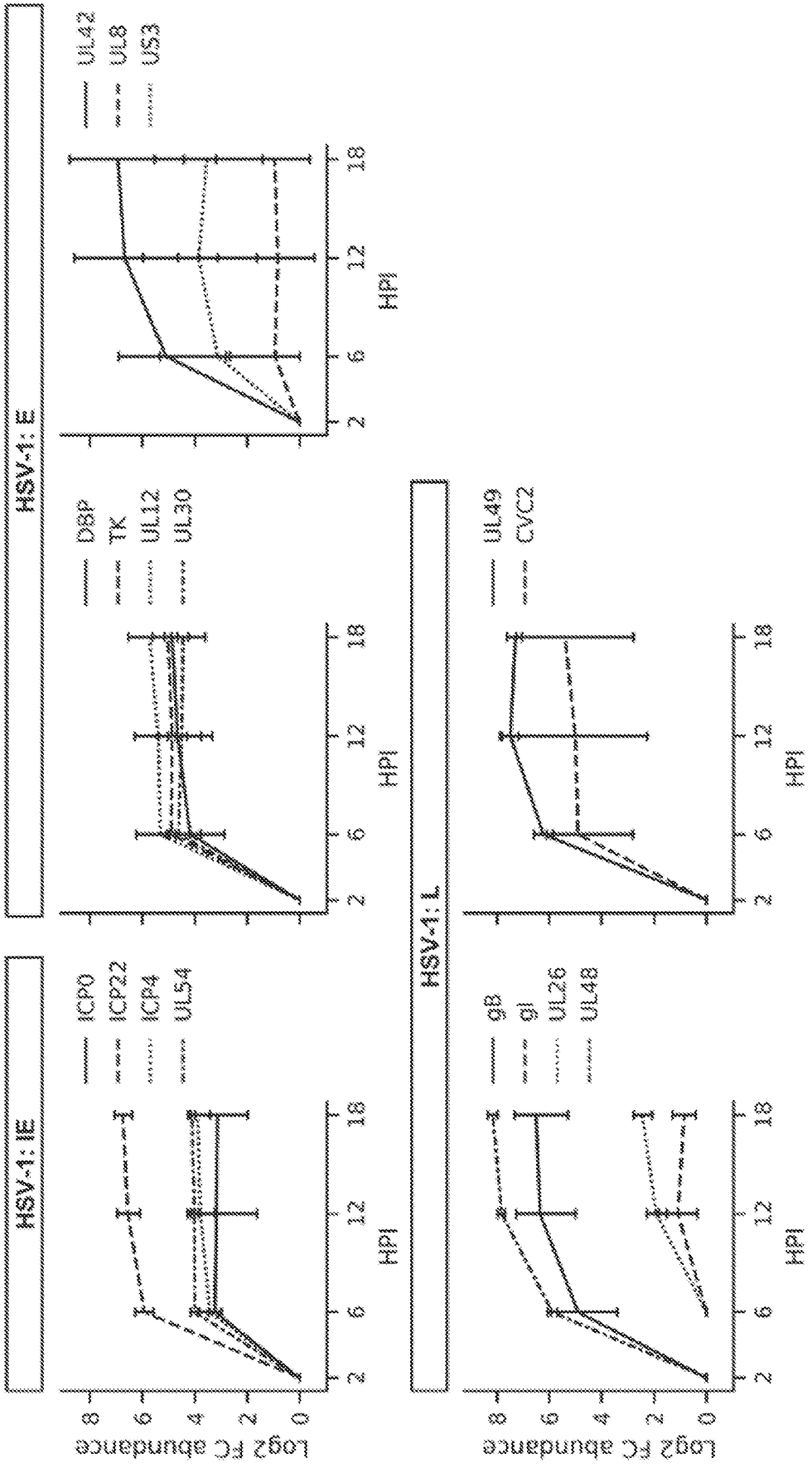

HSV-1: IE
HSV-1: E
HSV-1: L
ICP0
ICP22
ICP4
UL54
DBP
TK
UL12
UL30
UL42
UL8
US3
gB
gI
UL26
UL48
UL49
CVC2
log2 FC abundance
HPI
0
2
4
6
8
2
6
12
18

FIG. 4B

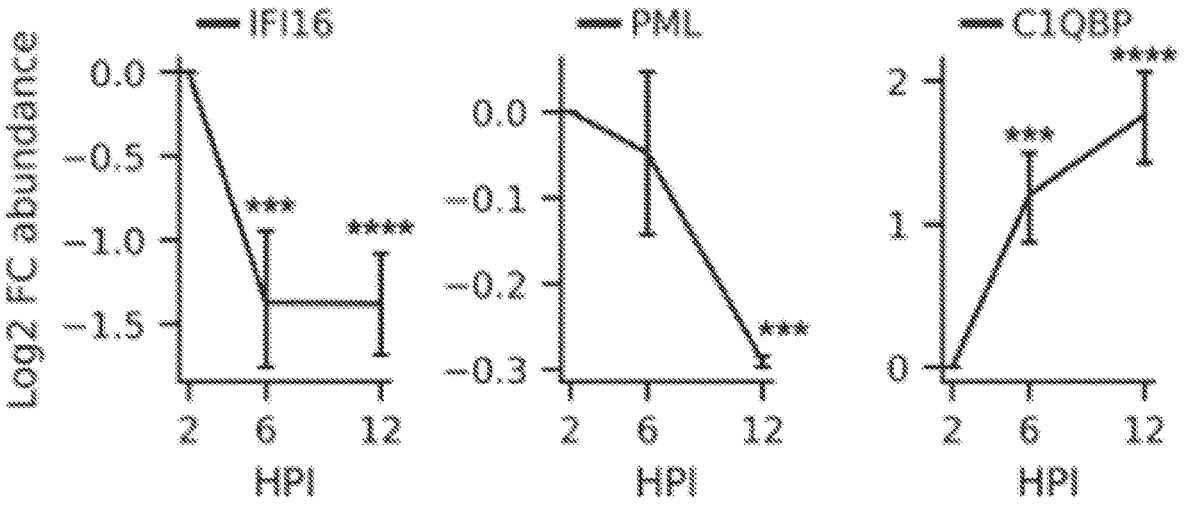

IFI16
PML
C1QBP
Log2 FC abundance
0.0
−0.5
−1.0
−1.5
0.0
−0.1
−0.2
−0.3
2
1
0
***
****
2
6
12
HPI

FIG. 4C

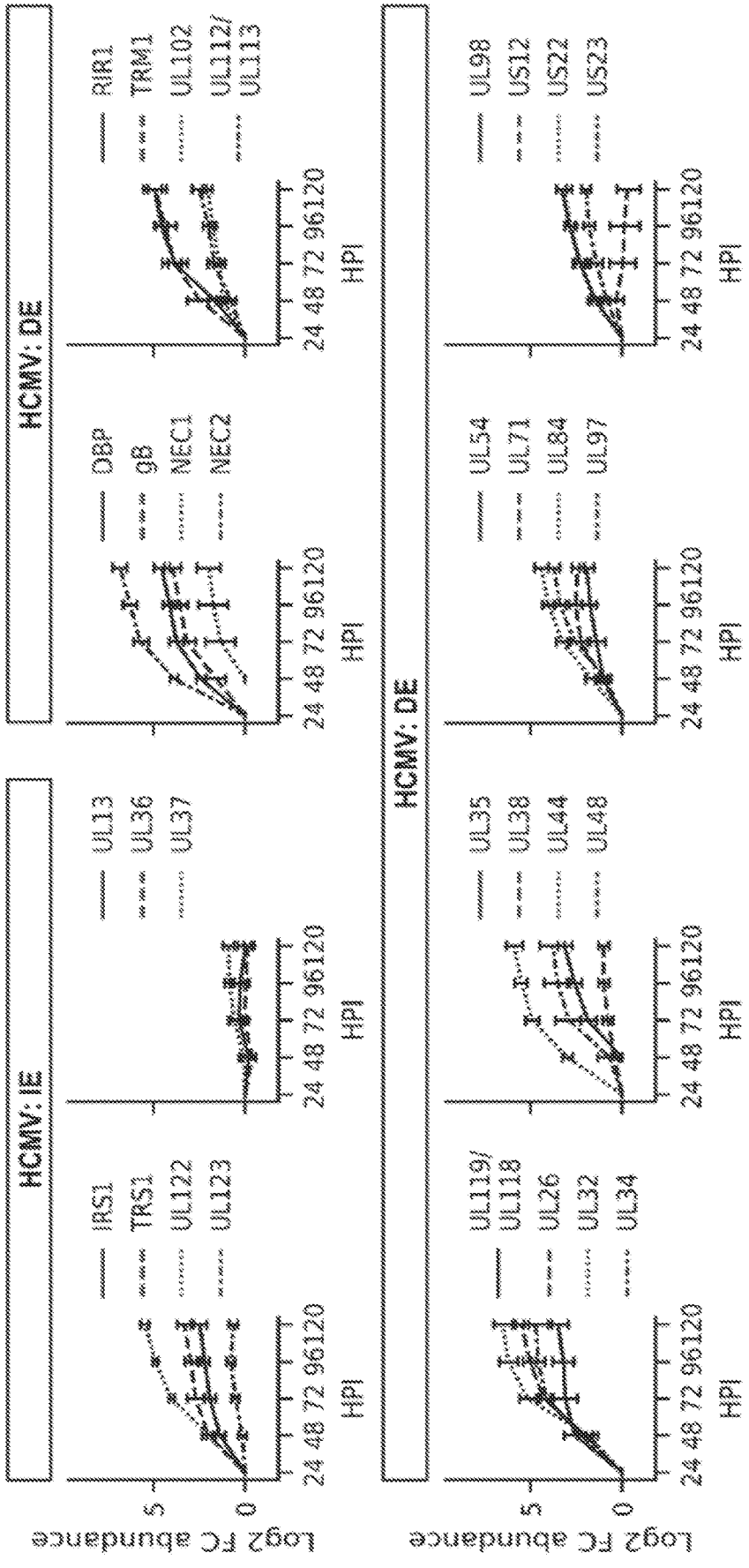

HCMV: IE
HCMV: DE
HCMV: DE
IRS1
TRS1
UL122
UL123
UL13
UL36
UL37
DBP
gB
NEC1
NEC2
RIR1
TRM1
UL102
UL112/
UL113
UL119/
UL118
UL26
UL32
UL34
UL35
UL38
UL44
UL48
UL54
UL71
UL84
UL97
UL98
US12
US22
US23
log2 FC abundance
5
0
24 48 72 96120
HPI

FIG. 4C cont'd

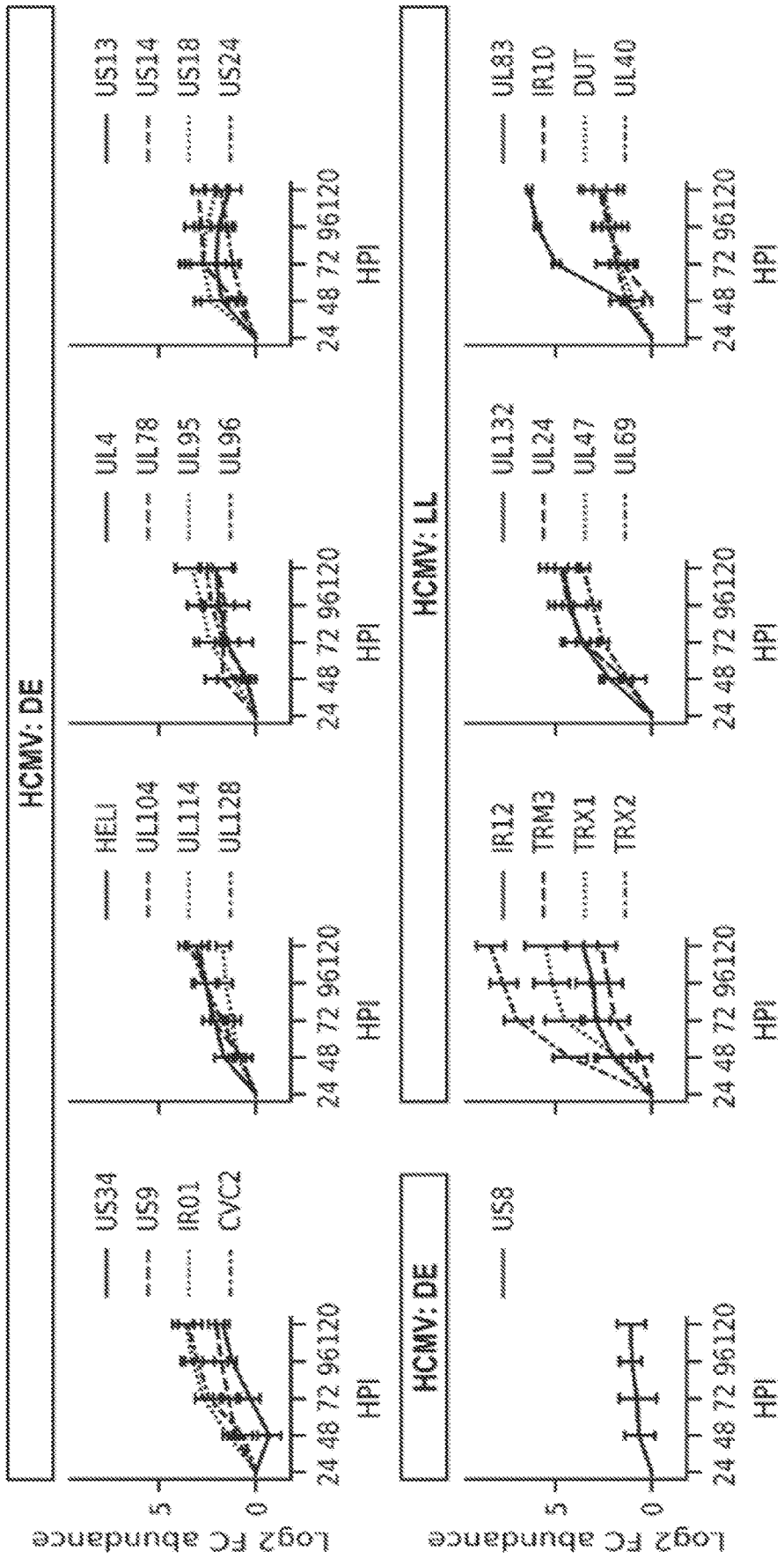

HCMV: DE
HCMV: LL
HCMV: DE
US34
US9
IR01
CVC2
HELI
UL104
UL114
UL128
UL4
UL78
UL95
UL96
US13
US14
US18
US24
US8
IR12
TRM3
TRX1
TRX2
UL132
UL24
UL47
UL69
UL83
IR10
DUT
UL40
log2 FC abundance
5
0
24 48 72 96120
HPI

FIG. 4C cont'd

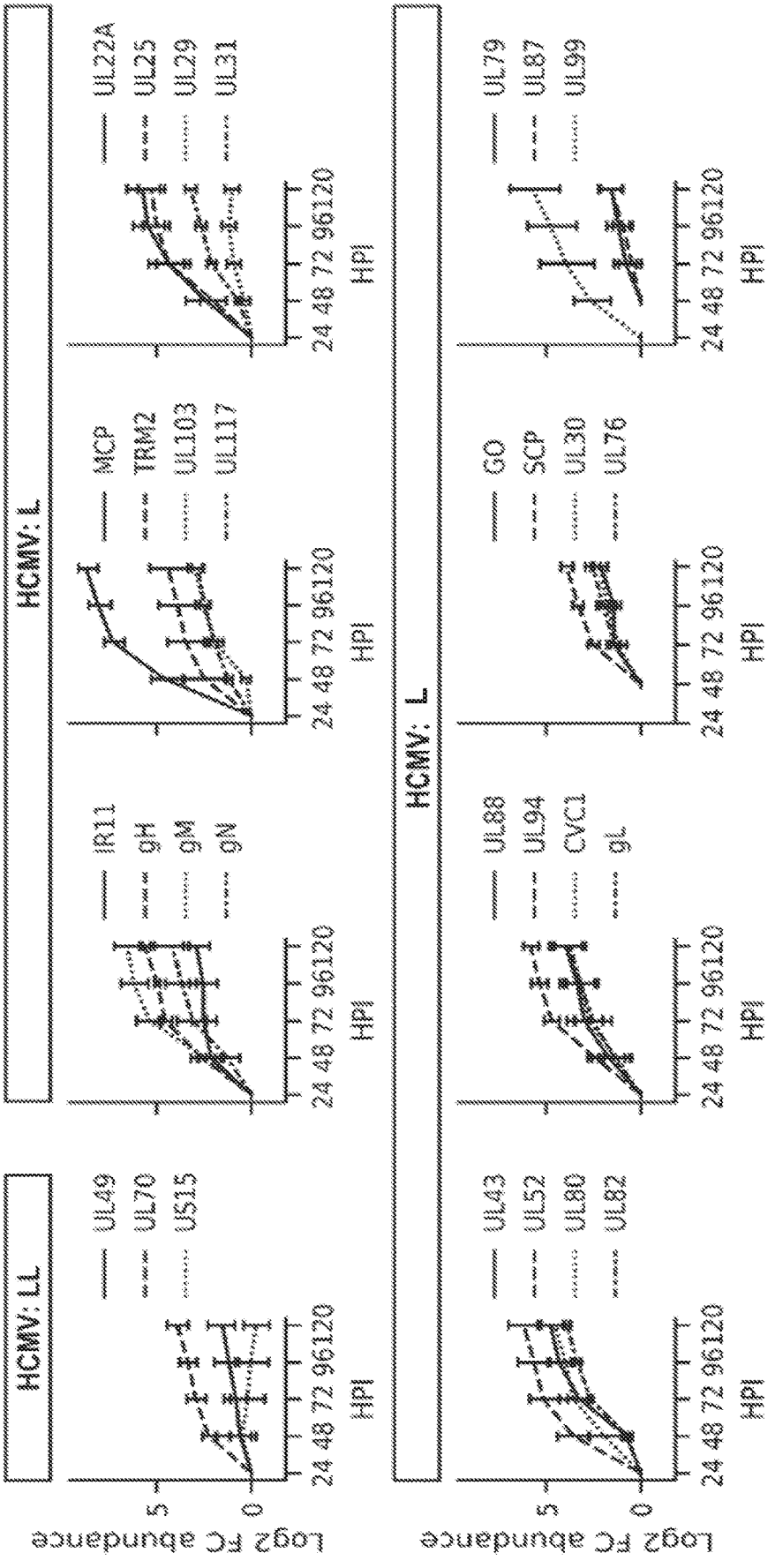

HCMV: LL
HCMV: L
HCMV: L
UL49
UL70
US15
IR11
gH
gM
gN
MCP
TRM2
UL103
UL117
UL22A
UL25
UL29
UL31
UL43
UL52
UL80
UL82
UL88
UL94
CVC1
gL
GO
SCP
UL30
UL76
UL79
UL87
UL99
log2 FC abundance
5
0
24 48 72 96120
HPI

FIG. 4D

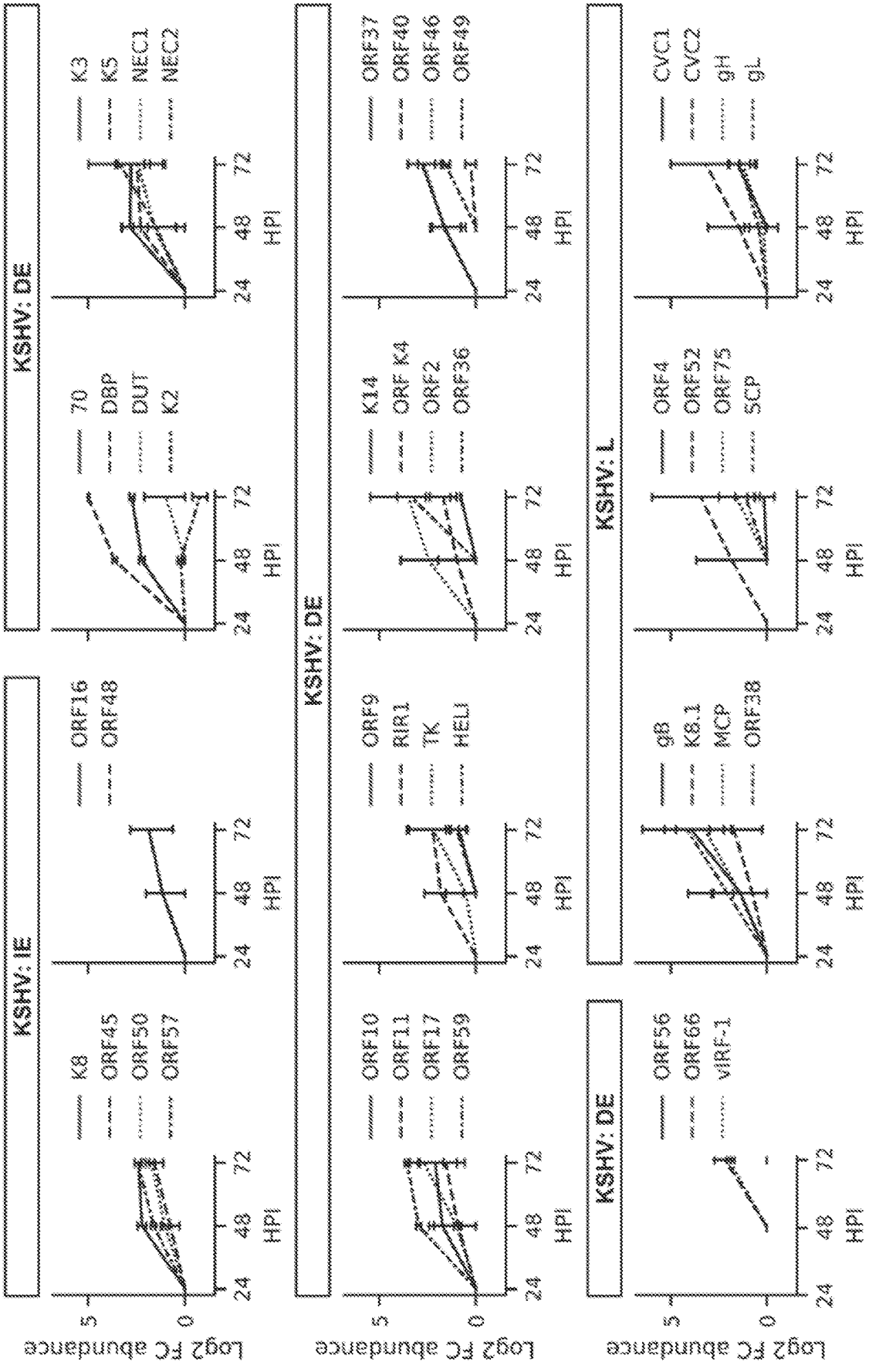

KSHV: IE
KSHV: DE
KSHV: DE
KSHV: L
KSHV: DE
K8
ORF45
ORF50
ORF57
ORF16
ORF48
70
DBP
DUT
K2
K3
K5
NEC1
NEC2
ORF10
ORF11
ORF17
ORF59
ORF9
RIR1
TK
HELI
K14
ORF K4
ORF2
ORF36
ORF37
ORF40
ORF46
ORF49
ORF56
ORF66
vIRF-1
gB
K8.1
MCP
ORF38
ORF4
ORF52
ORF75
SCP
CVC1
CVC2
gH
gL
Log2 FC abundance
HPI
24
48
72
5
0

FIG. 4D, cont'd

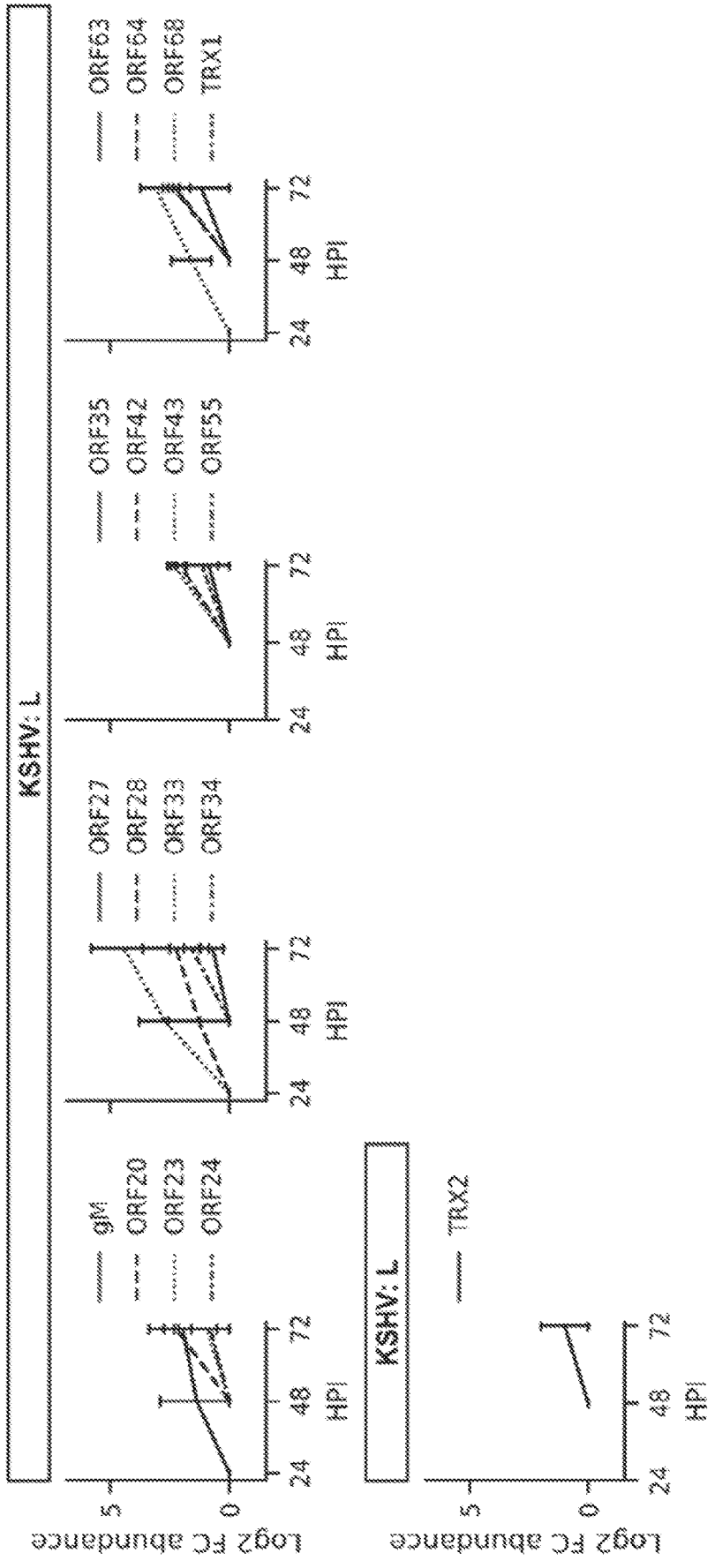

KSHV: L
gM
ORF20
ORF23
ORF24
ORF27
ORF28
ORF33
ORF34
ORF35
ORF42
ORF43
ORF55
ORF63
ORF64
ORF68
TRX1
KSHV: L
TRX2
log2 FC abundance
5
0
24
48
72
HPI

FIG. 5A

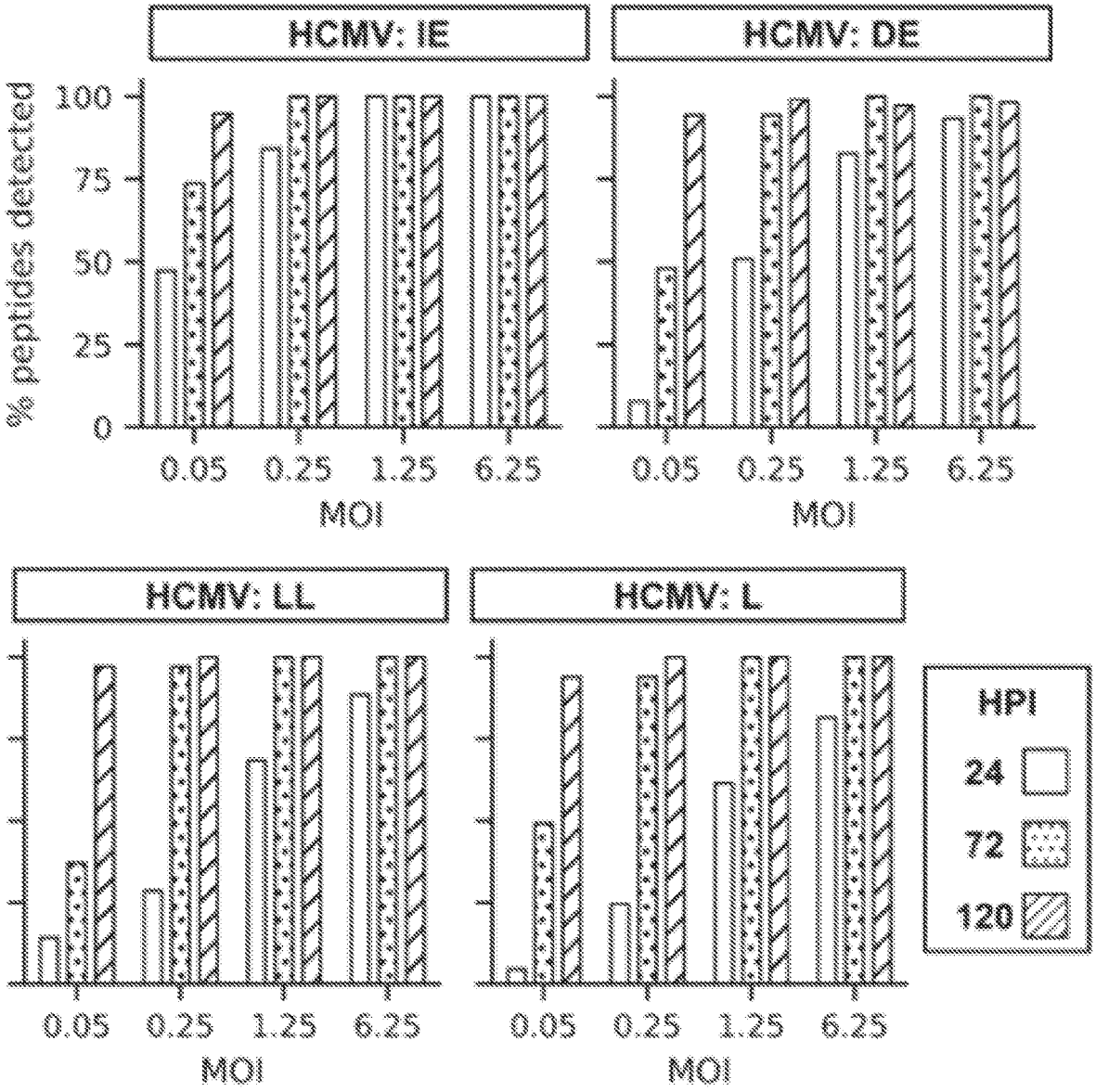

HCMV: IE
HCMV: DE
% peptides detected
100
75
50
25
0
0.05
0.25
1.25
6.25
MOI
HCMV: LL
HCMV: L
HPI
24
72
120

FIG. 5B

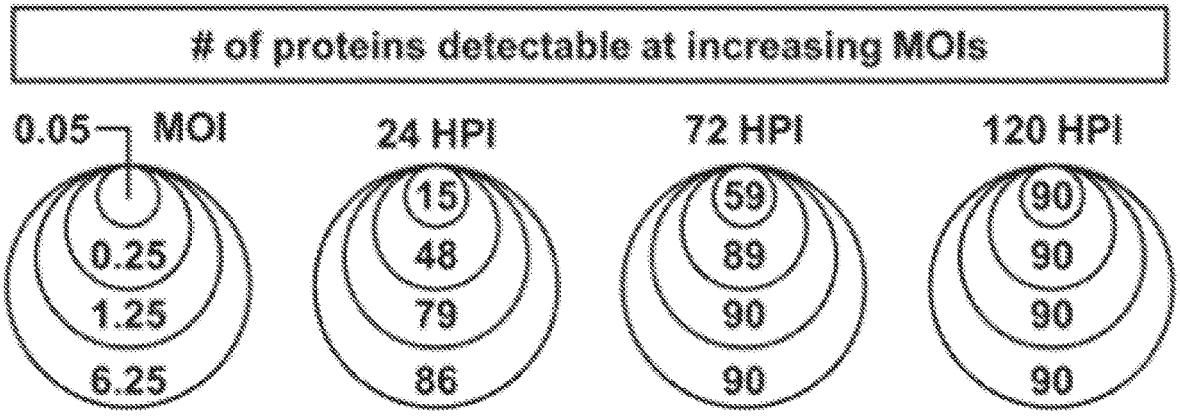

# of proteins detectable at increasing MOIs
0.05 MOI
0.25
1.25
6.25
24 HPI
15
48
79
86
72 HPI
59
89
90
90
120 HPI
90
90
90
90

FIG. 5C

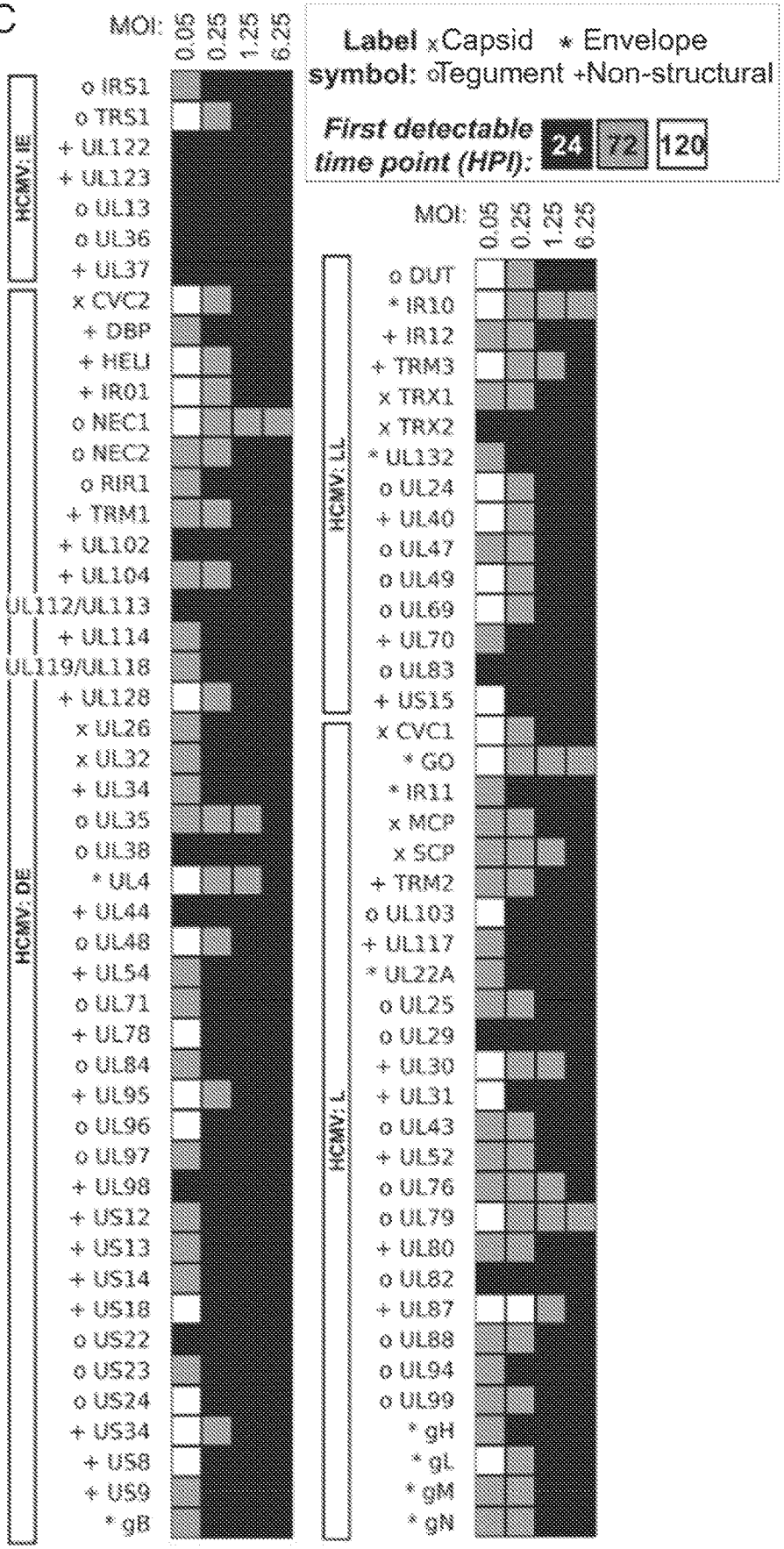

MOI: 0.05 0.25 1.25 6.25
Label symbol: x Capsid * Envelope o Tegument + Non-structural
First detectable time point (HPI): 24 72 120
HCMV: IE
o IRS1
o TRS1
+ UL122
+ UL123
o UL13
o UL36
+ UL37
HCMV: DE
x CVC2
+ DBP
+ HELI
+ IR01
o NEC1
o NEC2
o RIR1
+ TRM1
+ UL102
+ UL104
+ UL112/UL113
+ UL114
+ UL119/UL118
+ UL128
x UL26
x UL32
+ UL34
o UL35
o UL38
* UL4
+ UL44
o UL48
+ UL54
o UL71
+ UL78
o UL84
+ UL95
o UL96
o UL97
+ UL98
+ US12
+ US13
+ US14
+ US18
o US22
o US23
o US24
+ US34
+ US8
+ US9
* gB
MOI: 0.05 0.25 1.25 6.25
HCMV: LL
o DUT
* IR10
+ IR12
+ TRM3
x TRX1
x TRX2
* UL132
o UL24
+ UL40
o UL47
o UL49
o UL69
+ UL70
o UL83
+ US15
HCMV: L
x CVC1
* GO
* IR11
x MCP
x SCP
+ TRM2
o UL103
+ UL117
* UL22A
o UL25
o UL29
+ UL30
+ UL31
o UL43
+ UL52
o UL76
o UL79
+ UL80
o UL82
+ UL87
o UL88
o UL94
o UL99
* gH
* gL
* gM
* gN

FIG. 5D

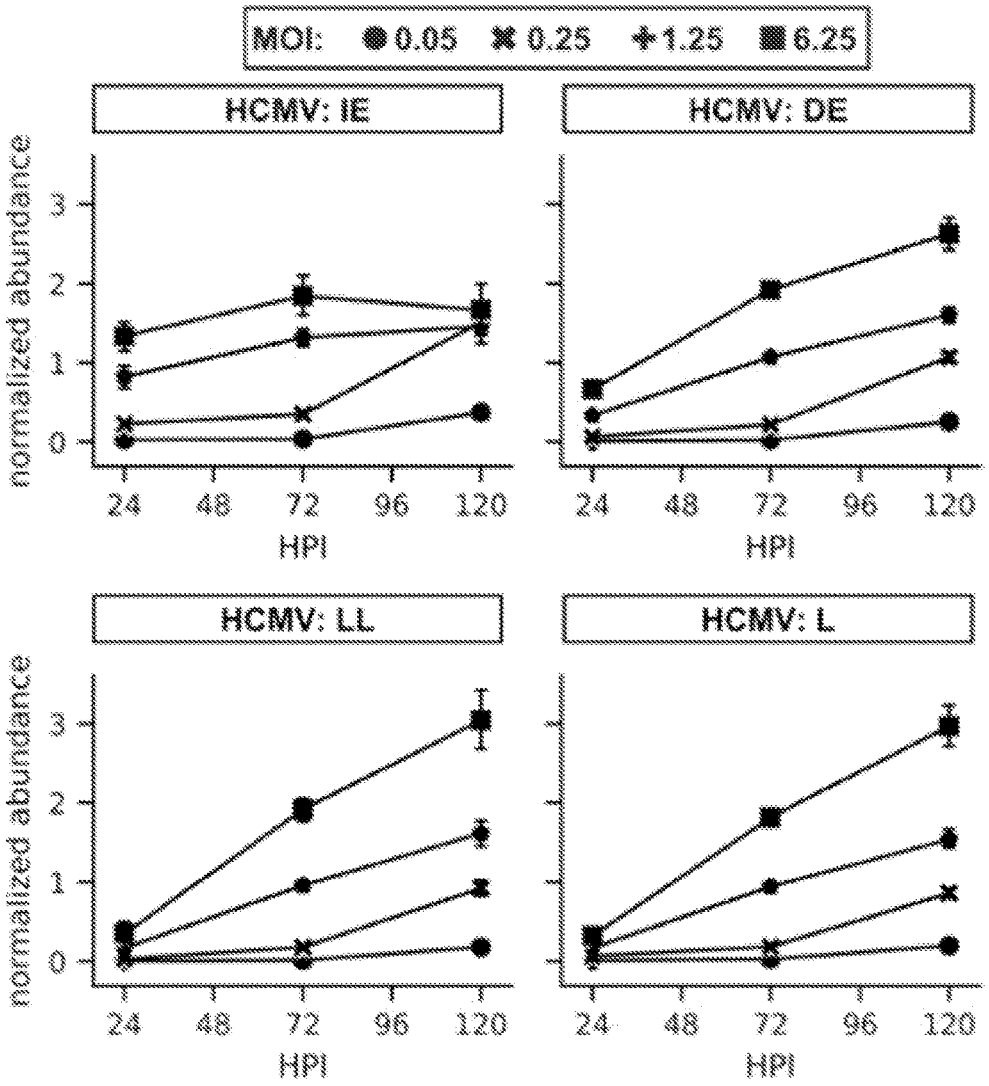

MOI: 0.05 0.25 1.25 6.25
HCMV: IE
HCMV: DE
HCMV: LL
HCMV: L
normalized abundance
0
1
2
3
24
48
72
96
120
HPI

FIG. 5E

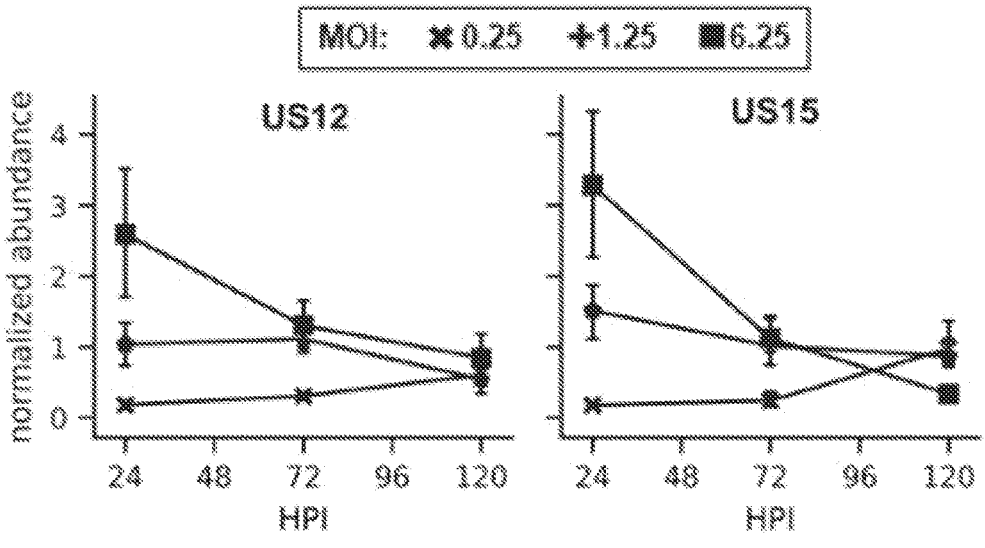

MOI: 0.25 1.25 6.25
US12
US15
normalized abundance
0
1
2
3
4
24
48
72
96
120
HPI

FIG. 6A

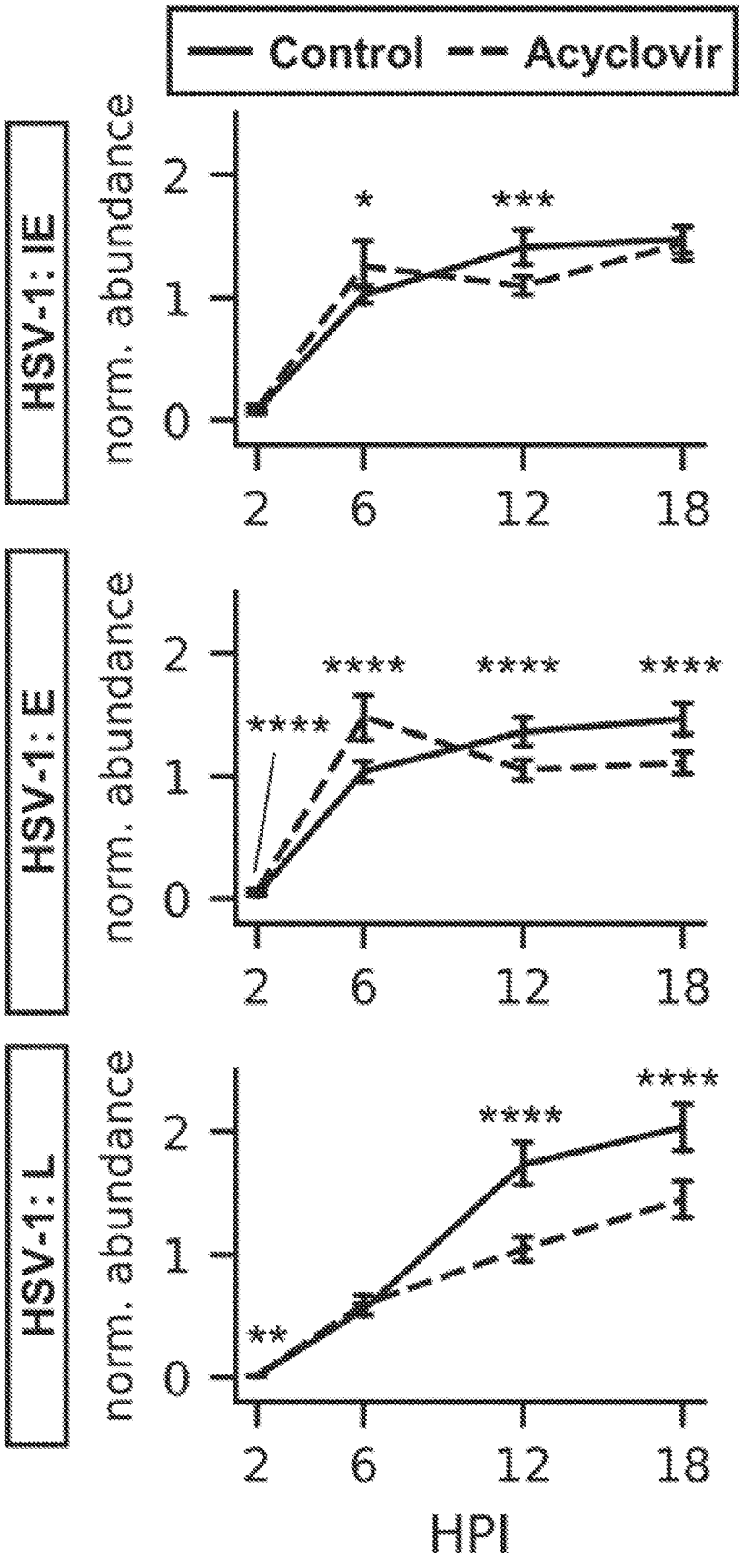

Control
Acyclovir
HSV-1: IE
HSV-1: E
HSV-1: L
norm. abundance
0
1
2
*
***
****
**
2
6
12
18
HPI

FIG. 6B

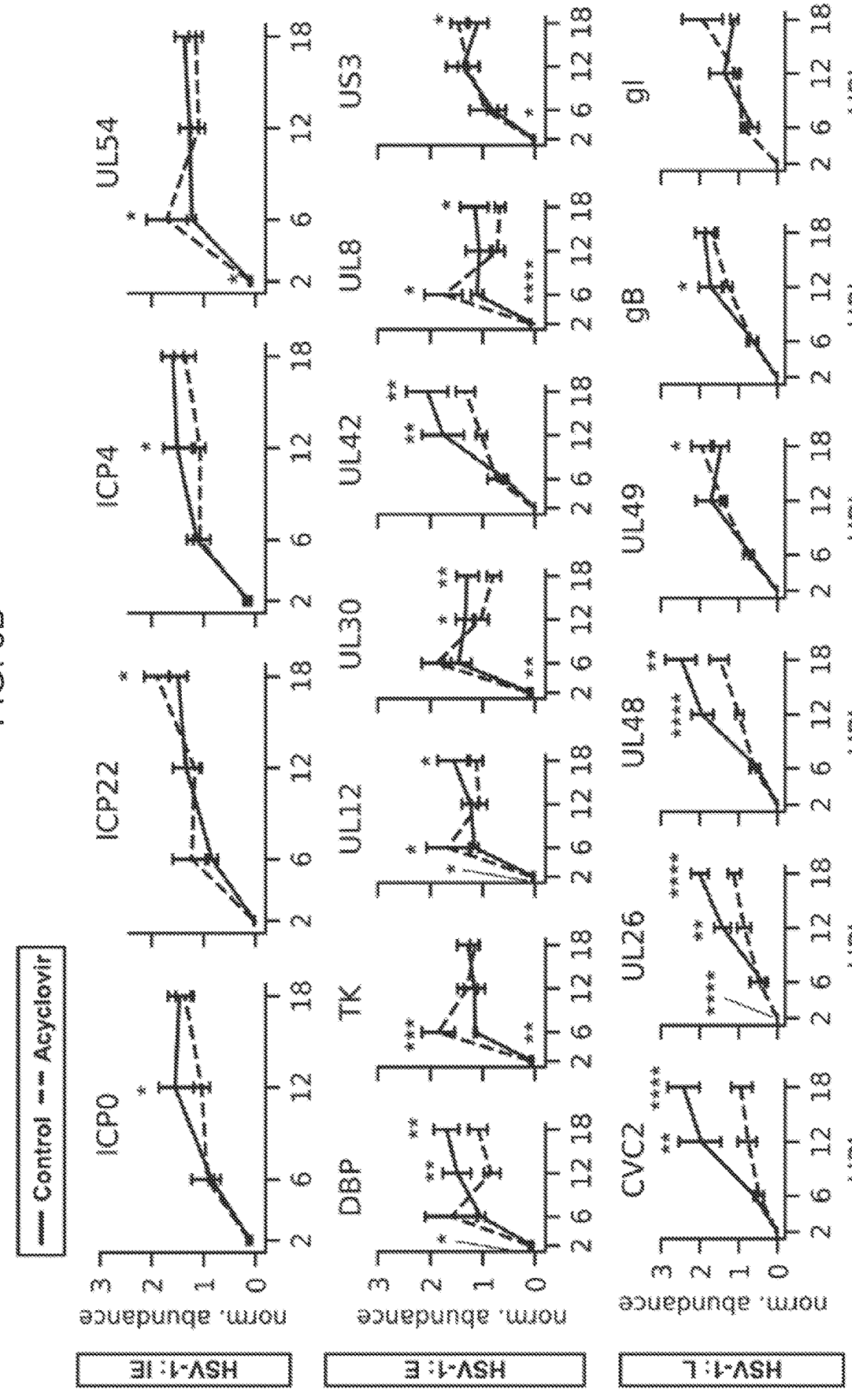
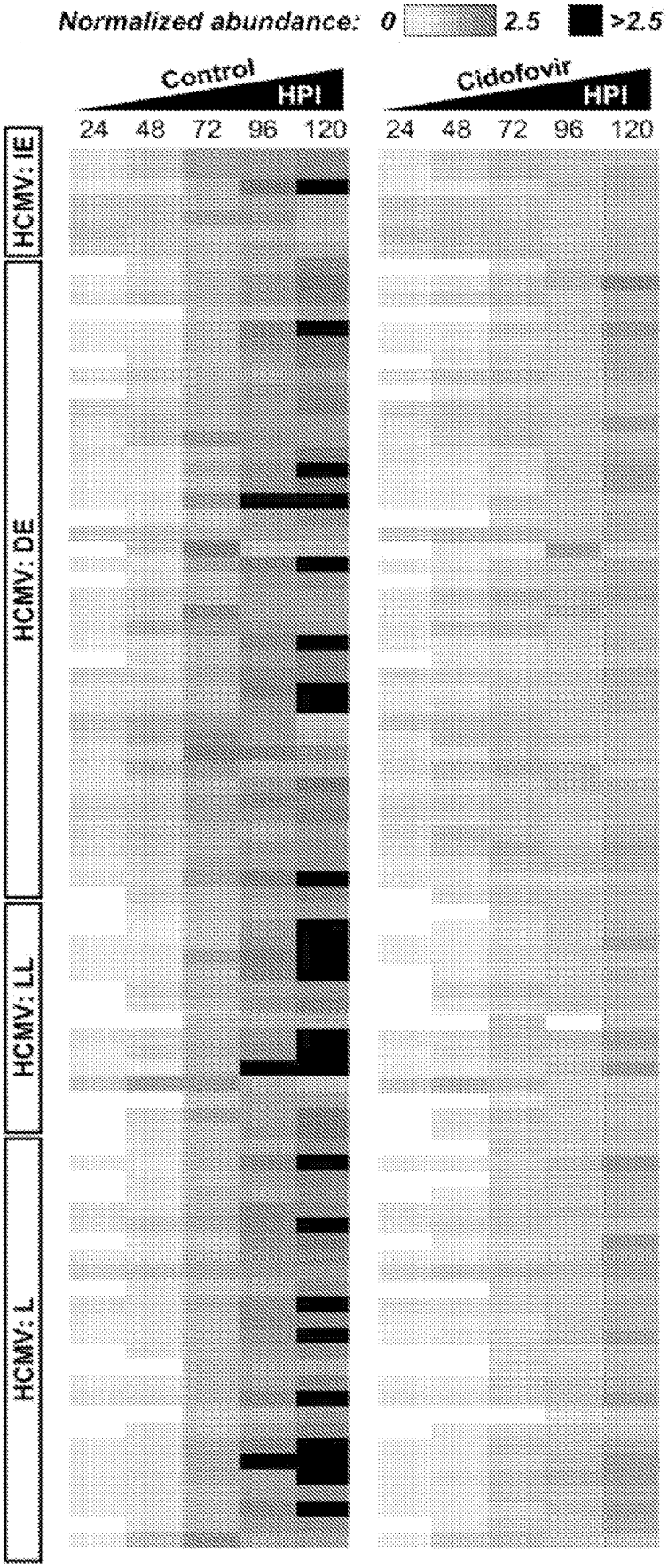

Control
Acyclovir
HSV-1: IE
HSV-1: E
HSV-1: L
norm. abundance
HPI
ICP0
ICP22
ICP4
UL54
DBP
TK
UL12
UL30
UL42
UL8
US3
CVC2
UL26
UL48
UL49
gB
gI

FIG. 6C


Normalized abundance: 0 2.5 >2.5
Control
HPI
24 48 72 96 120
Cidofovir
HPI
24 48 72 96 120
HCMV: IE
HCMV: DE
HCMV: LL
HCMV: L

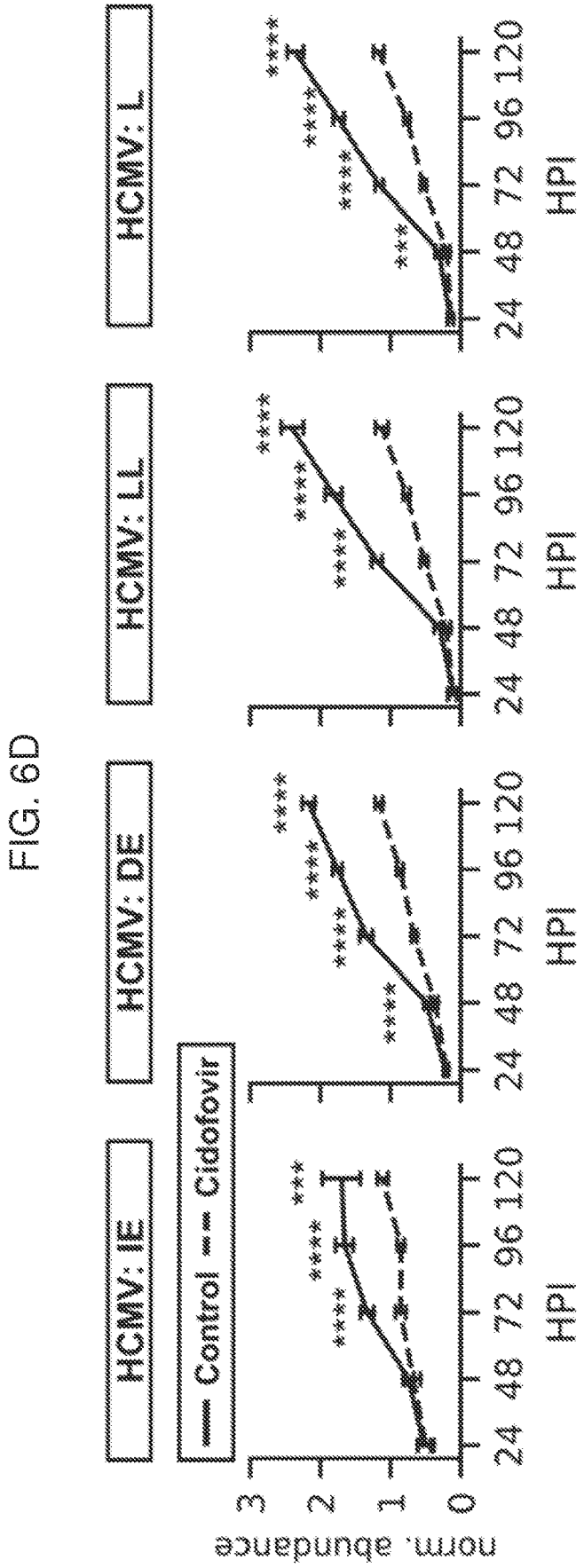

HCMV: IE
HCMV: DE
HCMV: LL
HCMV: L
Control
Cidofovir
norm. abundance
0
1
2
3
24
48
72
96
120
HPI
****
***

FIG. 6D

FIG. 6E

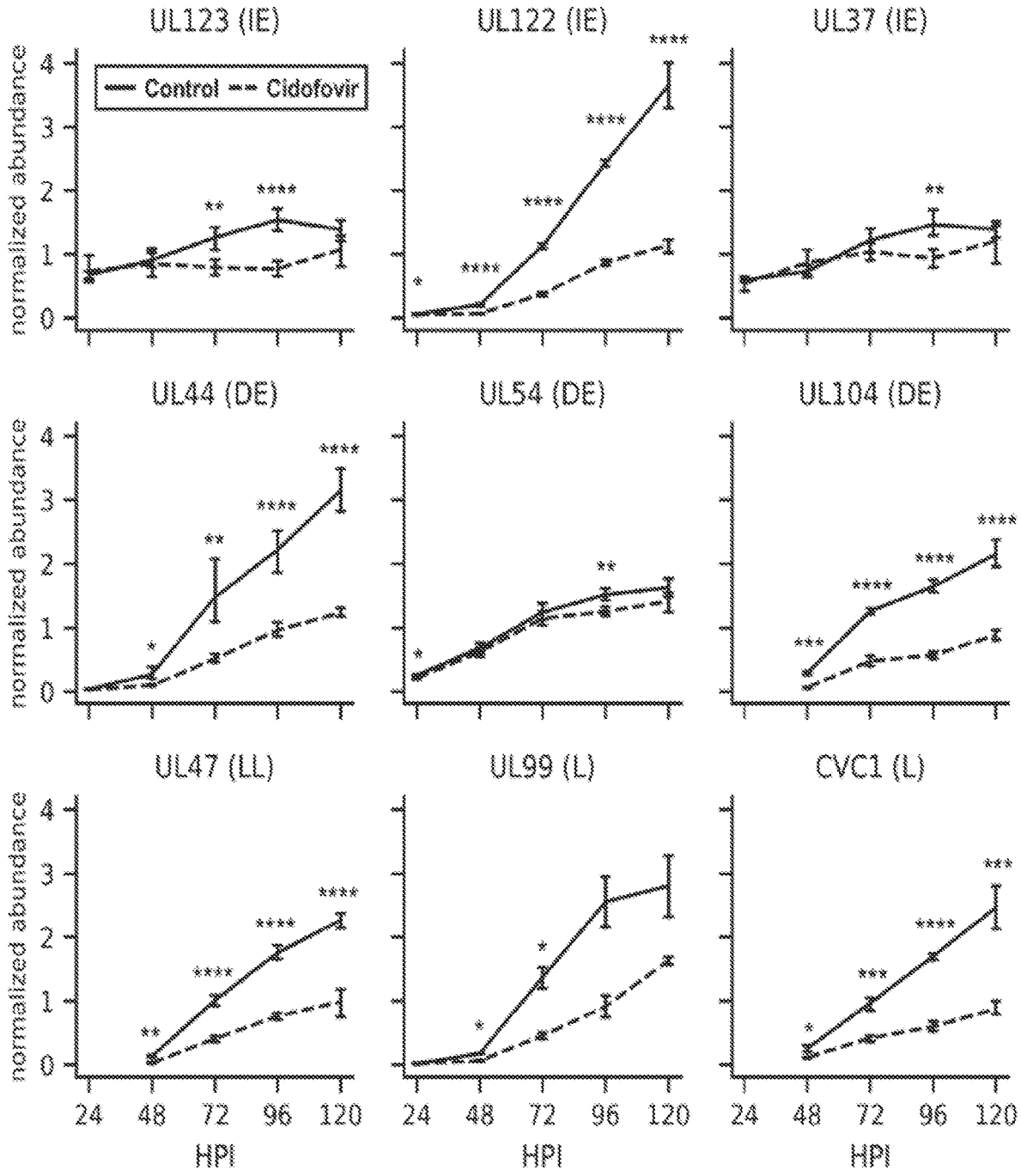

UL123 (IE)
UL122 (IE)
UL37 (IE)
UL44 (DE)
UL54 (DE)
UL104 (DE)
UL47 (LL)
UL99 (L)
CVC1 (L)
Control
Cidofovir
normalized abundance
HPI
24
48
72
96
120

FIG. 7A

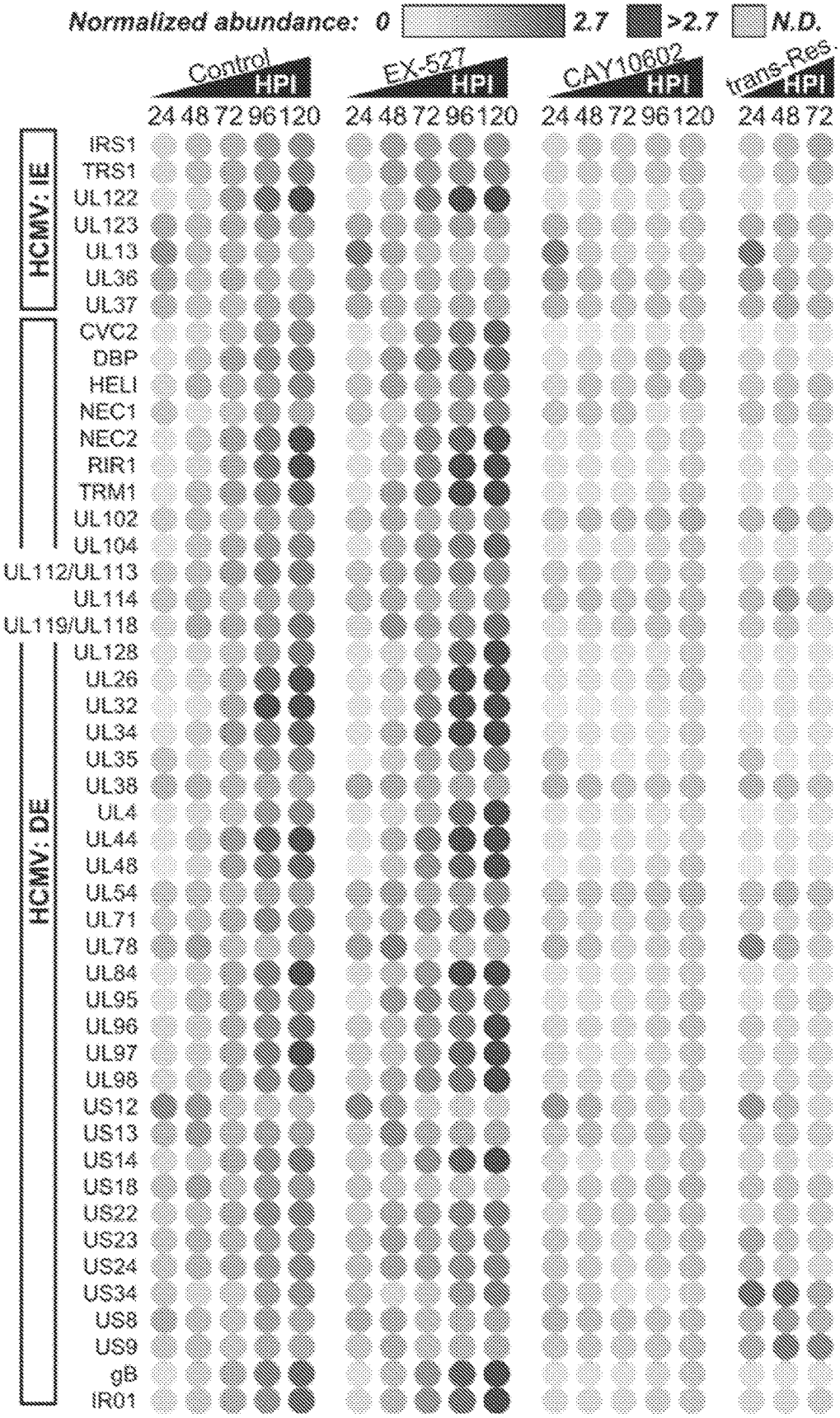

Normalized abundance: 0
2.7
>2.7
N.D.
Control
EX-527
CAY10602
trans-Res.
HPI
24 48 72 96 120
24 48 72 96 120
24 48 72 96 120
24 48 72
HCMV: IE
HCMV: DE
IRS1
TRS1
UL122
UL123
UL13
UL36
UL37
CVC2
DBP
HELI
NEC1
NEC2
RIR1
TRM1
UL102
UL104
UL112/UL113
UL114
UL119/UL118
UL128
UL26
UL32
UL34
UL35
UL38
UL4
UL44
UL48
UL54
UL71
UL78
UL84
UL95
UL96
UL97
UL98
US12
US13
US14
US18
US22
US23
US24
US34
US8
US9
gB
IR01

FIG. 7A cont'd

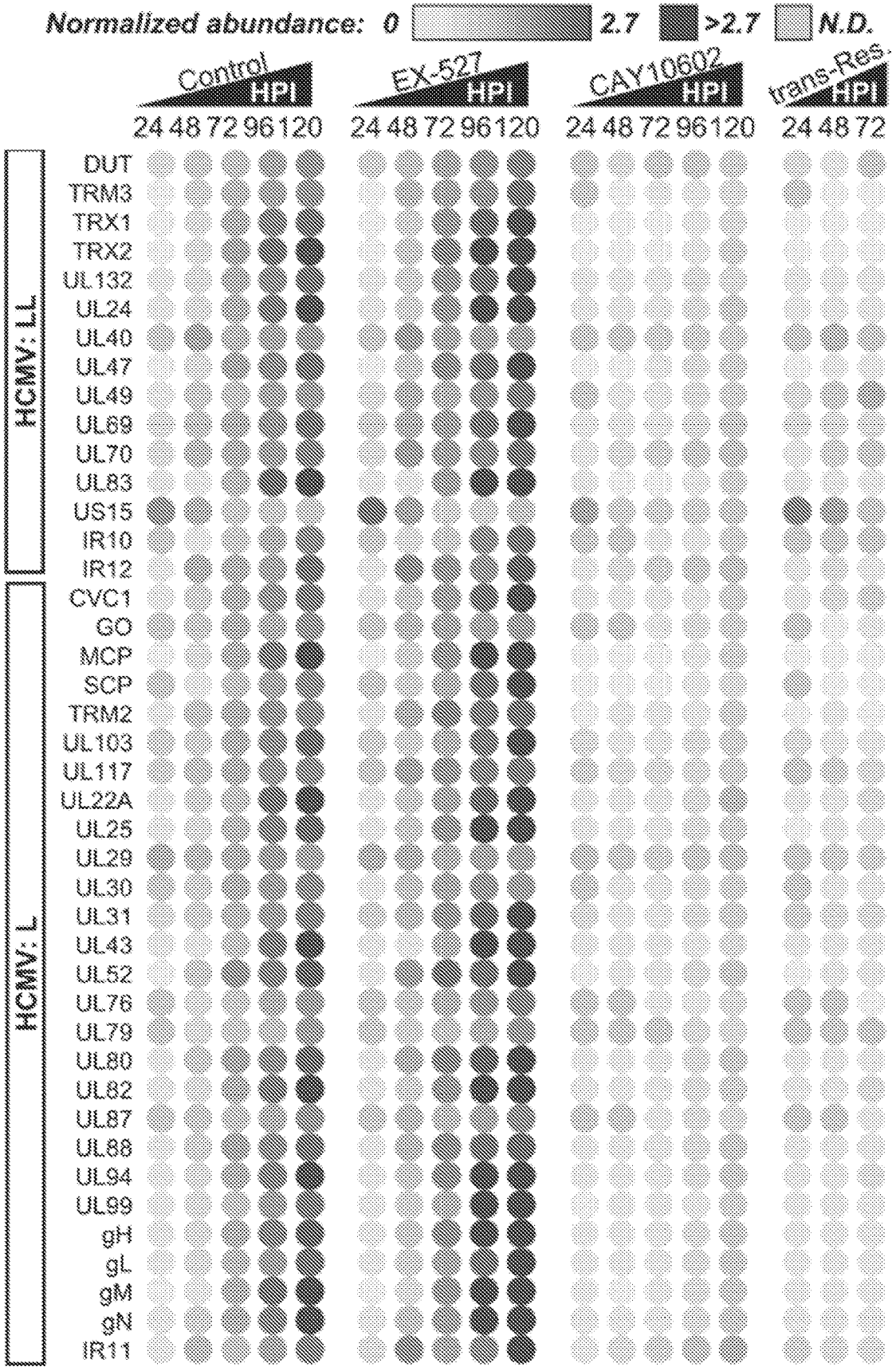

Normalized abundance: 0
2.7
>2.7
N.D.
Control
EX-527
CAY10602
trans-Res.
HPI
24 48 72 96 120
24 48 72 96 120
24 48 72 96 120
24 48 72
HCMV: LL
HCMV: L
DUT
TRM3
TRX1
TRX2
UL132
UL24
UL40
UL47
UL49
UL69
UL70
UL83
US15
IR10
IR12
CVC1
GO
MCP
SCP
TRM2
UL103
UL117
UL22A
UL25
UL29
UL30
UL31
UL43
UL52
UL76
UL79
UL80
UL82
UL87
UL88
UL94
UL99
gH
gL
gM
gN
IR11

FIG. 7B

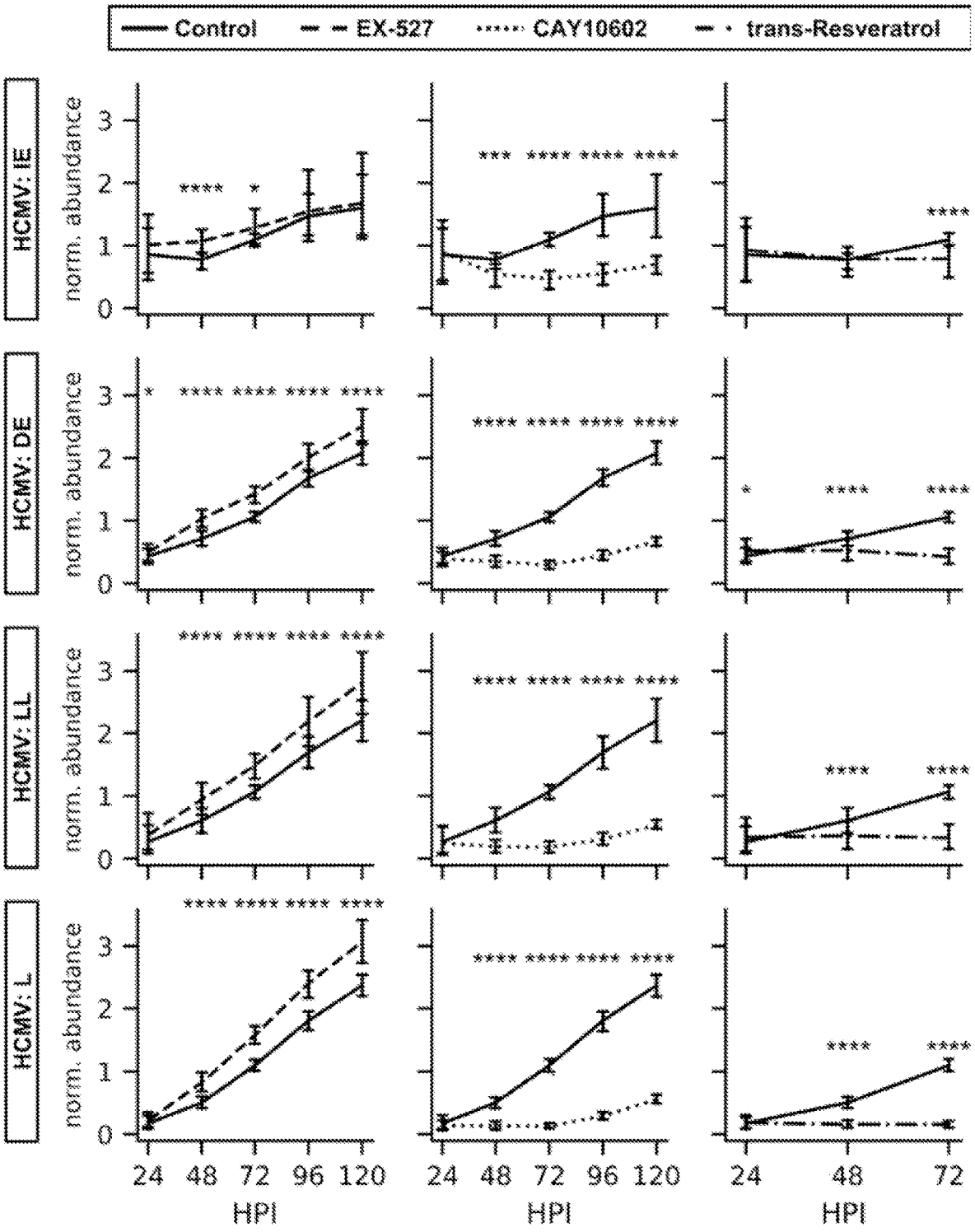

Control
EX-527
CAY10602
trans-Resveratrol
HCMV: IE
HCMV: DE
HCMV: LL
HCMV: L
norm. abundance
HPI
24 48 72 96 120
24 48 72

FIG. 7C

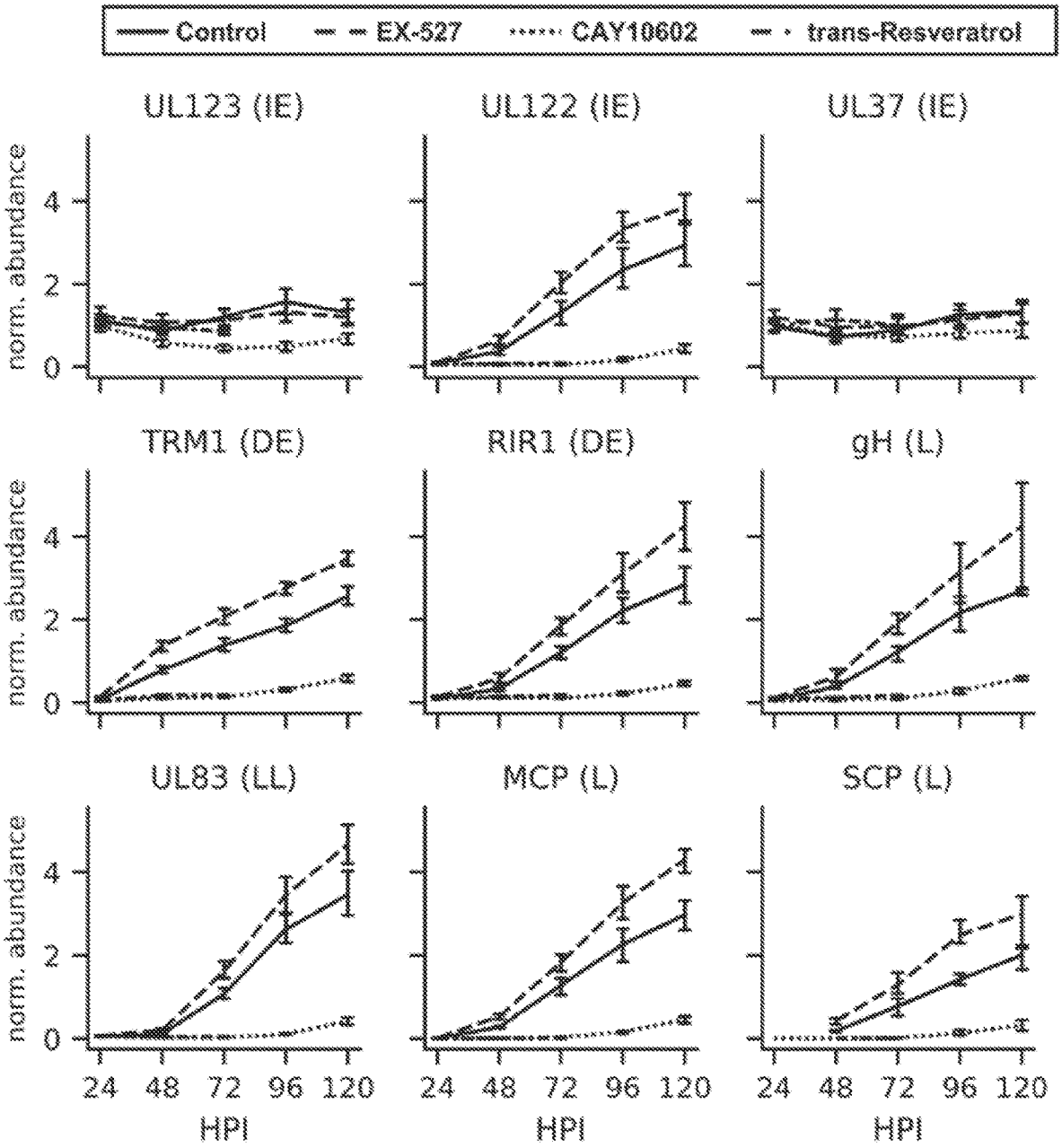

Control
EX-527
CAY10602
trans-Resveratrol
UL123 (IE)
UL122 (IE)
UL37 (IE)
TRM1 (DE)
RIR1 (DE)
gH (L)
UL83 (LL)
MCP (L)
SCP (L)
norm. abundance
0
2
4
24 48 72 96 120
HPI

FIG. 8A

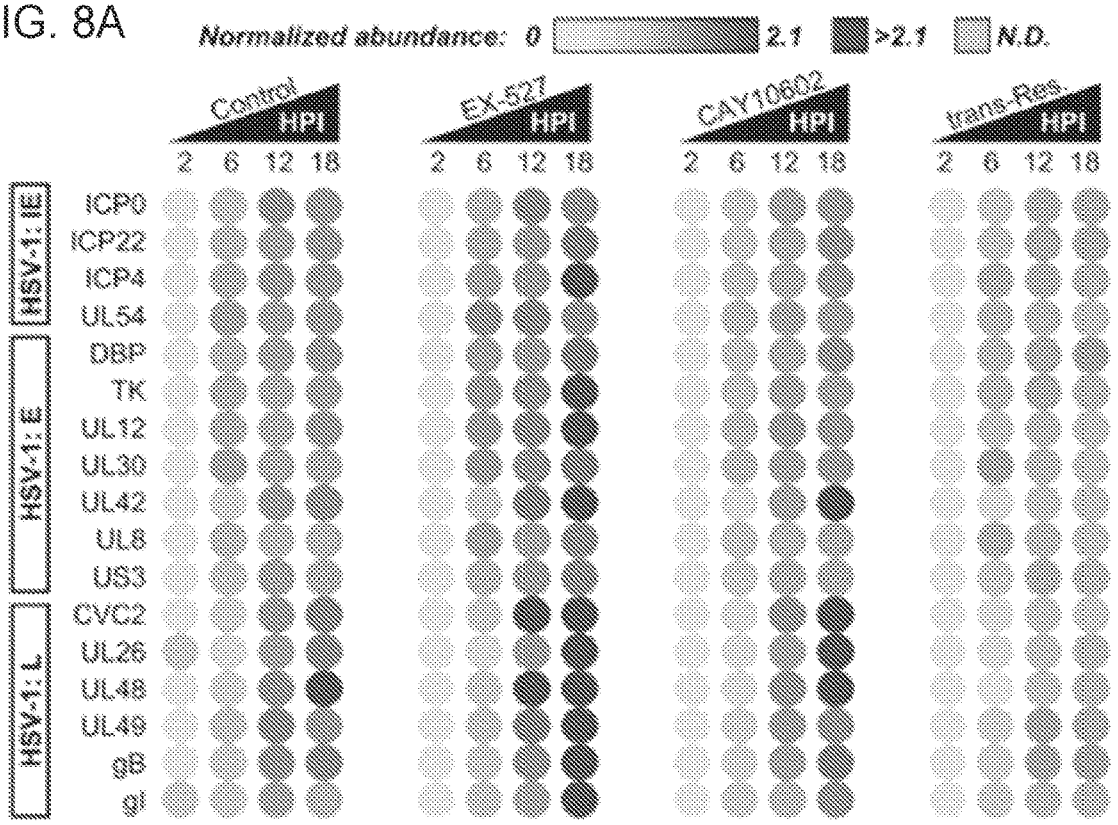

Normalized abundance: 0
2.1
>2.1
N.D.
Control
EX-527
CAY10602
trans-Res.
HPI
2 6 12 18
HSV-1: IE
HSV-1: E
HSV-1: L
ICP0
ICP22
ICP4
UL54
DBP
TK
UL12
UL30
UL42
UL8
US3
CVC2
UL26
UL48
UL49
gB
gI

FIG. 8B

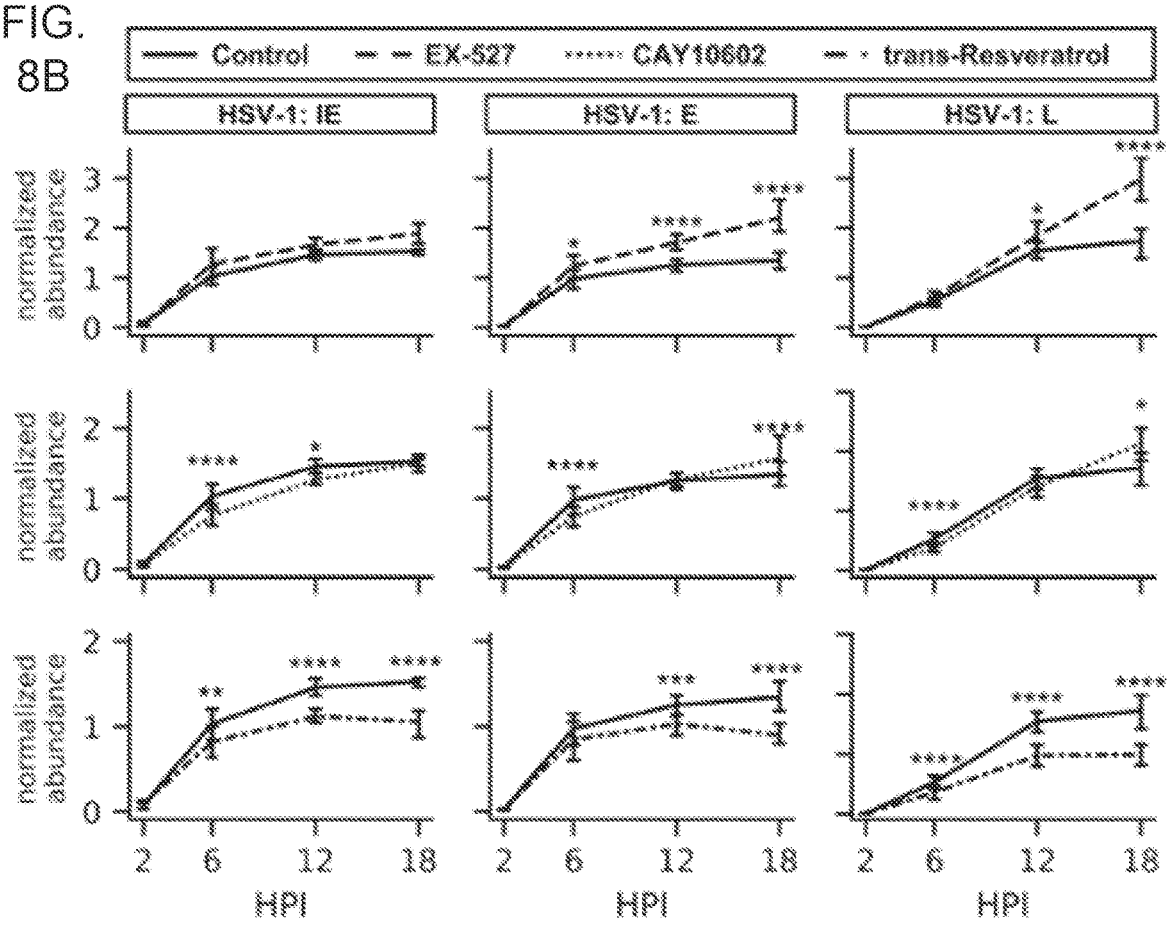

Control
EX-527
CAY10602
trans-Resveratrol
HSV-1: IE
HSV-1: E
HSV-1: L
normalized abundance
HPI
2 6 12 18

FIG. 8C

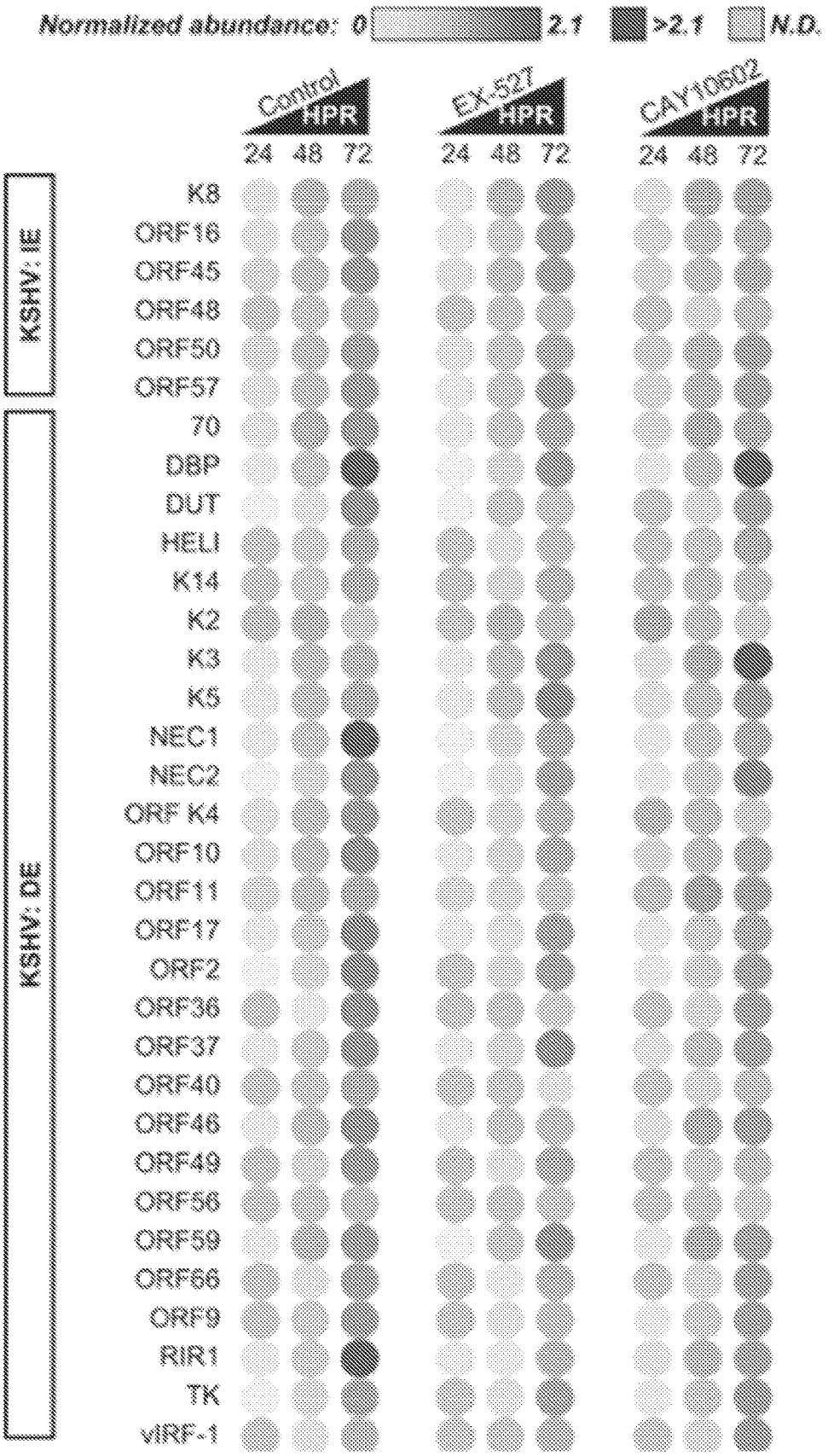

Normalized abundance: 0
2.1
>2.1
N.D.
Control
EX-527
CAY10602
HPR
24 48 72
KSHV: IE
KSHV: DE
K8
ORF16
ORF45
ORF48
ORF50
ORF57
70
DBP
DUT
HELI
K14
K2
K3
K5
NEC1
NEC2
ORF K4
ORF10
ORF11
ORF17
ORF2
ORF36
ORF37
ORF40
ORF46
ORF49
ORF56
ORF59
ORF66
ORF9
RIR1
TK
vIRF-1

FIG. 8C cont'd

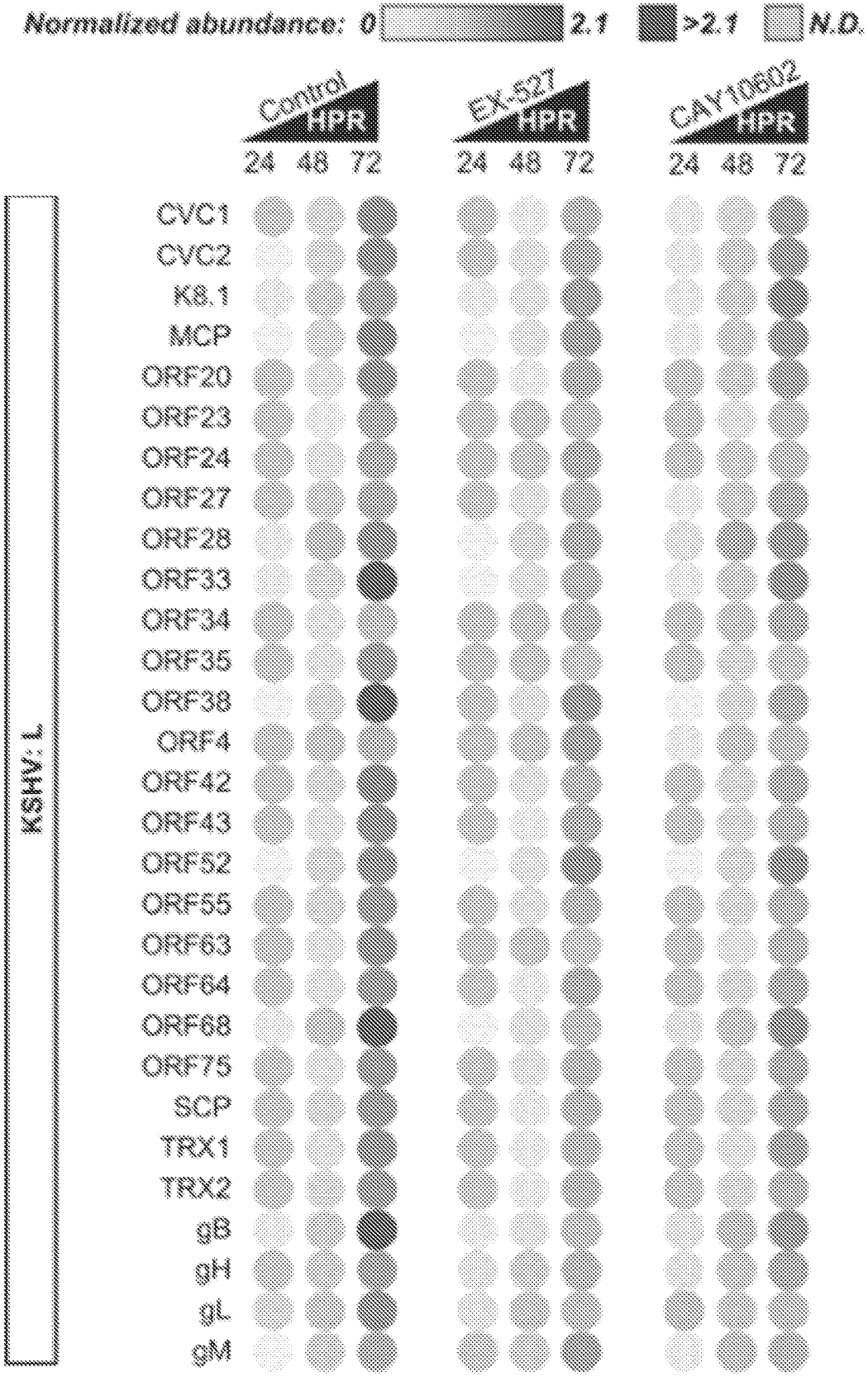

Normalized abundance: 0
2.1
>2.1
N.D.
Control
HPR
EX-527
HPR
CAY10602
HPR
24 48 72
24 48 72
24 48 72
KSHV: L
CVC1
CVC2
K8.1
MCP
ORF20
ORF23
ORF24
ORF27
ORF28
ORF33
ORF34
ORF35
ORF38
ORF4
ORF42
ORF43
ORF52
ORF55
ORF63
ORF64
ORF68
ORF75
SCP
TRX1
TRX2
gB
gH
gL
gM

FIG. 8D

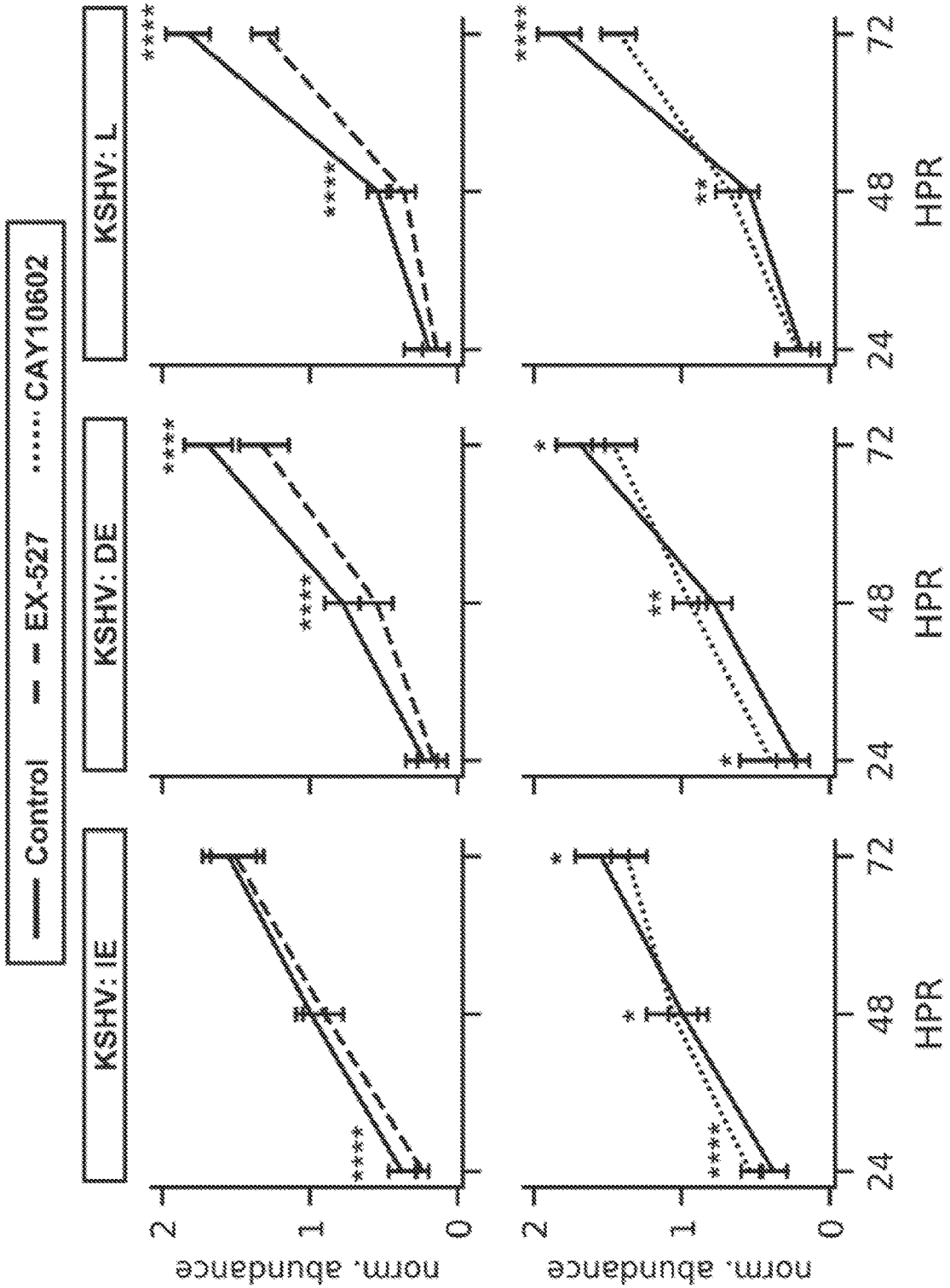
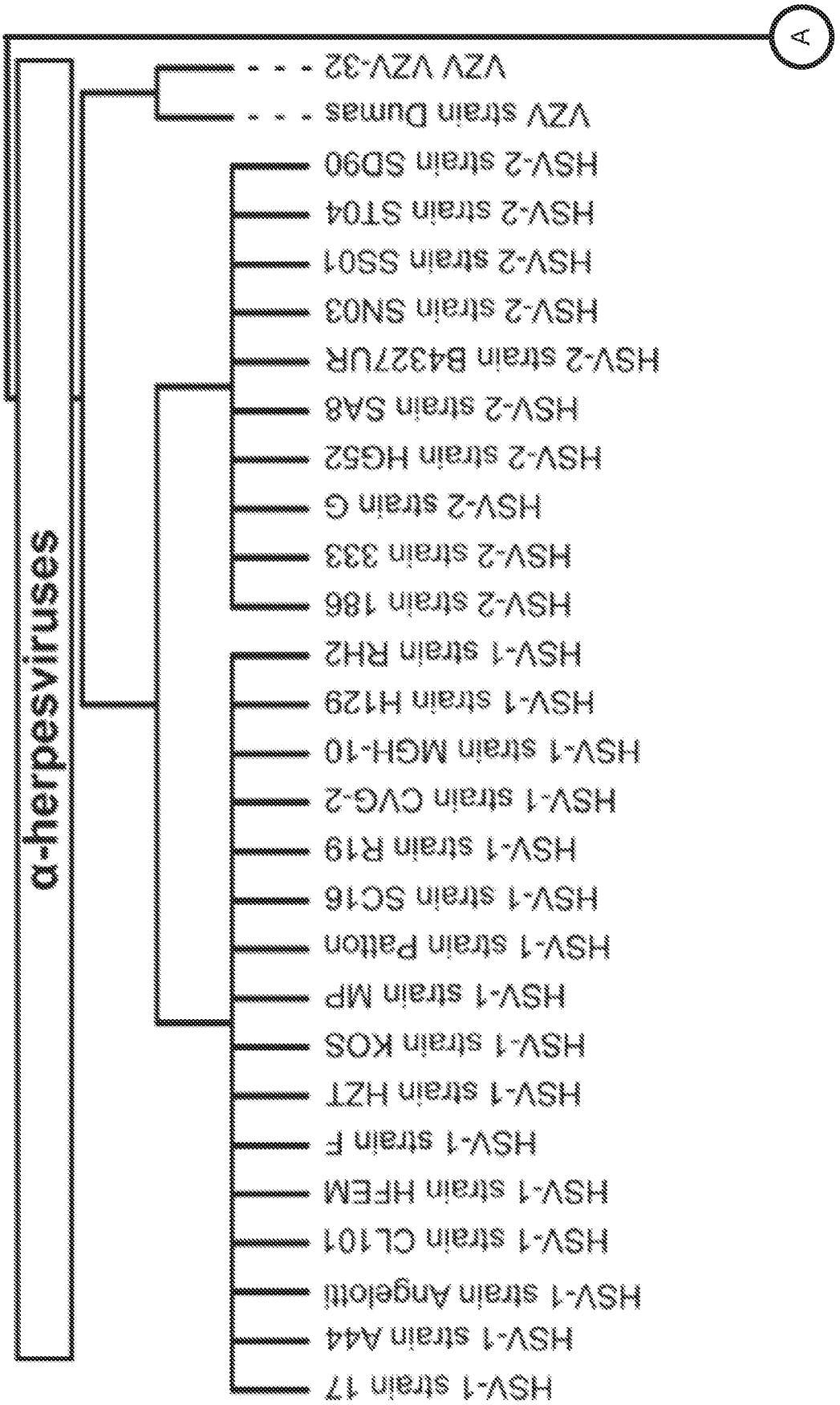

Control
EX-527
CAY10602
KSHV: IE
KSHV: DE
KSHV: L
norm. abundance
HPR
24
48
72
0
1
2
*
**
***
****

FIG. 9A


A
α-herpesviruses
VZV VZV-32
VZV strain Dumas
HSV-2 strain SD90
HSV-2 strain ST04
HSV-2 strain SS01
HSV-2 strain SN03
HSV-2 strain B4327UR
HSV-2 strain SA8
HSV-2 strain HG52
HSV-2 strain G
HSV-2 strain 333
HSV-2 strain 186
HSV-1 strain RH2
HSV-1 strain H129
HSV-1 strain MGH-10
HSV-1 strain CVG-2
HSV-1 strain R19
HSV-1 strain SC16
HSV-1 strain Patton
HSV-1 strain MP
HSV-1 strain KOS
HSV-1 strain HZT
HSV-1 strain F
HSV-1 strain HFEM
HSV-1 strain CL101
HSV-1 strain Angelotti
HSV-1 strain A44
HSV-1 strain 17

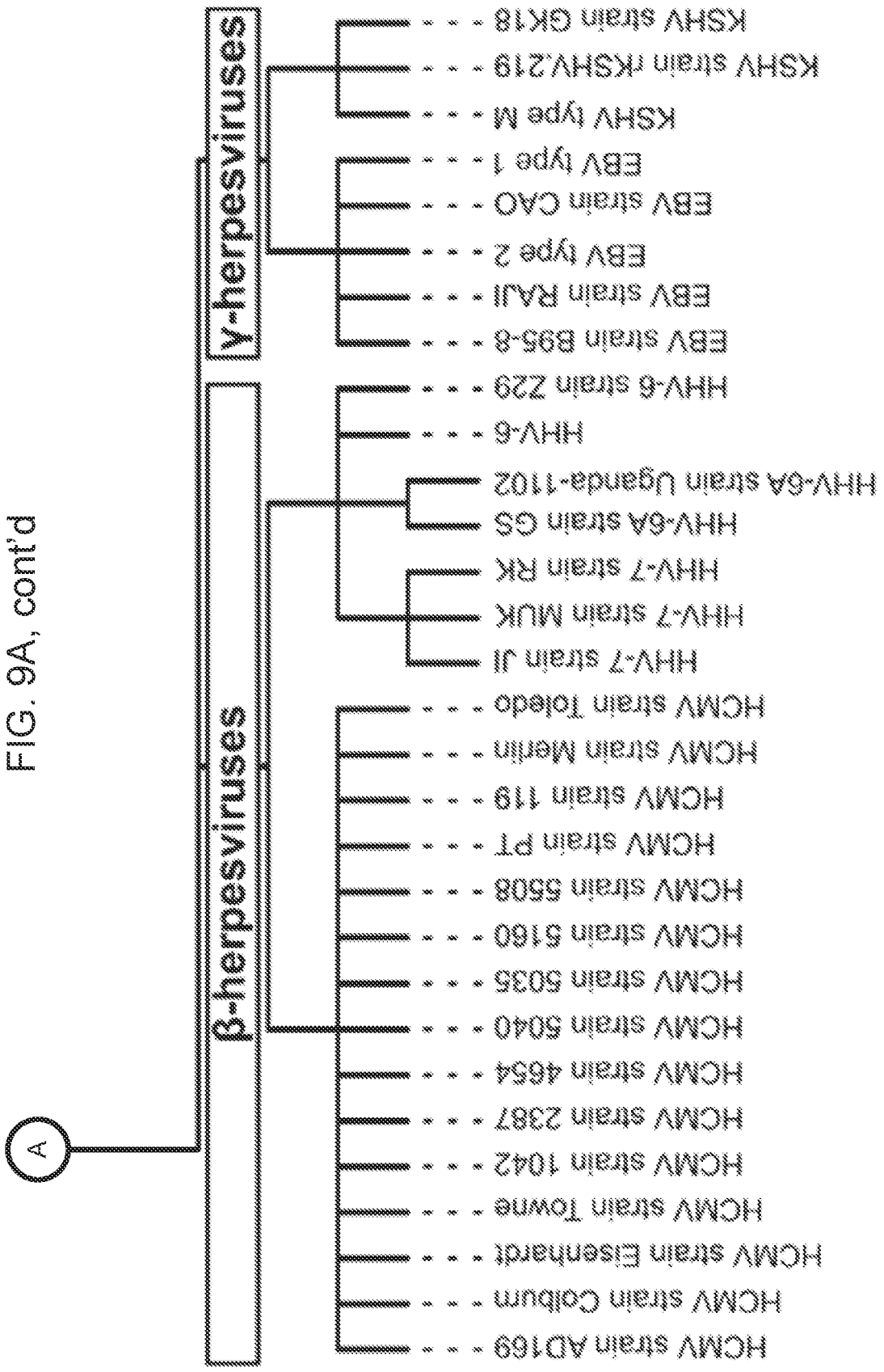

A
β-herpesviruses
γ-herpesviruses
HCMV strain AD169
HCMV strain Colburn
HCMV strain Eisenhardt
HCMV strain Towne
HCMV strain 1042
HCMV strain 2387
HCMV strain 4654
HCMV strain 5040
HCMV strain 5035
HCMV strain 5160
HCMV strain 5508
HCMV strain PT
HCMV strain 119
HCMV strain Merlin
HCMV strain Toledo
HHV-7 strain JI
HHV-7 strain MLK
HHV-7 strain RK
HHV-6A strain GS
HHV-6A strain Uganda-1102
HHV-6
HHV-6 strain Z29
EBV strain B95-8
EBV strain RAJI
EBV type 2
EBV strain CAO
EBV type 1
KSHV type M
KSHV strain rKSHV.219
KSHV strain GK18

FIG. 9A, cont'd

FIG. 9B

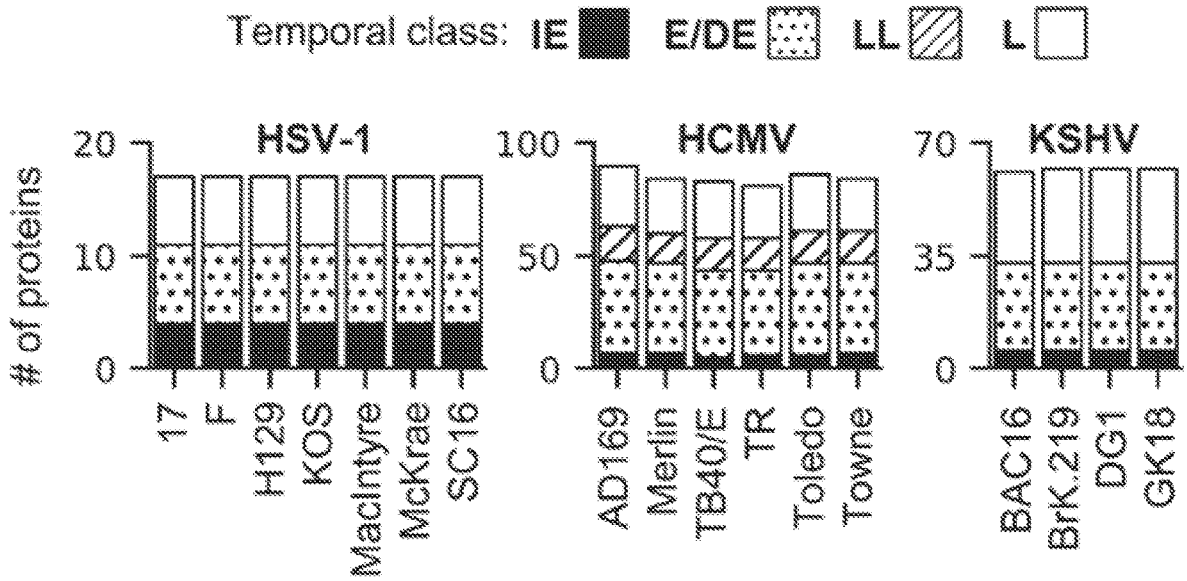

Temporal class: IE E/DE LL L
# of proteins
HSV-1
HCMV
KSHV
20
10
0
100
50
0
70
35
0
17
F
H129
KOS
MacIntyre
McKrae
SC16
AD169
Merlin
TB40/E
TR
Toledo
Towne
BAC16
BrK.219
DG1
GK18

FIG. 9C

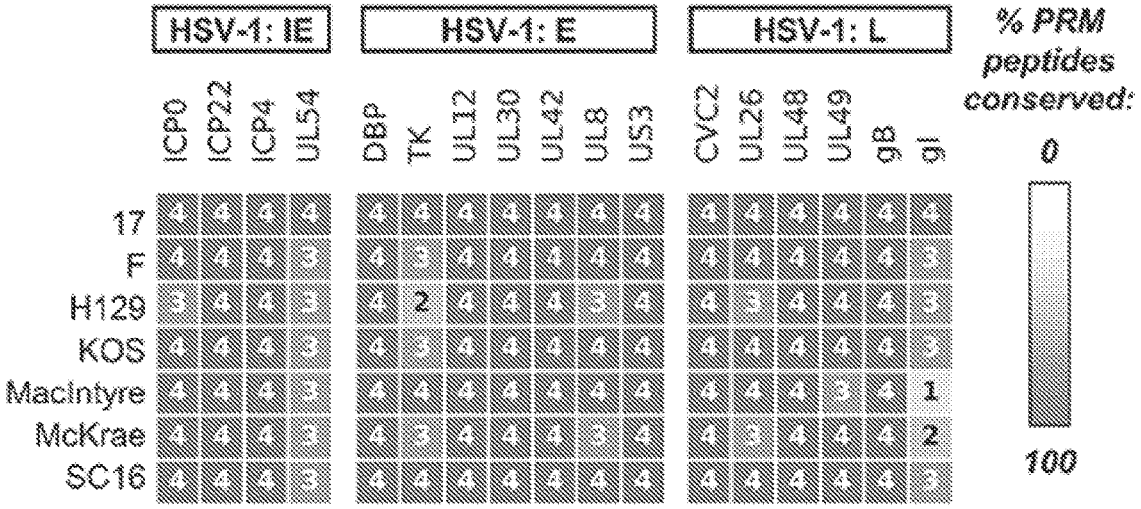

HSV-1: IE
HSV-1: E
HSV-1: L
% PRM peptides conserved:
0
100
ICP0
ICP22
ICP4
UL54
DBP
TK
UL12
UL30
UL42
UL8
US3
CVC2
UL26
UL48
UL49
gB
gI
17
F
H129
KOS
MacIntyre
McKrae
SC16

FIG. 9D

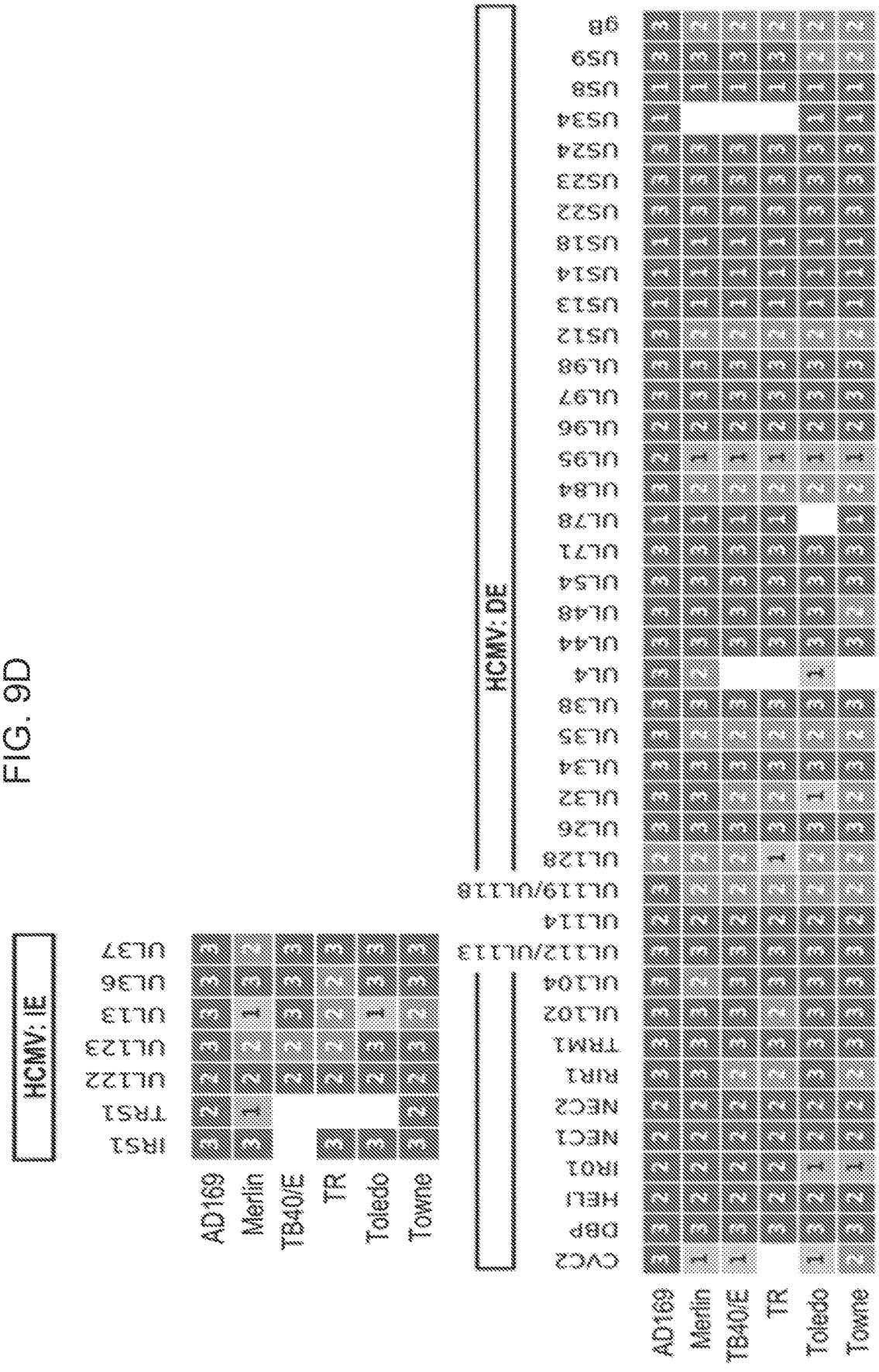

HCMV; IE
IRS1
TRS1
UL122
UL123
UL13
UL36
UL37
AD169
Merlin
TB40/E
TR
Toledo
Towne
HCMV; DE
CVC2
DBP
HEL
IRO1
NEC1
NEC2
RIR1
TRM1
UL102
UL104
UL112/UL113
UL114
UL119/UL118
UL128
UL26
UL32
UL34
UL35
UL38
UL4
UL44
UL48
UL54
UL71
UL78
UL84
UL95
UL96
UL97
UL98
US12
US13
US14
US18
US22
US23
US24
US34
US8
US9
gB
AD169
Merlin
TB40/E
TR
Toledo
Towne

FIG. 9D cont'd

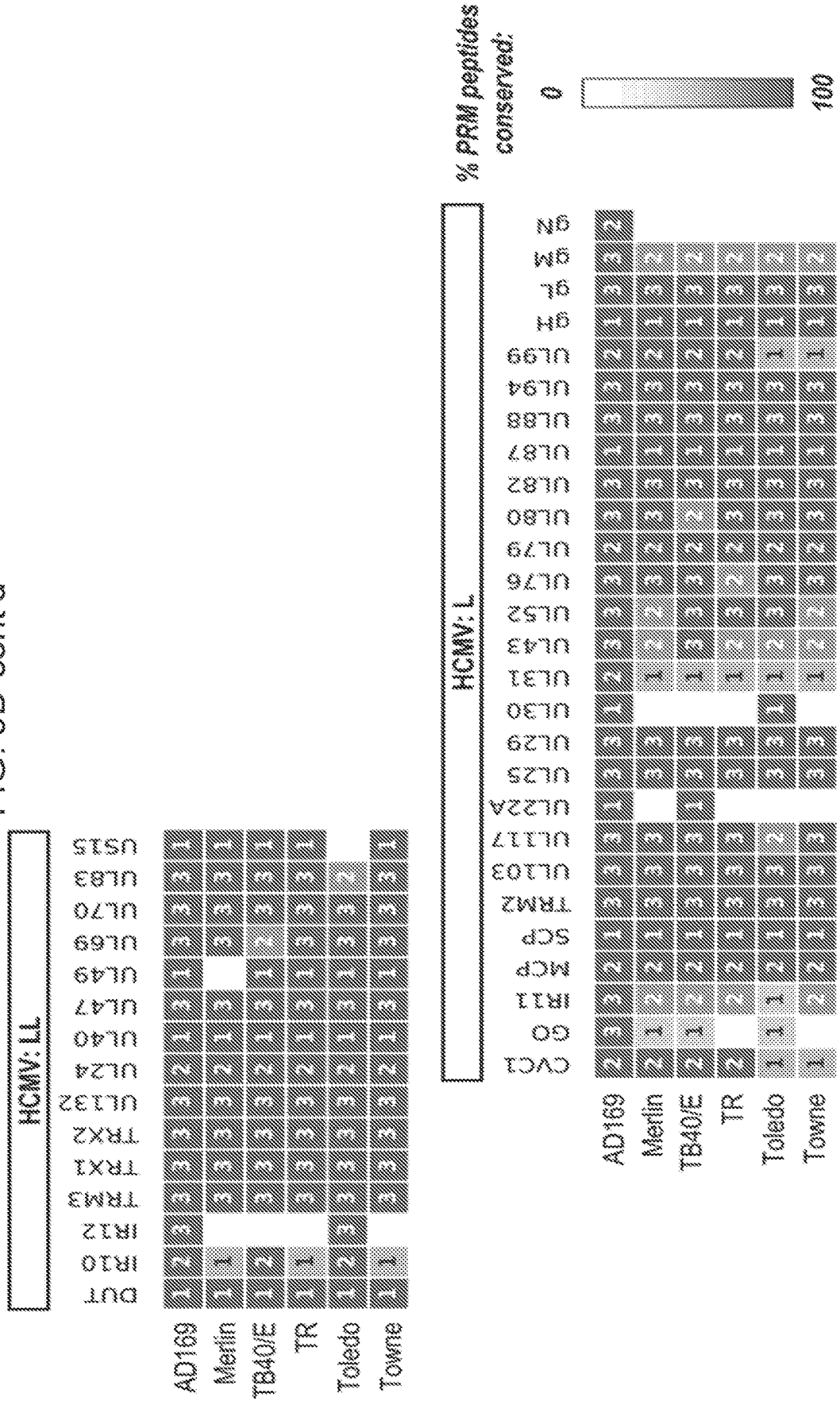
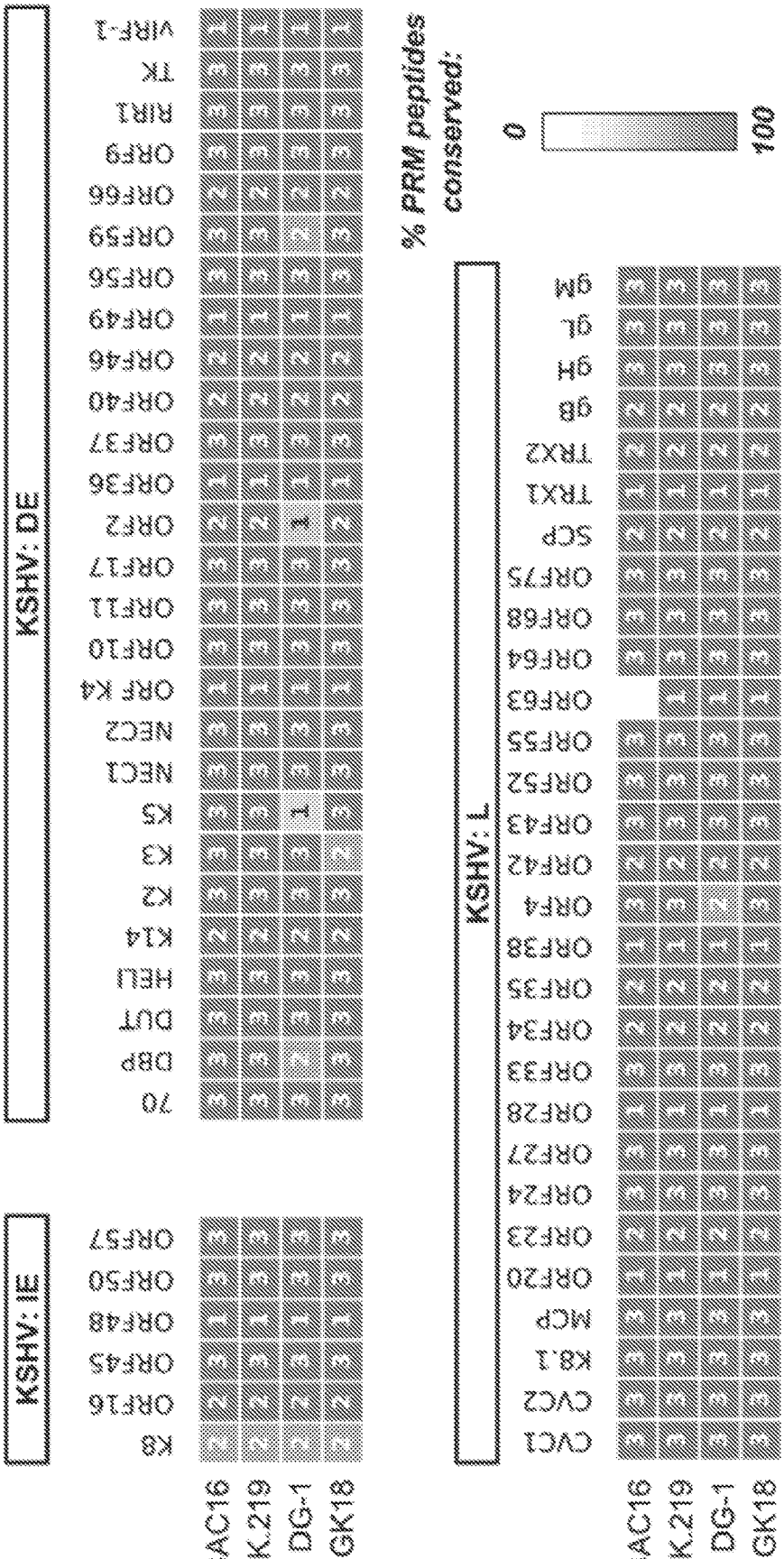

HCMV: LL
HCMV: L
% PRM peptides conserved:
0
100
AD169
Merlin
TB40/E
TR
Toledo
Towne
DUT
IR10
IR12
TRM3
TRX1
TRX2
UL132
UL24
UL40
UL47
UL49
UL69
UL70
UL83
US15
CVC1
GO
IR11
MCP
SCP
TRM2
UL103
UL117
UL22A
UL25
UL29
UL30
UL31
UL43
UL52
UL76
UL79
UL80
UL82
UL87
UL88
UL94
UL99
gH
gL
gM
gN

FIG. 9E


KSHV: IE
KSHV: DE
KSHV: L
% PRM peptides conserved:
0
100
BAC16
BrK.219
DG-1
GK18
K8
ORF16
ORF45
ORF48
ORF50
ORF57
70
DBP
DUT
HELI
K14
K2
K3
K5
NEC1
NEC2
ORF K4
ORF10
ORF11
ORF17
ORF2
ORF36
ORF37
ORF40
ORF46
ORF49
ORF56
ORF59
ORF66
ORF9
RIR1
TK
VIRF-1
CVC1
CVC2
K8.1
MCP
ORF20
ORF23
ORF24
ORF27
ORF28
ORF33
ORF34
ORF35
ORF38
ORF4
ORF42
ORF43
ORF52
ORF55
ORF63
ORF64
ORF68
ORF75
SCP
TRX1
TRX2
gB
gH
gL
gM

METHOD FOR DETECTION AND QUANTITATIVE MONITORING OF INFECTIONS WITH HERPESVIRUSES

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0001] This invention was made with government support under Grant No. GM114141 awarded by the National Institutes of Health. The government has certain rights in the invention.

INCORPORATION BY REFERENCE TO ANY PRIORITY APPLICATIONS

[0002] Any and all applications for which a foreign or domestic priority claim is identified in the Application Data Sheet as filed with the present application are hereby incorporated by reference under 37 CFR 1.57.

FIELD OF THE DISCLOSURE

[0003] The present disclosure relates generally to compositions, devices, systems, and methods for detection and quantification of herpesvirus infection. Embodiments of the disclosure describe methods of identifying and using protein signatures of herpesvirus infection, as well as exemplary protein signatures for use in such methods.

BACKGROUND OF THE DISCLOSURE

[0004] Herpesviruses infect up to 90% of the population and are dangerous in immunocompromised individuals and pregnant women. However, there are currently no effective non-toxic antiviral treatments or vaccines for these viruses. The replication of herpesviruses in host cells and the spread of infection to neighboring cells relies on a finely controlled virus replication cycle with a temporally tuned cascade of viral gene expression.

[0005] Despite the importance of herpesvirus infection, there exists an on-going need for methods to detect viral proteins or quantitatively track herpesvirus infections. Few antibodies specific for herpesvirus proteins are available, which inhibits accurate detection and tracking of herpesvirus infections.

SUMMARY OF THE DISCLOSURE

[0006] In order to effectively identify potential antiviral compounds, as well as gain an understanding of their impact on specific stages of a viral infection, described herein is development of a novel assay to monitor viral proteins from herpesviruses, such as the important human pathogens HSV-1 (an alpha herpesvirus), HMCV (a beta herpesvirus), and KSHV (a gamma herpesvirus). The described assays offer accurate detection and quantification of viral proteins from all distinct temporal classes (also referred to as kinetic classes) of viral replication (immediate-early (alpha), early (beta), and late (gamma)). These assays can be used to effectively screen and characterize potential antiviral compounds and any other infection modulators, as well as to gain mechanistic insights for instance by identifying the stage of infection and specific viral proteins affected by a compound. This is highly relevant for pharmaceutical companies and in clinical and biological research settings.

[0007] This disclosure describes the development of a method to assess the effects of small molecule treatment (or other perturbations) on herpesvirus infections by directly monitoring the temporal production and abundance levels of viral proteins. Assay embodiments described herein focus on herpesviruses due to the clear unmet medical need that they represent. This method is demonstrated herein for the three groups of herpesviruses (alpha, beta and gamma), including herpes simplex virus type 1 (HSV-1), human cytomegalovirus (HCMV) and Kaposi's sarcoma-associated herpesvirus (KSHV). The methods describe herein address at least three aims: (1) provide assays that allow accurate monitoring of the different temporal stages of viral infections, (2) enable use of these assays to screen for potential drugs that directly inhibit viral replication, determining the precise infection time point when these small molecules act, and (3) provide kits useful with the described assays.

[0008] One embodiment is an assay, including: obtaining a sample including: a cell or tissue infected with a herpesvirus, an extract from a cell or tissue infected with a herpesvirus, or a protein preparation from a cell or tissue infected with a herpesvirus; determining the abundance level of a plurality of herpesvirus proteins in the sample using parallel reaction monitoring (PRM) to quantify signature peptide(s) corresponding to the herpesvirus proteins; wherein the herpesvirus is HSV-1 and the signature peptides are selected from peptides in Table 1; or the herpesvirus is HCMV and the signature peptides are selected from peptides in Table 2; or the herpesvirus is KSHV and the signature peptides are selected from peptides in Table 3.

[0009] In examples of the assay embodiments, for at least the one herpesvirus protein for which the abundance level is determined, at least two signature peptides are quantified.

[0010] In examples of the assay embodiments, determining the abundance level of the plurality of herpesvirus proteins using PRM includes subjecting the sample to liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS).

[0011] In examples of the assay embodiments, the plurality of herpesvirus proteins includes at least one herpesvirus protein from each temporal class of viral replication for that herpesvirus.

[0012] In examples of the assay embodiments, the cell or tissue infected with the herpesvirus is a human cell or human tissue.

[0013] In examples of the assay embodiments, the plurality of herpesvirus proteins constitutes approximately 30-70%, or 50-80%, of the predicted viral proteome.

[0014] Also provided are time course assay embodiments, which assays involve repeating a herpesvirus protein assay as describe herein a plurality of times, where for each repetition the sample is obtained at a different timepoint in a time course. By way of example, the different timepoints in some instances are different times post infection of the cell or tissue with the herpesvirus. For instance, the different times after infection of the cell or tissue with the herpesvirus include at least one time from each state of a replication cycle of the herpesvirus. In yet other examples, the different timepoints are different times post exposure of the cell or tissue to a compound or a genetic or environmental variable.

[0015] Another provided embodiment is an exposure or dosage course assay (that is, an assay that is sampled across multiple exposures or dosages), the assay including: repeating a herpesvirus protein assay as described herein a plurality of times, where for each repetition the sample is obtained from a cell or tissue that has been exposed to a

different compound or condition or a different dosage of a compound or a condition. By way of example, the different compounds include one or more of known antiviral compounds, proposed antiviral compounds, test compounds, small molecule drugs or drug candidates, or siRNAs or other biologically active non-coding RNAs. For instance, the known antiviral compounds may include one or more of acyclovir, ganciclovir, another nucleoside, penciclovir, famciclovir, valacyclovir, valganciclovir, cidofovir, another nucleotide phosphonate, fomivirsen, or foscarnet. In additional examples of the exposure or dosage course, the different compounds can include honokiol.

[0016] In additional embodiments of the exposure or dosage course, the different exposures include one or more of genetic modification of the cell or tissue, genetic modification of the herpesvirus, environmental conditions, or cell or tissue growth or harvesting conditions. For instance, the genetic modification of the cell or tissue includes knock out or up-regulation of one or more host factors.

[0017] Yet another embodiment is a method for quantification of herpesvirus proteins from multiple temporal classes of viral replication, which method includes: subjecting a cell sample or cell extract to parallel reaction monitoring (PRM) to generate abundance data; analyzing the abundance data to quantify signature peptide(s) corresponding to at least one herpesvirus protein from each of at least two temporal classes of viral replication; and providing the quantified peptide(s) results from the analyzing to a database, a computer memory, a display, a printer, or another output device; wherein the herpesvirus is HSV-1 and the signature peptides are selected from peptides in Table 1; or the herpesvirus is HCMV and the signature peptides are selected from peptides in Table 2; or the herpesvirus is KSHV and the signature peptides are selected from peptides in Table 3.

[0018] Also described is use of any of the assays of the disclosure to: screen drug candidates as modulators of viral infection; analyze the stage of infection at which a test compound acts; determine what functional family(s) of viral proteins are affected by a drug or drug candidate; characterize viral and/or host responses to viral infection; characterize viral and/or host responses to drug treatment; or characterize viral and/or host responses to genetic manipulation of either the viral genome or the host genome.

[0019] Another embodiment is a kit for use with an assay or use embodiment, which kit includes: parameters for performing the assay for a target herpesvirus, a set of heavy isotope labeled peptides for use as controls, and a USB drive or other non-transitory computer readable medium containing software for assay analysis and/or standardized report generation. In examples of this kit embodiment, the target herpesvirus is HSV-1 and the set of heavy isotope labeled peptides includes: at least two signature peptides in Table 1; at least one signature peptide for each protein in Table 1; or at least one signature peptide from Table 1 for at least one protein from each temporal stage of HSV-1 viral replication. In further examples of the kit embodiment, the target herpesvirus is HCMV and the set of heavy isotope labeled peptides includes: at least two signature peptides in Table 2; at least one signature peptide for each protein in Table 2; or at least one signature peptide from Table 2 for at least one protein from each temporal stage of HCMV viral replication. In yet further examples, the target herpesvirus is KSHV and the set of heavy isotope labeled peptides includes: at least two signature peptides in Table 3; at least one signature peptide for each protein in Table 3; or at least one signature peptide from Table 3 for at least one protein from each temporal stage of KSHV viral replication.

[0020] Another embodiment is a service, the service including: performing an assay or a use as described herein on one or more biological samples provided by another/a third party (such as a researcher, a medical practitioner, and so forth). By way of example, such a service may be carried out for a fee. Optionally, results of the assay analysis may be provided to the third party by way of internet or other computerized correspondence.

[0021] This disclosure also provides assays, such as quantitative assays, for herpesviral proteins, substantially as described herein.

[0022] Yet another embodiment is a non-naturally occurring, labeled peptide having the amino acid sequence of a peptide in Table 1, Table 2, or Table 3. In examples of this non-naturally occurring, labeled peptide embodiment, the label enables the peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0023] Also described is a collection of non-naturally occurring, labeled signature peptides specific for HSV-1, the collection including: at least one peptide from Table 1 for each of the 60 proteins listed in Table 1; at least two peptides from Table 1 for each of the 60 proteins listed in Table 1; at least three peptides from Table 1 for each of the 60 proteins listed in Table 1; at least one peptide from Table 1 for at least one protein listed in Table 1 from each temporal stage of HSV-viral replication; at least 60 of the peptides listed in Table 1; more than 60 of the peptides listed in Table 1; at least 30 of the peptides listed in Table 1; at least 50 of the peptides listed in Table 1; at least 60 of the peptides listed in Table 1; substantially all of the peptides listed in Table 1; or all of the peptides listed in Table 1; wherein each peptide in the collection includes a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0024] Also described is a collection of non-naturally occurring, labeled signature peptides specific for HCMV, the collection including: at least one peptide from Table 2 for each of the 90 proteins listed in Table 2; at least two peptides from Table 2 for a plurality of the 90 proteins listed in Table 2; at least three peptides from Table 2 for a plurality of the 90 proteins listed in Table 2; at least one peptide from Table 2 for at least one protein listed in Table 2 from each temporal stage of HCMV-viral replication; at least 90 of the peptides listed in Table 2; more than 90 of the peptides listed in Table 2; at least 30 of the peptides listed in Table 2; at least 50 of the peptides listed in Table 2; at least 100 of the peptides listed in Table 2; at least 150 of the peptides listed in Table 2; at least 200 of the peptides listed in Table 2; substantially all of the peptides listed in Table 2; or all of the peptides listed in Table 2; wherein each peptide in the collection includes a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0025] Also described is a collection of non-naturally occurring, labeled signature peptides specific for KSHV, the

collection including: at least one peptide from Table 3 for each of the 62 proteins listed in Table 3; at least two peptides from Table 3 for a plurality of the 62 proteins listed in Table 3; at least three peptides from Table 3 for a plurality of the 62 proteins listed in Table 3; at least one peptide from Table 3 for at least one protein listed in Table 3 from each temporal stage of KSHV-viral replication; at least 62 of the peptides listed in Table 3; more than 62 of the peptides listed in Table 3; at least 30 of the peptides listed in Table 3; at least 50 of the peptides listed in Table 3; at least 75 of the peptides listed in Table 3; at least 100 of the peptides listed in Table 3; at least 150 of the peptides listed in Table 3; substantially all of the peptides listed in Table 3; or all of the peptides listed in Table 3; wherein each peptide in the collection includes a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0026] In any of the embodiments of non-naturally occurring, labeled signature peptides, the label on at least one peptide in the collection may include a heavy isotope. In some examples, all of the peptides in the collection include a heavy isotope.

DESCRIPTION OF THE DRAWINGS

[0027] One or more of the drawings submitted herewith are better understood in color, which is not available in patent application publications at the time of filing. Applicant considers the color versions of the drawings as part of the original submission and reserve the right to present color images of the drawings in later proceedings.

[0028] FIG. **1**. Representative workflow for signature detection of viral proteins by targeted mass spectrometry. First, a library of peptides unique to the proteins of interest and signature information derived from their mass spectrometry (MS) analysis is generated and experimentally validated. Next, this signature information is used for targeted MS analyses by parallel reaction monitoring (PRM). This offers accurate detection and quantification of the proteins of interest during the progression of infection, and can be implemented in any cell or tissue sample. This system can also be employed across different analysis labs, as the peptides provide self-balancing internal controls useful no matter who carries out the analysis.

[0029] FIG. **2**. is a computer architecture diagram showing one illustrative computer hardware architecture for implementing a computing device that might be utilized to implement aspects of the various embodiments presented herein. For instance, a computing device may be useful in recording, processing, analyzing, and/or presenting information including the quantification of peptide(s) indicative of the presence and/or quantity of a virus such as a herpesvirus. A computing device may be useful in analysis of raw information provided by a mass spectrophotometer, for instance in order to calculate protein level (in absolute or relative numbers) based on the quantification of one or more signature peptide(s) corresponding to that protein.

[0030] FIGS. **3**A-**3**F: Developing and validating TRUSTED, a PRM-based method for monitoring HSV-1, HCMV, and KSHV viral proteins (FIG. **3**A) Schematic representation of the herpesvirus replication cycle consisting of stages of entry, viral gene expression, genome replication, and the assembly and egress of newly formed virus particles. Timeline below the schematic depicts the relative time scale of replication in hours post-infection (HPI) for the alpha, beta, and gamma-herpesviruses HSV-1, HCMV, and KSHV, respectively. (FIG. **3**B) Overview of the PRM assay development process and its subsequent applications. (FIG. **3**C) Table of PRM assay specifications and protein targets. (FIG. **3**D) Traces of maximum concurrent precursors vs. retention time (RT) for different RT windows. Dashed grey line denotes **30** concurrent precursors, which is the maximum number of precursors that can be monitored at a given RT in a single injection to achieve reliable quantitation with the instrument settings utilized in this study. (FIG. **3**E) Normalized abundances across infection time for selected host proteins used for data normalization. (FIG. **3**F) Coefficient of variation (CV) between normalized abundance values. (Left) CV across different peptides from a given protein within the same biological replicate. (Middle) CV across biological replicates for a given peptide. (Right) Overall CV for a given protein across peptides and biological replicates. Note: Data is derived from experiments conducted under wild type infection conditions (HSV-1 and HCMV: MOI=3; KSHV: 100% reactivation) and error bars represent a 95% confidence interval (CI) across biological replicates (HSV-1: n=2; HCMV: n=7; KSHV: n=2).

[0031] FIGS. **4**A-**4**D: Herpesvirus PRM assay captures the signature temporal cascade of viral gene expression Abundance plots of: HSV-1 viral proteins (FIG. **4**A), HSV-1 host proteins (FIG. **4**B), HCMV viral proteins (FIG. **4**C), and KSHV viral proteins (FIG. **4**D). Plots of proteins are stratified by temporal expression class (IE=immediate early; DE=delayed early; E=early; LL=leaky late; L=late). Protein abundance levels are represented as fold-change (log-2) relative to the first time point at which peptides were detected. Data is derived from experiments conducted under wild type infection conditions (HSV-1 and HCMV: MOI=3; KSHV: 100% reactivation) and error bars represent a 95% CI across biological replicates (HSV-1: n=2; HCMV: n=7; KSHV: n=2). Significance was determined by two-tailed Student's t-test; *$p<0.05$, ** $p<0.01$, *** $p<0.001$, and **** $p<0.0001$.

[0032] FIGS. **5**A-**5**E: Differing levels of infection (MOI) are robustly detected via PRM (FIG. **5**A) Percent of HCMV peptides detected at different time points across increasing amounts of input virus (multiplicities of infection; MOI); in each set (MOI level), the bars represent 24, 72, and 102 hours post infection (HPI) from left to right. A peptide was considered to be "detected" if it was observed in at least one biological replicate (n=3). (FIG. **5**B) Number of viral proteins detected at increasing MOIs. All reported values are inclusive; i.e. all proteins detected at the previous MOI were also detected at the next MOI. (FIG. **5**C) Time point of first detection for HCMV proteins at increasing MOIs. The symbol preceding protein gene names corresponds to the part of the virion they are reported to associate with. (FIG. **5**D) Average HCMV protein abundance across infection time for increasing amounts of input virus (MOI), stratified by temporal class. Error bars represent a 95% CI across biological replicates (n=3). (FIG. **5**E) Protein abundance plots of HCMV proteins US12 and US15 at increasing MOIs. Error bars represent a 95% CI across biological replicates (n=3). Key: IE=Immediate Early, DE=Delayed Early, LL=Leaky Late, and L=Late Early.

[0033] FIGS. **6**A-**6**E: PRM application to investigations of clinically employed herpesvirus antiviral drugs (FIGS. **6**A-**6**B) Normalized protein abundance plots of HSV-1 pro-

tein levels during treatment with 1 μM acyclovir or DMSO (control) averaged across protein expression temporality classes (FIG. **6**A) or individual proteins (FIG. **6**B). (FIG. **6**C) Heatmap of HCMV protein levels after treatment with 1 μM cidofovir or PBS (control); the corresponding numerical values are provided in Table FIG. **6**C. (FIG. **6**D) Average HCMV protein abundance following 1 μM cidofovir or PBS (control) treatment stratified by protein expression temporality. (FIG. **6**E) Selected individual HCMV protein plots after 1 μM cidofovir or PBS (control) treatment. Error bars represent a 95% CI across biological replicates (HSV-1: n=2; HCMV: n=2). Significance was determined by two-tailed Student's t-test; *p<0.05, ** p<0.01, *** p<0.001, and **** p<0.0001.

[0034] FIGS. **7**A-**7**C: Modulation of sirtuin enzymatic activity regulates HCMV viral protein levels (FIG. **7**A) Heatmap of average HCMV protein levels after treatment with 10 μM EX-527, 12.5 μM CAY10602, 50 μM trans-Resveratrol (trans-Res.), or DMSO (control); N.D.=not detected; the corresponding numerical values are provided in Table FIG. **7**A. (FIG. **7**B) Average mean normalized (left) or log-2-fold-change (right; treatment/control) HCMV protein abundances following 10 μM EX-527, 12.5 μM CAY10602, 50 μM trans-Resveratrol, or DMSO (control) treatment stratified by protein expression temporality. (FIG. **7**C) Selected individual HCMV protein plots after 10 μM EX-527, 12.5 μM CAY10602, 50 μM trans-Resveratrol, or DMSO (control) treatment. Error bars represent a 95% CI across biological replicates (n=3). Significance was determined by two-tailed Student's t-test; *p<0.05, ** p<0.01, *** p<0.001, and **** p<0.0001.

[0035] FIGS. **8**A-**8**D: Modulation of sirtuin enzymatic activity differentially regulates HSV-1 and KSHV viral protein levels throughout infections (FIG. **8**A) Heatmap of average HSV-1 protein levels after treatment with 10 μM EX-527, 12.5 μM CAY10602, 50 μM trans-Resveratrol (trans-Res.), or DMSO (control); N.D.=not detected; the corresponding numerical values are provided in Table FIG. **8**A. (FIG. **8**B) Mean normalized HSV-1 protein abundances following 10 μM EX-527, 12.5 μM CAY10602, 50 μM trans-Resveratrol, or DMSO treatment stratified by protein expression temporality. (FIG. **8**C) Heatmap of average KSHV protein levels after treatment with 10 μM EX-527, 12.5 μM CAY10602, or DMSO (control); N.D.=not detected; the corresponding numerical values are provided in Table FIG. **8**C. (FIG. **8**D) Mean normalized KSHV protein abundances following 10 μM EX-527, 12.5 μM CAY10602, or DMSO (control) treatment stratified by protein expression temporality. Significance was determined by two-tailed Student's t-test; *p<0.05, ** p<0.01, *** p<0.001, and **** p<0.0001. Note: trans-Resveratrol was toxic at 50 μM to the iSLK.219 cell line, so its effect on KSHV protein levels could not be measured.

[0036] FIGS. **9**A-**9**E: Conservation of TRUSTED peptides indicates assay utility across several laboratory and clinical virus strains (FIG. **9**A) Phylogenetic tree of human herpesviruses from strains annotated in the NCBI taxonomy database. (FIGS. **9**B-**9**E) Predicted conservation of PRM assay peptides and proteins across different species and strains of human herpesviruses as represented by potential peptide sequences reported in complete genome sequences deposited in the NCBI nucleotide database. Peptides were only considered to be conserved if they matched with 100% identity to a consecutive string of amino acids in a given computationally translated nucleotide sequence. (FIG. **9**B) Number of proteins in the PRM assays that are conserved across different human herpesvirus strains. Any protein with at least one conserved peptide is depicted and protein representation by temporal class is shown as a stacked bar graph. (FIGS. **9**C-**9**E) Numbers of conserved peptides for all proteins targeted in the PRM assays for HSV-1 (FIG. **9**C; corresponding numerical values provided in Table FIG. **9**C), HCMV (FIG. **9**D; corresponding numerical values provided in Table FIG. **9**D), and KSHV (FIG. **9**E; corresponding numerical values provided in Table FIG. **9**E). The number of conserved peptides is denoted within each box and its color corresponds to the percent of peptides that are conserved for a given protein.

REFERENCE TO SEQUENCES

[0037] The amino acid sequences described herein are shown using standard letter abbreviations, as defined in 37 C.F.R. § 1.822. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included in embodiments where it would be appropriate. A computer readable text file, entitled P172-0004US_SeqList created on or about Jan. 18, 2023, with a file size of 116 KB, contains the sequence listing for this application and is hereby incorporated by reference in its entirety.

[0038] Information about sequences in the Sequence Listing is provided in the following three Tables. Temporality abbreviations: IE=Immediate Early, DE=Delayed Early, LL=Leaky Late, and L=Late Early; and Virion component abbreviations: NS=non-structural, E=envelope, T=tegument, C=Capsid.

TABLE 1

List of Signature Peptides for The Identification of HSV-1 Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO:
1	P04296	DBP	E	NS	Major DNA-binding protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = DBP PE = 1 SV = 1	1-4
2	P10211	gB	L	E	Envelope glycoprotein B OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gB PE = 1 SV = 1	5-8
3	P06487	gI	L	E	Envelope glycoprotein I OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gI PE = 1 SV = 1	9-12
4	P08393	ICPO	IE	T	E3 ubiquitin-protein ligase ICP0 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = ICPO PE = 1 SV = 1	13-17

TABLE 1-continued

List of Signature Peptides for The Identification of HSV-1 Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO:
5	P04485	ICP22	IE	NS	Transcriptional regulator ICP22 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = ICP22 PE = 1 SV = 1	18-21
6	P08392	ICP4	IE	T	Major viral transcription factor ICP4 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = ICP4 PE = 1 SV = 1	22-27
7	P03176	TK	E	T	Thymidine kinase OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = TK PE = 1 SV = 4	28-31
8	P04294	UL12	E	NS	Alkaline nuclease OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL12 PE = 1 SV = 1	32-37
9	P10210	UL26	L	C	Capsid scaffolding protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL26 PE = 1 SV = 1	38-42
10	P04293	UL30	E	NS	DNA polymerase catalytic subunit OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL30 PE = 1 SV = 2	43-46
11	P10226	UL42	E	NS	DNA polymerase processivity factor OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL42 PE = 1 SV = 1	47-50
12	P06492	UL48	L	T	Tegument protein VP16 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL48 PE = 1 SV = 1	51-54
13	P10233	UL49	L	T	Tegument protein VP22 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL49 PE = 1 SV = 1	55-58
14	P10238	UL54	IE	NS	mRNA export factor OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL54 PE = 1 SV = 1	59-62
15	P10192	UL8	E	NS	DNA helicase/primase complex-associated protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL8 PE = 1 SV = 1	63-66
16	P04413	US3	E	T	Serine/threonine-protein kinase US3 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = US3 PE = 1 SV = 1	67-70
17	P10209	CVC2	L	C	Capsid vertex component 2 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = CVC2 PE = 1 SV = 1	71-76
18	P10201	CVC1	L	C	Capsid vertex component 1 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = CVC1 PE = 1 SV = 1	77-79
19	P10234	DUT	E	T	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = DUT PE = 3 SV = 1	80-83
20	P10228	gC	L	E	Envelope glycoprotein C OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gC PE = 1 SV = 1	84-87
21	Q69091	gD	L	E	Envelope glycoprotein D OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gD PE = 1 SV = 1	88-92
22	P04488	gE	L	E	Envelope glycoprotein E OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gE PE = 1 SV = 1	93-96
23	P06484	gG	L	E	Envelope glycoprotein G OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gG PE = 3 SV = 1	97
24	P06477	gH	L	E	Envelope glycoprotein H OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gH PE = 1 SV = 1	98-101
25	P68331	gk	L	E	Envelope glycoprotein K OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gK PE = 1 SV = 1	102-103
26	P04288	gM	L	E	Envelope glycoprotein M OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = gM PE = 1 SV = 1	104-107
27	P10189	HELI	E	NS	DNA replication helicase OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = HELI PE = 3 SV = 3	108-109

TABLE 1-continued

List of Signature Peptides for The Identification of HSV-1 Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO:
28	P06491	MCP	L	C	Major capsid protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = MCP PE = 1 SV = 1	110-115
29	P10215	NEC1	L	NS	Nuclear egress protein 1 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = NEC1 PE = 1 SV = 1	116-118
30	P10218	NEC2	L	NS	Nuclear egress protein 2 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = NEC2 PE = 1 SV = 1	119-123
31	P08543	RIR1	E	NS	Ribonucleoside-diphosphate reductase large subunit OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = RIR1 PE = 1 SV = 2	124-126
32	P10224	RIR2	E	NS	Ribonucleoside-diphosphate reductase small subunit OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = RIR2 PE = 3 SV = 1	127-130
33	P10219	SCP	L	C	Small capsomere-interacting protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = SCP PE = 1 SV = 1	131
34	P32888	TRX1	L	C	Triplex capsid protein 1 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = TRX1 PE = 1 SV = 1	132-136
35	P10202	TRX2	L	C	Triplex capsid protein 2 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = TRX2 PE = 1 SV = 1	137-141
36	P04291	UL14	L	T	Tegument protein UL14 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL14 PE = 1 SV = 2	142
37	P10200	UL16	L	T	Cytoplasmic envelopment protein 2 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL16 PE = 1 SV = 1	143-145
38	P10186	UL2	E	NS	Uracil-DNA glycosylase OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL2 PE = 1 SV = 1	146-150
39	P10205	UL21	L	T	Tegument protein UL21 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL21 PE = 1 SV = 1	151-156
40	P10208	UL24	L	NS	Protein UL24 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL24 PE = 1 SV = 1	157
41	P10187	UL3	L	NS	Nuclear phosphoprotein UL3 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL3 PE = 3 SV = 1	158
42	P10216	UL32	L	NS	Packaging protein UL32 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL32 PE = 1 SV = 1	159-160
43	P10220	UL36	L	T	Large tegument protein deneddylase OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL36 PE = 1 SV = 1	161-165
44	P10221	UL37	L	T	Inner tegument protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL37 PE = 1 SV = 1	166-171
45	P10188	UL4	L	T	Nuclear protein UL4 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL4 PE = 3 SV = 1	172
46	P10225	UL41	L	T	Virion host shutoff protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL41 PE = 1 SV = 1	173-178
47	P10229	UL45	L	E	Envelope protein UL45 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL45 PE = 3 SV = 1	179
48	P10230	UL46	L	T	Tegument protein UL46 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL46 PE = 1 SV = 2	180-184
49	P10231	UL47	L	T	Tegument protein UL47 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL47 PE = 1 SV = 1	185-189
50	P10235	UL51	L	T	Tegument protein UL51 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL51 PE = 1 SV = 1	190-191

TABLE 1-continued

List of Signature Peptides for The Identification of HSV-1 Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO:
51	P10236	UL52	E	NS	DNA primase OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL52 PE = 1 SV = 1	192-93
52	P10240	UL56	E	E	Protein UL56 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL56 PE = 1 SV = 2	194-195
53	P10190	UL6	E	C	Portal protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL6 PE = 1 SV = 1	196-198
54	P10191	UL7	L	T	Cytoplasmic envelopment protein 1 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL7 PE = 1 SV = 1	199-203
55	P10193	UL9	L	NS	Replication origin-binding protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = UL9 PE = 1 SV = 1	204
56	P06486	US10	E	T	Virion protein US10 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = US10 PE = 1 SV = 1	205-207
57	P04487	US11	L	T	Accessory factor US11 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = US11 PE = 1 SV = 1	208-211
58	P03170	US12	IE	NS	ICP47 protein OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = US12 PE = 1 SV = 2	212
59	P06485	US2	L	T	Protein US2 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = US2 PE = 1 SV = 3	213-217
60	P06481	US9	E	E	Envelope protein US9 OS = Human herpesvirus 1 (strain 17) OX = 10299 GN = US9 PE = 1 SV = 1	218-219

TABLE 2

List of Signature Peptides for The Identification of HCMV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s):
1	P16810	IRL12	LL	NS	Uncharacterized protein IRL12 OS = Human cytomegalovirus (strain AD169) OX = 10360 PE = 4 SV = 1	220-225
2	P16809	IR11	L	E	Viral Fc-gamma receptor-like protein IR11 OS = Human cytomegalovirus (strain AD169) OX = 10360 PE = 3 SV = 1	226-231
3	P17147	DBP	DE	NS	Major DNA-binding protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = DBP PE = 1 SV = 1	232-234
4	P06473	gB	DE	E	Envelope glycoprotein B OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = gB PE = 1 SV = 1	235-237
5	P12824	gH	L	E	Envelope glycoprotein H OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = gH PE = 1 SV = 1	238-239
6	P16733	gM	L	E	Envelope glycoprotein M OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = gM PE = 1 SV = 1	240-242
7	P16795	gN	L	E	Envelope glycoprotein N OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = gN PE = 1 SV = 1	243-244
8	P09715	IRS1	IE	T	Protein IRS1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = IRS1 PE = 1 SV = 1	245-247
9	P16729	MCP	L	C	Major capsid protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = MCP PE = 1 SV = 1	248-250
10	P16794	NEC1	DE	T	Nuclear egress protein 1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = NEC1 PE = 1 SV = 1	251-252
11	P16791	NEC2	DE	T	Nuclear egress protein 2 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = NEC2 PE = 1 SV = 1	253-254

TABLE 2-continued

List of Signature Peptides for The Identification of HCMV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s):
12	P16782	RIR1	DE	T	Ribonucleoside-diphosphate reductase large subunit-like protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = RIR1 PE = 3 SV = 1	255-257
13	P16724	TRM1	DE	NS	Tripartite terminase subunit 1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = TRM1 PE = 3 SV = 1	258-260
14	P16792	TRM2	L	NS	Tripartite terminase subunit 2 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = TRM2 PE = 3 SV = 1	261-263
15	P16732	TRM3	LL	NS	Tripartite terminase subunit 3 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = TRM3 PE = 1 SV = 1	264-266
16	P09695	TRS1	IE	T	Protein HHLF1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = TRS1 PE = 1 SV = 1	267-268
17	P16783	TRX1	LL	C	Triplex capsid protein 1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = TRX1 PE = 1 SV = 1	269-271
18	P16728	TRX2	LL	C	Triplex capsid protein 2 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = TRX2 PE = 1 SV = 1	272-274
19	P16827	UL102	DE	NS	DNA helicase/primase complex-associated protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL102 PE = 2 SV = 2	275-277
20	P16734	UL103	L	T	Cytoplasmic envelopment protein 1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL103 PE = 3 SV = 1	278-280
21	P17151	UL112/ UL113	DE	NS	Early phosphoprotein p84 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL112/UL113 PE = 1 SV = 2	281-283
22	P16770	UL117	L	NS	Protein UL117 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL117 PE = 3 SV = 1	284-286
23	P16739	UL119/ UL118	DE	NS	Viral Fc-gamma receptor-like protein UL119 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL119/UL118 PE = 2 SV = 2	287-289
24	P19893	UL122	IE	NS	Viral transcription factor IE2 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL122 PE = 1 SV = 2	290-291
25	P13202	UL123	IE	NS	55 kDa immediate-early protein 1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL123 PE = 1 SV = 1	292-294
26	P16755	UL13	IE	T	Uncharacterized protein UL13 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL13 PE = 3 SV = 1	295-297
27	P69338	UL132	LL	E	Envelope glycoprotein UL132 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL132 PE = 3 SV = 1	298-300
28	P16845	UL22A	L	E	Glycoprotein UL22A OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL22A PE = 3 SV = 2	301
29	P16760	UL24	LL	T	Protein UL24 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL24 PE = 3 SV = 3	302-303
30	P16761	UL25	L	T	Phosphoprotein 85 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL25 PE = 3 SV = 1	304-306
31	P16762	UL26	DE	T	Tegument protein UL26 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL26 PE = 3 SV = 2	307-309
32	P16764	UL29	L	T	Uncharacterized protein UL29 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL29 PE = 3 SV = 1	310-312
33	P16848	UL31	L	NS	Uncharacterized protein UL31 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL31 PE = 3 SV = 2	313-314
34	P08318	UL32	DE	C	Large structural phosphoprotein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL32 PE = 1 SV = 1	315-317

TABLE 2-continued

List of Signature Peptides for The Identification of HCMV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s):
35	P16812	UL34	DE	NS	Transcriptional regulator UL34 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL34 PE = 3 SV = 2	318-320
36	P16766	UL35	DE	T	Protein UL35 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL35 PE = 1 SV = 1	321-323
37	P16767	UL36	IE	T	Uncharacterized protein UL36 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL36 PE = 3 SV = 1	324-326
38	P16778	UL37	IE	NS	UL37 immediate early glycoprotein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL37 PE = 1 SV = 2	327-329
39	P16779	UL38	DE	T	Apoptosis inhibitor UL38 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL38 PE = 3 SV = 1	330-332
40	P16781	UL43	L	T	Tegument protein UL43 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL43 PE = 3 SV = 2	333-335
41	P16790	UL44	DE	NS	DNA polymerase processivity factor OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL44 PE = 1 SV = 1	336-338
42	P16784	UL47	LL	T	Inner tegument protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL47 PE = 3 SV = 2	339-341
43	P16785	UL48	DE	T	Large tegument protein deneddylase OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL48 PE = 3 SV = 1	342-344
44	P16793	UL52	L	NS	Packaging protein UL32 homolog OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL52 PE = 3 SV = 1	345-347
45	P08546	UL54	DE	T	DNA polymerase catalytic subunit OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL54 PE = 1 SV = 2	348-350
46	P16749	UL69	LL	T	mRNA export factor ICP27 homolog OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL69 PE = 1 SV = 1	351-353
47	P16823	UL71	DE	T	Tegument protein UL51 homolog OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL71 PE = 1 SV = 2	354-356
48	P16753	UL80	L	NS	Capsid scaffolding protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL80 PE = 1 SV = 1	357-359
49	P06726	UL82	L	T	Protein pp71 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL82 PE = 1 SV = 2	360-362
50	P06725	UL83	LL	T	65 kDa phosphoprotein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL83 PE = 1 SV = 2	363-365
51	P16727	UL84	DE	T	Protein UL84 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL84 PE = 1 SV = 1	366-368
52	P16731	UL88	L	T	Protein UL88 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL88 PE = 3 SV = 1	369-371
53	P16800	UL94	L	T	Cytoplasmic envelopment protein 2 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL94 PE = 1 SV = 1	372-374
54	P16788	UL97	DE	T	Serine/threonine protein kinase UL97 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL97 PE = 1 SV = 1	375-377
55	P16789	UL98	DE	NS	Alkaline nuclease OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL98 PE = 3 SV = 2	378-380
56	P09721	US12	DE	NS	Uncharacterized protein HVLF6 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US12 PE = 3 SV = 1	381-383
57	P09722	US22	DE	T	Early nuclear protein HWLF1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US22 PE = 3 SV = 2	384-386
58	P09701	US23	DE	T	Tegument protein US23 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US23 PE = 3 SV = 2	387-389

TABLE 2-continued

List of Signature Peptides for The Identification of HCMV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s):
59	P09709	US34	DE	NS	Protein US34 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US34 PE = 3 SV = 1	390
60	P09729	US9	DE	NS	Unique short US9 glycoprotein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US9 PE = 3 SV = 1	391-393
61	P16808	IRL10	LL	E	Protein IRL10 OS = Human cytomegalovirus (strain AD169) OX = 10360 PE = 3 SV = 1	394-397
62	P09710	HKLF1	DE	NS	Uncharacterized protein HKLF1 OS = Human cytomegalovirus (strain AD169) OX = 10360 PE = 3 SV = 1	398-400
63	P16799	CVC1	L	C	Capsid vertex component 1 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = CVC1 PE = 3 SV = 1	401-402
64	P16726	CVC2	DE	C	Capsid vertex component 2 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = CVC2 PE = 3 SV = 1	403-405
65	P16824	DUT	LL	T	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = DUT PE = 3 SV = 1	406
66	P16832	gL	L	E	Envelope glycoprotein L OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = gL PE = 1 SV = 2	407-409
67	P16750	GO	L	E	Glycoprotein O OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = GO PE = 1 SV = 1	410-412
68	P16736	HELI	DE	NS	DNA replication helicase OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = HELI PE = 3 SV = 1	413-414
69	Q7M6N6	SCP	L	C	Small capsomere-interacting protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = SCP PE = 1 SV = 1	415
70	P16735	UL104	DE	NS	Portal protein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL104 PE = 3 SV = 2	416-418
71	P16769	UL114	DE	NS	Uracil-DNA glycosylase OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL114 PE = 3 SV = 1	419-420
72	P16837	UL128	DE	NS	Uncharacterized protein UL 128 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL128 PE = 1 SV = 2	421-423
73	P16765	UL30	L	NS	Uncharacterized protein UL30 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL30 PE = 3 SV = 1	424
74	P17146	UL4	DE	E	Early glycoprotein GP48 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL4 PE = 3 SV = 1	425-427
75	P16780	UL40	LL	NS	Protein UL40 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL40 PE = 1 SV = 1	428
76	P16786	UL49	LL	NS	Uncharacterized protein UL49 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL49 PE = 3 SV = 1	429
77	P17149	UL70	LL	NS	DNA primase OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL70 PE = 1 SV = 2	430-432
78	P16725	UL76	L	T	Protein UL76 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL76 PE = 2 SV = 1	433-435
79	P16751	UL78	DE	NS	Uncharacterized protein UL78 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL78 PE = 4 SV = 1	436
80	P16752	UL79	L	T	Protein UL79 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL79 PE = 3 SV = 1	437-438
81	P16730	UL87	L	NS	Protein UL87 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL87 PE = 3 SV = 1	439
82	P16801	UL95	DE	NS	Protein UL95 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL95 PE = 3 SV = 1	440-441

TABLE 2-continued

List of Signature Peptides for The Identification of HCMV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s):
83	P16787	UL96	DE	T	Protein UL96 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL96 PE = 3 SV = 2	442-443
84	P13200	UL99	L	T	Cytoplasmic envelopment protein 3 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = UL99 PE = 1 SV = 3	444-445
85	P09720	US13	DE	NS	Uncharacterized protein HVLF5 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US13 PE = 3 SV = 1	446
86	P09719	US14	DE	NS	Uncharacterized protein HVLF4 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US14 PE = 3 SV = 2	447
87	P09718	US15	LL	NS	Uncharacterized protein HVLF3 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US15 PE = 3 SV = 2	448
88	P69334	US18	DE	NS	Transmembrane protein US18 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US18 PE = 3 SV = 1	449
89	P09700	US24	DE	T	Tegument protein US24 OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US24 PE = 3 SV = 3	450-452
90	P09730	US8	DE	NS	Unique short US8 glycoprotein OS = Human cytomegalovirus (strain AD169) OX = 10360 GN = US8 PE = 3 SV = 2	453

TABLE 3

List of Signature Peptides for The Identification of KSHV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s)
1	P90463	70	DE	NS	Thymidylate synthase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = 70 PE = 1 SV = 1	454-456
2	Q2HRD3	DBP	DE	NS	Major DNA-binding protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = DBP PE = 1 SV = 1	457-459
3	Q2HR78	DUT	DE	T	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = DUT PE = 3 SV = 1	460-462
4	F5HB81	gB	L	E	Envelope glycoprotein B OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = gB PE = 1 SV = 1	463-464
5	Q2HRC7	K2	DE	T	Viral interleukin-6 homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = K2 PE = 1 SV = 1	465-467
6	P90495	K3	DE	T	E3 ubiquitin-protein ligase MIR1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = K3 PE = 1 SV = 1	468-470
7	P90489	K5	DE	NS	E3 ubiquitin-protein ligase MIR2 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = K5 PE = 1 SV = 1	471-473
8	Q2HR82	K8	IE	NS	E3 SUMO-protein ligase K-bZIP OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = K8 PE = 1 SV = 1	474-476
9	F5HB98	K8.1	L	E	Protein K8.1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = K8.1 PE = 3 SV = 1	477-479
10	Q2HRA7	MCP	L	C	Major capsid protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = MCP PE = 3 SV = 1	480-482
11	F5H982	NEC1	DE	NS	Nuclear egress protein 1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = NEC1 PE = 1 SV = 1	483-485
12	F5HA27	NEC2	DE	NS	Nuclear egress protein 2 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = NEC2 PE = 1 SV = 1	486-488

TABLE 3-continued

List of Signature Peptides for The Identification of KSHV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s)
13	Q2HRC9	ORF10	DE	NS	Protein ORF10 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF10 PE = 4 SV = 1	489-491
14	Q2HRC8	ORF11	DE	T	Protein ORF11 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF11 PE = 4 SV = 1	492-494
15	Q2HRB6	ORF17	DE	T	Capsid scaffolding protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF17 PE = 1 SV = 1	495-497
16	F5HHY1	ORF38	L	T	Cytoplasmic envelopment protein 3 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF38 PE = 3 SV = 1	498
17	Q2HRD4	ORF4	L	NS	Complement control protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF4 PE = 3 SV = 1	499-501
18	F5HDE4	ORF45	IE	T	Protein ORF45 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF45 PE = 1 SV = 1	502-504
19	F5HCV3	ORF50	IE	NS	Putative transcription activator ORF50 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF50 PE = 3 SV = 1	505-507
20	Q2HR80	ORF52	L	T	Tegument protein ORF52 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF52 PE = 1 SV = 1	508-510
21	Q2HR75	ORF57	IE	NS	mRNA export factor ICP27 homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF57 PE = 1 SV = 1	511-513
22	F5HID2	ORF59	DE	NS	DNA polymerase processivity factor OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF59 PE = 3 SV = 1	514-516
23	Q9QR70	ORF75	L	T	Protein ORF75 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF75 PE = 4 SV = 1	517-519
24	Q2HRD0	ORF9	DE	T	DNA polymerase catalytic subunit OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF9 PE = 3 SV = 1	520-522
25	Q2HR67	RIR1	DE	NS	Ribonucleoside-diphosphate reductase large subunit OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = RIR1 PE = 3 SV = 1	523-525
26	Q2HR63	SCP	L	C	Small capsomere-interacting protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = SCP PE = 1 SV = 1	526-527
27	F5HB62	TK	DE	T	Thymidine kinase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = TK PE = 3 SV = 1	528-530
28	F5HB39	CVC1	L	C	Capsid vertex component 1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = CVC1 PE = 3 SV = 1	531-533
29	Q2HRB3	CVC2	L	C	Capsid vertex component 2 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = CVC2 PE = 3 SV = 1	534-536
30	F5HAK9	gH	L	E	Envelope glycoprotein H OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = gH PE = 1 SV = 1	537-539
31	F5HDB7	gL	L	E	Envelope glycoprotein L OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = gL PE = 1 SV = 1	540-542
32	F5HDD0	gM	L	E	Envelope glycoprotein M OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = gM PE = 1 SV = 1	543-545
33	Q2HR89	HELI	DE	NS	DNA replication helicase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = HELI PE = 3 SV = 1	546-548
34	P0C788	K14	DE	NS	OX-2 membrane glycoprotein homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = K14 PE = 1 SV = 1	549-550
35	Q98157	ORF K4	DE	NS	Viral macrophage inflammatory protein 2 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF K4 PE = 1 SV = 1	551
36	F5HGJ3	ORF16	IE	NS	Apoptosis regulator Bcl-2 homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF16 PE = 1 SV = 1	552-553

TABLE 3-continued

List of Signature Peptides for The Identification of KSHV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s)
37	Q2HRC6	ORF2	DE	NS	Putative Dihydrofolate reductase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF2 PE = 3 SV = 1	554-555
38	Q2HRB2	ORF20	L	NS	Protein UL24 homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF20 PE = 2 SV = 1	556
39	F5HIM6	ORF23	L	T	Protein ORF23 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF23 PE = 3 SV = 1	557-558
40	F5HFD2	ORF24	L	T	Protein ORF24 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF24 PE = 3 SV = 1	559-561
41	F5HDY6	ORF27	L	E	Protein ORF27 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF27 PE = 4 SV = 1	562-564
42	F5HI25	ORF28	L	E	Protein ORF28 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF28 PE = 4 SV = 1	565
43	F5HEF2	ORF33	L	T	Cytoplasmic envelopment protein 2 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF33 PE = 3 SV = 1	566-568
44	Q2HR98	ORF34	L	NS	Protein UL95 homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF34 PE = 3 SV = 1	569-570
45	F5HCD4	ORF35	L	T	Protein ORF35 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF35 PE = 4 SV = 1	571-572
46	F5HGH5	ORF36	DE	T	Protein ORF36 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF36 PE = 1 SV = 1	573
47	Q2HR95	ORF37	DE	NS	Shutoff alkaline exonuclease OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF37 PE = 1 SV = 1	574-576
48	Q2HR92	ORF40	DE	NS	DNA helicase/primase complex-associated protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF40 PE = 3 SV = 1	577-578
49	F5HAI6	ORF42	L	T	Cytoplasmic envelopment protein 1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF42 PE = 3 SV = 1	579-580
49	F5HAI6	ORF42	L	T	Cytoplasmic envelopment protein 1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF42 PE = 3 SV = 1	580
50	F5HGK9	ORF43	L	C	Portal protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF43 PE = 3 SV = 1	581-583
51	F5HFA1	ORF46	DE	NS	Uracil-DNA glycosylase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF46 PE = 3 SV = 1	584-585
52	Q2HR85	ORF48	IE	T	Tegument protein ORF48 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF48 PE = 3 SV = 1	586
53	Q2HR83	ORF49	DE	NS	Protein ORF49 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF49 PE = 3 SV = 1	587
54	F5H9W9	ORF55	L	T	Tegument protein ORF55 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF55 PE = 3 SV = 1	588-590
55	F5HIN0	ORF56	DE	T	DNA primase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF56 PE = 3 SV = 1	591-593
56	F5HEU7	ORF63	L	T	Inner tegument protein OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF63 PE = 3 SV = 1	594
57	Q2HR64	ORF64	L	T	Large tegument protein deneddylase OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF64 PE = 3 SV = 1	595-597
58	F5HG20	ORF66	DE	NS	Protein ORF66 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF66 PE = 3 SV = 1	598-599
59	F5HF47	ORF68	L	E	Packaging protein UL32 homolog OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = ORF68 PE = 3 SV = 1	600-602

TABLE 3-continued

List of Signature Peptides for The Identification of KSHV Proteins:

#	Protein Accession	Protein Gene	temporality	component virion	Protein Description	SEQ ID NO(s)
60	F5H8Y5	TRX1	L	C	Triplex capsid protein 1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = TRX1 PE = 3 SV = 1	603
61	F5HGN8	TRX2	L	C	Triplex capsid protein 2 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = TRX2 PE = 3 SV = 1	604-605
62	F5HF68	VIRF-1	DE	T	VIRF-1 OS = Human herpesvirus 8 type P (isolate GK18) OX = 868565 GN = VIRF-1 PE = 1 SV = 1	606

DETAILED DESCRIPTION

[0039] Herpesviruses infect up to 90% of the population and are dangerous in immune-compromised individuals and pregnant women. However, effective non-toxic antiviral treatments or vaccines for these viruses are currently lacking. The replication of a herpesvirus in an infected cell and the spread of infection to neighboring cells rely on a finely controlled lifecycle with a temporally tuned cascade of viral gene expression.

[0040] In order to effectively identify potential virus modulatory compounds, as well as gain an understanding of their impact on specific stages of a viral infection, described herein is a novel assay format to monitor viral proteins from herpesviruses. These assays offer the accurate detection and quantification of viral proteins from all distinct temporal classes of viral replication. Three exemplary assays have been designed for the specific detection of three herpesviruses: herpes simplex virus 1 (HSV1), human cytomegalovirus (HCMV), and Kaposi's sarcoma-associated herpesvirus (KSHV). These assays can be utilized in combination with drug treatments, genetic modifications, or other perturbations to assess the impact of the intervention on viral protein production. Given the temporal nature of herpesvirus infection, the acquired protein abundance measurements made available using these assays provide information regarding the stage of infection (e.g. entry, viral genome replication, assembly, egress) that is affected, the specific viral proteins that are impacted, as well as additional mechanistic understanding of how a given compound or other perturbation impacts viral replication. Thus, the provided methods can be used as either primary or secondary screens for the purposes of anti-viral drug discovery, as well as in vaccine development assays.

[0041] Described herein is the development of a novel series of assays to determine the protein abundance levels of viral proteins during the progression of herpesvirus infections. These assays can be used to support the discovery of antiviral compounds, as well as other purposes. Liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) is used to perform a targeted mass spectrometry technique called parallel reaction monitoring (PRM) to quantitatively monitor signature peptides from target proteins (FIG. **1**). A "signature" peptide in this context refers to a peptide that can be used to distinguish one protein from all others in a sample.

[0042] While these assays have been designed on a quadrupole-Orbitrap instrument platform, they can easily be ported to additional instrument platforms (including the triple quadrupole instrumentation favored by industry and clinical facilities) with minimal modification and time investment. Thus, transfer of this technology to interested commercial entities will be readily achieved.

[0043] Noteworthy, mass spectrometry instruments are now part of the common infrastructure of academic, industry, and clinical settings. Almost all pharmaceutical and clinical companies currently either have a mass spectrometry group in house or a close relationship with a mass spectrometry contract research organization, and thus will be able to easily make use of this assay.

[0044] As exemplified herein, three assays have been developed for monitoring viral proteins in HSV-1, HCMV, and KSHV, monitoring up to 60 (see Table 1), up to 90 (see Table 2), and up to 62 (see Table 3) viral proteins from each virus, respectively. In each case, this constitutes approximately 50-80% of the predicted viral proteome. In Tables 1-3, many of the viral proteins are associated with more than one (that is, two, three, or four) signature peptides. While measurement of more than one signature peptide (including all of the listed signature peptides) for any one protein may provide the most redundant data for detection and/or quantification of the corresponding protein, it is understood that fewer than all of the provided peptides may be used in some embodiments. Thus, specific embodiments include assays in which only one signature peptide is detected for each viral protein being monitored, as well as assays in which two or more signature peptides are detected for one or more viral proteins being monitored.

[0045] In example herpesvirus PRM assay methods shown herein, cell pellets were lysed in 2% SDS, 100 mM NaCl, 0.5 mM EDTA, 50 mM Tris, pH 8.2, and 50 μg of protein was reduced and alkylated with 25 mM TCEP and 50 mM CAM respectively for 20 min at 70° C. Proteins were then precipitated via methanol chloroform precipitation (Wessel & Flugg, *Anal Biochem.* 138(1):141-143, 1984), resuspended in 50 mM HEPES, pH 8.2 and digested overnight with trypsin (50:1 protein:enzyme w/w ratio). Digested peptides were desalted by SDB-RPS StageTip as previously described (Lum et al., *Cell Syst.,* 7(6):627-242, 2018; Greco et al., *Methods Mol Biol* 1410:39-63, 2016; Federspiel & Cristea, *Methods Mol Biol.,* 1977:115-143, 2019).

[0046] Peptides (1.0 μg on column) were analyzed by LC-MS/MS using a Dionex Ultimate 3000 UHPLC coupled online to an EASYSpray ion source and a Q Exactive HF. Peptides were separated on an EASYSpray C18 column (75 μm×25 cm) heated to 50° C. using a linear gradient of 5% B to 32% B over 60 min at a flow rate of 250 nL/min and were ionized at 1.7 kv. Mobile phase A consisted of 0.1% FA in H_2O and mobile phase B consisted of 0.1% FA, 2.9% H_2O in ACN.

[0047] The PRM method was controlled by a peptide inclusion list with retention time windows of 6 min for selected precursor ions. The PRM method consisted of MS2 scans that were acquired at a resolution of 30,000 with an AGC setting of 1e5, an MIT of 60 ms, an isolation window of 0.8 m/z, fixed first mass of 125.0 m/z, and normalized collision energy of 27 recorded in profile.

[0048] The PRM assay was developed and analyzed using the open-source software Skyline (Maclean et al., *Bioinformatics* 26(7):966-968, 2010). Summed area under the curve of 3-4 transitions per peptide was used for quantitation. Targeted peptides were normalized to host protein loading control peptides. Peptide values for each sample were scaled to the average of each peptide across all runs. The average of multiple peptides was used as the inferred value for the protein measurement when more than one peptide was quantified (Federspiel et al., *PLoS Biol.* 17(9):e3000437. Doi: 10.1371/journal.pbio.3000437). PRM quantitation data were graphed using the Python Seaborn and Matplotlib libraries.

[0049] The assays provided herein can be expanded to complete coverage of each viral proteome, as well as to incorporate host proteins useful as markers of infection. Importantly, in each assay, viral proteins from every temporal class (e.g., immediate early (IE), early (E), and late (L) genes for HSV-1; IE, delayed early (DE), leaky late (LL), and L genes for HCMV, and IE, DE, and L genes for KSHV) can be monitored based on the systems provided herein. Concurrent with the addition of more protein targets, it is also possible to scale down the number of cells used in the assays, from ~150,000 to ~10,000 cells, thereby facilitating automation, as well as reducing cost.

[0050] Another important consideration for a screening assay is the speed at which the information can be acquired. The current assays can be completed in one to two hours for each time point, and the expanded assays are designed to stay within this short timeframe.

[0051] Also contemplated as a component is the development of an automated pipeline for data analysis that will allow users to analyze the acquired data and generate standardized reports with the click of a button. Using the existing automation capabilities of the open-source data analysis tool Skyline, in conjunction with custom written code, a simple user interface can be provided for each targeted assay. This will allow non-expert users to analyze and interpret their data quickly and easily. The output of this analysis pipeline will be a report with defined structure and components to allow for simple reporting and tracking, as well as for direct comparisons of results run at different times or laboratories and by different users.

[0052] It is demonstrated herein that the described assays can be used to effectively screen small molecule modulators of viral infection (Example 1). These screens can readily be expanded to a range of antiviral compounds, which will demonstrate the broad value of this assay and enhance its marketability.

[0053] As an initial demonstration of the use of this assay for testing compounds, sirtuin modulators have been assessed. Based on earlier work related to whether a single therapeutic strategy can be used to inhibit the infection with different viruses, in collaboration with others, a class of human enzymes called sirtuins was identified that have broad-spectrum antiviral functions against a range of DNA and RNA viruses, including herpesviruses (Koyunku et al., *mBio* 5:6):302249-14, 2014). Building on this prior work, described herein is use of the newly developed assay system to investigate an activator (CAY10602) and an inhibitor (EX-527) of sirtuin 1 to better define the precise stage of infection when these molecules impact HCMV replication (Example 1).

[0054] Using this assay, it was found that CAY10602 inhibits early stages of infection, as the levels of viral immediate early proteins were reduced (Example 1). Furthermore, this inhibitory effect was maintained throughout infection, as the levels of delayed-early and late viral proteins were also affected. However, the impact on the immediate early viral proteins was more pronounced for a specific subset of viral proteins. Therefore, the herein-described assay has the ability to not only pinpoint the stage of infection when a compound acts, but also the specific functional family of viral proteins that are affected. This is important for understanding the potential downstream impact of a compound on virus-induced alterations on cellular pathways. This assay also showed that EX-527 slightly elevates viral protein production.

[0055] The described screen can also readily be expanded to analysis of other compounds, for instance that are either antiviral (i.e., with therapeutic potential) or enhance virus infectivity (i.e., for vaccine development). For instance, other sirtuin activators that inhibit viral infection, and for which the specifics of their impact on virus replication remain unknown, may be tested. A range of other antiviral compounds can also be tested, as well as genetic manipulations (knockouts and over-expressions) known to affect viral infection. Altogether, this will prove the value of these assays as screening tools for compounds that modulate virus infections, determining not only if an intervention will inhibit viral replication, but also when during infection this inhibition takes place and via which specific viral proteins.

[0056] Also contemplated as embodiments are ready-to-use kits that will provide some or optionally all the components needed to perform an assay described herein. For instance, three kits can be provided, one each for HSV-1, HCMV, and KSHV. Embodiments of each kit will include the parameters for performing the assay for the target virus, a set of heavy isotope labeled peptides that can be added to every sample run, and a USB drive or other non-transitory computer readable medium containing software develop for assayed analysis and standardized report generation. The inclusion of a heavy labeled peptide corresponding to each of the signature viral and host peptides that have been selected for the kit/assay allows for rapid and easy transfer of the assay across different instrument platforms, and further enhances the accuracy of the quantification. The licensing of the assays (and preparation of the kits) can be performed in a modular fashion based on which virus(es) a prospective client is interested in. It is also contemplated that analysis of samples can be provided using with the described platform, for instance as a service provided through a Mass Spectrometry Facility (e.g., the Princeton Facility) if a client desires.

[0057] Current techniques for monitoring herpesvirus lifecycle progression are limited compared to the method described herein. The predominant technologies for monitoring protein levels during viral infection are western blotting and ELISA assays. Both rely on the generation of high-quality antibodies and are relatively expensive, time intensive, and not amenable to multiplex analysis. Antibod-

ies frequently have cross-reactivity with other proteins, thereby impacting the confidence of the measurement. Also, western blotting is inherently more variable, affecting the accuracy of the quantification. Currently, for high-throughput analysis of gene products during viral infection, microarray technology is used, which measures mRNA levels in infected samples. While this does allow for multiplexed analysis of many targets, it does not measure the actual resulting protein level, and thus does not measure the molecule most closely associated with the infection phenotype. The assays described here enable more direct high-throughput measurements of the molecules of interest, with greater precision and accuracy than antibody-based techniques. Importantly, these methods can be easily transferred to interested commercial partners and are not locked into any individual analysis platform. Thus, the described assays will be useful to industry and readily commercialized.

[0058] Representative Computer Architecture.

[0059] FIG. **2** shows an example computer architecture for a computer **700** capable of executing program components for detecting and measuring peptide level(s) in a herpesvirus assay described herein, and for calculating viral protein quantity in accordance with such assays. The computer architecture shown in FIG. **2** illustrates a conventional server computer, workstation, desktop computer, laptop, tablet, network appliance, digital cellular phone, smart watch, or other computing device, and may be utilized to execute any of the software components presented herein. For example, the computer architecture shown in FIG. **2** may be utilized to execute software components for performing operations as described herein. The computer architecture shown in FIG. **2** might also be utilized to implement a computing device, or any other of the computing systems described herein.

[0060] The computer **700** includes a baseboard **702**, or "motherboard," which is a printed circuit board to which a multitude of components or devices may be connected by way of a system bus or other electrical communication paths. In one illustrative example, one or more central processing units ("CPUs") **704** operate in conjunction with a chipset **706**. The CPUs **704** may be standard programmable processors that perform arithmetic and logical operations necessary for the operation of the computer **700**.

[0061] The CPUs **704** perform operations by transitioning from one discrete, physical state to the next through the manipulation of switching elements that differentiate between and change these states. Switching elements may generally include electronic circuits that maintain one of two binary states, such as flip-flops and electronic circuits that provide an output state based on the logical combination of the states of one or more other switching elements, such as logic gates. These basic switching elements may be combined to create more complex logic circuits, including registers, adders-subtractors, arithmetic logic units, floating-point units and the like.

[0062] The chipset **706** provides an interface between the CPUs **704** and the remainder of the components and devices on the baseboard **702**. The chipset **706** may provide an interface to a RAM **708**, used as the main memory in the computer **700**. The chipset **706** may further provide an interface to a computer-readable storage medium such as a read-only memory ("ROM") **710** or non-volatile RAM ("NVRAM") for storing basic routines that help to startup the computer **700** and to transfer information between the various components and devices. The ROM **710** or NVRAM may also store other software components necessary for the operation of the computer **700** in accordance with the description herein.

[0063] The computer **700** may operate in a networked environment using logical connections to remote computing devices and computer systems through a network, such as the network **720**. The chipset **706** may include functionality for providing network connectivity through a network interface controller ("NIC") **712**, such as a mobile cellular network adapter, WiFi network adapter or gigabit Ethernet adapter. The NIC **712** is capable of connecting the computer **700** to other computing devices over the network **720**. It should be appreciated that multiple NICs **712** may be present in the computer **700**, connecting the computer to other types of networks and remote computer systems.

[0064] The computer **700** may be connected to a mass storage device **718** that provides non-volatile storage for the computer. The mass storage device **718** may store system programs, application programs, other program modules and data, which have been described in greater detail herein. The mass storage device **718** may be connected to the computer **700** through a storage controller **714** connected to the chipset **706**. The mass storage device **718** may consist of one or more physical storage units. The storage controller **714** may interface with the physical storage units through a serial attached SCSI ("SAS") interface, a serial advanced technology attachment ("SATA") interface, a fiber channel ("FC") interface, or other type of interface for physically connecting and transferring data between computers and physical storage units.

[0065] The computer **700** may store data on the mass storage device **718** by transforming the physical state of the physical storage units to reflect the information being stored. The specific transformation of physical state may depend on various factors, in different implementations of this description. Examples of such factors may include, but are not limited to, the technology used to implement the physical storage units, whether the mass storage device **718** is characterized as primary or secondary storage and the like.

[0066] For example, the computer **700** may store information to the mass storage device **718** by issuing instructions through the storage controller **714** to alter the magnetic characteristics of a particular location within a magnetic disk drive unit, the reflective or refractive characteristics of a particular location in an optical storage unit, or the electrical characteristics of a particular capacitor, transistor, or other discrete component in a solid-state storage unit. Other transformations of physical media are possible without departing from the scope and spirit of the present description, with the foregoing examples provided only to facilitate this description. The computer **700** may further read information from the mass storage device **718** by detecting the physical states or characteristics of one or more particular locations within the physical storage units.

[0067] In addition to the mass storage device **718** described above, the computer **700** may have access to other computer-readable storage media to store and retrieve information, such as program modules, data structures, or other data. It will be appreciated by those skilled in the art that computer-readable storage media is any available media that provides for the non-transitory storage of data and that may be accessed by the computer **700**.

[0068] By way of example, and not limitation, computer-readable storage media may include volatile and non-volatile, removable and non-removable media implemented in any method or technology. Computer-readable storage media includes, but is not limited to, RAM, ROM, erasable programmable ROM ("EPROM"), electrically-erasable programmable ROM ("EEPROM"), flash memory or other solid-state memory technology, compact disc ROM ("CD-ROM"), digital versatile disk ("DVD"), high definition DVD ("HD-DVD"), BLU-RAY, or other optical storage, magnetic cassettes, magnetic tape, magnetic disk storage or other magnetic storage devices, or any other medium that can be used to store the desired information in a non-transitory fashion.

[0069] The mass storage device **718** may store an operating system **730** utilized to control the operation of the computer **700**. According to one example, the operating system comprises the LINUX operating system. According to another example, the operating system comprises the WINDOWS® SERVER operating system from MICROSOFT Corporation. According to another example, the operating system comprises the iOS operating system from Apple. According to another example, the operating system comprises the Android operating system from Google or its ecosystem partners. According to further examples, the operating system may comprise the UNIX operating system. It should be appreciated that other operating systems may also be utilized. The mass storage device **718** may store other system or application programs and data utilized by the computer **700**, such as components that include the data manager **740**, the flow manager **750** and/or any of the other software components and data described herein. The mass storage device **718** might also store other programs and data not specifically identified herein.

[0070] In one example, the mass storage device **718** or other computer-readable storage media is encoded with computer-executable instructions that, when loaded into the computer **700**, create a special-purpose computer capable of implementing one or more of the embodiments or examples described herein. These computer-executable instructions transform the computer **700** by specifying how the CPUs **704** transition between states, as described above. According to one example, the computer **700** has access to computer-readable storage media storing computer-executable instructions which, when executed by the computer **700**, perform one or more of the various processes described herein. The computer **700** might also include computer-readable storage media for performing any of the other computer-implemented operations described herein.

[0071] The computer **700** may also include one or more input/output controllers **716** for receiving and processing input from a number of input devices, such as a keyboard, a mouse, a touchpad, a touch screen, an electronic stylus, or other type of input device. Similarly, the input/output controller **716** may provide output to a display, such as a computer monitor, a flat-panel display, a digital projector, a printer, a plotter, or other type of output device. It will be appreciated that the computer **700** may not include all of the components shown in FIG. **2**, may include other components that are not explicitly shown in FIG. **2**, or may utilize an architecture completely different than that shown in FIG. **2**.

[0072] Further, the processes discussed herein may be implemented in hardware, software, or a combination thereof. In the context of software, the described operations represent computer-executable instructions stored on one or more computer-readable storage media that, when executed by one or more hardware processors, perform the recited operations. Generally, computer-executable instructions include routines, programs, objects, components, data structures, and the like that perform particular functions or implement particular abstract data types. Those having ordinary skill in the art will readily recognize that certain steps or operations illustrated in the figures above may be eliminated, combined, or performed in an alternate order. Any steps or operations may be performed serially or in parallel (unless context requires one or the other). Furthermore, the order in which the operations are described is not intended to be construed as a limitation.

[0073] Embodiments may be provided as a software program or computer program product including a non-transitory computer-readable storage medium having stored thereon instructions (in compressed or uncompressed form) that may be used to program a computer (or other electronic device) to perform processes or methods described herein. The computer-readable storage medium may be one or more of an electronic storage medium, a magnetic storage medium, an optical storage medium, a quantum storage medium, and so forth. For example, the computer-readable storage media may include, but is not limited to, hard drives, floppy diskettes, optical disks, read-only memories (ROMs), random access memories (RAMs), erasable programmable ROMs (EPROMs), electrically erasable programmable ROMs (EEPROMs), flash memory, magnetic or optical cards, solid-state memory devices, or other types of physical media suitable for storing electronic instructions. Further, embodiments may also be provided as a computer program product including a transitory machine-readable signal (in compressed or uncompressed form). Examples of machine-readable signals, whether modulated using a carrier or unmodulated, include, but are not limited to, signals that a computer system or machine hosting or running a computer program can be configured to access, including signals transferred by one or more networks. For example, the transitory machine-readable signal may comprise transmission of software by the Internet.

[0074] Separate instances of these programs can be executed on or distributed across any number of separate computer systems. Thus, although certain steps have been described as being performed by certain devices, software programs, processes, or entities, this need not be the case, and a variety of alternative implementations will be understood by those having ordinary skill in the art.

[0075] Additionally, those having ordinary skill in the art readily recognize that the techniques described above can be utilized in a variety of devices, environments, and situations. Although the subject matter has been described in language specific to structural features or methodological acts, it is to be understood that the subject matter defined in the appended claims is not necessarily limited to the specific features or acts described. Rather, the specific features and acts are disclosed as exemplary forms of implementing the claims.

[0076] The Exemplary Embodiments below, and the exemplary methods described herein, are included to demonstrate particular embodiments of the disclosure. Those of ordinary skill in the art should recognize in light of the present disclosure that many changes can be made to the

specific embodiments disclosed herein and still obtain a like or similar result without departing from the spirit and scope of the disclosure.

EXEMPLARY EMBODIMENTS

[0077] 1. An assay, including: obtaining a sample including: a cell or tissue infected with a herpesvirus, an extract from a cell or tissue infected with a herpesvirus, or a protein preparation from a cell or tissue infected with a herpesvirus; determining the abundance level of a plurality of herpesvirus proteins in the sample using parallel reaction monitoring (PRM) to quantify signature peptide(s) corresponding to the herpesvirus proteins; wherein the herpesvirus is HSV-1 and the signature peptides are selected from peptides in Table 1; or the herpesvirus is HCMV and the signature peptides are selected from peptides in Table 2; or the herpesvirus is KSHV and the signature peptides are selected from peptides in Table 3.

[0078] 2. The assay of embodiment 1, wherein for at least the one herpesvirus protein for which the abundance level is determined, at least two signature peptides are quantified.

[0079] 3. The assay of embodiment 1, wherein determining the abundance level of the plurality of herpesvirus proteins using PRM includes subjecting the sample to liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS).

[0080] 4. The assay of embodiment 1, wherein the plurality of herpesvirus proteins includes at least one herpesvirus protein from each temporal class of viral replication for that herpesvirus.

[0081] 5. The assay of embodiment 1, wherein the cell or tissue infected with the herpesvirus is a human cell or human tissue.

[0082] 6. The assay of embodiment 1, wherein the plurality of herpesvirus proteins constitutes approximately 30-70%, or 50-80%, of the predicted viral proteome.

[0083] 7 A time course assay, including: repeating the assay of embodiment 1 a plurality of times, where for each repetition the sample is obtained at a different timepoint in a time course.

[0084] 8. The time course assay of embodiment 7, where the different timepoints are different times post infection of the cell or tissue with the herpesvirus.

[0085] 9. The time course assay of embodiment 8, wherein the different times after infection of the cell or tissue with the herpesvirus include at least one time from each state of a replication cycle of the herpesvirus.

[0086] 10. The time course assay of embodiment 7, where the different timepoints are different times post exposure of the cell or tissue to a compound or environmental variable.

[0087] 11. An exposure or dosage course assay, including: repeating the assay of embodiment 1 a plurality of times, where for each repetition the sample is obtained from a cell or tissue that has been exposed to a different compound or condition or a different dosage of a compound or a condition.

[0088] 12. The exposure or dosage course assay of embodiment 11, wherein the different compounds include one or more of known antiviral compounds, proposed antiviral compounds, test compounds, small molecule drugs or drug candidates, or siRNAs or other biologically active non-coding RNAs.

[0089] 13. The exposure or dosage course assay of embodiment 12, wherein the known antiviral compounds include one or more of acyclovir, ganciclovir, another nucleoside, penciclovir, famciclovir, valacyclovir, valganciclovir, cidofovir, another nucleotide phosphonate, fomivirsen, or foscarnet.

[0090] 14. The exposure or dosage course assay of embodiment 11, wherein different compounds include honokiol.

[0091] 15. The exposure or dosage course assay of embodiment 11, wherein the different include one or more of genetic modification of the cell or tissue, genetic modification of the herpesvirus, environmental conditions, or cell or tissue growth or harvesting conditions.

[0092] 16. The exposure or dosage course assay of embodiment 15, wherein the genetic modification of the cell or tissue includes knock out or up-regulation of one or more host factors.

[0093] 17. A method for quantification of herpesvirus proteins from multiple temporal classes of viral replication, including: subjecting a cell sample or cell extract to parallel reaction monitoring (PRM) to generate abundance data; analyzing the abundance data to quantify signature peptide(s) corresponding to at least one herpesvirus protein from each of at least two temporal classes of viral replication; and providing the quantified peptide(s) results from the analyzing to a database, a computer memory, a display, a printer, or another output device; wherein the herpesvirus is HSV-1 and the signature peptides are selected from peptides in Table 1; or the herpesvirus is HCMV and the signature peptides are selected from peptides in Table 2; or the herpesvirus is KSHV and the signature peptides are selected from peptides in Table 3.

[0094] 18. Use of any of the assays of embodiments 1-17, to: screen drug candidates as modulators of viral infection; analyze the stage of infection at which a test compound acts; determine what functional family(s) of viral proteins are affected by a drug or drug candidate; characterize viral and/or host responses to viral infection; characterize viral and/or host responses to drug treatment; or characterize viral and/or host responses to genetic manipulation of either the viral genome or the host genome.

[0095] 19. A kit for use with an assay of any one of embodiments 1-16 or the use of embodiment 18, including: parameters for performing the assay for a target herpesvirus, a set of heavy isotope labeled peptides for use as controls, and a USB drive or other non-transitory computer readable medium containing software for assay analysis and/or standardized report generation.

[0096] 20. The kit of embodiment 19, wherein the target herpesvirus is HSV-1 and the set of heavy isotope labeled peptides includes: at least two signature peptides in Table 1; at least one signature peptide for each protein in Table 1; or at least one signature peptide from Table 1 for at least one protein from each temporal stage of HSV-1 viral replication.

[0097] 21. The kit of embodiment 19, wherein the target herpesvirus is HCMV and the set of heavy isotope

labeled peptides includes: at least two signature peptides in Table 2; at least one signature peptide for each protein in Table 2; or at least one signature peptide from Table 2 for at least one protein from each temporal stage of HCMV viral replication.

[0098] 22. The kit of embodiment 19, wherein the target herpesvirus is KSHV and the set of heavy isotope labeled peptides includes: at least two signature peptides in Table 3; at least one signature peptide for each protein in Table 3; or at least one signature peptide from Table 3 for at least one protein from each temporal stage of KSHV viral replication.

[0099] 23. A service, including: performing the assay of any one of embodiments 1-17 or the use of embodiment 18 on one or more biological samples provided by another.

[0100] 24. A quantitative assay for herpesviral proteins, substantially as described herein.

[0101] 25. A non-naturally occurring, labeled peptide having the amino acid sequence of a peptide in Table 1, Table 2, or Table 3.

[0102] 26. The non-naturally occurring, labeled peptide of embodiment 25, wherein the label enables the peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0103] 27. A collection of non-naturally occurring, labeled signature peptides specific for HSV-1, including: at least one peptide from Table 1 for each of the 60 proteins listed in Table 1; at least two peptides from Table 1 for each of the 60 proteins listed in Table 1; at least three peptides from Table 1 for each of the 60 proteins listed in Table 1; at least one peptide from Table 1 for at least one protein listed in Table 1 from each temporal stage of HSV-viral replication; at least 60 of the peptides listed in Table 1; more than 17 of the peptides listed in Table 1; at least 30 of the peptides listed in Table 1; at least 50 of the peptides listed in Table 1; at least 60 of the peptides listed in Table 1; substantially all of the peptides listed in Table 1; or all of the peptides listed in Table 1; wherein each peptide in the collection includes a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0104] 28. A collection of non-naturally occurring, labeled signature peptides specific for HCMV, including: at least one peptide from Table 2 for each of the 90 proteins listed in Table 2; at least two peptides from Table 2 for a plurality of the 90 proteins listed in Table 2; at least three peptides from Table 2 for a plurality of the 90 proteins listed in Table 2; at least one peptide from Table 2 for at least one protein listed in Table 2 from each temporal stage of HCMV-viral replication; at least 90 of the peptides listed in Table 2; more than 90 of the peptides listed in Table 2; at least 30 of the peptides listed in Table 2; at least 50 of the peptides listed in Table 2; at least 100 of the peptides listed in Table 2; at least 150 of the peptides listed in Table 2; at least 200 of the peptides listed in Table 2; substantially all of the peptides listed in Table 2; or all of the peptides listed in Table 2; wherein each peptide in the collection includes a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0105] 29. A collection of non-naturally occurring, labeled signature peptides specific for KSHV, including: at least one peptide from Table 3 for each of the 62 proteins listed in Table 3; at least two peptides from Table 3 for a plurality of the 62 proteins listed in Table 3; at least three peptides from Table 3 for a plurality of the 62 proteins listed in Table 3; at least one peptide from Table 3 for at least one protein listed in Table 3 from each temporal stage of KSHV-viral replication; at least 62 of the peptides listed in Table 3; more than 62 of the peptides listed in Table 3; at least 30 of the peptides listed in Table 3; at least 50 of the peptides listed in Table 3; at least 75 of the peptides listed in Table 3; at least 100 of the peptides listed in Table 3; at least 150 of the peptides listed in Table 3; substantially all of the peptides listed in Table 3; or all of the peptides listed in Table 3; wherein each peptide in the collection includes a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

[0106] 30. The peptide collection of any one of embodiments 27-29, wherein the label on at least one peptide in the collection includes a heavy isotope.

Example 1: A Trusted Targeted Mass Spectrometry Assay for Pan-Herpesvirus Protein Detection

[0107] The presence and abundance of viral proteins within host cells are part of the essential signatures of the cellular stages of viral infections. Viral proteins are either brought into host cells by infectious particles or expressed at specific steps of the replication cycle. However, methods that can comprehensively detect and quantify these proteins are still limited, particularly for viruses with large protein coding capacity. Here, a mass spectrometry-based Targeted herpesviRUS proTEin Detection (TRUSTED) assay was designed and experimentally validated for monitoring human viruses representing the three Herpesviridae subfamilies—herpes simplex virus type 1 (HSV-1), human cytomegalovirus (HCMV), and Kaposi's sarcoma-associated herpesvirus (KSHV). Assay applicability was demonstrated for 1) capturing the temporal cascades of viral replication, 2) detecting proteins throughout a range of virus concentrations, 3) assessing the effects of clinical therapeutic agents, 4) characterizing the impact of sirtuin-modulating compounds, and 5) studies using different laboratory and clinical viral strains.

[0108] As evidenced by the global burden of viral infectious disease, there is a need for methods that can quickly and accurately detect viral infections and monitor their progression in both laboratory and clinical settings. An indicator of the presence of a viral infection and the stage of a replication cycle is the expression and abundance of viral proteins (Greco et al., Annu. Rev. Virol. 1, 581-604, 2014; Gruffat et al., Front. Microbiol. 7, 2016). Numerous human viruses proceed through their replication cycle by initiating a temporal cascade of viral gene expression, and the expression of different viral proteins can provide signatures of infection progression. However, the genome size and subsequent number of proteins expressed by different viruses

varies widely. For example, viruses range from those expressing a single polyprotein that is cleaved into 10-20 individual proteins (e.g. hepatitis C virus, coronaviruses, poliovirus, etc.) to those with hundreds (e.g. human cytomegalovirus (HCMV)) or thousands (e.g. pandoravirus) of predicted open reading frames (Philippe et al., Science 341, 281-286, 2013; Spall et al., Semin. Virol. 8, 15-23, 1997; Stern-Ginossar et al., Science 338, 1088-1093, 2012). Consequently, it can be challenging to comprehensively monitor viral protein levels for viruses with large protein coding capacity, given that the complexity of such a detection method would scale with the size of the viral proteome. Additionally, the study of viruses with large proteomes has historically suffered from the especially small percentage of viral proteins for which commercially produced antibodies are available.

[0109] Among these large viruses are herpesviruses, which first emerged over 200 million years ago, and consequently have coevolved with humans and other hosts into modernity. This long history of virus-host co-evolution has allowed these viruses to acquire relatively large proteomes (70-250 putative proteins) that facilitate their diverse means for co-opting cellular processes and evading host defense mechanisms. The herpesvirus family consists of three subfamilies of alpha-, beta-, and gamma-herpesviruses—each of which encompass prevalent human pathogens that establish latent, life-long infections that can sporadically reactivate to cause acute disease. For example, alpha-herpesviruses, like herpes simplex virus type I (HSV-1) and type II (HSV-2), cause symptoms ranging from skin lesions to deadly encephalitis (Whitley & Roizman, Lancet 357, 1513-1518, 2001) and the beta-herpesvirus HCMV is linked to cardiac disease (Courivaud et al., J. Infect. Dis. 207, 1569-1575, 2013) and is the leading cause of virally induced birth defects (Cheeran et al., Clin. Microbiol. Rev. 22, 99-126, 2009). Furthermore, some herpesviruses can exacerbate infections with other viral agents. For example, HSV-2 increases the likelihood of contraction and spread of human immunodeficiency virus (HIV-1) (Zhu et al., Nat. Med. 15, 886-892, 2009), and the gamma-herpesvirus Kaposi's sarcoma-associated herpesvirus (KSHV) is the leading cause of cancer in untreated HIV-infected individuals (Mesri et al., Nat. Rev. Cancer 10, 707-719, 2010). However, despite their prevalence as human pathogens and the global health burden of herpesvirus-induced diseases, the available antiviral treatments suffer from toxicity issues (Adair et al., South. Med. J. 87, 1227-1231, 1994; Asahi et al., Eur. J. Neurol. 16, 457-460, 2009; Bedard et al., Antimicrob. Agents Chemother. 43, 557-567, 1999) and vaccines for these viruses do not exist.

[0110] In addition to sharing a proclivity for causing critical diseases, herpesviruses also share a common structure and replication cycle (FIG. **3**A). As enveloped, double-stranded DNA viruses, herpesviruses enter the cell, traffic to the nucleus where they replicate their viral genomes, and finally package this newly synthesized viral DNA into progeny virions that can egress from the cell to continue the infection cycle (Adler et al., Trends Microbiol. 25, 229-241, 2017). Although many of these stages are shared between these viruses, they complete their replication cycles over different lengths of time. For example, HSV-1 replicates in under 24 hours, while KSHV takes ~3 days, and HCMV takes 4-5 days. Despite these differences, a shared characteristic feature of herpesvirus replication is the tightly regulated temporal cascade of viral gene expression that ensues following viral entry into the cell, which can include the expression of immediate early (IE), early (E), delayed early (DE), leaky late (LL), and late (L) classes of viral genes (Honess & Roizman, J. Virol. 14, 8-19, 1974; Schulz & Chang, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), Chapter 28, 2007; Stinski, J. Virol. 26, 686-701, 1978). Consequently, monitoring the levels of herpesvirus proteins not only allows establishment of the presence of infection, but also the stage at which a particular sample is in the infection cycle. The monitoring of few IE, DE, or L marker proteins is standard for assessing replication progression. Traditionally, common methods for monitoring herpesvirus replication include antibody-based techniques such as Western blot (Omoto & Mocarski, J. Virol. 87, 8651-8664, 2013; Sheng & Cristea, PLOS Pathog. 17, e1009506, 2021) and ELISA (Inoue et al., Clin. Diagn. Lab. Immunol. 7, 427-435, 2000) or nucleic acid-based approaches such as microarrays (Bresnahan & Shenk, Science 288, 2373-2376, 2000 Polson et al., Cancer Res. 62, 4525-4530, 2002) and RNA-seq (Boldogköi et al., Sci. Data 5, 1-14, 2018; Wyler et al., Nat. Commun. 10, 1-14, 2019). However, each of these methods suffers from drawbacks including that RNA-based approaches frequently do not accurately reflect the protein abundances which drive cellular phenotypes (Ruggles et al., Mol. Cell. Proteomics 16, 959-981, 2017; Vogel & Marcotte, Nat. Rev. Genet. 13, 227-232, 2012; Zhang et al., Nature 513, 382-387, 2014) and that antibodies against viral proteins often either do not exist or are insufficiently characterized. Being able to accurately monitor the abundances of most viral proteins would provide the ability to comprehensively characterize specific stages of infection and to identify the temporal regulation of viral effectors that inhibit host defense factors and modulate cellular processes. Such a detection method would also allow for the screening of small molecules for their potential anti- or pro-viral activities and discovering their putative viral targets.

[0111] Targeted mass spectrometry (MS) offers a robust method to directly detect and quantify specific proteins of interest with high sensitivity and accuracy. Targeted MS methods, such as parallel reaction monitoring (PRM) and selected reaction monitoring (SRM), rely on the curation of libraries of peptides that fulfill a series of detection requirements, such as being unique to a given protein, well-ionized, and amenable to chromatography separation and MS/MS fragmentation during the nLC-MS/MS analysis. Such libraries provide signature peptides for an array of proteins of interest. With iterative development and validation steps, these methods can be scaled up for high throughput monitoring of hundreds of proteins in a single run (Ebhardt et al., Proteomics 15, 3193-3208, 2015; Lum et al., Cell Syst. 7, 627-642.e6, 2018). Once such a library is developed, these targeted MS approaches can be implemented on several mass spectrometry instrumentation platforms and within different experimental workflows. Ultimately, the established detection parameters for these signature peptides are readily transferrable to other research, clinical, or industry labs.

[0112] Here, a PRM detection library was designed and experimentally validated for the broad detection of viral proteins from all three herpesvirus families: the alpha-herpesvirus HSV-1, the beta-herpesvirus HCMV, and the gamma-herpesvirus KSHV. This assay is called TRUSTED

(Targeted herpesviRUS proTEin Detection). The breadth of proteins monitored by the method captures the temporal cascades of the replication cycles of these viruses. The targeted MS assay accurately quantified the effects of clinically relevant antiviral agents, further capturing their precise temporal regulation of specific viral proteins. Further establishing the applicability of this method for characterizing small molecule compounds, the effects of drugs that modulate the antiviral activity of sirtuin proteins was investigate. Finally, a computational analysis of peptide conservation was performed, demonstrating the applicability of TRUSTED across different viral strains, including laboratory and clinical isolates. Overall, this method provides a sensitive, reliable, and scalable assay for monitoring herpesvirus protein levels and has been deposited online to the PRIDE repository to be readily implementable by other research groups. These results support the broad applicability of these assays for probing viral protein abundances in a wide variety of model systems and contexts, including antiviral drug screening, detecting infections in clinical settings, and genetic manipulations of virus or host factors.

Results

A Targeted Mass Spectrometry Assay for Detecting and Quantifying Signature Alpha-, Beta-, and Gamma-Herpesvirus Proteins

[0113] Considering the biological and clinical relevance of herpesviruses and the lack of methods to comprehensively monitor herpesvirus protein expression in laboratory and clinical settings, a targeted PRM-based assay was developed that offers the ability to systematically quantify viral protein abundances during HSV-1, HCMV, and KSHV infections. To accomplish this, infections were performed in human fibroblast cells for HSV-1 and HCMV, and used a latently-infected cell model (iSLK.219) that can be reactivated to study lytic KSHV infection (Myoung & Ganem, J. Virol. Methods 174, 12-21, 2011). Although both of these cell types represent standard model systems for the study of each aforementioned infection, the assay was designed to be readily applicable to other cell culture models or tissues.

[0114] To capture the various temporal stages of these virus replication cycles, proteins across all classes of herpesvirus gene expression and different virion components were targeted. Detection of canonical markers of infection progression was focused on for each virus, as was detection of viral proteins with diverse cellular functions and localizations. The assays were designed to monitor peptides generated by trypsin digestion given the widespread use and accessibility of this enzyme in experimental workflows. Additionally, it was found that the predicted lysine/arginine content of these viruses, as well as their predicted tryptic peptide content, was well suited to MS analysis. Moving forward, a set of signature peptides was manually curated for each virus by performing an iterative process of exploratory, data-dependent MS analyses of infected samples and experimental validation of peptide detection and reliability by PRM (FIG. **3**B). To further advance the method to monitor proteins and peptides not identified in the exploratory analyses, existing literature and peptide databases were also queried for previously detected viral peptides and attempted to validate these via unscheduled PRM injections. The majority of the HSV-1, HCMV, and KSHV proteins were represented in these assays by 2-4 peptides ranging from 6-36 amino acids in length, with few additional viral proteins being captured by only one experimentally validated peptide. As a result, this allowed for the monitoring of peptides from viral proteins belonging to all temporal classes of viral genes for all three viruses, representing the IE, DE, E, LL, and L replication stages, as well as components of the virion (e.g. capsid, tegument, and envelope proteins) (FIG. **3**C, Tables 1-3).

[0115] Overall, these assays measure the levels of proteins representing 50-80% of the reported proteomes for each virus. Of the three viruses discussed here, HSV-1 expresses the smallest number of proteins and replicates in the fastest amount of time. This HSV-1 PRM assay quantifies up to 60 viral proteins with 3-4 peptides being monitored for most targets. Comparatively, HCMV and KSHV express substantially more proteins, and these assays monitor up to 90 and up to 62 viral proteins, respectively. Moreover, greater than 50% of the proteins quantified by the assays represent targets without commercially available antibodies.

[0116] The assay monitors these viral peptides of interest using 6-minute retention time windows across a series of one (HSV-1 and KSHV) or two (HCMV) 60-minute injections using ~1.5 μg of input sample (FIG. **3**D). To reliably quantify protein abundance across different biological samples, the assay leverages internal reference standard peptides that help account for variability in input material due to natural variation in sample preparation and other factors. To serve this purpose several ubiquitously expressed cytoskeletal factors were chosen, including tubulin (TUBA1A), myosin 5A (MYOSA), and a myosin II heavy chain (MYH9), which exhibit stable expression levels throughout infection (FIG. **3**E, Tables 1-3). After normalizing for differences in input sample, measurements were obtained that were reproducible and exhibited low mass errors for the relative protein abundances across the different infections. Coefficients of variation (CVs) averaged less than 30% across peptides corresponding to a given protein and across different biological replicates (FIG. **3**F). Altogether, this process culminated in the establishment of virus-specific peptide libraries that proved effective at robustly detecting HSV-1, HCMV, and KSHV peptides during wild type infections. Given the robustness and accuracy of detection offered by targeted mass spectrometry, this assay was named TRUSTED (Targeted herpesviRUS proTEin Detection).

Herpesvirus PRM Assay Captures the Signature Temporal Cascade of Viral Gene Expression

[0117] An essential aspect of herpesvirus replication is the temporal cascade of gene expression that ensues following viral entry into cells. Having demonstrated that the assays can accurately detect viral proteins, whether it can also capture the temporality of their abundances during the progression of infection was next assessed. For HSV-1, infected fibroblasts were harvested at 2, 6, 12, and 18 hours post-infection (HPI), while for HCMV cells at 24, 48, 72, 96, and 120 HPI were collected. For KSHV, the latent virus was reactivated in iSLK.219 cells and collected samples at 24, 48, and 72 hours post-reactivation (HPR). For each virus, these time points represent the specific stages of virus gene expression (immediate early through late), virion assembly, and egress. Measurements of protein levels at each time point demonstrated the sequential nature of viral protein levels, as expected from the well-established cascades of

gene expression that are characteristic of herpesvirus infections (depicted as fold-change in FIG. **4**).

[0118] For HSV-1 infection, viral protein levels increased throughout the course of infection, with an approximately 32-fold median increase observed at 18 HPI relative to the first time point of detection for each protein (FIG. **4**A). To further confirm the adequate progression through infection, this PRM assay was also designed to include peptides from host factors known to be inhibited or repurposed by HSV-1 (FIG. **4**B). Indeed, in accordance with previous studies (Boutell et al., J. Virol. 76, 841-850, 2002; Johnson et al., Virol. 87, 5005-5018, 2013; Liu et al., J. Virol. 89, 8982-8998, 2015; Orzalli et al., Proc. Natl. Acad. Sci. U.S.A 109, 2012), virus-induced degradation of the defense factors, interferon-inducible protein 16 (IFI16) and PML, and an increase in the levels of the pro-viral host protein C1QBP (p32) were observed.

[0119] During HCMV infection, viral protein levels increased up to 1000-fold, with a median increase of ~10-fold by 120 HPI (FIG. **4**C). It was also noted that some HCMV IE proteins (UL13, UL36, UL37, and UL123) exhibited less induction (<2-fold, on average), compared to most other HCMV proteins. This agrees with literature reports that many of these IE proteins are highly induced early upon infection, afterwards maintaining similar levels throughout the virus replication cycle (Jean Beltran et al., Cell Syst. 3, 361-373, 2016; Lu & Everett, J. Virol. 89, 3062-3075, 2015; McCormick et al., J. Virol. 77, 631-641, 2003).

[0120] The reactivation of KSHV led to milder temporal increases of ~4-fold by 72 HPR (FIG. **4**D). Like most HSV-1 and HCMV proteins, KSHV protein levels also generally increased following reactivation, with the exception of the DE protein K2, which was decreased by ~40% by 72 HPR. This agrees with a previous study showing that K2 is robustly expressed in latently infected iSLK.219 cells, but its levels are decreased following reactivation (Park et al., Sci. Rep. 9, 1-13, 2019).

Differing Levels of Infection (MOI) are Robustly Detected Via PRM

[0121] Having established that the TRUSTED assays reliably capture herpesvirus temporal gene expression, the performance of the assay in recognizing different infection levels, i.e. the number of incoming viral particles per cell (multiplicity of infection; MOI) was characterized. To this end, PRM was performed on cells that were subjected to increasing amounts of HCMV virus by infecting at MOIs of 0.05, 0.25, 1.25, and 6.25. Even at low MOIs (MOI=0.05 or 0.25), it was found that nearly all of the targeted peptides and proteins reached detectable levels by 120 HPI (FIGS. **5**A-**5**C). At higher levels of infection (MOI=1.25 or 6.25) all were detectable even earlier, by 24-72 HPI. Among the proteins that were detectable at low MOIs early during infection were IE proteins, such as UL122, UL123, UL13, UL36, and UL37, as well as the most abundant HCMV viral tegument protein, UL83 (FIG. **6**C) (Murphy et al., Proc. Natl. Acad. Sci. U.S.A 100, 14976-14981, 2003; Varnum et al., J. Virol. 78, 10960-10966, 2004). As expected, for most proteins, abundance increased with increasing MOI (FIG. **5**D) and the extent of this increase was approximately linear with respect to the theoretical percent of cells infected at a given MOI. However, a subset of proteins within the US12 family did not conform to this pattern, including US12 (DE) and US15 (LL) (FIG. **5**E). Proteins within the US12 family are known for their immunomodulatory capacity and have previously been shown to be targeted for lysosomal degradation (Fielding et al., Elife 6, 2017). As such, their decrease in abundance at high MOIs is perhaps unsurprising—yet, these results demonstrating that these proteins do not appear to be degraded at low MOIs suggest that there may be a previously unappreciated threshold of US12 family protein expression that must be reached before these proteins are targeted for degradation. Overall, these results demonstrate that these PRM assays are applicable to wide range of MOIs, with low MOIs being closer to physiological levels and high MOIs being commonly employed in research studies (e.g., for achieving synchronous infections).

PRM Application to Investigations of Clinically Employed Herpesvirus Antiviral Drugs

[0122] To demonstrate the utility of the PRM assays for screening antiviral compounds, viral protein abundance dynamics upon treatment with canonical herpesvirus antiviral drugs was next monitored. Fibroblast cells were treated with acyclovir (ACV) or cidofovir (CDV), two compounds used in the clinic as treatments for HSV-1 and HCMV infections, respectively (Kimberlin & Whitley, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), pp. 1153-1174, 2007; Lurain & Chou, Clin. Microbiol. Rev. 23, 689-712, 2010). Both ACV and CDV hinder viral replication by acting as nucleoside (ACV) or nucleotide (CDV) analogues that selectively inhibit viral DNA polymerases (Biron, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), pp. 1219-1250, 2007). Both drugs target the same viral process, yet ACV is a more potent inhibitor of HSV-1 than HCMV and the converse is true for CDV (Kimberlin & Whitley, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), pp. 1153-1174, 2007; Lurain & Chou, Clin. Microbiol. Rev. 23, 689-712, 2010). Although their mechanism of action and impact on virus production are well-established, how these drugs broadly affect the landscape of viral protein abundances remains less understood, with the exception of a proteomics study performed for HSV-1 after ACV treatment (Bell et al., J. Proteome Res. 12, 1820-1829, 2013). Therefore, whether the PRM assay can provide context to viral protein regulation upon drug treatment during HSV-1 and HCMV infection was investigated. Given their mechanism of action, it was expected that following ACV or CDV treatment viral protein levels would be decreased after DNA replication is inhibited, which occurs around 6 HPI for HSV-1 and 24 HPI for HCMV. Indeed, upon treatment with 1 μM ACV (IC_{50}=2-3 μM in MRC5 cells (Bacon et al., J. Antimicrob. Chemother. 37:303-313, 1996; Brandi et al., Life Sci. 69:1285-1290, 2001; Leary et al., Antimicrob. Agents Chemother. 46:762-768, 2002)), a decrease was observed of ~20% and ~35% by and after 12 HPI in levels of E and L HSV-1 proteins, respectively (FIGS. **6**A-**6**B). Among these, a significant reduction in the levels of many HSV-1 proteins known to be involved in viral DNA replication was noted, such as DBP, UL42, UL30, UL8, and UL12, as well as UL48, which is a major activator of viral gene expression (Cohan & Frappier, Virus Res. 298, 2021; Roizman & Campadelli-Fiume, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), pp. 70-92, 2007).

Yet, little effect was observed for IE proteins. Considering that L gene expression is directly dependent on successful DNA replication (Honess & Roizman, J. Virol. 14, 8-19, 1974), it is perhaps anticipated that these proteins would show a more robust response to ACV treatment. It was also noted that among E and L proteins, only a subset were significantly downregulated upon ACV treatment, which is in agreement with a previous study showing that IE proteins are broadly unaffected and only a subset of E and L HSV-1 proteins are decreased by ACV treatment (Bell et al., J. Proteome Res. 12, 1820-1829, 2013).

[0123] In contrast to the varied response to ACV, upon treatment of HCMV-infected cells with 1 μM CDV (IC_{50}≈0.5 μM in MRC5 cells (Beadle et al., Antimicrob. Agents Chemother. 46, 2381-2386, 2002; Scott et al., Antimicrob. Agents Chemother. 51, 89-94, 2007)) substantial decreases were observed in HCMV protein levels across all temporal classes of gene expression (FIGS. **6**C-**6**E). By 72 HPI more than 85% of the proteins monitored exhibited decreases of at least 35% compared to the PBS control. Moreover, among all 90 proteins, only a single protein, UL54, was decreased by less than 20% across all time points, further underscoring the global effects of CDV treatment on HCMV protein expression (FIG. **6**E). Nevertheless, a phenotype that was conserved from these observations of ACV treatment was that IE genes were relatively less impacted by CDV treatment compared to other gene classes. In both cases, this likely reflects the relative independence of IE gene expression, as these proteins are characterized by their ability to be transcribed in the absence of de novo protein synthesis (Roizman & Zhou, Virology 479-480, 562-567, 2015). An exception to this observation, however, was that the abundance of the IE protein UL122 was decreased by ~70% by 120 HPI. This observation may be explained by the fact that the UL122 locus produces at least two alternative protein isoforms that are expressed from alternative downstream promoters, and these isoforms are expressed with late kinetics and depend on successful viral genome replication (Puchtler & Stamminger, J. Virol. 65, 6301-6306, 1991; Stenberg et al., J. Virol. 63, 2699-2708, 1989). The peptides monitored by this PRM assay are within the C-terminal region of the UL122 protein, and thus common to both full-length UL122 and these shorter isoforms.

Modulation of Antiviral Sirtuin Enzymatic Activity Differentially Regulates Viral Protein Levels During Herpesvirus Infections

[0124] In addition to those targeting DNA replication, a variety of other small molecules have been shown to impact herpesvirus production. These include compounds that target sirtuin proteins, which has previously been shown to exhibit antiviral activity against several viruses, including HSV-1 and HCMV (Koyuncu et al., MBio 5, 2014). Sirtuins are a diverse family of seven (SIRT1-7) NAD^+-dependent deacetylases and deacylases that regulate a range of cellular processes including metabolism, the cell cycle, and gene expression (Choi & Mostoslaysky, Curr. Opin. Genet. Dev. 26, 24-32, 2014; Michan & Sinclair, Biochem. J. 404, 1-13, 2007). Accumulating evidence during infections with both DNA and RNA viruses suggests that sirtuins could serve as potential targets for therapeutic intervention (Budayeva et al., J. Virol. 90, 5-8, 2016). It was previously established that using EX-527 or CAY10602 compounds to inhibit or activate SIRT1 enzymatic activity results in increased or decreased HCMV titers, respectively (Koyuncu et al., MBio 5, 2014). Similarly, the broad-spectrum activator of sirtuins, trans-Resveratrol, decreased HCMV titers. The effects of these drugs on the HCMV viral proteome, however, have not been fully investigated, nor has their impact on HSV-1 or KSHV replication and viral protein levels been tested.

[0125] To characterize the effects of SIRT1 activation or inhibition on viral protein levels during HCMV infection, cells were treated with 10 μM EX-527, 12.5 μM CAY10602, or 50 μM trans-Resveratrol and performed the PRM assay. At these concentrations, an increase (EX-527) or decrease (CAY10602 and trans-Resveratrol) of ~50% in HCMV titers (Koyuncu et al., MBio 5, 2014) had previously been observed. Of the small subset of proteins that had previously quantified been by western blot (UL123, UL26, and UL99) following CAY10602 and trans-Resveratrol treatment (Koyuncu et al., MBio 5, 2014), the PRM results were in agreement with previous observations; UL123 levels were unchanged at 24 HPI, UL26 levels were decreased at 48 HPI, and UL99 levels were robustly decreased by 72 HPI (FIG. **7**A). However, these results also revealed that treatment with the sirtuin-activating compounds CAY10602 and trans-Resveratrol induces a global decrease of ~70% by 120 HPI in viral protein levels (FIGS. **7**A-**7**C). Decreased levels are already observed for IE proteins, in particular for UL122 and UL13. These effects become progressively compounded for DE, LL, and L proteins, an observation similar to the results following CDV treatment. A number of viral proteins (e.g., NEC1, UL76, UL79, UL87, and IR10) become undetectable at early HPIs, displaying delayed expression kinetics upon treatment with sirtuin activators. For most viral proteins, the sirtuin-modulatory effects became more pronounced as the infection progressed. In contrast, EX-527 treatment produced a moderate increase (~20-40%) in viral protein levels, and these effects were primarily observed for DE, LL, and L proteins (FIGS. **7**A-**7**C). Overall, these results match the previously reported changes in virus titers (Koyuncu et al., MBio 5, 2014), suggesting that alterations in protein levels contribute to the effect of sirtuin-modulatory compounds on virus production.

[0126] The next question asked was whether treatment with these compounds, at the same concentrations, would also impact viral protein levels in the context of HSV-1 infection and KSHV reactivation. Similar to EX-527 treatment during HCMV infection, an ~60% increase in E and L HSV-1 protein levels was observed by late time points of infection (FIGS. **8**A-**8**B). On the other hand, trans-Resveratrol decreased protein levels by ~30-40% and CAY10602 treatment reduced HSV-1 protein levels only moderately at 6 HPI, with levels recovering later in infection. These findings following trans-Resveratrol treatment in fibroblasts agrees with another study that found that, upon a similar treatment, the levels of several monitored viral proteins were reduced in HSV-1-infected neurons (Leyton et al., Virus Res. 205, 63-72, 2015). Among the proteins that were detected, the viral transactivators ICP4 and UL48 (VP16) were strongly upregulated upon EX-527 treatment and downregulated by trans-Resveratrol treatment. Given their essential roles in stimulating viral IE gene expression (Fan et al., Front. Microbiol. 11, 1910, 2020; Roizman & Campadelli-Fiume, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), pp. 70-92, 2007), it is possible that regulation of ICP4 and UL48

levels could serve as a toggle for modulating HSV-1 gene expression at a more global level in a SIRT1-dependent manner.

[0127] Finally, for KSHV, the CAY10602 and EX-527 treatments led to contrasting effects compared to the HCMV and HSV-1 results (FIGS. **8**C-**8**D). Although their changes were subtle (<10%), only seven viral proteins (ORF4, ORF24, ORF37, ORF52, ORF57, ORF59, and gM) displayed a pattern that included both increased and decreased abundances upon treatment with sirtuin inhibitor and activator, respectively. Overall, EX-527 treatment resulted in decreased protein levels at all reactivation time points tested, in particular for DE and L proteins. CAY10602 slightly increased protein levels at early time points (i.e., 24 and 48 HPR), while resulting in decreased proteins levels at the latest time point post-reactivation (i.e., 72 HPR). However, it is of note that most of these changes, although passing significance thresholds, were relatively mild in terms of the fold-change reached. The one exception is the overall decrease in virus protein abundances (by 20-30%) observed for both EX-527 and CAY10602 at 72 HPR.

[0128] Altogether, these results confirm and augment understanding of how sirtuin activity-modulating treatments impact protein expression throughout the course of HCMV, HSV-1 and KSHV infections. These results also demonstrate the ability of these assays to contextualize the effects of small molecule treatments, both at the individual and global viral protein levels.

Conservation of TRUSTED Peptides Indicates Assay Utility Across Diverse Virus Strains

[0129] An important consideration when developing a detection assay is its broad applicability—in the current exemplar case, whether this PRM assay is suitable for detecting viral proteins upon infection with a range of HSV-1, HCMV, and KSHV strains. Several laboratory and clinical strains are implemented for the study of each of these viruses, and many have readily accessible complete genome sequences available in online databases (e.g., NCBI, Ensembl). To therefore address the applicability of the assay to different strains (FIG. **9**A), a computational analysis was performed of potential peptide sequences represented by the genomes of different HSV-1, HCMV, and KSHV strains in the NCBI nucleotide database to determine the extent of conservation for peptides targeted by the PRM assay. As expected, the analysis demonstrated that ~100% of the PRM peptides were conserved for HSV-1 strain 17 and HCMV strain AD169, the model strains upon which the PRM assays were developed (FIGS. **9**B-**9**D). A direct comparison to the precise type of KSHV virus produced by the cell line used in this study (iSLK.219) was not possible given the lack of a fully sequenced genome in the NCBI database. However, nearly full conservation was observed when compared to BrK.219, a B-cell line latently infected with the same type of KSHV (rKSHV.219) that is also harbored by iSLK.219 cells (Kati et al., J. Virol. Methods 217, 79-86, 2015) (FIGS. **9**B and **9**E).

[0130] Next the peptide sequences targeted by the TRUSTED assay were compared to those predicted to be present in other HSV-1 strains: F, H129, KOS, MacIntyre, McKrae, and SC16. Among all of these strains near 100% conservation was observed for most proteins targeted by the assay, supporting its broader use for studies with a range of HSV-1 strains. The one exception was the glycoprotein gI (FIG. **9**C). Although PRM peptides targeting this viral protein were available for all analyzed strains, most conservation was observed between 17, F, H129, KOS, and SC16 strains, where three-to-four of the optimized PRM peptides for gI were fully conserved. Alternatively, one-to-two peptides were available for the McIntyre and McKrae strains. This is in accordance with previous reports showing that gI exhibits relatively high levels of variation across different HSV-1 strains (Watson et al., Virology 433, 528-537, 2012).

[0131] Similarly, for both HCMV and KSHV >90% conservation was observed among the different strains assessed in this analysis. A comparison of laboratory/high-passage (AD169 and Towne) and clinical/low-passage (Toledo, TR, TB40/E, and Merlin) strains of HCMV demonstrated strong conservation across most proteins, with more than 85% of the proteins targeted by the PRM assay having at least one conserved peptide across all strains tested. Similar levels of conservation were observed for the different KSHV strains assessed, which included the laboratory strain BAC16, which was developed for KSHV recombinant virus production (Brulois et al., J. Virol. 86, 9708-9720, 2012), as well as two clinical strains GK18 and DG-1. An important limitation of this analysis, however, is that protein segments resulting from alternative splicing are not captured by this computationally predicted peptide sequences. For both HCMV and KSHV, it was observed that there was one protein for each virus with peptides targeted by the PRM assays that were not predicted to be conserved across any of the strains. In both cases, the proteins in question (UL128 for HCMV and K8 for KSHV) are known to be produced as the result of alternative splicing, and thus were not detected by this analysis. Despite this, overall, these results indicate that the PRM assay developed and described herein will be applicable across a range of virus strains and has the capacity to extend beyond cell culture experiments.

Discussion

[0132] Here, TRUSTED, a targeted MS assay for detecting and quantifying proteins from three model viruses across herpesvirus subfamilies, is presented. The described assays for alpha-, beta-, and gamma-herpesviruses allow for a comprehensive overview of replication cycle progression, while simultaneously quantifying locus-specific changes covering much of the proteomes of these herpesviruses. By applying this technique, 1) the temporal characteristics of the herpesvirus gene expression cascade was captured, 2) a new perspective on canonical herpesvirus treatments has been provided, 3) its applicability to screening anti- and pro-viral compounds, as shown for the modulation of SIRT1 antiviral function, has been examined, and 4) its utility across different laboratory and clinical viral strains was proposed. Ultimately, this approach is broadly applicable to investigating the progression of herpesvirus replication in diverse model systems and in the context of a wide variety of perturbations including small-molecule treatment, antiviral screening, and genetic perturbations.

[0133] An important driver for the development of this assay was the lack of commercially available antibodies for a majority of the proteins expressed by these large viruses. By employing targeted MS, viral peptide levels were able to be directly measured in an antibody-independent manner. An equally important driver was the need for methods that provide high throughput detection of viral proteins. In comparison to standard antibody-based methods (e.g., west-

ern blot, ELISA), this assay also has the advantage of being highly parallelized, able to simultaneously measure a vast number of viral proteins. Although mRNA measurements also offer throughput, it is known that transcript levels do not always reflect the levels of functional protein products (Ruggles et al., Mol. Cell. Proteomics 16, 959-981, 2017; Vogel & Marcotte, Nat. Rev. Genet. 13, 227-232, 2012; Zhang et al., Nature 513, 382-387, 2014). The described HSV-1, HCMV and KSHV detection assays include peptides from viral proteins belonging to all temporal classes of viral genes, representing the IE, DE, E, LL, and L replication stages of these viruses. Therefore, an informed snapshot of the virus replication state is obtained at a previously unattainable level in 1-2 injections onto the instrument.

[0134] The provided herpesvirus detection assays benefit from other advantages characteristic for targeted MS, such as its affordability compared to purchasing equivalent number of antibodies or ELISA kits. Additionally, the detection parameters established for these herpesvirus proteins are readily exportable for use by other groups in a wide variety of model systems (e.g., different cell lines, tissues, animal models). In each of these contexts, it may be necessary to optimize the sample preparation procedure, for example by altering lysis conditions, but the overall parameters of the PRM assays are unlikely to need adjusting. With the exception of the rare scenario where one or more of the normalizing human proteins (e.g., TUBA1A, MYOSA, MHY9) are not expressed or their levels are substantially altered by infection, the peptides targeted in each assay should be readily detected for virus strains where these peptide sequences are conserved. Furthermore, experiments using low MOIs suggest the promise of these assays for detecting viral proteins in clinical samples, and future experiments would be needed to support their use in this context. The continuous increase in access to mass spectrometry instrumentation within academic, industry, and clinical settings further expands the ability to implement these targeted MS assays in a variety of biological and medical investigations.

[0135] Following the development of these assays, their performance was validated both in the context of canonical herpesvirus treatments and investigation of other potential antiviral compounds. In doing this, known, as well as previously unappreciated, aspects were uncovered of the effects of the canonical treatments, ACV and CDV, which act as inhibitors of virally encoded DNA polymerases (Biron, In Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis, (Cambridge University Press), pp. 1219-1250, 2007). For both of these established drugs, a reduction in late gene expression was observed during HSV-1 and HCMV infections. However, in contrast to the decreased levels of IE and E proteins that were detected at early time points following CDV treatment during HCMV infection, these results indicate that the expression of IE and E HSV-1 genes increase at 6 HPI after ACV treatment. This has been observed previously (Furman & McGuirt, Antimicrob. Agents Chemother. 23, 332-334, 1983), and a possible explanation for this effect is that when DNA replication is inhibited by ACV, a greater fraction of viral genomes are available for IE and E gene transcription, since they are not actively being used to replicate new viral genomes. However, this increase in viral gene expression for ACV-treated cells relative to control cells could only occur at early time points of infection since the successful replication of viral genomes in control cells later during the infection cycle would ultimately overcome this effect. Alternatively, the increase in HSV-1 gene expression at early time points following ACV treatment could indicate a viral feedback response to the blockage in DNA synthesis, whereby increasing the production of DNA polymerase subunits and processing factors helps to overcome the blockage. Furthermore, this increase could be accomplished through a global increase in protein synthesis rates, as 6 HPI roughly coincides with the peak abundance of these particular IE and E transcripts (Harkness et al., J. Virol. 88, 6847-6861, 2014). Consistent with this model, an increase in total cellular protein synthesis rates was observed at the concentration of ACV used in the study (Furman & McGuirt, Antimicrob. Agents Chemother. 23, 332-334, 1983). Overall, these results not only capture the changes in viral protein abundances that are likely to underlie and result from the antiviral activity of these polymerase-inhibiting drugs, but also further underscore the complex regulation of viral protein levels.

[0136] Having assessed the performance of the TRUSTED assays for investigating clinically employed compounds, its applicability for characterizing putative anti- and pro-viral small molecule compounds was tested. As previously shown that the sirtuin family of NAD-deacetylases can restrict herpesvirus replication (Koyuncu et al., MBio 5, 2014), the assays were applied to determine the effects of modulating sirtuin activity on viral protein levels. Although siRNA knockdown or small-molecular modulation of SIRT1 has been shown to affect HCMV titers in a manner consistent with an antiviral role for SIRT1 (Koyuncu et al., MBio 5, 2014), it is not known how these effects are mediated or whether these changes in viral titer are also evident at the HCMV protein level. Here, this was indeed found to be the case, as treatment of HCMV-infected cells with the SIRT1 activators CAY10602 or trans-Resveratrol resulted in a global reduction in viral protein production by 48 HPI. Additionally, treatment with the SIRT1 inhibitor EX-527 was shown to increase HCMV protein levels, particularly toward the end of the virus replication cycle. Altogether, these results establish that SIRT1 enzymatic activity modulates HCMV protein expression—yet, whether these effects are mediated directly or indirectly remains to be investigated. Considering that one of the main targets of SIRT1 is histones, it is possible that SIRT1 enzymatic activity directly regulates viral protein expression by deacetylating histones on viral genomes (Cliffe & Knipe, J. Virol. 82, 12030-12038, 2008; Murphy et al., EMBO J. 21, 1112-1120, 2002; Zalckvar et al., Proc. Natl. Acad. Sci. U.S.A 110, 13126-13131, 2013). Alternatively, it remains to be seen whether SIRT1 can regulate the acetylation status of HCMV proteins, thereby impacting their levels and functions. It is also possible, however, that these effects are indirectly mediated SIRT1. For example, it is well established that SIRT1 deacetylates and inhibits the transcription factor NFκB (Kauppinen et al., Cell. Signal. 25, 1939-1948, 2013), which is essential for driving HCMV protein expression from the major immediate early promoter (MIEP) (Hancock & Nelson, Virol. 1, 2017). Consistent with this notion decreases in UL122 (IE2) and UL123 (IE1) levels were observed upon CAY10602 and trans-Resveratrol treatment, perhaps due to differential MIEP activity. Moreover, considering the robust and global reduction in HCMV protein levels observed following SIRT1 activation by CAY10602 or trans-Resveratrol, it follows that these effects

could be driven by altering the levels of essential viral transcription factors like UL122 and UL123.

[0137] Ultimately, the impact of SIRT1 modulation on herpesvirus protein levels appears to be broad in nature, as an effect on viral protein levels during HSV-1 infection upon treatments with SIRT1 activators and inhibitors was also observed. Both in the case of HSV-1 and HCMV, it was found that modulating SIRT1 activity with small molecule compounds altered the levels of master viral transcriptional activators, such as ICP4 and UL48 (VP16) for HSV-1 and UL122 and UL123 for HCMV. However, the investigation of the effects of CAY10602 and EX-527 treatment on KSHV protein levels did not follow this pattern. For the KSHV infection model used in this study, reactivation is achieved, in part, by treating with sodium butyrate (NaB). NaB is a broad inhibitor of class I and II HDACs that promotes KSHV reactivation by strongly inhibiting HDAC-mediated silencing of the major lytic transactivator RTA (ORF50) (Lu et al., J Virol 77, 11425-11435, 2003). It has similarly been shown that SIRT1 regulates the reactivation of KSHV via a parallel mechanism (Li et al., J. Virol. 88, 6355-6367, 2014). Notably, the experiments demonstrating a role for SIRT1 in maintaining KSHV latency were performed in a reactivation model different than the one used in this study. As the established protocol for achieving robust KSHV reactivation in the iSLK.219 cell line uses relatively high levels of NaB (Hartenian et al., PLoS Patho. 16, e1008269, 2020), it is possible that the antiviral effects of SIRT1 on the RTA locus are negligible in this context. Therefore, considering the wealth of other SIRT1 targets, as well as the known pleiotropic effects of NaB, one would not necessarily expect the effects of modulating SIRT1 enzymatic activity in a NaB background to properly recapitulate its known antiviral role. Yet, despite the limitation of this reactivation workflow, in combination with the reported role for SIRT1 in regulating RTA, these results suggest that SIRT1 is poised to globally regulate herpesvirus protein levels, perhaps via the regulation of essential viral transcription factor levels.

[0138] In summary, this Example demonstrated the value of these TRUSTED assays for globally detecting and quantifying viral proteins from the three main Herpesviridae subfamilies with high accuracy and throughput. These targeted detection methods can offer information about virus biology, as well as provide the means to monitor the effects of small molecules or genetic perturbations in the context of infections. Given the promise for their broad applicability to a range of biological contexts and viral strains, these assays are believed to be of widespread utility. This assay enables development of additional targeted MS assays for the detection of diverse viral pathogens, as well as development of highly needed repositories of signature peptide for virus detection.

Data and Code Availability

[0139] Skyline data analysis files and raw mass spectrometry data have been deposited to PanoramaWeb at online at panoramaweb.org/HerpesvirusPRM.url and are associated with the ProteomeXchange identifier PXD025879. The above data can be accessed with a reviewer account (email: panorama+reviewer29@proteinms.net, password: sUkA-lhPS).

Star Methods

Cell Lines and Primary Cultures

[0140] MRC5 primary human fibroblasts (HFs) (ATCC CCL-171) were used as the model system for HSV-1 and HCMV infections and were cultured in complete growth medium (DMEM supplemented with 10% fetal bovine serum and 1% penicillin-streptomycin antibiotics) at 37° C. and 5% CO_2. iSLK.219 cells harboring latent KSHV (a gift from Dr. Britt Glaunsinger, University of California, Berkeley) were grown in complete growth medium supplemented with 500 μg/ml hygromycin (ThermoFisher Scientific, 10687010) at 37° C. and 5% CO_2. All cells were used for experiments within a maximum of 10 passages.

Virus Strains and Infections

[0141] Wild type HSV-1 strain 17+ (a gift from Beate Sodeik, Hannover Medical School, Hannover, Germany) was propagated as previously described (Diner et al., 2015). Briefly, PO stocks were generated by electroporating pBAC-HSV-1 into U-2 OS cells. Working stocks were then generated from the PO stock by infecting U-2 OS cells at a low level (~0.001 PFU/cell) and virus was collected ~3 days later when cells exhibited 100% cytopathic effect. In a similar manner, wild type HCMV strain AD169 was produced from BAC electroporation into HFs and working stocks were propagated by infecting HFs at a low level. In both cases, cell-associated virus was released by sonication, combined with supernatant virus, then concentrated by ultracentrifugation (20,000 rpm, 2 hours, 4° C. with SW28 swinging bucket rotor [Beckman Coulter]) over a 10% ficoll (HSV-1) or 20% sorbitol (HCMV) cushion. Virus stock titers were determined by plaque assay for HSV-1 or tissue culture infectious dose ($TCID_{50}$) for HCMV and infections were performed at a multiplicity of infection (MOI) of 3. KSHV infections were performed by reactivating iSLK.219 cells with 1 mM sodium butyrate (Sigma-Aldrich, B5887) and 1 μg/ml doxycycline (Sigma, D9891), which resulted in 100% reactivation after 72 hours.

Small Molecule Treatments and Sample Collection

[0142] Acyclovir (Cayman Chemical, 14160), cidofovir (Cayman Chemical, 13113), EX-527 (Cayman Chemical, 10009798), CAY10602 (Cayman Chemical, 10009796), and trans-Resveratrol (Cayman Chemical, 70675) were resuspended in DMSO (acyclovir, EX-527, CAY10602, trans-Resveratrol) or PBS (cidofovir) to generate 2000× stocks that were stored at −80° C. 12 hours prior to virus infection or reactivation, cells were treated with either the small molecule drug or DMSO/PBS control at an equivalent volume. Cell culture concentrations of each drug were as follows: acyclovir (1 μM), cidofovir (1 μM), EX-527 (10 μM), CAY10602 (12.5 μM), and trans-Resveratrol (50 μM). For infection cycles lasting longer than 24 hours, small molecule drugs were re-added to the cell culture medium every 24 hours. Upon collection, cells were rinsed with PBS, scraped into a microcentrifuge tube, pelleted by centrifugation, and rinsed again with PBS. After the addition of 2 μl of protease inhibitor cocktail (Sigma, P8340) sample pellets were snap frozen in liquid nitrogen and stored at −80° C. until ready for mass spectrometry analysis.

Selection of Target Proteins and Peptides for Targeted Mass Spectrometry Analysis Via Parallel Reaction Monitoring

[0143] For all three viral infection models, initial data-dependent analysis runs using the same chromatography conditions as the targeted analyses were performed on the latest timepoint collected in order to identify as many viral proteins and peptides as possible. These identifications were compared to a FASTA file containing the complete viral proteomes of all three viruses plus the human proteome using Skyline (MacLean et al., Bioinformatics 26, 966-968, 2010). Up to four proteotypic peptides for each viral protein detected were selected. In cases where more than three unique peptides were available, peptides were prioritized for selection based first on originating from different regions of the protein and second based on eluting at different points in the chromatogram. Additional peptide selection for proteins not found via data-dependent analysis was performed by successively running unscheduled targeted runs for up to 30 peptides at a time. Peptides initially detected via targeted analysis were confirmed by both manual inspection and automated database search using Sequest HT and Proteome Discoverer™ 2.3. While not every viral protein was detected for each virus, proteins representing all of the temporal classes of viral protein expression are present in the final targeted method.

Protein Sample Preparation for PRM Analysis

[0144] HCMV and KSHV samples: Frozen cell pellets were resuspended in lysis buffer (4% SDS, 50 mM Tris pH 7.5, 100 mM NaCl, 0.5 mM EDTA) and lysed by repeated steps of incubation at 95° C. for 3 min. followed by sonication in a cup-horn sonicator for 20 pulses. Protein concentration was determined by BCA assay and 50-100 μg of protein was then reduced and alkylated at 70° C. for 20 min. using 25 mM TCEP (Thermo Fisher #77720) and 50 mM 2-chloroacetamide (MP Biomedicals #ICN15495580). Protein was then extracted by methanol-chloroform precipitation, resuspended in 25 mM HEPES buffer (pH 8.2), and digested for 16 hours at 37° C. using a 1:50 ratio of trypsin to protein (w/w). The resulting peptides were then adjusted to 1% trifluoroacetic acid (TFA) and desalted using the StageTip method (Rappsilber et al., *Nat. Protoc.* 2(8):1896-1906, 2007) with C18 material (3M #2215). Finally, bound peptides were washed with 0.5% TFA, eluted with 70% acetonitrile (ACN) and 0.5% formic acid (FA), dried via SpeedVac™ (ThermoFisher), and resuspended in 1% FA and 1% ACN to a concentration of 0.75 μg/μl for peptide LC-MS/MS analysis.

[0145] HSV-1 samples: Due to a smaller amount of available starting sample and to demonstrate assay applicability to other peptide preparation methods, HSV-1 samples were prepared using S-Trap (Protifi, C02-micro-80) following the manufacturers protocol. Briefly, samples were resuspended in lysis buffer (9% SDS, 50 mM Tris pH 7.5, 100 mM NaCl, 0.5 mM EDTA) and lysed by repeated steps of incubation at 95° C. for 3 min. followed by sonication in a cup-horn sonicator for 20 pulses. Protein concentration was determined by BCA assay and 30 μg of protein was adjusted to a volume of 40 μl and reduced and alkylated at 70° C. for 20 min. using 25 mM TCEP and 50 mM 2-chloroacetamide. Samples were then acidified to a final concentration of 1.2% aqueous phosphoric acid, mixed with 165 μl of wash buffer solution (90% methanol, 100 mM triethanolamine bicarbonate [TEAB] pH 7.1), and loaded onto the S-trap column. Next, samples were washed 5× with 150 μl of wash buffer, and a 1 hour on-column digestion was performed at 47° C. using a 1:25 ratio of trypsin to protein (w/w) in 25 μl of 25 mM TEAB (pH 8). Digested peptides were then eluted with sequential addition of 40 μl of 25 mM TEAB (pH 8), 40 μl of 0.2% FA, and 70 μl of 50% ACN in 0.2% FA. Finally, pooled elutions were dried via SpeedVac and resuspended in 1% FA and 1% ACN to a concentration of 0.75 μg/μl for peptide LC-MS/MS analysis.

Peptide LC-MS/MS Analysis

[0146] Samples prepared for parallel reaction monitoring (PRM) analysis were analyzed on a Q Exactive HF mass spectrometer (ThermoFisher Scientific) coupled to an EASYSpray ion source (ThermoFisher Scientific). Peptides were resolved for nLC-MS/MS analysis using a Dionex Ultimate 3000 nanoRSLC (ThermoFisher Scientific) equipped with a 25 cm EASYSpray C18 column (ThermoFisher Scientific, ES902). Peptides (1.5 μg) were separated by reverse phase chromatography with solvents A (0.1% formic acid) and B (90% acetonitrile, 0.1% formic acid) at a flow rate of 250 nL/min using a two-phase linear gradient of 2-22% solvent B for 45 min and 22-38% Solvent B for 15 min and were ionized at 1.7 kV. A single duty cycle consisted of an MS-SIM scan (400-2000 m/z range, 15,000 resolution, 15 ms max injection time (MIT), 3×10^6 automatic gain control (AGC) target) followed by 30 PRM scans (30,000 resolution, 60 ms MIT, 1×10^5 AGC target, 0.8 m/z isolation window, normalized collision energy (NCE) of 27, 125 m/z fixed first mass) and spectrum data were recorded in profile. Acquisition was controlled by a scheduled inclusion list using 6 min retention time windows. For HSV-1 and KSHV, all peptides were acquired in a single run. For HCMV, the peptide inclusion list was split in half and two injections per sample were made in order to obtain sufficient scans across the peak.

PRM Data Processing and Analysis

[0147] Raw files containing PRM spectra were imported into Skyline and peak quality for all peptides monitored was assessed manually and compared to a reference spectral library. Peptides without convincing spectra or spectra with excessive interference were manually discarded. Following quality control, peptide abundance was calculated from the summed area under the curve (total peak area) for the top three most abundant transition ions per peptide and peptide quantification was exported as a csv file for programmatic analysis in Python. To normalize for differences in input sample, peptide abundances were scaled such that the values of global standard peptides were equivalent, on average, across all input files (e.g. conditions, replicates, injections, etc.). For example, if a single global standard peptide is considered, its summed peak area in a given file is divided by the mean summed peak area across all input files. For each input file, the average of these mean normalized values is then calculated across all global standard peptides that were monitored. Finally, the total peak area values for all peptides monitored by the assay are divided by the input file-specific scaling factor calculated via the above procedure. For data visualization and subsequent analysis, peptide values were then scaled to their mean across replicates, time points, and treatments (where applicable). In some cases, the

log-2 fold change for all peptides was also calculated relative to either the first time point that a given peptide was detected (FIG. **4**) or relative to a control treatment (FIGS. **6-8**).

Analysis of PRM Peptide Conservation Across Herpesvirus Species and Strains

[0148] Peptide conservation analysis was performed by downloading all herpesvirus-associated complete genomes from the NCBI nucleotide database. Potential peptide sequences were then generated for both strands in all reading frames and compared to each peptide targeted by the PRM assay to determine if a given peptide could be produced from a given genome. For virus strains with more than one reported, complete genome deposited in the database, peptides were considered to be conserved as long as they were computationally detected in at least one of these genomes.

Programs, Software, and Statistics

[0149] Data processing and analyses were performed using Python 3.7 in conjunction with Pandas, NumPy, SciPy, Seaborn, and Matplotlib libraries. Significance was determined by two-tailed Student's t-test using the Python SciPy library unless otherwise stated. Where applicable: *$p<0.05$, ** $p<0.01$, *** $p<0.001$, and **** $p<0.0001$. Figures where constructed in Microsoft PowerPoint.

[0150] As will be understood by one of ordinary skill in the art, each embodiment disclosed herein can comprise, consist essentially of or consist of its particular stated element, step, ingredient or component. Thus, the terms "include" or "including" should be interpreted to recite: "comprise, consist of, or consist essentially of." The transition term "comprise" or "comprises" means includes, but is not limited to, and allows for the inclusion of unspecified elements, steps, ingredients, or components, even in major amounts. The transitional phrase "consisting of" excludes any element, step, ingredient or component not specified. The transition phrase "consisting essentially of" limits the scope of the embodiment to the specified elements, steps, ingredients or components and to those that do not materially affect the embodiment. A material effect, in this context, is an alteration of composition or method that results in a statistically significant change in detection or monitoring or measuring of protein level(s) associates with a herpes virus infection.

[0151] Unless otherwise indicated, all numbers expressing quantities of ingredients, properties such as molecular weight, reaction conditions, and so forth used in the specification and claims are to be understood as being modified in all instances by the term "about." Accordingly, unless indicated to the contrary, the numerical parameters set forth in the specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques. When further clarity is required, the term "about" has the meaning reasonably ascribed to it by a person skilled in the art when used in conjunction with a stated numerical value or range, i.e. denoting somewhat more or somewhat less than the stated value or range, to within a range of ±20% of the stated value; ±19% of the stated value; ±18% of the stated value; ±17% of the stated value; ±16% of the stated value; ±15% of the stated value; ±14% of the stated value; ±13% of the stated value; ±12% of the stated value; ±11% of the stated value; ±10% of the stated value; ±9% of the stated value; ±8% of the stated value; ±7% of the stated value; ±6% of the stated value; ±5% of the stated value; ±4% of the stated value; ±3% of the stated value; ±2% of the stated value; or ±1% of the stated value.

[0152] Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements.

[0153] The terms "a," "an," "the" and similar referents used in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

[0154] Groupings of alternative elements or embodiments of the invention disclosed herein are not to be construed as limitations. Each group member may be referred to and claimed individually or in any combination with other members of the group or other elements found herein. It is anticipated that one or more members of a group may be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is deemed to contain the group as modified thus fulfilling the written description of all Markush groups used in the appended claims.

[0155] Certain embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Of course, variations on these described embodiments will become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventor expects skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

[0156] Furthermore, numerous references have been made to patents, printed publications, journal articles, other writ-

ten text, and web site content throughout this specification (referenced materials herein). Each of the referenced materials are individually incorporated herein by reference in their entirety for their referenced teaching(s), as of the filing date of the first application in the priority chain in which the specific reference was included. For instance, with regard to chemical compounds and nucleic acid or amino acids sequences referenced herein that are available in a public database, the information in the database entry is incorporated herein by reference as of the date that the database identifier was first included in the text of an application in the priority chain.

[0157] It is to be understood that the embodiments of the invention disclosed herein are illustrative of the principles of the present invention. Other modifications that may be employed are within the scope of the invention. Thus, by way of example, but not of limitation, alternative configurations of the present invention may be utilized in accordance with the teachings herein. Accordingly, the present invention is not limited to that precisely as shown and described.

[0158] The particulars shown herein are by way of example and for purposes of illustrative discussion of the preferred embodiments of the present invention only and are presented in the cause of providing what is believed to be the most useful and readily understood description of the principles and conceptual aspects of various embodiments of the invention. In this regard, no attempt is made to show structural details of the invention in more detail than is necessary for the fundamental understanding of the invention, the description taken with the drawings and/or examples making apparent to those skilled in the art how the several forms of the invention may be embodied in practice.

[0159] Definitions and explanations used in the present disclosure are meant and intended to be controlling in any future construction unless clearly and unambiguously modified in the example(s) or when application of the meaning renders any construction meaningless or essentially meaningless. In cases where the construction of the term would render it meaningless or essentially meaningless, the definition should be taken from Webster's Dictionary, 11th Edition or a dictionary known to those of ordinary skill in the art, such as the Oxford Dictionary of Biochemistry and Molecular Biology, 2nd Edition (Ed. Anthony Smith, Oxford University Press, Oxford, 2006), and/or A Dictionary of Chemistry, 8th Edition (Ed. J. Law & R. Rennie, Oxford University Press, 2020).

Table FIG. 6C, part 1 of 2: Numerical values corresponding heatmap in FIG. 6C.

Protein	Protein		treatment PBS timepoint				
Gene	Acc'n	Tempor	24	48	72	96	120
IRS1	P09715	IE	0.250785	0.756381	1.451441	1.694721	2.004621
TRS1	P09695	IE	0.140825	0.676574	1.620029	1.723719	2.095501
UL122	P19893	IE	0.068637	0.209524	1.124834	2.43485	3.650415
UL123	P13202	IE	0.681151	0.907494	1.262795	1.539325	1.386181
UL13	P16755	IE	0.631837	0.8794	1.604159	1.73045	1.131117
UL36	P16767	IE	0.918981	0.843071	1.080198	1.279079	1.009684
UL37	P16778	IE	0.592152	0.73698	1.219448	1.463375	1.390296
CVC2	P16726	DE		0.258661	1.08198	1.299644	2.147224
DBP	P17147	DE	0.052836	0.349198	1.213731	1.65021	2.421545
HELI	P16736	DE	0.106083	0.572051	1.197691	1.778849	2.358703
NEC1	P16794	DE			0.720243	1.034519	1.569651
NEC2	P16791	DE	0.01666	0.225026	1.185219	2.090479	2.671696
RIR1	P16782	DE	0.049137	0.212205	1.222715	1.994853	2.493298
TRM1	P16724	DE		0.2566	1.023039	1.600806	2.309575
UL102	P16827	DE	0.304174	0.846621	1.275958	1.424813	1.674066
UL104	P16735	DE		0.295404	1.262875	1.650401	2.151989
UL112/UL113	P17151	DE	0.413674	0.504576	1.26149	1.587395	2.269971
UL114	P16769	DE	0.301202	0.753335	1.180486	1.59813	1.698169
UL119/UL118	P16739	DE	0.10991	0.870682	1.79184	1.722192	1.787611
UL128	P16837	DE	0.147551	0.221898	0.918828	1.577666	2.480548
UL26	P16762	DE	0.05108	0.207762	1.360138	1.944208	2.5785
UL32	P08318	DE	0.024197	0.078473	1.053011	1.971722	2.471693
UL34	P16812	DE	0.053016	0.287237	1.698087	2.581309	2.860096
UL35	P16766	DE		0.108128	0.734779	1.502527	2.102323
UL38	P16779	DE	0.514737	0.744087	1.274677	1.528141	1.607453
UL4	P17146	DE		0.544291	2.277638	0.978331	1.120444
UL44	P16790	DE	0.032732	0.273312	1.48212	2.215076	3.148486
UL48	P16785	DE		0.163114	1.03521	1.661073	1.995695
UL54	P08546	DE	0.258098	0.687352	1.243172	1.520513	1.631654
UL71	P16823	DE	0.208212	0.63463	2.012666	1.605904	1.554933
UL78	P16751	DE	0.17223	1.147585	1.601803	1.706453	1.776326
UL84	P16727	DE	0.083629	0.333997	1.234403	2.136399	2.84944
UL95	P16801	DE		0.313896	1.206258	1.705688	2.373253
UL96	P16787	DE	0.348955	0.52491	1.380551	2.184377	2.372318
UL97	P16788	DE	0.178576	0.353446	1.277154	2.27615	2.999907
UL98	P16789	DE	0.176646	0.596109	1.240219	1.934312	2.69132
US12	P09721	DE	0.586568	1.114854	1.63054	1.753413	0.990584
US13	P09720	DE	0.322888	1.099342	1.996525	1.661279	1.262476
US14	P09719	DE	0.221282	0.512589	2.33877	2.260259	1.998401

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Table FIG. 6C, part 1 of 2: Numerical values corresponding heatmap in FIG. 6C.

Protein	Protein		treatment PBS timepoint				
Gene	Acc'n	Tempor	24	48	72	96	120
US18	P69334	DE	0.237715	1.196709	1.802059	1.409431	1.403785
US22	P09722	DE	0.161242	0.648367	1.385537	1.774462	2.428785
US23	P09701	DE	0.333897	0.751452	1.431044	2.043794	2.078385
US24	P09700	DE	0.447468	0.660882	1.430814	1.732604	2.296272
US8	P09730	DE	0.425692	0.981054	1.301518	1.332339	1.735514
US9	P09729	DE	0.276947	0.630381	1.258728	1.680793	1.988449
gB	P06473	DE	0.067202	0.323045	1.371855	1.533585	1.879769
sp|P09710|IR01_HCMVA	P09710	DE	0.166694	0.458022	1.583051	2.36612	2.899611
DUT	P16824	LL		0.426446	1.015092	1.607234	2.217037
TRM3	P16732	LL		0.194632	1.042872	1.348334	1.685798
TRX1	P16783	LL		0.105044	0.934396	1.699969	2.709225
TRX2	P16728	LL	0.009752	0.103028	1.017941	1.932234	3.225171
UL132	P69338	LL	0.053565	0.228255	1.465775	2.209159	2.693363
UL24	P16760	LL	0.065362	0.195111	1.156665	2.082414	2.653938
UL40	P16780	LL		0.454859	1.227951	1.429929	2.019743
UL47	P16784	LL		0.136439	1.009136	1.752108	2.265806
UL49	P16786	LL			0.907803	1.163751	1.30788
UL69	P16749	LL	0.127901	0.333797	1.146749	1.856518	2.622016
UL70	P17149	LL	0.081415	0.533152	1.306058	1.974665	2.738696
UL83	P06725	LL	0.032366	0.077552	1.264046	2.529601	2.893248
US15	P09718	LL	0.667066	1.513413	1.807614	1.313109	0.911894
sp|P16808|IR10_HCMVA	P16808	LL			1.000214	1.548755	1.585485
sp|P16810|IR12_HCMVA	P16810	LL		0.42267	1.455845	1.495767	2.393318
CVC1	P16799	L		0.25608	0.966758	1.701526	2.474723
GO	P16750	L		0.235202	1.13264	1.34771	2.068163
MCP	P16729	L	0.007966	0.104896	1.096994	2.126841	3.451037
SCP	Q7M6N6	L		0.10908	0.84193	1.562422	2.21031
TRM2	P16792	L		0.216727	1.131495	1.396104	1.901399
UL103	P16734	L	0.215361	0.271472	1.214228	2.021008	2.195014
UL117	P16770	L	0.222897	0.602105	1.297717	2.062811	2.903952
UL22A	P16845	L		0.146262	0.789563	1.946351	2.404015
UL25	P16761	L	0.027601	0.177959	1.227902	1.824382	2.137984
UL29	P16764	L	0.455785	0.733505	1.294604	1.6468	1.727337
UL30	P16765	L		0.260338	0.811393	1.296451	2.099247
UL31	P16848	L	0.219951	0.302142	1.190181	1.931344	2.945038
UL43	P16781	L	0.072227	0.138191	1.019467	1.976613	2.372416
UL52	P16793	L	0.009554	0.273543	1.072243	1.839262	2.881923
UL76	P16725	L		0.175862	0.925197	1.483273	2.073458
UL79	P16752	L			1.212119	1.353885	1.323589
UL80	P16753	L	0.009843	0.247173	1.222493	1.512581	2.233543
UL82	P06726	L	0.195721	0.300115	1.109869	2.061503	2.947351
UL87	P16730	L			0.800856	1.240519	1.854068
UL88	P16731	L		0.200969	0.969586	1.573311	2.277961
UL94	P16800	L	0.028986	0.221683	1.345914	2.222315	3.391382
UL99	P13200	L	0.017936	0.179753	1.361859	2.557756	2.805152
gH	P12824	L	0.043819	0.29768	1.391606	1.621845	2.88984
gL	P16832	L	0.034155	0.252536	1.028485	1.573971	2.115138
gM	P16733	L	0.056971	0.113649	1.185737	2.025884	2.634662
gN	P16795	L		0.224573	1.120667	1.644274	2.012461
sp|P16809|IR11_HCMVA	P16809	L	0.063932	0.984503	1.916477	1.425699	1.4745

Table FIG. 6C, part 2 of 2: Numerical values corresponding heatmap in FIG. 6C.

Protein	Protein		treatment CDV timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
IRS1	P09715	IE	0.199986	0.54076	1.017395	0.95363	1.003233
TRS1	P09695	IE	0.110313	0.402986	0.901374	0.789285	1.103319
UL122	P19893	IE	0.053644	0.075626	0.373843	0.8676	1.141027
UL123	P13202	IE	0.73244	0.851492	0.792374	0.773245	1.073504
UL13	P16755	IE	0.513069	0.781242	0.85747	0.796458	1.074796
UL36	P16767	IE	0.988532	0.93035	0.881822	0.833989	1.234293

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Table FIG. 6C, part 2 of 2: Numerical values corresponding heatmap in FIG. 6C.

Protein	Protein		treatment CDV timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
UL37	P16778	IE	0.546603	0.865743	1.037712	0.936036	1.211654
CVC2	P16726	DE			0.229796	0.881199	0.958843
DBP	P17147	DE	0.04283	0.238596	0.780163	1.215436	2.035455
HELI	P16736	DE	0.102356	0.410569	0.713135	0.613421	1.12763
NEC1	P16794	DE			0.245633	0.664107	1.120549
NEC2	P16791	DE	0.015902	0.085671	0.691913	0.973118	1.797276
RIR1	P16782	DE	0.049612	0.106458	0.44297	0.847813	1.313438
TRM1	P16724	DE		0.118782	0.544402	0.834651	1.312144
UL102	P16827	DE	0.291728	0.785271	1.111084	0.933199	1.353088
UL104	P16735	DE		0.062375	0.485231	0.57286	0.893783
UL112/UL113	P17151	DE	0.334496	0.516317	0.713059	0.74387	0.879487
UL114	P16769	DE	0.30253	0.642947	1.007798	0.974251	1.541152
UL119/UL118	P16739	DE	0.075406	0.387858	0.917847	0.720627	0.867826
UL128	P16837	DE	0.147215	0.163049	0.315652	0.811144	1.192616
UL26	P16762	DE	0.049544	0.107348	0.497253	1.007169	1.563873
UL32	P08318	DE	0.016161	0.031134	0.230341	0.855086	1.478301
UL34	P16812	DE	0.053761	0.101766	0.575404	0.684934	0.944404
UL35	P16766	DE			0.334648	0.664653	1.132697
UL38	P16779	DE	0.500743	0.749414	0.934287	0.874868	1.271594
UL4	P17146	DE		0.074474	0.081455	1.514433	0.634991
UL44	P16790	DE	0.032501	0.095565	0.519712	0.965386	1.23511
UL48	P16785	DE		0.043328	0.466482	0.754106	1.099828
UL54	P08546	DE	0.215351	0.624271	1.148686	1.255569	1.415334
UL71	P16823	DE	0.297774	0.389946	0.767965	1.299094	1.228876
UL78	P16751	DE	0.183363	0.653348	1.047713	0.790342	0.920837
UL84	P16727	DE	0.082702	0.129705	0.394805	0.777919	1.217286
UL95	P16801	DE		0.12153	0.333455	0.55959	0.727477
UL96	P16787	DE	0.338998	0.359515	0.511079	0.714223	1.265073
UL97	P16788	DE	0.168506	0.250163	0.525763	0.833774	1.136561
UL98	P16789	DE	0.178545	0.356072	0.674095	1.01228	1.140401
US12	P09721	DE	0.639747	0.719166	1.060776	0.668834	0.661029
US13	P09720	DE	0.217406	0.725446	1.061914	0.874107	0.778618
US14	P09719	DE	0.190274	0.284909	0.81128	0.684521	0.697716
US18	P69334	DE	0.316053	0.762455	1.076368	1.116389	0.679037
US22	P09722	DE	0.170113	0.400723	0.758502	1.104873	1.167395
US23	P09701	DE	0.343519	0.497448	0.711426	0.785243	1.023792
US24	P09700	DE	0.29728	0.475328	0.665269	0.783188	1.043264
US8	P09730	DE	0.331677	0.909091	1.064029	0.779572	1.139513
US9	P09729	DE	0.230799	0.611225	1.072598	0.907894	1.342186
gB	P06473	DE	0.051334	0.189332	0.724313	0.995867	1.203063
sp|P09710|IR01_HCMVA	P09710	DE	0.15142	0.216371	0.452832	0.496683	0.784905
DUT	P16824	LL		0.29049	0.62746	0.782325	1.033917
TRM3	P16732	LL			0.491309	0.702517	0.985491
TRX1	P16783	LL		0.01277	0.336317	0.840918	1.114209
TRX2	P16728	LL	0.008754	0.019515	0.361876	0.84128	1.493121
UL132	P69338	LL	0.040479	0.113114	0.451618	0.688745	0.867732
UL24	P16760	LL		0.107038	0.392259	0.708459	1.171435
UL40	P16780	LL		0.390533	0.781149	0.746709	0.949128
UL47	P16784	LL		0.030524	0.411373	0.760447	0.987849
UL49	P16786	LL			0.594833		0.6463
UL69	P16749	LL	0.167573	0.255881	0.675926	0.90319	1.466744
UL70	P17149	LL	0.068242	0.314259	0.743004	0.832734	1.254916
UL83	P06725	LL	0.03389	0.037905	0.42756	1.026985	1.676848
US15	P09718	LL	0.587918	1.200814	0.889925	0.610799	0.497447
sp|P16808|IR10_HCMVA	P16808	LL			0.274276	0.685864	0.905406
sp|P16810|IR12_HCMVA	P16810	LL		0.210264	0.687537	0.572596	0.762004
CVC1	P16799	L		0.114247	0.407893	0.599964	0.877464
GO	P16750	L			0.600957	0.567844	0.820979
MCP	P16729	L	0.009303	0.014442	0.400636	0.875489	1.664133
SCP	Q7M6N6	L			0.373261	0.67795	1.225047
TRM2	P16792	L		0.061302	0.550456	0.834268	1.243658
UL103	P16734	L	0.236005	0.195378	0.564237	0.898964	1.157411
UL117	P16770	L	0.198288	0.387502	0.586738	0.585824	0.837033
UL22A	P16845	L		0.070247	0.419873	0.584165	1.639524
UL25	P16761	L	0.023156	0.064258	0.460618	0.844308	1.445088
UL29	P16764	L	0.435242	0.630488	0.854916	0.892122	1.329202
UL30	P16765	L			0.411482	0.544486	0.912512
UL31	P16848	L	0.263208	0.237948	0.422259	0.6245	1.093568

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Table FIG. 6C, part 2 of 2: Numerical values corresponding heatmap in FIG. 6C.

Protein	Protein		treatment CDV timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
UL43	P16781	L	0.068983	0.09529	0.240246	0.777663	1.1093
UL52	P16793	L	0.013908	0.086712	0.465787	0.876604	1.492921
UL76	P16725	L			0.303513	0.420981	0.739568
UL79	P16752	L			0.471315	0.558584	0.8598
UL80	P16753	L	0.007269	0.040807	0.658131	1.01737	1.248889
UL82	P06726	L	0.21355	0.214759	0.494683	0.993159	1.469289
UL87	P16730	L				0.318733	0.571648
UL88	P16731	L		0.050213	0.428913	0.682707	0.808781
UL94	P16800	L	0.031925	0.092581	0.547424	0.852067	1.265724
UL99	P13200	L	0.017968	0.065129	0.455047	0.911138	1.628261
gH	P12824	L	0.033031	0.130388	0.754226	1.267968	1.569596
gL	P16832	L	0.032043	0.069084	0.507315	0.675982	1.175407
gM	P16733	L	0.022403	0.031186	0.476981	0.996641	1.476228
gN	P16795	L		0.07597	0.514066	0.694728	1.395662
sp|P16809|IR11_HCMVA	P16809	L	0.041091	0.502024	0.869003	0.696092	0.763362

Table FIG. 7A, part one of three: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment DMSO timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
IRS1	P09715	IE	0.393104	0.879093	1.037837	1.489751	1.798934
TRS1	P09695	IE	0.289694	0.930518	1.175334	1.667247	2.06192
UL122	P19893	IE	0.0896	0.36789	1.311	2.35221	2.93474
UL123	P13202	IE	1.117581	0.869304	1.200658	1.576622	1.313666
UL13	P16755	IE	1.808719	0.867179	0.94627	0.972491	0.833624
UL36	P16767	IE	1.269471	0.756912	1.10423	0.969856	0.935186
UL37	P16778	IE	0.977619	0.710908	0.879852	1.258002	1.321659
CVC2	P16726	DE	0.033036	0.234398	0.843682	1.473524	1.742806
DBP	P17147	DE	0.202937	0.725404	1.308883	1.802648	2.135764
HELI	P16736	DE	0.375325	1.004965	0.970409	1.405546	1.842887
NEC1	P16794	DE		0.199916	0.714128	1.415099	1.255646
NEC2	P16791	DE	0.047283	0.56915	1.416441	2.121626	2.94629
RIR1	P16782	DE	0.093042	0.331684	1.198452	2.209886	2.829697
TRM1	P16724	DE	0.071195	0.781348	1.377334	1.848543	2.558026
UL102	P16827	DE	0.506281	0.822891	0.764576	1.238179	1.430991
UL104	P16735	DE	0.079816	0.602142	1.160453	1.57307	1.94716
UL112/UL113	P17151	DE	0.490921	0.922144	1.447385	1.953647	2.151198
UL114	P16769	DE	0.687095	0.979833	0.824552	1.255677	1.361339
UL119/UL118	P16739	DE	0.279099	1.149815	1.104291	1.524356	2.198141
UL128	P16837	DE	0.136473	0.235374	0.610776	1.378586	2.301731
UL26	P16762	DE	0.09088	0.315592	1.083849	2.344631	3.355264
UL32	P08318	DE	0.021045	0.136302	1.176787	2.926972	3.259442
UL34	P16812	DE	0.131957	0.571032	1.532516	2.115785	2.611207
UL35	P16766	DE		0.236243	0.856154	1.481481	1.945895
UL38	P16779	DE	1.024826	1.00979	1.031389	1.23675	1.211252
UL4	P17146	DE	0.050876	0.262743	0.665275	1.547969	1.940969
UL44	P16790	DE	0.09404	0.591005	1.585129	2.60947	2.75765
UL48	P16785	DE	0.023599	0.305841	1.395709	2.145967	2.608366
UL54	P08546	DE	0.728126	0.878315	0.8278	1.21377	1.404576
UL71	P16823	DE	0.543242	0.784585	1.155059	2.000245	2.086693
UL78	P16751	DE	0.978204	1.333013	0.774078	0.786681	1.413302
UL84	P16727	DE	0.154744	0.485524	1.196259	2.1062	2.969434
UL95	P16801	DE	0.133557	0.791183	1.273922	1.697682	2.092853
UL96	P16787	DE	0.395194	0.498143	1.105626	1.818972	2.420627
UL97	P16788	DE	0.323982	0.407571	1.106745	2.107496	2.743195
UL98	P16789	DE	0.343372	0.711319	1.204941	1.86116	2.486448
US12	P09721	DE	1.845409	1.611546	0.6772	0.709222	0.878613
US13	P09720	DE	0.952303	1.582174	1.073425	1.468487	1.311741
US14	P09719	DE	0.385377	0.526746	1.238294	1.713375	2.325983
US18	P69334	DE	0.913165	1.421354	0.897768	1.553597	1.663655
US22	P09722	DE	0.466248	0.889126	1.16792	1.961626	2.12487

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Table FIG. 7A, part one of three: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment DMSO timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
US23	P09701	DE	0.707085	0.951967	1.043903	1.466673	1.83079
US24	P09700	DE	0.727117	1.032747	1.10738	1.502221	1.903099
US34	P09709	DE	0.64941	0.266953	0.560355	1.338793	1.752423
US8	P09730	DE	1.182054	0.910335	0.737573	1.31192	1.171373
US9	P09729	DE	0.613619	0.881808	0.738144	1.10986	1.178805
gB	P06473	DE	0.143939	0.487999	1.176069	2.064371	2.610523
IR01	P09710	DE	0.301458	0.667166	1.138179	1.658432	2.429139
DUT	P16824	LL	0.340306	0.70037	0.881236	1.309266	1.788989
TRM3	P16732	LL	0.005785	0.492149	1.080037	1.458589	1.800428
TRX1	P16783	LL	0.010183	0.233817	1.214315	2.083469	2.464961
TRX2	P16728	LL	0.004367	0.293278	1.359655	2.369769	3.039143
UL132	P69338	LL	0.105837	0.394871	1.148245	1.989573	2.449843
UL24	P16760	LL	0.125926	0.321343	1.126095	2.281626	2.925485
UL40	P16780	LL	0.629045	1.327183	1.060654	1.37884	1.494983
UL47	P16784	LL	0.010151	0.367838	1.322829	2.012307	2.474483
UL49	P16786	LL	0.129139	0.606789	0.873072	1.323194	1.633429
UL69	P16749	LL	0.279007	0.764161	1.269773	1.81729	2.431475
UL70	P17149	LL	0.267492	1.035599	1.102485	1.537487	2.080954
UL83	P06725	LL	0.045577	0.106815	1.074583	2.613546	3.459602
US15	P09718	LL	1.736876	1.136256	0.634881	0.703388	0.711988
IR10	P16808	LL		0.100867	0.661253	1.105537	2.018289
IR12	P16810	LL	0.095529	1.214211	1.160935	1.395809	2.36916
CVC1	P16799	L	0.113008	0.52015	1.127732	1.738645	2.302152
GO	P16750	L		0.579512	1.151258	1.199106	1.809305
MCP	P16729	L	0.004831	0.26752	1.273651	2.260747	2.96467
SCP	Q7M6N6	L		0.173111	0.773711	1.410959	2.005696
TRM2	P16792	L	0.046195	0.928792	1.460667	2.100253	2.25531
UL103	P16734	L	0.494035	0.480031	1.135776	1.946469	2.565965
UL117	P16770	L	0.429142	0.826665	1.220833	1.768765	1.872085
UL22A	P16845	L	0.043747	0.430408	0.925235	2.382229	2.972968
UL25	P16761	L	0.035989	0.331394	1.053009	2.102861	2.66582
UL29	P16764	L	1.124493	0.981446	1.255175	1.517049	1.390968
UL30	P16765	L		0.522517	1.145859	1.589368	1.953842
UL31	P16848	L	0.345362	0.572116	1.05512	1.579286	2.14508
UL43	P16781	L	0.103108	0.149933	0.772934	2.205217	3.10558
UL52	P16793	L	0.028902	0.702339	1.713372	2.124829	2.676017
UL76	P16725	L		0.352753	0.753033	1.163988	1.574809
UL79	P16752	L		0.398017	0.703113	0.912349	1.622292
UL80	P16753	L	0.048682	0.688282	1.35164	1.881246	2.543808
UL82	P06726	L	0.174561	0.287136	1.187686	2.276051	2.817713
UL87	P16730	L		0.704093	0.768952	1.234206	1.820823
UL88	P16731	L	0.045945	0.559472	1.466787	1.883565	2.473639
UL94	P16800	L	0.064895	0.30074	1.187478	2.143727	2.755272
UL99	P13200	L	0.036289	0.289185	0.786987	1.578262	2.299944
gH	P12824	L	0.070326	0.373848	1.219586	2.167575	2.675225
gL	P16832	L	0.048344	0.370447	0.934334	1.631913	2.483173
gM	P16733	L	0.019516	0.203496	1.135467	2.477414	3.039096
gN	P16795	L	0.172056	0.558447	1.172849	2.127828	2.950601
IR11	P16809	L	0.170317	0.995013	0.820773	1.338677	2.149723

Table FIG. 7A, part 2 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment EX-527 timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
IRS1	P09715	IE	0.591008	1.40896	1.45297	1.541626	1.656193
TRS1	P09695	IE	0.371537	1.435856	1.526488	1.764696	1.945819
UL122	P19893	IE	0.105395	0.63015	2.032761	3.33355	3.843622
UL123	P13202	IE	1.225628	1.057823	1.119377	1.31216	1.196422
UL13	P16755	IE	2.222267	1.115289	0.847079	0.757733	0.636139
UL36	P16767	IE	1.389102	0.885226	1.039287	0.974351	1.141714

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Table FIG. 7A, part 2 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment				
			EX-527	EX-527	EX-527	EX-527	EX-527
			timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
UL37	P16778	IE	1.192159	0.956982	0.971239	1.136804	1.293862
CVC2	P16726	DE	0.047747	0.476888	1.581313	2.030158	2.650395
DBP	P17147	DE	0.2975	1.313526	1.848136	2.320553	2.344675
HELI	P16736	DE	0.594308	1.451514	1.217401	1.542745	1.963409
NEC1	P16794	DE		0.466789	1.354085	1.524392	1.901636
NEC2	P16791	DE	0.069187	0.912545	1.890826	2.626156	3.323789
RIR1	P16782	DE	0.134451	0.57444	1.849171	3.098451	4.254559
TRM1	P16724	DE	0.135066	1.362245	2.072084	2.748651	3.47803
UL102	P16827	DE	0.733659	1.14895	0.965547	1.31481	1.703236
UL104	P16735	DE	0.0733	0.994871	1.634889	2.027069	2.632987
UL112/UL113	P17151	DE	0.608859	1.27523	1.652788	1.839454	1.752987
UL114	P16769	DE	0.830077	1.236007	0.981175	1.280067	1.561763
UL119/UL118	P16739	DE	0.402952	1.772877	1.333697	1.79256	2.466528
UL128	P16837	DE	0.123328	0.321942	0.930985	2.352975	3.323697
UL26	P16762	DE	0.116606	0.504816	1.482611	2.920353	4.14742
UL32	P08318	DE	0.030696	0.296457	1.867211	3.24201	3.991019
UL34	P16812	DE	0.220402	0.944509	2.267205	2.939025	3.253491
UL35	P16766	DE	0.014946	0.408894	1.180604	1.818817	2.282807
UL38	P16779	DE	1.285338	1.288563	1.137121	1.209506	1.30009
UL4	P17146	DE	0.066462	0.394409	1.091592	2.418042	3.577224
UL44	P16790	DE	0.114289	0.981904	2.041512	2.948001	3.235758
UL48	P16785	DE	0.029578	0.584717	1.786399	2.510836	3.146015
UL54	P08546	DE	0.99575	1.35587	1.105452	1.36112	1.68656
UL71	P16823	DE	0.753104	1.147403	1.660189	2.01117	2.29427
UL78	P16751	DE	1.348929	2.165044	0.723823	0.909449	1.081154
UL84	P16727	DE	0.241799	0.851559	1.673742	2.852737	3.937379
UL95	P16801	DE	0.209806	1.60345	1.943516	2.053504	2.186525
UL96	P16787	DE	0.522785	0.765395	1.376677	2.029292	2.905683
UL97	P16788	DE	0.416199	0.678445	1.499966	2.599692	3.557208
UL98	P16789	DE	0.426328	1.17023	1.698151	2.285939	2.735892
US12	P09721	DE	1.996846	1.435294	0.450758	0.418455	0.544134
US13	P09720	DE	0.585645	1.946569	1.1408	1.119837	1.262922
US14	P09719	DE	0.429486	0.776683	1.819842	2.676913	3.370413
US18	P69334	DE					
US22	P09722	DE	0.552733	1.298633	1.376625	1.85749	2.04501
US23	P09701	DE	0.908004	1.45506	1.204828	1.489183	1.808652
US24	P09700	DE	0.82496	1.445037	1.338863	1.689468	1.927756
US34	P09709	DE	0.777937	0.306615	0.625002	1.486055	2.076057
US8	P09730	DE	1.120794	1.147072	0.837019	1.053235	1.167256
US9	P09729	DE	0.725543	1.169757	0.777427	0.996418	1.115877
gB	P06473	DE	0.174584	0.763851	1.749207	2.685096	3.300573
IR01	P09710	DE	0.264282	1.063209	1.623899	2.376679	2.882245
DUT	P16824	LL	0.466081	0.892085	1.314353	1.795798	2.090512
TRM3	P16732	LL	0.018774	1.02261	1.588103	2.116128	2.654605
TRX1	P16783	LL	0.011353	0.499105	1.766105	2.613623	3.502978
TRX2	P16728	LL	0.006257	0.607848	2.026974	3.214779	4.315337
UL132	P69338	LL	0.133087	0.481624	1.752206	2.465814	2.837893
UL24	P16760	LL	0.174373	0.494823	1.69841	3.16897	4.18348
UL40	P16780	LL	0.742979	1.547923	1.310339	1.304801	1.300485
UL47	P16784	LL	0.019991	0.664088	1.8425	2.452856	2.88063
UL49	P16786	LL	0.304803	1.186641	1.150344	1.688097	2.22546
UL69	P16749	LL	0.418877	1.222353	1.612025	2.424229	3.274744
UL70	P17149	LL	0.374438	1.660989	1.540933	1.912518	2.340356
UL83	P06725	LL	0.063099	0.197338	1.617085	3.439916	4.663234
US15	P09718	LL	2.346331	1.4624	0.533046	0.516143	0.764521
IR10	P16808	LL		0.271878	0.746938	1.991968	2.411238
IR12	P16810	LL	0.207656	1.93902	1.710055	1.771738	2.686219
CVC1	P16799	L	0.183779	0.727911	1.553613	2.453429	3.146933
GO	P16750	L		1.033524	1.460731	1.415713	1.549275
MCP	P16729	L	0.005908	0.526119	1.815522	3.25922	4.298434
SCP	Q7M6N6	L		0.417337	1.29177	2.484876	2.983501
TRM2	P16792	L	0.106868	1.377131	2.616844	2.797888	2.914212
UL103	P16734	L	0.52735	0.565809	1.285224	2.322211	3.020124
UL117	P16770	L	0.679446	1.44872	1.692004	2.148533	2.302078
UL22A	P16845	L	0.065004	0.628413	1.343917	2.572579	4.430641
UL25	P16761	L	0.057212	0.629548	1.727173	2.732889	4.208425
UL29	P16764	L	1.141514	1.20704	1.247057	1.398225	1.420313

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Table FIG. 7A, part 2 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment EX-527 timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
UL30	P16765	L	0.134401	0.806592	1.440981	1.746032	1.615107
UL31	P16848	L	0.4765	1.032585	1.699196	2.532274	3.731496
UL43	P16781	L	0.099059	0.191361	1.150285	2.873035	4.456903
UL52	P16793	L	0.064504	1.489052	2.338652	2.489357	2.793375
UL76	P16725	L		0.615674	1.295207	1.685269	2.070391
UL79	P16752	L		0.532744	0.879508	1.266501	1.77947
UL80	P16753	L	0.065986	1.21443	2.042597	2.684956	2.976453
UL82	P06726	L	0.182723	0.501821	1.820873	3.011921	3.82947
UL87	P16730	L		0.973663	0.966077	1.353789	1.964296
UL88	P16731	L	0.065985	0.988493	1.88573	2.357611	2.658042
UL94	P16800	L	0.110697	0.603771	1.910088	2.903675	3.756646
UL99	P13200	L	0.064869	0.476312	1.185196	2.77835	3.121477
gH	P12824	L	0.102358	0.612662	1.920063	3.132675	4.259949
gL	P16832	L	0.061456	0.54747	1.391021	2.425249	3.085682
gM	P16733	L	0.02138	0.336849	1.720709	3.14536	4.05328
gN	P16795	L	0.205163	0.833859	1.551963	2.766087	3.549374
IR11	P16809	L	0.30782	1.840514	1.308304	1.957091	2.909996

Table FIG. 7A, part 3 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment CAY10602 timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
IRS1	P09715	IE	0.393856	0.581292	0.562487	0.782088	0.878562
TRS1	P09695	IE	0.264166	0.445964	0.528428	0.714633	0.793278
UL122	P19893	IE	0.059973	0.05121	0.054268	0.164207	0.433233
UL123	P13202	IE	0.983063	0.567181	0.445102	0.475776	0.679516
UL13	P16755	IE	2.054705	0.440516	0.360393	0.298632	0.426274
UL36	P16767	IE	1.409841	0.911679	0.601021	0.583624	0.811172
UL37	P16778	IE	1.032019	0.755659	0.719049	0.801743	0.871547
CVC2	P16726	DE	0.01787	0.027105	0.03983	0.171402	0.286394
DBP	P17147	DE	0.175602	0.321512	0.391041	0.794094	1.236905
HELI	P16736	DE	0.338898	0.633026	0.570933	0.801698	0.992441
NEC1	P16794	DE				0.0869	0.244647
NEC2	P16791	DE	0.039686	0.070707	0.11001	0.288565	0.519505
RIR1	P16782	DE	0.093968	0.115661	0.109921	0.209787	0.45765
TRM1	P16724	DE	0.040874	0.1031	0.1317	0.313364	0.580927
UL102	P16827	DE	0.534341	0.78656	0.762628	0.90061	1.127833
UL104	P16735	DE	0.039031	0.073986	0.100476	0.306681	0.59692
UL112/UL113	P17151	DE	0.523554	0.423049	0.380833	0.511353	0.678676
UL114	P16769	DE	0.670445	0.770946	0.651681	0.788251	0.901107
UL119/UL118	P16739	DE	0.219773	0.340151	0.419498	0.669471	0.906369
UL128	P16837	DE	0.11131	0.067294	0.047277	0.193737	0.537015
UL26	P16762	DE	0.072733	0.080212	0.102274	0.282802	0.732739
UL32	P08318	DE	0.019523	0.02022	0.026785	0.116798	0.361664
UL34	P16812	DE	0.113716	0.079061	0.090479	0.223108	0.475984
UL35	P16766	DE		0.007792	0.028712	0.125242	0.264786
UL38	P16779	DE	0.975481	0.813938	0.583926	0.667221	0.79167
UL4	P17146	DE	0.037361	0.071277	0.067649	0.212807	0.363478
UL44	P16790	DE	0.064739	0.089135	0.078867	0.176004	0.369143
UL48	P16785	DE	0.011748	0.034428	0.0801	0.280715	0.623851
UL54	P08546	DE	0.608876	0.717827	0.663928	0.907533	1.076395
UL71	P16823	DE	0.439031	0.345939	0.305392	0.475372	0.645052
UL78	P16751	DE	0.975463	0.713386	0.361614	0.423462	0.609856
UL84	P16727	DE	0.101209	0.075753	0.087852	0.232838	0.562785
UL95	P16801	DE	0.076253	0.143747	0.156969	0.311984	0.601709
UL96	P16787	DE	0.387012	0.258265	0.263185	0.411203	0.805568
UL97	P16788	DE	0.281246	0.172616	0.168695	0.303747	0.606391
UL98	P16789	DE	0.30052	0.379642	0.296671	0.467359	0.731457
US12	P09721	DE	1.67214	0.944636	0.42388	0.450544	0.468652
US13	P09720	DE	0.683816	0.912323	0.535105	0.889536	0.889014

-continued

Table FIG. 7A, part 3 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein		treatment CAY10602 timepoint				
Gene	Acc'n	Tempor.	24	48	72	96	120
US14	P09719	DE	0.395719	0.158868	0.155875	0.344664	0.665223
US18	P69334	DE	0.533463	0.536669	0.541546	0.928291	1.010493
US22	P09722	DE	0.396613	0.54202	0.481265	0.623066	0.77635
US23	P09701	DE	0.677624	0.428294	0.393282	0.530356	0.775833
US24	P09700	DE	0.619953	0.419988	0.311425	0.484959	0.818338
US34	P09709	DE	0.798142	0.411833	0.206614	0.212461	0.416762
US8	P09730	DE	1.056746	0.890473	0.579385	0.680108	0.785804
US9	P09729	DE	0.626989	0.611748	0.564904	0.7084	0.852919
gB	P06473	DE	0.113671	0.096711	0.102184	0.284986	0.658201
IR01	P09710	DE	0.27398	0.315724	0.258781	0.457469	0.558401
DUT	P16824	LL		0.258241			0.544689
TRM3	P16732	LL		0.016945	0.036583	0.163805	0.382985
TRX1	P16783	LL	0.0077	0.006112	0.020991	0.10701	0.339807
TRX2	P16728	LL	0.005245	0.006041	0.021927	0.142292	0.440109
UL132	P69338	LL	0.104428	0.096623	0.128671	0.229987	0.401115
UL24	P16760	LL	0.113689	0.115463	0.11656	0.236289	0.590661
UL40	P16780	LL	0.640295	0.629994	0.472709	0.538386	0.561222
UL47	P16784	LL	0.008892	0.020231	0.060079	0.233051	0.52868
UL49	P16786	LL		0.187047	0.164335	0.265126	0.561868
UL69	P16749	LL	0.220265	0.161545	0.206227	0.350776	0.610094
UL70	P17149	LL	0.188217	0.393742	0.419399	0.610433	0.846022
UL83	P06725	LL	0.04505	0.020484	0.020481	0.100194	0.409142
US15	P09718	LL	1.317916	0.516807	0.432643	0.45761	0.618698
IR10	P16808	LL			0.035575	0.205656	0.44946
IR12	P16810	LL	0.068108	0.290824	0.449695	0.69096	0.796962
CVC1	P16799	L	0.061193	0.111536	0.096785	0.225234	0.517324
GO	P16750	L			0.059887	0.244254	0.423632
MCP	P16729	L	0.004968	0.006609	0.026238	0.148166	0.449652
SCP	Q7M6N6	L	0.004248	0.004793	0.014999	0.124623	0.316896
TRM2	P16792	L	0.019806	0.056653	0.079497	0.189958	0.48826
UL103	P16734	L	0.357808	0.156695	0.092753	0.248852	0.520817
UL117	P16770	L	0.436212	0.382954	0.315065	0.395142	0.544234
UL22A	P16845	L	0.043823	0.101509	0.214966	0.348455	0.946211
UL25	P16761	L	0.038885	0.062398	0.095999	0.235287	0.508109
UL29	P16764	L	0.833637	0.755564	0.505968	0.667421	0.814801
UL30	P16765	L		0.153757	0.143097	0.235511	0.406439
UL31	P16848	L	0.327923	0.144514	0.144678	0.246161	0.527495
UL43	P16781	L	0.060882	0.049915	0.031757	0.053129	0.229447
UL52	P16793	L	0.015673	0.051106	0.119127	0.322407	0.616075
UL76	P16725	L			0.031921	0.151271	0.366014
UL79	P16752	L				0.329911	0.399809
UL80	P16753	L	0.036298	0.035881	0.060522	0.267357	0.591225
UL82	P06726	L	0.184316	0.106086	0.104185	0.256563	0.556114
UL87	P16730	L			0.090288	0.264554	0.328096
UL88	P16731	L	0.038308	0.087535	0.16855	0.392623	0.633948
UL94	P16800	L	0.086256	0.074295	0.114538	0.277603	0.580289
UL99	P13200	L	0.029596	0.051654	0.055125	0.175331	0.474914
gH	P12824	L	0.049246	0.063364	0.103196	0.283512	0.584909
gL	P16832	L	0.037266	0.051915	0.082463	0.262318	0.576832
gM	P16733	L	0.034853	0.024148	0.062423	0.265256	0.650841
gN	P16795	L	0.156426	0.11178	0.112219	0.29996	0.64289
IR11	P16809	L	0.104426	0.370685	0.43444	0.907473	1.205348

TABLE

FIG. 7A, part 4 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein	Tempo-	treatment Resveratrol timepoint		
Gene	Acc'n	rality	24	48	72
IRS1	P09715	IE	0.529956	0.867139	1.155143
TRS1	P09695	IE	0.290693	0.712253	1.081477

TABLE-continued

FIG. 7A, part 4 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein	Protein	Tempo-	treatment Resveratrol timepoint		
Gene	Acc'n	rality	24	48	72
UL122	P19893	IE	0.065837	0.071551	0.098803
UL123	P13202	IE	1.053418	0.949379	0.857325

TABLE-continued

FIG. 7A, part 4 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein Gene	Protein Acc'n	Tempo-rality	treatment Resveratrol timepoint 24	48	72
UL13	P16755	IE	2.215506	0.664646	0.477702
UL36	P16767	IE	1.360005	1.044813	0.81251
UL37	P16778	IE	0.979705	1.143145	0.998048
CVC2	P16726	DE	0.024159	0.04895	0.05308
DBP	P17147	DE	0.260316	0.317438	0.203067
HELI	P16736	DE	0.523923	0.703469	0.762553
NEC1	P16794	DE			
NEC2	P16791	DE	0.050306	0.134738	0.231033
RIR1	P16782	DE	0.122928	0.146687	0.169564
TRM1	P16724	DE	0.049604	0.174351	0.173559
UL102	P16827	DE	0.888975	1.270298	1.099634
UL104	P16735	DE	0.07335	0.109096	0.110828
UL112/UL113	P17151	DE	0.360105	0.454537	0.391216
UL114	P16769	DE	0.800814	1.321974	1.097195
UL119/UL118	P16739	DE	0.559619	0.636653	0.22415
UL128	P16837	DE	0.080346	0.035958	0.037134
UL26	P16762	DE	0.087447	0.092237	0.087004
UL32	P08318	DE	0.02724	0.064069	0.098338
UL34	P16812	DE	0.109583	0.126462	0.194478
UL35	P16766	DE		0.026531	0.066803
UL38	P16779	DE	0.969075	0.806915	0.657148
UL4	P17146	DE	0.027921	0.10705	0.18632
UL44	P16790	DE	0.059105	0.096567	0.10768
UL48	P16785	DE	0.021937	0.053935	0.076903
UL54	P08546	DE	0.629525	0.946427	0.892148
UL71	P16823	DE	0.525154	0.366053	0.420088
UL78	P16751	DE	1.895865	1.069589	0.437089
UL84	P16727	DE	0.140603	0.148911	0.180674
UL95	P16801	DE	0.067564	0.291435	0.48866
UL96	P16787	DE	0.47273	0.386106	0.280409
UL97	P16788	DE	0.365199	0.373237	0.288369
UL98	P16789	DE	0.297907	0.341223	0.261442
US12	P09721	DE	1.672542	0.896436	0.270936
US13	P09720	DE	0.547645	0.592286	0.506371
US14	P09719	DE	0.388327	0.230434	0.141255
US18	P69334	DE			
US22	P09722	DE	0.337908	0.537142	0.565354
US23	P09701	DE	1.208648	0.598219	0.5216
US24	P09700	DE	1.018754	0.485704	0.34223
US34	P09709	DE	2.474791	2.409233	1.230564
US8	P09730	DE	0.985558	1.342671	1.040625
US9	P09729	DE	1.11978	2.242142	1.96586
gB	P06473	DE	0.203534	0.199137	0.207817
IR01	P09710	DE	0.239462	0.332489	0.449532

TABLE-continued

FIG. 7A, part 4 of 4: Numerical values corresponding heatmap in FIG. 7A.

Protein Gene	Protein Acc'n	Tempo-rality	treatment Resveratrol timepoint 24	48	72
DUT	P16824	LL	0.381506	0.226187	
TRM3	P16732	LL		0.024259	0.027495
TRX1	P16783	LL	0.007402	0.012593	0.019945
TRX2	P16728	LL	0.006335	0.010032	0.019982
UL132	P69338	LL	0.151863	0.202743	0.215042
UL24	P16760	LL	0.115035	0.104562	0.107209
UL40	P16780	LL	0.681605	1.097644	0.685119
UL47	P16784	LL	0.013143	0.042567	0.088278
UL49	P16786	LL	0.380113	0.910012	1.208807
UL69	P16749	LL	0.259004	0.302363	0.375791
UL70	P17149	LL	0.215131	0.55462	0.682003
UL83	P06725	LL	0.048684	0.036714	0.038456
US15	P09718	LL	2.089457	1.334174	0.686865
IR10	P16808	LL			
IR12	P16810	LL	0.130465	0.261383	0.181978
CVC1	P16799	L	0.133548	0.333945	0.429535
GO	P16750	L		0.020748	0.038813
MCP	P16729	L	0.005554	0.008603	0.011437
SCP	Q7M6N6	L		0.008886	0.004632
TRM2	P16792	L	0.012358	0.034579	0.02287
UL103	P16734	L	0.386143	0.148924	0.129388
UL117	P16770	L	0.74394	0.49095	0.303232
UL22A	P16845	L	0.068781	0.218774	0.262339
UL25	P16761	L	0.021733	0.07603	0.126454
UL29	P16764	L	0.698949	0.564767	0.475613
UL30	P16765	L		0.140005	0.13441
UL31	P16848	L	0.443437	0.321745	0.359492
UL43	P16781	L	0.062104	0.068869	0.072844
UL52	P16793	L	0.02488	0.097745	0.114328
UL76	P16725	L			0.026096
UL79	P16752	L			
UL80	P16753	L	0.036415	0.041819	0.054043
UL82	P06726	L	0.202418	0.219099	0.281263
UL87	P16730	L			0.038618
UL88	P16731	L	0.051737	0.094011	0.15546
UL94	P16800	L	0.102746	0.181131	0.240157
UL99	P13200	L	0.048054	0.098972	0.137407
gH	P12824	L	0.086512	0.123344	0.171651
gL	P16832	L	0.037563	0.058173	0.077717
gM	P16733	L	0.040469	0.047109	0.069545
gN	P16795	L	0.185358	0.084823	0.071192
IR11	P16809	L	0.409211	0.32185	0.253003

Table FIG. 8A, part 1 of 4: Numerical values corresponding heatmap in FIG. 8A.

Protein Gene	Protein Acc'n	Temporality	treatment DMSO timepoint 2	6	12	18
ICP0	P08393	IE	0.091601	0.831262	1.617589	1.556848
ICP22	P04485	IE	0.015224	0.877639	1.389603	1.548126
ICP4	P08392	IE	0.115776	1.116858	1.482325	1.570898
UL54	P10238	IE	0.081053	1.295314	1.341291	1.435079
DBP	P04296	E	0.035458	0.956676	1.374226	1.572022
TK	P03176	E	0.037772	1.117986	1.132964	1.25255
UL12	P04294	E	0.016795	1.117311	1.187313	1.505661
UL30	P04293	E	0.054658	1.347601	1.228628	1.204441
UL42	P10226	E	0.004685	0.471087	1.467427	1.717706
UL8	P10192	E	0.019022	1.00542	0.970042	1.04424
US3	P04413	E	0.012863	0.819327	1.406379	1.113226
CVC2	P10209	L	0.008226	0.473372	1.575599	1.951277

-continued

Table FIG. 8A, part 1 of 4: Numerical values corresponding heatmap in FIG. 8A.

Protein	Protein		treatment DMSO timepoint			
Gene	Acc'n	Temporality	2	6	12	18
UL26	P10210	L		0.327125	1.253707	1.799956
UL48	P06492	L	0.007555	0.438116	1.694589	2.178714
UL49	P10233	L	0.00999	0.724138	1.813934	1.542657
gB	P10211	L	0.013898	0.608248	1.680034	1.844084
gI	P06487	L		0.587287	1.273557	1.038478

Table FIG. 8A, part 2 of 4: Numerical values corresponding heatmap in FIG. 8A.

Protein	Protein		treatment EX527 timepoint			
Gene	Acc'n	Temporality	2	6	12	18
ICP0	P08393	IE	0.130747	0.933884	1.772462	1.714264
ICP22	P04485	IE	0.014161	1.072249	1.535313	1.978738
ICP4	P08392	IE	0.091539	1.324896	1.510708	2.197023
UL54	P10238	IE	0.048592	1.758885	1.814059	1.637077
DBP	P04296	E	0.024651	1.405336	1.56787	2.002195
TK	P03176	E	0.026538	1.44938	1.751106	2.225822
UL12	P04294	E	0.011959	1.502629	1.841384	2.271776
UL30	P04293	E	0.031238	1.509631	1.753595	2.062508
UL42	P10226	E	0.002331	0.597451	2.035243	3.214178
UL8	P10192	E	0.023466	1.251577	1.371002	1.783501
US3	P04413	E	0.01288	0.947623	1.573214	1.817608
CVC2	P10209	L	0.007823	0.543283	2.235611	3.555849
UL26	P10210	L	0.005455	0.354121	1.506767	2.826692
UL48	P06492	L	0.006829	0.561339	2.26784	3.714222
UL49	P10233	L	0.00849	0.802131	1.954359	2.145436
gB	P10211	L	0.01179	0.622509	1.744297	2.559837
gI	P06487	L	0.006707	0.76479	1.288333	3.078023

Table FIG. 8A, part 3 of 4: Numerical values corresponding heatmap in FIG. 8A.

Protein	Protein		treatment CAY CAY CAY CAY timepoint			
Gene	Acc'n	Temporality	2	6	12	18
ICP0	P08393	IE	0.109689	0.559876	1.404967	1.467764
ICP22	P04485	IE	0.012207	0.691448	1.221374	1.666293
ICP4	P08392	IE	0.086075	0.801731	1.191422	1.57662
UL54	P10238	IE	0.051547	0.952677	1.257328	1.313714
DBP	P04296	E	0.023522	0.758127	1.208481	1.69295
TK	P03176	E	0.028755	0.863711	1.310912	1.303696
UL12	P04294	E	0.013418	0.896401	1.438763	1.546526
UL30	P04293	E	0.036594	0.980419	1.369071	1.587575
UL42	P10226	E	0.002416	0.351432	1.383397	2.445713
UL8	P10192	E	0.016257	0.791325	1.049431	1.213886
US3	P04413	E	0.011643	0.601446	1.132041	1.20266
CVC2	P10209	L	0.008425	0.340462	1.678938	2.616954
UL26	P10210	L	0.00159	0.222366	1.267067	2.207433
UL48	P06492	L	0.007094	0.297847	1.650076	2.515001
UL49	P10233	L	0.007747	0.461708	1.472174	1.715462
gB	P10211	L	0.011622	0.382347	1.390461	1.982212
gI	P06487	L	0.006169	0.556999	1.015615	1.740746

Table FIG. 8A, part 4 of 4: Numerical values corresponding heatmap in FIG. 8A.

Protein Gene	Protein Acc'n	Temporality	treatment Res timepoint 2	Res 6	Res 12	Res 18
ICP0	P08393	IE	0.16223	0.533334	1.107601	1.159238
ICP22	P04485	IE	0.015004	0.742905	1.240564	1.213186
ICP4	P08392	IE	0.107283	1.06342	1.100592	1.049477
UL54	P10238	IE	0.0667	0.94154	1.026143	0.814809
DBP	P04296	E	0.021206	0.912071	1.230058	1.251509
TK	P03176	E	0.038321	0.970655	1.239877	0.980627
UL12	P04294	E	0.017633	0.741797	0.887778	0.742468
UL30	P04293	E	0.038758	1.353173	1.001291	0.792639
UL42	P10226	E	0.003041	0.286649	0.774309	0.783726
UL8	P10192	E	0.017105	1.056303	0.912267	0.825867
US3	P04413	E	0.016047	0.615979	1.156352	0.945653
CVC2	P10209	L	0.010031	0.259173	0.706668	0.600989
UL26	P10210	L	0.003453	0.198554	0.754941	0.889843
UL48	P06492	L	0.007183	0.181626	0.841061	0.927547
UL49	P10233	L	0.009894	0.428049	1.282968	1.225547
gB	P10211	L	0.012795	0.509822	1.285611	1.305631
gI	P06487	L	0.00718	0.570458	0.956029	1.002501

TABLE

FIG. 8C, part 1 of 3: Numerical values corresponding heatmap in FIG. 8C.

Protein Gene	Protein Acc'n	Tempor.	treatment Mock timepoint 24	48	72
K8	Q2HR82	IE	0.250872	1.161807	1.324475
ORF16	F5HGJ3	IE	0.311661	0.822163	1.70263
ORF45	F5HDE4	IE	0.520839	1.002488	1.812888
ORF48	Q2HR85	IE			1.147799
ORF50	F5HCV3	IE	0.485292	0.996571	1.574245
ORF57	Q2HR75	IE	0.324399	0.983233	1.720653
70	P90463	DE	0.279352	1.284666	1.843208
DBP	Q2HRD3	DE	0.075075	0.927189	2.373527
DUT	Q2HR78	DE	0	0.277177	1.960806
HELI	Q2HR89	DE		0.631028	1.393923
K14	P0C788	DE		0.761589	1.321663
K2	Q2HRC7	DE	1.066088	1.260581	0.644392
K3	P90495	DE	0.155329	1.075289	1.152274
K5	P90489	DE	0.211893	1.031406	1.428942
NEC1	F5H982	DE	0.161504	0.882364	2.19039
NEC2	F5HA27	DE	0.027672	0.494326	1.832928
ORF K4	Q98157	DE	0.340771	1.060912	1.679899
ORF10	Q2HRC9	DE	0.255515	1.052553	1.983122
ORF11	Q2HRC8	DE	0.560045	1.054019	1.319391
ORF17	Q2HRB6	DE	0.148286	0.694125	2.044174
ORF2	Q2HRC6	DE	0.050944	0.561067	2.014536
ORF36	F5HGH5	DE		0.219931	1.974033
ORF37	Q2HR95	DE	0.216816	0.772489	1.886544
ORF40	Q2HR92	DE		0.873853	1.382555
ORF46	F5HFA1	DE	0.233529	0.993466	1.975631
ORF49	Q2HR83	DE		0.556444	1.721273
ORF56	F5HIN0	DE			1.106301
ORF59	F5HID2	DE	0.148183	1.162132	1.756203
ORF66	F5HG20	DE		0.368537	1.519143
ORF9	Q2HRD0	DE		0.769739	1.690263
RIR1	Q2HR67	DE	0.175293	0.773715	2.737441
TK	F5HB62	DE	0.049232	0.456436	1.495669
vIRF-1	F5HF68	DE		0.288905	1.136165
CVC1	F5HB39	L		0.534377	1.933347
CVC2	Q2HRB3	L	0.031014	0.56842	1.950497
K8.1	F5HB98	L	0.155327	0.619327	1.48734
MCP	Q2HRA7	L	0.039025	0.585137	2.015966

TABLE-continued

FIG. 8C, part 1 of 3: Numerical values corresponding heatmap in FIG. 8C.

Protein Gene	Protein Acc'n	Tempor.	treatment Mock timepoint 24	48	72
ORF20	Q2HRB2	L		0.404988	1.893899
ORF23	F5HIM6	L		0.132345	1.442602
ORF24	F5HFD2	L		0.404033	1.336459
ORF27	F5HDY6	L		0.631181	1.380048
ORF28	F5HI25	L	0.151046	0.986466	1.906399
ORF33	F5HEF2	L	0.06944	0.600258	3.017602
ORF34	Q2HR98	L		0.396368	1.124734
ORF35	F5HCD4	L		0.320572	1.789647
ORF38	F5HHY1	L	0.028723	0.546813	2.338524
ORF4	Q2HRD4	L		0.847298	1.12695
ORF42	F5HAI6	L		0.50304	2.051213
ORF43	F5HGK9	L		0.395142	1.979972
ORF52	Q2HR80	L	0.012767	0.543412	1.890341
ORF55	F5H9W9	L		0.599361	1.738063
ORF63	F5HEU7	L		0.342482	1.872595
ORF64	Q2HR64	L		0.359751	1.802176
ORF68	F5HF47	L	0.165706	0.823673	2.220449
ORF75	Q9QR70	L		0.398109	1.824131
SCP	Q2HR63	L		0.520672	1.740542
TRX1	F5H8Y5	L		0.419094	1.876895
TRX2	F5HGN8	L		0.449372	1.704811
gB	F5HB81	L	0.153946	0.673606	2.522058
gH	F5HAK9	L	0.898514	0.700489	1.634211
gL	F5HDB7	L	0.570127	0.789326	1.980407
gM	F5HDD0	L	0.0522	0.693253	1.350728

TABLE

FIG. 8C, part 2 of 3: Numerical values corresponding heatmap in FIG. 8C.

Protein	Protein		treatment EX timepoint		
Gene	Acc'n	Tempor.	24	48	72
K8	Q2HR82	IE	0.201633	1.14801	1.69662
ORF16	F5HGJ3	IE	0.234168	0.686419	1.622655
ORF45	F5HDE4	IE	0.264585	0.979881	1.541031
ORF48	Q2HR85	IE			1.065234
ORF50	F5HCV3	IE	0.313215	0.847011	1.365736
ORF57	Q2HR75	IE	0.171769	0.839816	1.721247
70	P90463	DE	0.132778	0.819533	1.404251
DBP	Q2HRD3	DE	0.03296	0.535677	1.722069
DUT	Q2HR78	DE	0		0.935547
HELI	Q2HR89	DE		0.326801	0.955653
K14	P0C788	DE		0.578306	1.286936
K2	Q2HRC7	DE	0.833204	1.205792	1.082347
K3	P90495	DE	0.092396	1.003864	1.842465
K5	P90489	DE	0.152053	0.968268	2.061201
NEC1	F5H982	DE	0.054822	0.451124	1.399405
NEC2	F5HA27	DE	0.015266	0.244264	1.532691
ORF K4	Q98157	DE		0.486906	1.191785
ORF10	Q2HRC9	DE	0.115198	0.580505	1.434879
ORF11	Q2HRC8	DE	0.45656	0.472621	0.779285
ORF17	Q2HRB6	DE	0.10648	0.404479	1.570592
ORF2	Q2HRC6	DE		0.437974	1.637422
ORF36	F5HGH5	DE			0.621963
ORF37	Q2HR95	DE	0.092797	0.529641	1.993645
ORF40	Q2HR92	DE			0.249163
ORF46	F5HFA1	DE	0.126543	0.833771	1.053783
ORF49	Q2HR83	DE		0.338501	1.413434
ORF56	F5HIN0	DE			
ORF59	F5HID2	DE	0.061268	0.795458	1.902301
ORF66	F5HG20	DE		0.146811	1.215235
ORF9	Q2HRD0	DE		0.4208	1.043832
RIR1	Q2HR67	DE	0.114925	0.172039	1.141737
TK	F5HB62	DE		0.392223	1.62304
vIRF-1	F5HF68	DE			1.269964
CVC1	F5HB39	L		0.194165	1.207429
CVC2	Q2HRB3	L		0.301861	1.371002
K8.1	F5HB98	L	0.223542	0.34868	1.653587
MCP	Q2HRA7	L	0.021274	0.281983	1.614703
ORF20	Q2HRB2	L		0.170939	1.391119
ORF23	F5HIM6	L			1.088129
ORF24	F5HFD2	L			1.416283
ORF27	F5HDY6	L		0.381594	1.216247
ORF28	F5HI25	L	0.060266	0.553673	1.419655
ORF33	F5HEF2	L	0.031752	0.321573	1.262954
ORF34	Q2HR98	L			1.264619
ORF35	F5HCD4	L			0.92449
ORF38	F5HHY1	L		0.426122	1.717284
ORF4	Q2HRD4	L		0.803217	1.529984
ORF42	F5HAI6	L		0.311363	1.238085
ORF43	F5HGK9	L		0.181894	1.438427
ORF52	Q2HR80	L	0.012366	0.364312	1.937347
ORF55	F5H9W9	L		0.305254	1.208399
ORF63	F5HEU7	L			0.845336
ORF64	Q2HR64	L		0.205695	1.343859
ORF68	F5HF47	L	0.061954	0.314714	1.081687
ORF75	Q9QR70	L		0.24762	1.15379
SCP	Q2HR63	L		0.206876	1.240679
TRX1	F5H8Y5	L		0.11445	1.134226
TRX2	F5HGN8	L		0.226945	1.17981
gB	F5HB81	L	0.097263	0.264001	1.046872
gH	F5HAK9	L	0.338935	0.662013	1.208988
gL	F5HDB7	L	0.414566	0.8375	1.053092
gM	F5HDD0	L		0.762034	1.656842

TABLE

FIG. 8C, part 3 of 3: Numerical values corresponding heatmap in FIG. 8C.

Protein	Protein		treatment CAY timepoint		
Gene	Acc'n	Tempor.	24	48	72
K8	Q2HR82	IE	0.388124	1.329386	1.499073
ORF16	F5HGJ3	IE	0.517516	1.053491	1.293577
ORF45	F5HDE4	IE	0.547881	1.041682	1.317436
ORF48	Q2HR85	IE		0.508965	1.106384
ORF50	F5HCV3	IE	0.651305	1.244527	1.522098
ORF57	Q2HR75	IE	0.564089	1.18637	1.488422
70	P90463	DE	0.451947	1.340581	1.443683
DBP	Q2HRD3	DE	0.11166	1.101957	2.119885
DUT	Q2HR78	DE		0.516316	1.581764
HELI	Q2HR89	DE		0.949235	1.476599
K14	P0C788	DE		1.065478	0.986027
K2	Q2HRC7	DE	1.41119	1.002016	0.677338
K3	P90495	DE	0.254321	1.3004	2.123664
K5	P90489	DE	0.333265	1.119622	1.69335
NEC1	F5H982	DE	0.170144	0.872546	1.432558
NEC2	F5HA27	DE	0.064413	0.712001	2.024777
ORF K4	Q98157	DE	1.155091	1.122112	0.63291
ORF10	Q2HRC9	DE	0.444376	1.064794	1.401755
ORF11	Q2HRC8	DE	1.08323	1.636782	1.51014
ORF17	Q2HRB6	DE	0.172963	0.745322	1.435201
ORF2	Q2HRC6	DE	0.089948	0.605622	1.49398
ORF36	F5HGH5	DE		0.582354	1.601718
ORF37	Q2HR95	DE	0.361123	1.032245	1.632392
ORF40	Q2HR92	DE		0.508197	1.007717
ORF46	F5HFA1	DE	0.357076	1.368402	1.653878
ORF49	Q2HR83	DE		0.642917	0.996682
ORF56	F5HIN0	DE			0.681096
ORF59	F5HID2	DE	0.226801	1.311835	1.635818
ORF66	F5HG20	DE		0.589573	1.52081
ORF9	Q2HRD0	DE	0.098675	0.760632	1.640208
RIR1	Q2HR67	DE	0.28733	1.143322	1.489698
TK	F5HB62	DE	0.114656	0.807848	1.823661
vIRF-1	F5HF68	DE		0.569482	1.735484
CVC1	F5HB39	L	0.119084	0.54238	1.505753
CVC2	Q2HRB3	L	0.100446	0.741668	1.689399
K8.1	F5HB98	L	0.16624	0.749003	2.095964
MCP	Q2HRA7	L	0.068842	0.675883	1.783281
ORF20	Q2HRB2	L		0.653535	1.48552
ORF23	F5HIM6	L		0.356252	1.008057
ORF24	F5HFD2	L		0.671061	0.980702
ORF27	F5HDY6	L	0.076732	0.767915	1.423831
ORF28	F5HI25	L	0.348909	1.404417	1.744692
ORF33	F5HEF2	L	0.144601	0.694402	1.851981
ORF34	Q2HR98	L		0.903414	1.310864
ORF35	F5HCD4	L		0.526872	0.806904
ORF38	F5HHY1	L	0.044738	0.586253	1.348275
ORF4	Q2HRD4	L	0.134492	0.849358	1.048987
ORF42	F5HAI6	L		0.554666	1.341633
ORF43	F5HGK9	L		0.44264	1.152873
ORF52	Q2HR80	L	0.017914	0.528212	1.884785
ORF55	F5H9W9	L		0.555562	1.237576
ORF63	F5HEU7	L		0.4013	1.209528
ORF64	Q2HR64	L		0.445928	1.451584
ORF68	F5HF47	L	0.266188	0.892474	1.892521
ORF75	Q9QR70	L		0.487687	1.318834
SCP	Q2HR63	L		0.529627	1.454643
TRX1	F5H8Y5	L		0.425996	1.586564
TRX2	F5HGN8	L		0.479186	1.161251
gB	F5HB81	L	0.343295	0.995086	1.747287
gH	F5HAK9	L	0.27268	0.903574	1.47578
gL	F5HDB7	L	1.031252	0.793627	1.027628
gM	F5HDD0	L	0.189537	1.115876	1.246972

Table FIG 9C: Numerical values corresponding heatmap in FIG. 9C.

Protein		HSV-1 strain*						
Gene	Tempor.	17	F	H129	KOS	MacIntyre	McKrae	Sc16
CVC2	L	4/100	4/100	4/100	4/100	4/100	4/100	4/100
DBP	E	4/100	4/100	4/100	4/100	4/100	4/100	4/100
ICP0	IE	4/100	4/100	3/75	4/100	4/100	4/100	4/100
ICP22	IE	4/100	4/100	4/100	4/100	4/100	4/100	4/100
ICP4	IE	4/100	4/100	4/100	4/100	4/100	4/100	4/100
TK	E	4/100	3/75	2/50	3/75	4/100	3/75	4/100
UL12	E	4/100	4/100	4/100	4/100	4/100	4/100	4/100
UL26	L	4/100	4/100	3/75	4/100	4/100	3/75	4/100
UL30	E	4/100	4/100	4/100	4/100	4/100	4/100	4/100
UL42	E	4/100	4/100	4/100	4/100	4/100	4/100	4/100
UL48	L	4/100	4/100	4/100	4/100	4/100	4/100	4/100
UL49	L	4/100	4/100	4/100	4/100	3/75	4/100	4/100
UL54	IE	4/100	3/75	3/75	3/75	3/75	3/75	3/75
UL8	E	4/100	4/100	3/75	4/100	4/100	3/75	4/100
US3	E	4/100	4/100	4/100	4/100	4/100	4/100	4/100
gB	L	4/100	4/100	4/100	4/100	4/100	4/100	4/100
gI	L	4/100	3/75	3/75	3/75	1/25	2/50	3/75

*Number of Conserved Peptides/Percentage of Conserved Peptides

Table FIG. 9D: Numerical values corresponding heatmap in FIG. 9D.

Protein		HCMV strain*					
Gene	Tempor.	AD169	Merlin	TB40	TR	Toledo	Towne
CVC1	L	2/66.6	2/66.6	2/66.6	2/66.6	1/33.3	1/33.3
CVC2	DE	3/100	1/33.3	1/33.3	0/0	2/66.6	2/66.6
DBP	DE	3/100	3/100	3/100	3/100	3/100	3/100
DUT	LL	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
GO	L	3/100	1/33.3	1/33.3	0/0	1/33.3	0/0
HELI	DE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
IR01	DE	2/66.6	2/66.6	2/66.6	2/66.6	1/33.3	1/33.3
IR10	LL	2/66.6	1/33.3	2/66.6	1/33.3	2/66.6	1/33.3
IR11	L	3/100	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
IR12	LL	3/100	0/0	0/0	0/0	3/100	0/0
IRS1	IE	3/100	3/100	0/0	3/100	3/100	3/100
MCP	L	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
NEC1	DE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
NEC2	DE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
RIR1	DE	3/100	3/100	2/66.6	2/66.6	3/100	2/66.6
SCP	L	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
TRM1	DE	3/100	3/100	3/100	3/100	3/100	3/100
TRM2	L	3/100	3/100	3/100	3/100	3/100	3/100
TRM3	LL	3/100	3/100	3/100	3/100	3/100	3/100
TRS1	IE	2/66.6	1/33.3	0/0	0/0	0/0	2/66.6
TRX1	LL	3/100	3/100	3/100	3/100	3/100	3/100
TRX2	LL	3/100	3/100	3/100	3/100	3/100	3/100
UL102	DE	3/100	3/100	3/100	2/66.6	3/100	3/100
UL103	L	3/100	3/100	3/100	3/100	3/100	3/100
UL104	DE	3/100	2/66.6	3/100	3/100	3/100	3/100
UL112/UL113	DE	3/100	3/100	3/100	3/100	3/100	
UL114	DE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL117	L	3/100	3/100	3/100	3/100	3/100	3/100
UL119/UL118	DE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	
UL122	IE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL123	IE	3/100	2/66.6	2/66.6	2/66.6	3/100	3/100
UL128	DE	2/66.6	2/66.6	2/66.6	1/33.3	2/66.6	2/66.6
UL13	IE	3/100	1/33.3	3/100	2/66.6	2/66.6	2/66.6
UL132	LL	3/100	3/100	3/100	3/100	3/100	3/100
UL22A	L	1/33.3	0/0	1/33.3	0/0	0/0	0/0
UL24	LL	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL25	L	3/100	3/100	3/100	3/100	3/100	3/100
UL26	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL29	L	3/100	3/100	3/100	3/100	3/100	3/100
UL30	L	1/33.3	0/0	0/0	0/0	1/33.3	0/0
UL31	L	2/66.6	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
UL32	DE	3/100	3/100	2/66.6	2/66.6	2/66.6	2/66.6
UL34	DE	3/100	3/100	3/100	3/100	3/100	3/100

-continued

Table FIG. 9D: Numerical values corresponding heatmap in FIG. 9D.

Protein		HCMV strain*					
Gene	Tempor.	AD169	Merlin	TB40	TR	Toledo	Towne
UL35	DE	3/100	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL36	IE	3/100	3/100	3/100	2/66.6	3/100	3/100
UL37	IE	3/100	2/66.6	3/100	3/100	3/100	3/100
UL38	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL4	DE	3/100	2/66.6	0/0	0/0	1/33.3	0/0
UL40	LL	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
UL43	L	3/100	2/66.6	3/100	2/66.6	2/66.6	2/66.6
UL44	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL47	LL	3/100	3/100	3/100	3/100	3/100	3/100
UL48	DE	3/100	3/100	3/100	3/100	3/100	2/66.6
UL49	LL	1/33.3	0/0	1/33.3	1/33.3	1/33.3	1/33.3
UL52	L	3/100	2/66.6	3/100	3/100	3/100	2/66.6
UL54	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL69	LL	3/100	3/100	2/66.6	3/100	3/100	3/100
UL70	LL	3/100	3/100	3/100	3/100	3/100	3/100
UL71	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL76	L	3/100	3/100	3/100	2/66.6	3/100	3/100
UL78	DE	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
UL79	L	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL80	L	3/100	3/100	2/66.6	3/100	3/100	3/100
UL82	L	3/100	3/100	3/100	3/100	3/100	3/100
UL83	LL	3/100	3/100	3/100	3/100	3/100	3/100
UL84	DE	3/100	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL87	L	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
UL88	L	3/100	3/100	3/100	3/100	3/100	3/100
UL94	L	3/100	3/100	3/100	3/100	3/100	3/100
UL95	DE	2/66.6	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
UL96	DE	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
UL97	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL98	DE	3/100	3/100	3/100	3/100	3/100	3/100
UL99	L	2/66.6	2/66.6	2/66.6	2/66.6	1/33.3	1/33.3
US12	DE	3/100	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
US13	DE	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
US14	DE	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
US15	LL	1/33.3	1/33.3	1/33.3	1/33.3	0/0	1/33.3
US18	DE	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
US22	DE	3/100	3/100	3/100	3/100	3/100	3/100
US23	DE	3/100	3/100	3/100	3/100	3/100	3/100
US24	DE	3/100	3/100	3/100	3/100	3/100	3/100
US34	DE	1/33.3	0/0	0/0	0/0	1/33.3	1/33.3
US8	DE	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
US9	DE	3/100	3/100	3/100	3/100	2/66.6	2/66.6
gB	DE	3/100	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
gH	L	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3	1/33.3
gL	L	3/100	3/100	3/100	3/100	3/100	3/100
gM	L	3/100	2/66.6	2/66.6	2/66.6	2/66.6	2/66.6
gN	L	2/66.6	0/0	0/0	0/0	0/0	0/0

*Number of Conserved Peptides/Percentage of Conserved Peptides

TABLE

FIG. 9E: Numerical values corresponding heatmap in FIG. 9E.

Protein		KSHV strain*			
Gene	Tempor.	BAC16	BrK	DG1	GK18
70	DE	3/100	3/100	3/100	3/100
CVC1	L	3/100	3/100	3/100	3/100
CVC2	L	3/100	3/100	3/100	3/100
DBP	DE	3/100	3/100	2/66.6	3/100
DUT	DE	3/100	3/100	3/100	3/100
HELI	DE	3/100	3/100	3/100	3/100
K14	DE	2/66.6	2/66.6	2/66.6	2/66.6
K2	DE	3/100	3/100	3/100	3/100
K3	DE	3/100	3/100	3/100	2/66.6
K5	DE	3/100	3/100	1/33.3	3/100
K8	IE	2/66.6	2/66.6	2/66.6	2/66.6

TABLE-continued

FIG. 9E: Numerical values corresponding heatmap in FIG. 9E.

Protein		KSHV strain*			
Gene	Tempor.	BAC16	BrK	DG1	GK18
K8.1	L	3/100	3/100	3/100	3/100
MCP	L	3/100	3/100	3/100	3/100
NEC1	DE	3/100	3/100	3/100	3/100
NEC2	DE	3/100	3/100	3/100	3/100
ORF K4	DE	1/33.3	1/33.3	1/33.3	1/33.3
ORF10	DE	3/100	3/100	3/100	3/100
ORF11	DE	3/100	3/100	3/100	3/100
ORF16	IE	2/66.6	2/66.6	2/66.6	2/66.6
ORF17	DE	3/100	3/100	3/100	3/100
ORF2	DE	2/66.6	2/66.6	1/33.3	2/66.6
ORF20	L	1/33.3	1/33.3	1/33.3	1/33.3

TABLE-continued

FIG. 9E: Numerical values corresponding heatmap in FIG. 9E.

Protein		KSHV strain*			
Gene	Tempor.	BAC16	BrK	DG1	GK18
ORF23	L	2/66.6	2/66.6	2/66.6	2/66.6
ORF24	L	3/100	3/100	3/100	3/100
ORF27	L	3/100	3/100	3/100	3/100
ORF28	L	1/33.3	1/33.3	1/33.3	1/33.3
ORF33	L	3/100	3/100	3/100	3/100
ORF34	L	2/66.6	2/66.6	2/66.6	2/66.6
ORF35	L	2/66.6	2/66.6	2/66.6	2/66.6
ORF36	DE	1/33.3	1/33.3	1/33.3	1/33.3
ORF37	DE	3/100	3/100	3/100	3/100
ORF38	L	1/33.3	1/33.3	1/33.3	1/33.3
ORF4	L	3/100	3/100	2/66.6	3/100
ORF40	DE	2/66.6	2/66.6	2/66.6	2/66.6
ORF42	L	2/66.6	2/66.6	2/66.6	2/66.6
ORF43	L	3/100	3/100	3/100	3/100
ORF45	IE	3/100	3/100	3/100	3/100
ORF46	DE	2/66.6	2/66.6	2/66.6	2/66.6
ORF48	IE	1/33.3	1/33.3	1/33.3	1/33.3
ORF49	DE	1/33.3	1/33.3	1/33.3	1/33.3
ORF50	IE	3/100	3/100	3/100	3/100
ORF52	L	3/100	3/100	3/100	3/100
ORF55	L	3/100	3/100	3/100	3/100

TABLE-continued

FIG. 9E: Numerical values corresponding heatmap in FIG. 9E.

Protein		KSHV strain*			
Gene	Tempor.	BAC16	BrK	DG1	GK18
ORF56	DE	3/100	3/100	3/100	3/100
ORF57	IE	3/100	3/100	3/100	3/100
ORF59	DE	3/100	3/100	2/66.6	3/100
ORF63	L	0/0	1/33.3	1/33.3	1/33.3
ORF64	L	3/100	3/100	3/100	3/100
ORF66	DE	2/66.6	2/66.6	2/66.6	2/66.6
ORF68	L	3/100	3/100	3/100	3/100
ORF75	L	3/100	3/100	3/100	3/100
ORF9	DE	3/100	3/100	3/100	3/100
RIR1	DE	3/100	3/100	3/100	3/100
SCP	L	2/66.6	2/66.6	2/66.6	2/66.6
TK	DE	3/100	3/100	3/100	3/100
TRX1	L	1/33.3	1/33.3	1/33.3	1/33.3
TRX2	L	2/66.6	2/66.6	2/66.6	2/66.6
gB	L	2/66.6	2/66.6	2/66.6	2/66.6
gH	L	3/100	3/100	3/100	3/100
gL	L	3/100	3/100	3/100	3/100
gM	L	3/100	3/100	3/100	3/100
vIRF-1	DE	1/33.3	1/33.3	1/33.3	1/33.3

*Number of Conserved Peptides/Percentage of Conserved Peptides

SEQUENCE LISTING

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-continued

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<210> SEQ ID NO 5
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<400> SEQUENCE: 5

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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 7

Phe Thr Val Ala Trp Asp Trp Val Pro Lys
1 5 10

<210> SEQ ID NO 8
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 8

Asn Asn Leu Glu Thr Thr Ala Phe His Arg
1 5 10

<210> SEQ ID NO 9
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 9

Ser His Pro Ser Thr Pro Pro Lys
1 5

<210> SEQ ID NO 10
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 10

Phe Val Gly Asp Gln Val Pro His Thr Thr Tyr Tyr Asp Gly Gly Val
1 5 10 15

Glu Leu Trp His Tyr Pro Met Gly His Lys
20 25

<210> SEQ ID NO 11
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

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<400> SEQUENCE: 11

Ala Thr Asp Ser Thr His Ser Pro Ala Tyr Pro Thr Leu Glu Leu Asn
1 5 10 15

Leu Ala Gln Gln Pro Leu Leu Arg
20

<210> SEQ ID NO 12
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 12

Val Val His Val Val Thr Val Thr Ala Cys Pro Arg
1 5 10

<210> SEQ ID NO 13
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 13

Gly Ser Gly Gly Pro Gly Val Glu Gly Gly His Gly Pro Ser Arg
1 5 10 15

<210> SEQ ID NO 14
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 14

His Pro Trp Ser Gly Glu Gln Gly Ala Ser Thr Arg
1 5 10

<210> SEQ ID NO 15
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 15

Asp Leu Pro Asp Ser Ser Asp Ser Glu Ala Glu Thr Glu Val Gly Gly
1 5 10 15

Arg

<210> SEQ ID NO 16
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 16

Ala Gly Thr Ala Val Asp Phe Ile Trp Thr Gly Asn Gln Arg
1 5 10

<210> SEQ ID NO 17
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 17

Tyr Leu Pro Ile Ser Gly Val Ser Ser Val Val Ala Leu Ser Pro Tyr
1 5 10 15

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Val Asn Lys

<210> SEQ ID NO 18
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 18

Leu Leu Gln Val Ser Gly Gly Thr Trp Gly Met His Leu Arg
1 5 10

<210> SEQ ID NO 19
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 19

Trp Thr Pro Asp Leu Gly Tyr Met Arg
1 5

<210> SEQ ID NO 20
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 20

Ala Pro Thr Pro Ser Ala Pro Ser Pro Asn Ala Met Leu Arg
1 5 10

<210> SEQ ID NO 21
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 21

Asp Gly Val Ile Phe Pro Lys
1 5

<210> SEQ ID NO 22
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 22

Ser Gly Ala Asp Ala Pro Gly Ser Asp Ala Arg
1 5 10

<210> SEQ ID NO 23
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 23

Val Ala Gly Gly Ser Glu Ala Ala Val Ala Ala Val Arg
1 5 10

<210> SEQ ID NO 24
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 24

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Ala Leu Leu Glu Pro Asp Asp Asp Ala Pro Pro Leu Val Leu Arg
1 5 10 15

<210> SEQ ID NO 25
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 25

Ala Pro Ala Ala Gly Thr Asp Ala Gly Glu Asp Ala Gly Asp Ala Val
1 5 10 15

Ser Pro Arg

<210> SEQ ID NO 26
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 26

Gly Pro Ser Ser Ala Ala Pro Ala Ala Pro Gly Arg
1 5 10

<210> SEQ ID NO 27
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 27

Asp Gly Tyr Val Ser Gly Glu Pro Trp Pro Gly Ala Gly Pro Pro Pro
1 5 10 15

Pro Gly Arg

<210> SEQ ID NO 28
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 28

Val Leu Gly Ala Ser Glu Thr Ile Ala Asn Ile Tyr Thr Thr Gln His
1 5 10 15

Arg

<210> SEQ ID NO 29
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 29

Val Tyr Gly Leu Leu Ala Asn Thr Val Arg
1 5 10

<210> SEQ ID NO 30
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 30

Asp Asp Ile Val Tyr Val Pro Glu Pro Met Thr Tyr Trp Arg
1 5 10

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<210> SEQ ID NO 31
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 31

Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys
1 5 10

<210> SEQ ID NO 32
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 32

Asp Ile His Gly Tyr Leu Ala Pro Val Pro Lys
1 5 10

<210> SEQ ID NO 33
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 33

His Thr Ile Ser Pro Val Ser Trp Ser Ser Gly Asp Leu Val Arg
1 5 10 15

<210> SEQ ID NO 34
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 34

Ala Asp Asp Gly Gly Glu Ala Gly Ala Asp Thr Arg
1 5 10

<210> SEQ ID NO 35
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 35

Ala Pro Leu Ala Ile Gly Pro Leu Trp Ala Arg
1 5 10

<210> SEQ ID NO 36
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 36

Gly Pro Asp Ser Pro Pro Lys
1 5

<210> SEQ ID NO 37
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 37

Leu Glu Asp Gly Ala Gly Ala Leu Gly Ala Ala Gly Pro Ser Lys
1 5 10 15

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<210> SEQ ID NO 38
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 38

Trp Ser Leu Val Ala Glu Arg
1 5

<210> SEQ ID NO 39
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 39

Gln Ala Gly Gly Gln Pro Ala Ala Gly Asp Pro Gly Val Arg
1 5 10

<210> SEQ ID NO 40
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 40

Ala Ala Asp Leu Phe Val Ser Gln Met Met Gly Ala Arg
1 5 10

<210> SEQ ID NO 41
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 41

Leu Gly Thr Ile Val Thr Tyr Asp Thr Gly Leu Asp Ala Ala Ile Ala
1 5 10 15

Pro Phe Arg

<210> SEQ ID NO 42
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 42

Leu Ala Ala Glu Ala Glu Leu Ala Leu Ser Gly Arg
1 5 10

<210> SEQ ID NO 43
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 43

Ile Pro Gln Ser Ser Pro Glu Glu Ala Val Leu Leu Asp Lys
1 5 10

<210> SEQ ID NO 44
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 44

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Glu Ser Leu Leu Ser Ile Leu Leu Arg
1 5

<210> SEQ ID NO 45
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 45

Leu Asn Ala Val Ala Glu Ala Val Leu Lys
1 5 10

<210> SEQ ID NO 46
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 46

Gly Ile Ser Ala Asp His Phe Glu Ala Glu Val Val Glu Arg
1 5 10

<210> SEQ ID NO 47
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 47

Asp Leu Pro Thr Gly Glu Ala Ser Pro Gly Ala Phe Ser Ala Phe Arg
1 5 10 15

<210> SEQ ID NO 48
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 48

Glu Glu Gly Val Ser Ser Ser Thr Ser Thr Gln Val Gln Ile Leu Ser
1 5 10 15

Asn Ala Leu Thr Lys
20

<210> SEQ ID NO 49
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 49

Val Glu Leu Ala Ile Thr Gly Gln Ala Pro Phe Arg
1 5 10

<210> SEQ ID NO 50
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 50

Thr Ser Leu Leu Asp Ser Leu Leu Val Met Gly Asp Arg
1 5 10

<210> SEQ ID NO 51
<211> LENGTH: 9

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<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 51

Glu His Leu Asn Leu Pro Leu Val Arg
1 5

<210> SEQ ID NO 52
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 52

Leu Ser Phe Leu Pro Ala Gly His Thr Arg
1 5 10

<210> SEQ ID NO 53
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 53

Asp Gly Leu Gly Leu Tyr Tyr Glu Ala Leu Ser Arg
1 5 10

<210> SEQ ID NO 54
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 54

Phe Leu Ser Thr Leu Pro Ser Asp Val Val Glu Trp Gly Asp Ala Tyr
1 5 10 15

Val Pro Glu Arg
20

<210> SEQ ID NO 55
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 55

Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly Arg
1 5 10

<210> SEQ ID NO 56
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 56

Leu His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro
1 5 10 15

Arg

<210> SEQ ID NO 57
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 57

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Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr Ile Arg
1 5 10 15

<210> SEQ ID NO 58
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 58

Phe Val Gln Tyr Asp Glu Ser Asp Tyr Ala Leu Tyr Gly Gly Ser Ser
1 5 10 15

Ser Glu Asp Asp Glu His Pro Glu Val Pro Arg
20 25

<210> SEQ ID NO 59
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 59

Gly Ser Glu Gln Pro Asp Pro Pro Gly Gly Gln Arg
1 5 10

<210> SEQ ID NO 60
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 60

Ala Pro Ala Ala Asp Thr Ile Asp Ala Thr Thr Arg
1 5 10

<210> SEQ ID NO 61
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 61

Val Ser Trp Glu Thr Leu Val Ala His Gly Pro Ser Leu Tyr Arg
1 5 10 15

<210> SEQ ID NO 62
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 62

Gly Val Ala Glu Ile Asp Tyr Ala Thr Leu Gly Val Gly Val Gly Glu
1 5 10 15

Lys

<210> SEQ ID NO 63
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 63

Gly Pro Ala Tyr Thr Thr Ala Ala Gly Val Val Arg
1 5 10

<210> SEQ ID NO 64

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<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 64

Gly Gly Ala Leu Leu Asp Ala Glu His Tyr Trp Arg
1 5 10

<210> SEQ ID NO 65
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 65

Ala Gln Leu Leu Ala Ala Leu Ala Asp Leu Gly Gly Ser Gly Leu Ala
1 5 10 15

Asp Pro His Gly Arg
20

<210> SEQ ID NO 66
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 66

Ala Ser Trp Gly Pro Pro Ala Ala Pro Arg
1 5 10

<210> SEQ ID NO 67
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 67

Tyr Gln Ala Asp Leu Tyr Thr Tyr Leu Ser Arg
1 5 10

<210> SEQ ID NO 68
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 68

Ala Gly Trp Tyr Thr Ser Thr Ser His Glu Ala Arg
1 5 10

<210> SEQ ID NO 69
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 69

Gln Leu Leu Ser Ala Val Asp Tyr Ile His Arg
1 5 10

<210> SEQ ID NO 70
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 70

Asp Glu Ile Gly Ala Thr Gly Phe Thr Ala Glu Glu Leu Asp Ala Met

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1 5 10 15

Asp Arg

<210> SEQ ID NO 71
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 71

Asn Phe Ile Thr Pro Glu Phe Pro Arg
1 5

<210> SEQ ID NO 72
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 72

Asp Phe Trp Met Ser Pro Val Phe Asn Leu Pro Arg
1 5 10

<210> SEQ ID NO 73
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 73

Gly Ala Ser Gly Ser Asp Ser Gly Ala Ile Lys
1 5 10

<210> SEQ ID NO 74
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 74

Gly His Asn Leu Phe Leu Trp Glu Asp Gln Thr Leu Leu Arg
1 5 10

<210> SEQ ID NO 75
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 75

Leu Thr Ala Leu Glu Leu Ile Asn Arg
1 5

<210> SEQ ID NO 76
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 76

Ala Pro Val Thr Phe Gly Asp Leu Leu Gly Arg
1 5 10

<210> SEQ ID NO 77
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

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<400> SEQUENCE: 77

Ala Ala Leu Gln Gly Gly Pro Arg
1 5

<210> SEQ ID NO 78
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 78

Ala Trp Leu Gly Glu Val Thr Arg
1 5

<210> SEQ ID NO 79
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 79

Val Val Pro Leu Gly Asp Asp Leu Pro Ala Arg
1 5 10

<210> SEQ ID NO 80
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 80

Gly Leu Leu Val Val Pro Thr Arg
1 5

<210> SEQ ID NO 81
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 81

Glu Ala Ile Ala Phe Leu Pro Lys
1 5

<210> SEQ ID NO 82
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 82

Val Ser Gly Asp Ser Gly Trp Ala Val Gly Arg
1 5 10

<210> SEQ ID NO 83
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 83

Gly Gly Gly Val Val Gln Leu Asn Leu Val Asn Arg
1 5 10

<210> SEQ ID NO 84
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

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<400> SEQUENCE: 84

Thr Thr Pro Thr Glu Pro Ala Ser Pro Pro Thr Thr Pro Lys Pro Thr
1 5 10 15

Ser Thr Pro Lys
20

<210> SEQ ID NO 85
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 85

Asp Ser Val Thr Phe Ser Arg
1 5

<210> SEQ ID NO 86
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 86

Ser Pro Pro Thr Ser Thr Pro Asp Pro Lys Pro Lys
1 5 10

<210> SEQ ID NO 87
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 87

Ala Thr Cys Thr Ala Ala Ala Tyr Tyr Pro Arg
1 5 10

<210> SEQ ID NO 88
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 88

Tyr Ala Leu Pro Leu Arg
1 5

<210> SEQ ID NO 89
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 89

Ser Leu Gly Ala Cys Pro Ile Arg
1 5

<210> SEQ ID NO 90
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 90

Ser Val Leu Leu Asn Ala Pro Ser Glu Ala Pro Gln Ile Val Arg
1 5 10 15

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<210> SEQ ID NO 91
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 91

Asp Leu Pro Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Arg
1 5 10 15

<210> SEQ ID NO 92
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 92

Tyr Ala Leu Val Asp Ala Ser Leu Lys
1 5

<210> SEQ ID NO 93
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 93

Thr Asp Phe Val Trp Gln Glu Arg
1 5

<210> SEQ ID NO 94
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 94

Asn Ala Val Val Glu Gln Pro Leu Pro Gln Arg
1 5 10

<210> SEQ ID NO 95
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 95

Val Ser Val Gly Glu Asp Val Ser Leu Leu Pro Ala Pro Gly Pro Thr
1 5 10 15

Gly Arg

<210> SEQ ID NO 96
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 96

Ser Leu Val Ile His Gly Val Arg
1 5

<210> SEQ ID NO 97
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 97

Asp Thr Leu Pro Gln Ser Pro Gly Pro Ala Phe Pro Leu Ala Glu Asp

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1 5 10 15

Val Glu Lys

<210> SEQ ID NO 98
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 98

Val Phe Val Leu Gly Ser Leu Thr Arg
1 5

<210> SEQ ID NO 99
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 99

Val Gly Asp Pro Ala Asp Glu Asn Pro Pro Gly Ala Leu Pro Gly Pro
1 5 10 15

Pro Gly Gly Pro Arg
20

<210> SEQ ID NO 100
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 100

Gln Pro Phe Leu Ala Gly Val Pro Ser Ala Val Gln Arg
1 5 10

<210> SEQ ID NO 101
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 101

Ala Leu Phe Tyr Ala Ser Ala Val Leu Arg
1 5 10

<210> SEQ ID NO 102
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 102

Ile Val Ser Ser Val Phe Leu Gln Tyr Pro Tyr Thr Lys
1 5 10

<210> SEQ ID NO 103
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 103

Met Val Ala Pro Ala Thr Tyr Leu Leu Asn Tyr Ala Gly Arg
1 5 10

<210> SEQ ID NO 104
<211> LENGTH: 29

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<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 104

His Arg Pro Ala Pro Gly Ser Pro Pro Gly Ile Pro Glu Tyr Ala Glu
1 5 10 15

Asp Pro Tyr Ala Ile Ser Tyr Gly Gly Gln Leu Asp Arg
20 25

<210> SEQ ID NO 105
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 105

Gly Val Leu Ser Gly Thr Tyr Leu Arg
1 5

<210> SEQ ID NO 106
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 106

Gly Gly Val Ala Val Pro Leu Arg
1 5

<210> SEQ ID NO 107
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 107

Gly Ser Pro Asp Ser Ala Pro Pro Thr Lys
1 5 10

<210> SEQ ID NO 108
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 108

Leu Asn Ser Ala Tyr Val Ala Met Ser Arg
1 5 10

<210> SEQ ID NO 109
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 109

Thr Thr Ser Ser Glu Phe Leu Arg
1 5

<210> SEQ ID NO 110
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 110

Ala Ala Gly Gly Val Tyr Ala Gly Asp Lys
1 5 10

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<210> SEQ ID NO 111
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 111

Tyr Leu Asp Asn Gly Arg
1 5

<210> SEQ ID NO 112
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 112

Ala Thr Leu Val Ala Glu Leu Lys
1 5

<210> SEQ ID NO 113
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 113

Ala Pro Pro Leu Ala Leu Leu Leu Pro Met Gln Arg
1 5 10

<210> SEQ ID NO 114
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 114

Leu Phe Asp Phe Phe Ser Arg
1 5

<210> SEQ ID NO 115
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 115

Leu Leu Gln Ser Phe Leu Lys
1 5

<210> SEQ ID NO 116
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 116

Ser Ser Ala Ala Gly Gly Thr Leu Gly Val Val Arg
1 5 10

<210> SEQ ID NO 117
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 117

Ser Leu Ser Val Pro Leu Val Lys

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1 5

<210> SEQ ID NO 118
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 118

Asp Ile Ser Phe Asp Gly Gly Leu Met Leu Glu Tyr Gln Arg
1 5 10

<210> SEQ ID NO 119
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 119

Glu Ala Tyr Gly Ala Glu Ala Gly Leu Gly Val Ala Gly Thr Gly Phe
1 5 10 15

Arg

<210> SEQ ID NO 120
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 120

Phe Met Gly Pro Glu Asp Ala Gly Arg
1 5

<210> SEQ ID NO 121
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 121

Gly Gly Asp Gly Glu Ala Gly Pro Tyr Ser Pro Ser Ser Leu Pro Ser
1 5 10 15

Arg

<210> SEQ ID NO 122
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 122

Val Gln Leu Ala Phe Arg
1 5

<210> SEQ ID NO 123
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 123

Leu Ile Val Pro Ser Thr Leu Arg
1 5

<210> SEQ ID NO 124
<211> LENGTH: 8
<212> TYPE: PRT

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<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 124

Phe Leu Gly Asp Ala Val Asn Arg
1 5

<210> SEQ ID NO 125
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 125

Asp Gly Glu Thr Leu Arg Pro Asn Thr Leu Leu Leu Lys
1 5 10

<210> SEQ ID NO 126
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 126

Ala Asp Gly Thr Leu Pro Ala Ser Thr Leu Val Arg
1 5 10

<210> SEQ ID NO 127
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 127

Leu Ser Glu Gly Glu Leu Ser Phe Tyr Arg
1 5 10

<210> SEQ ID NO 128
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 128

Val Asp Trp Leu Glu Ala Arg
1 5

<210> SEQ ID NO 129
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 129

Val Thr Cys Gln Ser Asn Asp Leu Ile Ser Arg
1 5 10

<210> SEQ ID NO 130
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 130

Val Tyr Gly Leu Phe Arg
1 5

<210> SEQ ID NO 131
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 131

Thr Tyr Ser Pro Phe Val Val Arg
1 5

<210> SEQ ID NO 132
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 132

Asn Pro Asp Phe Pro Leu Ala Gly Leu Ala Ala Asn Pro Gln Thr Pro
1 5 10 15

Arg

<210> SEQ ID NO 133
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 133

Ala Gly Thr Leu Leu Leu Ala Leu Arg
1 5

<210> SEQ ID NO 134
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 134

Gly Gly Ala Ala Leu Ile Gly Ser Pro Arg
1 5 10

<210> SEQ ID NO 135
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 135

Asp Thr Ala Gly Gln Gly Leu Leu Arg
1 5

<210> SEQ ID NO 136
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 136

Gly Leu Glu Pro Ala Leu Glu Arg
1 5

<210> SEQ ID NO 137
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 137

Val Val Phe Leu Pro Thr Ile Arg
1 5

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<210> SEQ ID NO 138
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 138

Phe Pro Ala Val Ile Thr Arg
1 5

<210> SEQ ID NO 139
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 139

Leu Asp Ser Leu Asp Leu Thr Leu Arg
1 5

<210> SEQ ID NO 140
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 140

Phe Pro Val Pro Leu Pro Ser Pro Leu Ala Arg
1 5 10

<210> SEQ ID NO 141
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 141

Val Cys Thr Phe Asp Gly Ala Ala Val Val Arg
1 5 10

<210> SEQ ID NO 142
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 142

Glu Gly Val Ser Thr Gln Asp Pro Arg
1 5

<210> SEQ ID NO 143
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 143

Ile Val Asn Ser Val Phe Val Trp Arg
1 5

<210> SEQ ID NO 144
<211> LENGTH: 34
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 144

Ala Ala Thr Pro Pro Glu Glu Thr Pro Asp Pro Thr Thr Glu Gln Leu
1 5 10 15

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Ala Glu Glu Pro Val Val Gly Glu Leu Asp Gly Ala Tyr Leu Val Pro
20 25 30

Ala Lys

<210> SEQ ID NO 145
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 145

Leu Gln Glu Val Val Gly Gly Arg
1 5

<210> SEQ ID NO 146
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 146

Asp Gly Val Leu Leu Leu Asn Thr Thr Leu Thr Val Lys
1 5 10

<210> SEQ ID NO 147
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 147

Phe Ser His Pro Ser Pro Leu Ser Lys
1 5

<210> SEQ ID NO 148
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 148

Ala Asn Val Pro Pro Pro Pro Ser Leu Arg
1 5 10

<210> SEQ ID NO 149
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 149

Glu Asp Val Phe Ser Trp Thr Arg
1 5

<210> SEQ ID NO 150
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 150

Asn Val Leu Ala Ala Val Lys
1 5

<210> SEQ ID NO 151
<211> LENGTH: 11
<212> TYPE: PRT

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<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 151

Thr Ser Pro Gly Val Leu Ile Ser Gly Leu Arg
1 5 10

<210> SEQ ID NO 152
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 152

Thr Asp Val Val Ile Thr Gly Arg
1 5

<210> SEQ ID NO 153
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 153

Leu Phe Gly Ser Ala Gly Ala Pro Arg
1 5

<210> SEQ ID NO 154
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 154

Leu Ser Pro Phe Pro Ala Leu Val Arg
1 5

<210> SEQ ID NO 155
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 155

Ala Ala Gly Tyr Leu Asp Val Leu Leu Thr Val Arg
1 5 10

<210> SEQ ID NO 156
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 156

Ala Pro Arg Pro Ile Ala Gly Ser Gly Ala Gly Ser Gly Gly Ala Gly
1 5 10 15

Ala Lys

<210> SEQ ID NO 157
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 157

Val Ser Gly Asn Ile Thr Ala Val Val Arg
1 5 10

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<210> SEQ ID NO 158
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 158

Gly Ala Ala Val Ala Ser Pro Asp Gln Pro Leu His Gly Gly Pro Glu
1 5 10 15

Arg

<210> SEQ ID NO 159
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 159

Ala Thr Leu Val Gly Ser Phe Ala Arg
1 5

<210> SEQ ID NO 160
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 160

Thr Asp Gly Gly Val Pro Gly Arg
1 5

<210> SEQ ID NO 161
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 161

Ser Ala Leu Ala Val Leu Ile Arg
1 5

<210> SEQ ID NO 162
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 162

Val Leu Pro Ala Phe Ser Ala Gly Gly Pro Pro Thr Arg
1 5 10

<210> SEQ ID NO 163
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 163

Val Ser Gly Gly Pro Gly Pro Leu Val Leu Arg
1 5 10

<210> SEQ ID NO 164
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 164

Leu Ala Gly Gly Leu Leu Glu Arg

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1 5

<210> SEQ ID NO 165
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 165

Ala Gly Ala Val Glu Glu Leu Gly Gly Arg
1 5 10

<210> SEQ ID NO 166
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 166

Leu Leu Ala Ser Leu Ala Gly Leu Arg
1 5

<210> SEQ ID NO 167
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 167

Phe Ser Ser Gly Gln Pro Ser Leu Leu Arg
1 5 10

<210> SEQ ID NO 168
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 168

Leu Gly Ala Leu Ile Thr Leu Leu Glu Pro Ala Ala Arg
1 5 10

<210> SEQ ID NO 169
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 169

Gly Val Leu Gln Asp Leu Ala Glu Arg
1 5

<210> SEQ ID NO 170
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 170

Gln Leu Glu Asp Ala Ile Val Leu Leu Arg
1 5 10

<210> SEQ ID NO 171
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 171

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Ala Leu Val Ala Ser Leu Ala Ser Leu Arg
1 5 10

<210> SEQ ID NO 172
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 172

Ala Ser Leu Thr Ser Ala Leu Pro Asp Ala Ala Gln Val Val His Val
1 5 10 15

Phe Glu Tyr Gly Thr Arg
20

<210> SEQ ID NO 173
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 173

Phe Leu Glu Gln Leu Arg
1 5

<210> SEQ ID NO 174
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 174

Ser Leu Phe Pro Ile Phe Val Thr Asp Arg
1 5 10

<210> SEQ ID NO 175
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 175

Gly Thr Ser Leu Ala Ser Gly Thr Arg
1 5

<210> SEQ ID NO 176
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 176

Ser Thr Glu Thr Arg Pro Pro Leu Pro Pro Ala Ala Gly Gly Thr Glu
1 5 10 15

Thr Arg

<210> SEQ ID NO 177
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 177

Gly Pro Trp Thr Leu Leu Lys
1 5

<210> SEQ ID NO 178

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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 178

Thr Gln Ala Pro Pro Pro Ala Phe Tyr Lys
1 5 10

<210> SEQ ID NO 179
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 179

Ser Ser Gly Tyr Trp Trp Val Ser Gly Asp Gly Ile Arg
1 5 10

<210> SEQ ID NO 180
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 180

Phe Leu Pro Leu Gly Gly Ser Pro Glu Ala Pro Ala Glu Thr Phe Ala
1 5 10 15

Arg

<210> SEQ ID NO 181
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 181

Leu Ala Asn Leu Trp Gln Thr Gly Lys
1 5

<210> SEQ ID NO 182
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 182

Ala Trp Phe Gly Ala Ala Leu Ala Ala Asp Leu Leu Arg
1 5 10

<210> SEQ ID NO 183
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 183

Val Tyr Glu Glu Ile Pro Trp Met Arg
1 5

<210> SEQ ID NO 184
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 184

Thr Gly Pro Pro Pro Pro Pro Leu Ser Pro Ser Pro Val Leu Ala Arg
1 5 10 15

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<210> SEQ ID NO 185
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 185

Gln Gly Gly Tyr Leu Gly Pro Val Asp Ala Arg
1 5 10

<210> SEQ ID NO 186
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 186

Val Glu Val Leu Glu Gly Arg
1 5

<210> SEQ ID NO 187
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 187

Ala Ile Leu Ala Ala Gly Leu Val Leu Gln Arg
1 5 10

<210> SEQ ID NO 188
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 188

Leu Leu Met Gly Asp Glu Gly Ala Ala Ala Leu Arg
1 5 10

<210> SEQ ID NO 189
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 189

Ala Thr Gly Leu Gly Gly Pro Pro Arg Pro
1 5 10

<210> SEQ ID NO 190
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 190

Ala Ala Val Pro Pro Ser Glu Ala Glu Pro Arg
1 5 10

<210> SEQ ID NO 191
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 191

Ser Ala Asp Val Leu Val Ser Gln Ala Ile Arg

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1 5 10

<210> SEQ ID NO 192
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 192

Gly Ala Ala Ala Ala Gly Phe Pro Leu Tyr Val Glu Arg
1 5 10

<210> SEQ ID NO 193
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 193

Glu Thr Leu Thr Glu Val Leu Gly Arg
1 5

<210> SEQ ID NO 194
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 194

Leu Val Ala Pro Pro Asp Ile Thr Arg
1 5

<210> SEQ ID NO 195
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 195

Ser Phe Gly Pro Gly Gly Leu Leu Ala Thr Pro Leu Phe Leu Pro Glu
1 5 10 15

Thr Arg

<210> SEQ ID NO 196
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 196

Glu Ala Asp Ile Ala Gly Val Ala Glu Arg
1 5 10

<210> SEQ ID NO 197
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 197

Val Phe Asp Thr Trp Arg
1 5

<210> SEQ ID NO 198
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

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<400> SEQUENCE: 198

Leu Ile Ile Asn Met Lys
1 5

<210> SEQ ID NO 199
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 199

Ser Leu Val Glu Ala Ala Glu Ala Ile Ser Gln Gln Thr Leu Leu Arg
1 5 10 15

<210> SEQ ID NO 200
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 200

Phe Thr Ala Thr Ser Ile Ala Arg
1 5

<210> SEQ ID NO 201
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 201

Phe Ser Leu Phe Asn Pro Arg
1 5

<210> SEQ ID NO 202
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 202

Leu Pro Gly Pro Pro Pro Arg
1 5

<210> SEQ ID NO 203
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 203

Ala Pro Leu Val Tyr Trp Trp Leu Ser Glu Thr Pro Lys
1 5 10

<210> SEQ ID NO 204
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 204

Ile Ile Trp Gly Glu Leu Phe Gly Val Gln Met Ala Lys
1 5 10

<210> SEQ ID NO 205
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

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<400> SEQUENCE: 205

Asp His Pro Glu Asn Leu Gly Asn Pro Glu Tyr Arg
1 5 10

<210> SEQ ID NO 206
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 206

Tyr Ala Pro Leu Ala Ser Pro Asp Pro Phe Ser Pro Gln His Gly Ala
1 5 10 15

Tyr Ala Arg

<210> SEQ ID NO 207
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 207

Leu Val His Thr Gln Trp Leu Arg
1 5

<210> SEQ ID NO 208
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 208

Val Gly Ala Asp Thr Thr Ile Ser Lys Pro Ser Glu Ala Val Arg Pro
1 5 10 15

Pro Thr Ile Pro Arg
20

<210> SEQ ID NO 209
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 209

Gly Asp Asn Asp Gln Ala Ala Gly Gln Cys Gly Asp Ser Gly Leu Leu
1 5 10 15

Arg

<210> SEQ ID NO 210
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 210

Met Ile Ser Gly Pro Pro Gln Arg
1 5

<210> SEQ ID NO 211
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 211

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Gly Val Pro Ser Ala Gly Met His Pro Arg
1 5 10

<210> SEQ ID NO 212
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 212

Thr Gly Gly Thr Val Thr Asp Ser Pro Arg
1 5 10

<210> SEQ ID NO 213
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 213

Thr Ser Val Asp Ala Ser Pro Ala Leu Trp Ser Phe Leu Leu Arg
1 5 10 15

<210> SEQ ID NO 214
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 214

Asp Gln Pro Ser Pro Pro Arg
1 5

<210> SEQ ID NO 215
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 215

Thr Pro Asp Ala Trp Val Gly Glu Pro Trp Ala Val Pro Thr Arg
1 5 10 15

<210> SEQ ID NO 216
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 216

Tyr Glu Tyr Gln Tyr Gly Val Val Leu Pro Gly Thr Asn Gly Arg
1 5 10 15

<210> SEQ ID NO 217
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 217

Gly Pro Gln Glu Thr Asp Pro Leu Ile Ala Val Arg
1 5 10

<210> SEQ ID NO 218
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 218

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Leu Ser Asp Pro Asn Ser Ser Ala Arg
1 5

<210> SEQ ID NO 219
<211> LENGTH: 34
<212> TYPE: PRT
<213> ORGANISM: Herpes simplex virus type 1

<400> SEQUENCE: 219

Ser Asp Met Ser Val Pro Leu Tyr Pro Thr Ala Ser Pro Val Ser Val
1 5 10 15

Glu Ala Tyr Tyr Ser Glu Ser Glu Asp Glu Ala Ala Asn Asp Phe Leu
20 25 30

Val Arg

<210> SEQ ID NO 220
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 220

Asn Ala His Thr Gln Ser Trp Tyr Trp Leu Arg
1 5 10

<210> SEQ ID NO 221
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 221

Tyr His Met Leu Gln Asp Thr Val Ser Glu Ser Glu Phe Ile Val Arg
1 5 10 15

<210> SEQ ID NO 222
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 222

Tyr Asn Thr Asp Ile Glu Asn Glu Asp Arg
1 5 10

<210> SEQ ID NO 223
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 223

Asn Ala His Thr Gln Ser Trp Tyr Trp Leu Arg
1 5 10

<210> SEQ ID NO 224
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 224

Tyr His Met Leu Gln Asp Thr Val Ser Glu Ser Glu Phe Ile Val Arg
1 5 10 15

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<210> SEQ ID NO 225
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 225

Tyr Asn Thr Asp Ile Glu Asn Glu Asp Arg
1 5 10

<210> SEQ ID NO 226
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 226

Val Val Val Thr Asp Ser Gln Glu Ala Asp Arg
1 5 10

<210> SEQ ID NO 227
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 227

Met Pro Pro Leu Cys Ile Ile Thr Asp Ala Tyr Lys
1 5 10

<210> SEQ ID NO 228
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 228

Met Pro Pro Leu Cys Ile Ile Thr Asp Ala Tyr Lys
1 5 10

<210> SEQ ID NO 229
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 229

Val Val Val Thr Asp Ser Gln Glu Ala Asp Arg
1 5 10

<210> SEQ ID NO 230
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 230

Thr Asp Leu Asp Thr Glu Pro Leu Leu Leu Thr Val Asp Gly Asp Leu
1 5 10 15

Gln

<210> SEQ ID NO 231
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 231

Thr Asp Leu Asp Thr Glu Pro Leu Leu Leu Thr Val Asp Gly Asp Leu

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1 5 10 15

Gln

<210> SEQ ID NO 232
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 232

Thr Ala Gly Val Pro Ala Pro Met Ala Ala Thr Val Ala Arg
1 5 10

<210> SEQ ID NO 233
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 233

Leu Val Tyr Leu Gln Ser Ser Ala Arg
1 5

<210> SEQ ID NO 234
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 234

Phe Leu Asn Asp Val Asp Ile Leu Gly Ser Phe Gly Arg
1 5 10

<210> SEQ ID NO 235
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 235

Ser Ser Asn Val Phe Asp Leu Glu Glu Ile Met Arg
1 5 10

<210> SEQ ID NO 236
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 236

Thr Met Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser Thr Arg
1 5 10 15

<210> SEQ ID NO 237
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 237

Asp Thr Ser Leu Gln Ala Pro Pro Ser Tyr Glu Glu Ser Val Tyr Asn
1 5 10 15

Ser Gly Arg

<210> SEQ ID NO 238
<211> LENGTH: 12
<212> TYPE: PRT

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<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 238

Gln Glu Glu Ala Gly Thr Glu Ile Ser Ile Pro Arg
1 5 10

<210> SEQ ID NO 239
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 239

Thr Thr Leu Leu Leu Tyr Pro Thr Ala Val Asp Leu Ala Lys
1 5 10

<210> SEQ ID NO 240
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 240

Tyr Gln Ala Leu Ala Thr Ala Ser Gly Glu Glu Val Ala Val Leu Ser
1 5 10 15

His His Asp Ser Leu Glu Ser Arg
20

<210> SEQ ID NO 241
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 241

Gly Met Ser Leu Asn Gln Ser Thr Arg
1 5

<210> SEQ ID NO 242
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 242

Ser Leu Phe Phe Phe Ser Arg
1 5

<210> SEQ ID NO 243
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 243

His Ala Asn Asp Asp Phe Tyr Lys
1 5

<210> SEQ ID NO 244
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 244

Leu Ser Ser Thr Thr His Asp Pro Asn Val Met Arg
1 5 10

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<210> SEQ ID NO 245
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 245

Glu Pro His Gly Gln Trp Glu Phe Met Phe Arg
1 5 10

<210> SEQ ID NO 246
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 246

Thr Leu Gly Leu Asp Leu Thr Thr Val Met Thr Glu Arg
1 5 10

<210> SEQ ID NO 247
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 247

Thr Gly Pro Gly Pro Pro Pro Leu Pro Pro Lys
1 5 10

<210> SEQ ID NO 248
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 248

Thr Ser Ala Gly Glu Glu Met Phe Glu Ala Leu Arg
1 5 10

<210> SEQ ID NO 249
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 249

Val Ala Ser Gly Ala Gly Leu Pro Thr Ser Arg
1 5 10

<210> SEQ ID NO 250
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 250

Asn Met Glu Gly Val Gln Val Val Ala Asp Arg
1 5 10

<210> SEQ ID NO 251
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 251

Leu Thr Leu His Asp Leu His Asp Ile Phe Arg
1 5 10

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<210> SEQ ID NO 252
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 252

Gln His Thr Cys Leu Asp Ile Ser Pro Tyr Gly Asn Glu Gln Val Ser
1 5 10 15

Arg

<210> SEQ ID NO 253
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 253

Ala Ala Ser Thr Ser Leu Ala Val Arg
1 5

<210> SEQ ID NO 254
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 254

Val Leu His Gln Asp Leu Val Gln Ala Thr Arg
1 5 10

<210> SEQ ID NO 255
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 255

Phe Glu Gly Glu Val Leu Glu Ser Val Leu Lys
1 5 10

<210> SEQ ID NO 256
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 256

Glu Leu Val Thr Glu Ala Val Val Trp Gly Asn Ala Arg
1 5 10

<210> SEQ ID NO 257
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 257

Val Ser Ser Gly Leu Ser Thr Phe Asn Pro Ala Gly Ala Thr Arg
1 5 10 15

<210> SEQ ID NO 258
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 258

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Ile Tyr Pro Glu Val Val Ala Gln Asn Arg
1 5 10

<210> SEQ ID NO 259
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 259

Glu Tyr Asn Leu Phe Thr Asp Ile Pro Glu Arg
1 5 10

<210> SEQ ID NO 260
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 260

Leu Met Asn Gly Phe Leu Tyr Arg
1 5

<210> SEQ ID NO 261
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 261

Val Tyr Asp Leu Leu Leu Pro Ser Leu Asp Ala Arg
1 5 10

<210> SEQ ID NO 262
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 262

Thr Gln Leu Leu Thr Ala Ile Val Ser Lys
1 5 10

<210> SEQ ID NO 263
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 263

Leu Met Asp Ile Asn Gly Ile Leu Glu Gly Lys
1 5 10

<210> SEQ ID NO 264
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 264

Asp Pro Gln Phe Gln Gln Ile Asn Asn Phe Met Thr Asp Phe Lys
1 5 10 15

<210> SEQ ID NO 265
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 265

Glu Ala Phe Asn Thr Ile Leu Gly Phe Leu Ala Gln Asn Thr Thr Lys
1 5 10 15

<210> SEQ ID NO 266
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 266

Tyr Ser Thr Leu Asn Thr Asn Ala Tyr Asp Tyr Phe Gly Lys
1 5 10

<210> SEQ ID NO 267
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 267

Asp Asp Glu Asp Trp Lys Pro Ser Arg
1 5

<210> SEQ ID NO 268
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 268

Val Thr Phe Ser Asn Ile Ala Thr His Tyr His Tyr Asn Ala Gln
1 5 10 15

<210> SEQ ID NO 269
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 269

Asp Pro Ala Asp Glu Asp Asn Glu Leu Val Thr Ala Leu Lys
1 5 10

<210> SEQ ID NO 270
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 270

Ala Ala Leu Gln Trp Leu Asp Leu Gly Pro His Leu Leu His Arg
1 5 10 15

<210> SEQ ID NO 271
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 271

Leu Asp Asn Phe Ser Val Glu Leu Gly Asp Phe Arg
1 5 10

<210> SEQ ID NO 272
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 272

Ala Ala Val Gln Gln Leu Gln Thr Ile Thr Phe Arg
1 5 10

<210> SEQ ID NO 273
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 273

Leu Val Ala Ala Val Val Pro Ile Pro Gln Arg
1 5 10

<210> SEQ ID NO 274
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 274

Leu Ala Leu Glu Asp Ser Ser Met Leu Leu Val Lys
1 5 10

<210> SEQ ID NO 275
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 275

Asp Tyr Leu Gly Pro Asp Leu Phe Glu Thr Gly Ala Ala Arg
1 5 10

<210> SEQ ID NO 276
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 276

Val Ser Val Ser Glu Leu Glu Ala Val Tyr Arg
1 5 10

<210> SEQ ID NO 277
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 277

Ser Leu Ala Val Asp Ala Gln His Ala Ala Lys
1 5 10

<210> SEQ ID NO 278
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 278

Leu Thr Gly Gln Asp Glu Ala His Ser Phe Ser Leu Lys
1 5 10

<210> SEQ ID NO 279
<211> LENGTH: 16
<212> TYPE: PRT

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<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 279

Gln Asn Val Met Ile Met Glu Pro Gln Val Leu Asp Phe Thr Val Arg
1 5 10 15

<210> SEQ ID NO 280
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 280

Gly Val Leu Glu Val His Thr Asp Phe Thr Arg
1 5 10

<210> SEQ ID NO 281
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 281

Val Pro Pro Asn Ser Gln Glu Ser Ala Ala Pro Gln Pro Pro Arg
1 5 10 15

<210> SEQ ID NO 282
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 282

Ile Leu His Gln Ser Val Asn Gln Thr Phe Asp Val Arg
1 5 10

<210> SEQ ID NO 283
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 283

Leu Leu Pro Glu Thr Ser Gly Gly Thr Val Val Val Asn His Ser Ser
1 5 10 15

Val Ala Arg

<210> SEQ ID NO 284
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 284

Tyr Val Phe Glu Glu Val Ser Arg
1 5

<210> SEQ ID NO 285
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 285

Phe Phe His Gln Asp Pro Asn Arg
1 5

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<210> SEQ ID NO 286
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 286

Tyr Ala Pro Leu Phe Ala Ser Lys
1 5

<210> SEQ ID NO 287
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 287

Ser Phe Thr Thr Thr Tyr Val Phe Ile Lys
1 5 10

<210> SEQ ID NO 288
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 288

Gly Pro Phe Thr Gln Val Gly Tyr Leu Ser Ala Phe Pro Pro Asp Asn
1 5 10 15

Glu Gly Lys

<210> SEQ ID NO 289
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 289

Leu Glu Glu Pro Val Glu Glu Lys
1 5

<210> SEQ ID NO 290
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 290

Gly Ile Gln Ile Ile Tyr Thr Arg
1 5

<210> SEQ ID NO 291
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 291

Ile Phe Ser Thr Asn Gln Gly Gly Phe Met Leu Pro Ile Tyr Glu Thr
1 5 10 15

Ala Ala Lys

<210> SEQ ID NO 292
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 292

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Val His Glu Pro Phe Glu Glu Met Lys
1 5

<210> SEQ ID NO 293
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 293

Leu Gly Gly Ala Leu Gln Ala Lys
1 5

<210> SEQ ID NO 294
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 294

Val Phe Ala Gln Tyr Ile Leu Gly Ala Asp Pro Leu Arg
1 5 10

<210> SEQ ID NO 295
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 295

Gln Gln Leu Thr Gly Glu Glu Thr Arg
1 5

<210> SEQ ID NO 296
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 296

Gln Asn Pro Ala Ala Glu Ala Gln Glu Leu Ala Val Ile Pro Pro Ala
1 5 10 15

Pro Thr Val Leu Arg
20

<210> SEQ ID NO 297
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 297

His Asp Ala Ser Glu Asn Ala Val Arg
1 5

<210> SEQ ID NO 298
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 298

Asp Trp Asp Glu Glu Glu Glu Ala Ser Ala Ala Arg
1 5 10

<210> SEQ ID NO 299
<211> LENGTH: 15

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<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 299

Asp Gly Asn Leu Asp Thr Ser Phe Val Asn Pro Asn Tyr Gly Arg
1 5 10 15

<210> SEQ ID NO 300
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 300

Gly Ser Pro Leu Thr Ile Glu Ser His Leu Ser Asp Asn Glu Glu Asp
1 5 10 15

Pro Ile Arg

<210> SEQ ID NO 301
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 301

Ser Val Thr Val Glu Gln Pro Ser Thr Ser Ala Asp Gly Ser Asn Thr
1 5 10 15

Thr Pro Ser Lys
20

<210> SEQ ID NO 302
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 302

Ala Trp Ser Leu Gly Leu Asp Thr Met Ala Arg
1 5 10

<210> SEQ ID NO 303
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 303

Phe Ser Gly His Asn Gly Ile Tyr Asp Arg
1 5 10

<210> SEQ ID NO 304
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 304

Asp Tyr Asn Val Leu Phe Tyr Thr Ala His Tyr Thr Ser Arg
1 5 10

<210> SEQ ID NO 305
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 305

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Ser Ala Thr Glu Asp Leu Asp Arg
1 5

<210> SEQ ID NO 306
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 306

Phe Val Leu Gln Asp Phe Asp Val Gln His Leu Arg
1 5 10

<210> SEQ ID NO 307
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 307

Leu Leu Val Val Thr Gln Gly Gln Leu Arg
1 5 10

<210> SEQ ID NO 308
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 308

Gly Leu Leu His Ser Tyr Phe Glu Asp Val Glu Arg
1 5 10

<210> SEQ ID NO 309
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 309

Ala Pro Asp Gly Gly Leu Asn Leu Asp Asp Phe Met Arg
1 5 10

<210> SEQ ID NO 310
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 310

Asp Leu Gly Leu Ser Ala Ser Met Leu Arg
1 5 10

<210> SEQ ID NO 311
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 311

Val Gly Leu Ala Leu Leu Ile Asp Asp Phe Arg
1 5 10

<210> SEQ ID NO 312
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 312

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Ser Ser Leu Tyr Glu Ala Asn Pro Glu Leu Arg
1 5 10

<210> SEQ ID NO 313
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 313

Thr Ala Glu Gln Glu Val Ala Ala Ala Asp Pro Glu Thr Gly Asn Glu
1 5 10 15

Arg

<210> SEQ ID NO 314
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 314

His Met Asp Pro Glu Gln Asp Tyr Arg
1 5

<210> SEQ ID NO 315
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 315

Asp Ala Ala Asp Glu Val Trp Ala Leu Arg
1 5 10

<210> SEQ ID NO 316
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 316

Asp Val Val Ala Leu Val Asn Phe Leu Arg
1 5 10

<210> SEQ ID NO 317
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 317

Ser Gly Thr Gly Pro Gln Pro Gly Ser Ala Gly Met Gly Gly Ala Lys
1 5 10 15

<210> SEQ ID NO 318
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 318

Ala Glu Pro Ser Val Ser Asn Asp Asp Gly Asn Gly Gly Glu Arg
1 5 10 15

<210> SEQ ID NO 319
<211> LENGTH: 9
<212> TYPE: PRT

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<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 319

Asp Asn Val Ala Gly Ser Ile Ser Lys
1 5

<210> SEQ ID NO 320
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 320

Glu Pro Pro Thr Pro Ala Asp Glu Leu Gln Thr Ala Val Ser Arg
1 5 10 15

<210> SEQ ID NO 321
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 321

Glu Gly Glu Leu Phe Phe Phe Ser Lys
1 5

<210> SEQ ID NO 322
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 322

Thr Gln Leu Asp Val Leu Tyr Ser Asp Pro Leu Lys
1 5 10

<210> SEQ ID NO 323
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 323

Ile Thr Thr Glu Thr Tyr His Leu Gln Arg
1 5 10

<210> SEQ ID NO 324
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 324

Gly Asp Val Glu Ser Leu Ser Ala Glu Val Thr Lys
1 5 10

<210> SEQ ID NO 325
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 325

Ser Ala Leu Gly Pro Phe Val Gly Lys
1 5

<210> SEQ ID NO 326
<211> LENGTH: 11

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<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 326

Asn Val Met Thr His Glu Glu Ala Glu Ser Arg
1 5 10

<210> SEQ ID NO 327
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 327

Leu Glu Asp Pro Leu Pro Pro Trp Leu Arg
1 5 10

<210> SEQ ID NO 328
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 328

Gln His Gly Val Ile Asp Gly Glu Asn Ser Glu Thr Glu Arg
1 5 10

<210> SEQ ID NO 329
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 329

Thr Pro Glu Val Asn Pro Ile Asp Ala Glu Gly Leu Ser Gly Leu Ala
1 5 10 15

Arg

<210> SEQ ID NO 330
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 330

Ile Pro Met Thr Phe Val Asp Arg
1 5

<210> SEQ ID NO 331
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 331

Gln Leu Val Leu Phe Met Thr Pro Lys
1 5

<210> SEQ ID NO 332
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 332

Ile Ser Trp Leu Glu Arg
1 5

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<210> SEQ ID NO 333
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 333

Val Tyr Val Tyr Ser Pro Val Val Glu Ser Leu Tyr Leu Val Ser Arg
1 5 10 15

<210> SEQ ID NO 334
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 334

Ser Ala Ser Leu Ser Phe Leu Asp Trp Pro Asp Gly Ser Val Thr Glu
1 5 10 15

Gly Val Arg

<210> SEQ ID NO 335
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 335

Phe Leu Leu Pro Val Gly Thr Val Ser Arg
1 5 10

<210> SEQ ID NO 336
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 336

Leu Ser Glu Pro Pro Thr Leu Ala Leu Arg
1 5 10

<210> SEQ ID NO 337
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 337

Ile Val Thr Glu His Asp Thr Leu Leu Tyr Val Ala Ser Arg
1 5 10

<210> SEQ ID NO 338
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 338

Asn Gly Leu Phe Ala Val Glu Asn Phe Leu Thr Glu Glu Pro Phe Gln
1 5 10 15

Arg

<210> SEQ ID NO 339
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 339

Val Thr Leu Ala Leu Glu Gln Ala Gln Arg
1 5 10

<210> SEQ ID NO 340
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 340

Glu Phe Leu Glu Ala Pro Trp Glu Ser Ala Pro Gln Pro Pro Arg
1 5 10 15

<210> SEQ ID NO 341
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 341

Asp Ala Ser Gly Leu Met Phe Pro Ile Ile Ser Thr Arg
1 5 10

<210> SEQ ID NO 342
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 342

Tyr Gln Gln Leu Val Asp Glu Val Glu Gln Glu Leu Lys
1 5 10

<210> SEQ ID NO 343
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 343

Phe Asn Gln Asp Leu Leu Ser Ala Leu Gln Gln Leu Ser Lys
1 5 10

<210> SEQ ID NO 344
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 344

Ile Asp Thr Gln Gln Glu Leu Thr Ala Ala Asp Arg
1 5 10

<210> SEQ ID NO 345
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 345

Leu Asp Ala Leu Ser Thr Ala Ser Glu Arg
1 5 10

<210> SEQ ID NO 346
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 346

Leu Val Asp Pro Thr Tyr Val Ile Asp Lys
1 5 10

<210> SEQ ID NO 347
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 347

Val Thr Asn Glu Ala Val Leu Phe Gly Arg
1 5 10

<210> SEQ ID NO 348
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 348

Gly Leu Thr Pro Gln Ala Leu Val Ala Arg
1 5 10

<210> SEQ ID NO 349
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 349

Glu Val Ile Ala Ser Val Gly Glu Leu Val Pro Glu Pro Arg
1 5 10

<210> SEQ ID NO 350
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 350

Ile Gly Glu Tyr Leu Leu Glu Gln Gly Phe Pro Val Tyr Glu Val Arg
1 5 10 15

<210> SEQ ID NO 351
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 351

Val Ala Ala Ser Ala Ser Val Pro Leu Asn Pro His Tyr Gly Lys
1 5 10 15

<210> SEQ ID NO 352
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 352

Ala Leu Gln Val Thr Gly Thr Pro Gln Phe Phe Asp Gln Phe Asp Thr
1 5 10 15

Asn Asn Ala Met Gly Thr Tyr Arg
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<210> SEQ ID NO 353
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 353

Thr Asp Pro Ala Thr Leu Thr Ala Tyr Asp Lys
1 5 10

<210> SEQ ID NO 354
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 354

Glu Leu Gln Ala Phe Leu Asp Glu Asn Phe Lys
1 5 10

<210> SEQ ID NO 355
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 355

Ile Leu Glu Ala Leu Asp Ile Leu Ile Leu Lys
1 5 10

<210> SEQ ID NO 356
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 356

Glu Ser Ala Pro Gln Glu Thr Leu Pro Thr Asn His Glu Arg
1 5 10

<210> SEQ ID NO 357
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 357

Asp Ser Pro Gly Gly Met Asp Glu Pro Pro Ser Gly Trp Glu Arg
1 5 10 15

<210> SEQ ID NO 358
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 358

Ser Asp Ser Tyr Gly Leu Leu Gly Asn Ser Val Asp Ala Leu Tyr Ile
1 5 10 15

Arg

<210> SEQ ID NO 359
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 359

His Phe Ala Asp Tyr Val Asp Pro His Tyr Pro Gly Trp Gly Arg

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1 5 10 15

<210> SEQ ID NO 360
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 360

Leu Ile Thr Asn Val Glu Gly Gly Ser Leu Glu Ala Gly Arg
1 5 10

<210> SEQ ID NO 361
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 361

Leu Leu Val Asp Leu Asn Asn Phe Gly Pro Arg
1 5 10

<210> SEQ ID NO 362
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 362

Thr Ala Ala Asp Ile Ser Ser Thr Leu Arg
1 5 10

<210> SEQ ID NO 363
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 363

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg
1 5 10

<210> SEQ ID NO 364
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 364

Gly Pro Gln Tyr Ser Glu His Pro Thr Phe Thr Ser Gln Tyr Arg
1 5 10 15

<210> SEQ ID NO 365
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 365

Ile Phe Ala Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys
1 5 10 15

<210> SEQ ID NO 366
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 366

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Tyr Ser Gly Ser Pro Gln Thr Ile Leu Thr Leu Thr Asp Lys
1 5 10

<210> SEQ ID NO 367
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 367

Ser Gly Ala Ala Asp Glu Gly Leu Glu Val Arg
1 5 10

<210> SEQ ID NO 368
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 368

Ser Val Ile Asp Gln Gln Leu Thr Arg
1 5

<210> SEQ ID NO 369
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 369

Ala Leu Leu Ala Asp Tyr Ala Glu Thr Phe Ser Pro Leu Gly Ser Phe
1 5 10 15

Thr Arg

<210> SEQ ID NO 370
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 370

Val Glu Glu Asn Asp Leu Val Asn Val Val Leu Arg
1 5 10

<210> SEQ ID NO 371
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 371

His Val Ile Trp Pro Gly Thr Ser Val Leu Trp Ala Pro Asp Val Val
1 5 10 15

Ile Thr Thr Val Gln Arg
20

<210> SEQ ID NO 372
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 372

Thr Asp Val Trp Asp Leu Val Lys
1 5

<210> SEQ ID NO 373

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<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 373

Val Glu Glu Pro Val Ser Arg
1 5

<210> SEQ ID NO 374
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 374

Thr Ala Ala Gln Val Thr Leu Gly Asp Gly Leu Asp Tyr His Ile Gly
1 5 10 15

Val Lys

<210> SEQ ID NO 375
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 375

Ala Ala Gly Glu Gln Gln Gln Pro Pro Ser Leu Val Gly Thr Gly Val
1 5 10 15

His Arg

<210> SEQ ID NO 376
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 376

Val Gly Gly Val Asp Ala Val Leu Glu Glu Asn Asp Val Glu Leu Arg
1 5 10 15

<210> SEQ ID NO 377
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 377

Leu Gly Gln Gly Ser Phe Gly Glu Val Trp Pro Leu Asp Arg
1 5 10

<210> SEQ ID NO 378
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 378

His Ala Val Ser Thr Val Leu Asp Arg
1 5

<210> SEQ ID NO 379
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 379

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Glu Tyr Leu Ala Asp Leu Leu Tyr Leu Asn Lys
1 5 10

<210> SEQ ID NO 380
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 380

His Gly Gly Ser Asp Asp Tyr Val Trp Leu Ser Arg
1 5 10

<210> SEQ ID NO 381
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 381

Val Thr Ala Pro Tyr Leu Arg
1 5

<210> SEQ ID NO 382
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 382

Thr Ala His Trp Leu Phe His Lys
1 5

<210> SEQ ID NO 383
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 383

Ser Val Gln His Phe Leu Trp Met Val Arg
1 5 10

<210> SEQ ID NO 384
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 384

Thr Leu Ser Met Leu Gln Gly Leu Tyr Leu Arg
1 5 10

<210> SEQ ID NO 385
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 385

Thr Glu Val Glu Pro Leu Leu Met Leu Gly Ser Ile Glu Gly Leu Arg
1 5 10 15

<210> SEQ ID NO 386
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 386

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Trp His Gly Ala Leu Gly Thr Ile Thr Arg
1 5 10

<210> SEQ ID NO 387
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 387

Trp Glu Asp Gly Ala Pro Thr Phe Thr Arg
1 5 10

<210> SEQ ID NO 388
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 388

Thr Glu Ala Glu Val Ser Glu Ala Glu Val Glu Ala Arg
1 5 10

<210> SEQ ID NO 389
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 389

Ile Asn Leu Asn Thr Asp Leu Ser Pro Glu Trp Val Lys
1 5 10

<210> SEQ ID NO 390
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 390

Ile Leu Pro Val Gly Ser Met Tyr Arg
1 5

<210> SEQ ID NO 391
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 391

Tyr Glu Thr Glu Leu Pro Gln Val Asp Ala Arg
1 5 10

<210> SEQ ID NO 392
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 392

Val Thr Pro Ser Asp Leu Glu Arg
1 5

<210> SEQ ID NO 393
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 393

Leu Ser Trp Ser Ser Asp Glu Ser Ser Ala Ser Ser Ser Ser Arg
1 5 10 15

<210> SEQ ID NO 394
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 394

Asn Asn Thr Gly Thr Glu Val Asp Gln Cys Leu Ala Tyr Arg
1 5 10

<210> SEQ ID NO 395
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 395

Val Ala Thr Asn Cys Leu Val Lys
1 5

<210> SEQ ID NO 396
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 396

Val Ala Thr Asn Cys Leu Val Lys
1 5

<210> SEQ ID NO 397
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 397

Asn Asn Thr Gly Thr Glu Val Asp Gln Cys Leu Ala Tyr Arg
1 5 10

<210> SEQ ID NO 398
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 398

Gln Pro Val Val Thr Leu Leu Leu Ala Arg
1 5 10

<210> SEQ ID NO 399
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 399

Gln Pro Val Val Thr Leu Leu Leu Ala Arg
1 5 10

<210> SEQ ID NO 400
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 400

Asp Gly Leu Ala Asp Trp Asn Val Val Arg
1 5 10

<210> SEQ ID NO 401
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 401

Val Thr Leu His Gly Leu Ala Gln Arg
1 5

<210> SEQ ID NO 402
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 402

Ser Ala Pro Lys Pro Gln Glu Leu Leu Phe Gly Pro Arg
1 5 10

<210> SEQ ID NO 403
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 403

Phe Thr Leu Ala Asp Leu Leu Gly Ser Asp Ala Val Ala Gly Gly Gly
1 5 10 15

Leu Pro Gly Gly Arg
20

<210> SEQ ID NO 404
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 404

Leu Leu Glu Asp Ala Ala Val Thr Met Arg
1 5 10

<210> SEQ ID NO 405
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 405

Gly Val Ile Gln His Leu Pro Gly Tyr Gly Thr Ile Thr Glu Glu Leu
1 5 10 15

Val Gln Glu Arg
20

<210> SEQ ID NO 406
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 406

Phe Trp Glu Thr Pro Thr Leu Ile Met Lys

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1 5 10

<210> SEQ ID NO 407
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 407

Ala Leu Leu Thr Leu Leu Ser Ser Asp Thr Ala Pro Arg
1 5 10

<210> SEQ ID NO 408
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 408

Val Asn Leu Pro Ala His Ser Arg
1 5

<210> SEQ ID NO 409
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 409

His Gln Leu Asp Pro Pro Leu Leu Arg
1 5

<210> SEQ ID NO 410
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 410

Ser Ile Met Ala Thr Gln Leu Arg
1 5

<210> SEQ ID NO 411
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 411

Thr Thr Pro Thr Ser Pro Ser Met Gly Phe Gln Arg
1 5 10

<210> SEQ ID NO 412
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 412

Gln Leu Glu Thr Thr Ile Ser Thr Lys
1 5

<210> SEQ ID NO 413
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 413

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His Val Pro Leu Ala Asp Ser Ala Val Ser His Glu Thr Leu Glu Arg
1 5 10 15

<210> SEQ ID NO 414
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 414

Ile Ile Asn Tyr Ser Gln Phe Val Asp His Asn Leu Ser Ser Glu Ile
1 5 10 15

Thr Lys

<210> SEQ ID NO 415
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 415

Met Ser Ser Leu Phe Asn Asp Lys
1 5

<210> SEQ ID NO 416
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 416

Thr Leu Phe Asp Thr Ile Thr Val Arg
1 5

<210> SEQ ID NO 417
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 417

Val Ala Asn Ala Pro Glu Val Arg
1 5

<210> SEQ ID NO 418
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 418

Leu Val Thr His Gln Gly Ala Glu Glu Ala Ile Val Tyr Ser Asn Tyr
1 5 10 15

Thr Val Glu Arg
20

<210> SEQ ID NO 419
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 419

Gly Ser Leu Leu Thr Pro Asp Glu Gln Ala Arg
1 5 10

<210> SEQ ID NO 420

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 420

Phe Leu Ser Leu Pro Asp His Asp Thr Val Leu Leu Arg
1 5 10

<210> SEQ ID NO 421
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 421

Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser Val Pro Tyr Arg
1 5 10

<210> SEQ ID NO 422
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 422

Leu Thr Ser Cys Asn Tyr Asn Pro Leu Tyr Leu Glu Ala Asp Gly Arg
1 5 10 15

<210> SEQ ID NO 423
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 423

Gly Ile Val Thr Thr Met Thr His Ser Leu Thr Arg
1 5 10

<210> SEQ ID NO 424
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 424

Val Leu Thr Asp Pro Glu Pro Ile Gln Ser Glu Ala Glu Gly Glu Asn
1 5 10 15

Lys

<210> SEQ ID NO 425
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 425

Thr Glu Asp Phe Leu His Trp Leu Leu Gly Trp Gly His Lys
1 5 10

<210> SEQ ID NO 426
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 426

Ser Ile Cys Ser Phe Phe Pro Lys
1 5

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<210> SEQ ID NO 427
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 427

Leu Gln Gly Asn Tyr Asn Glu Gln His Tyr Arg
1 5 10

<210> SEQ ID NO 428
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 428

Ser Leu Gly Val Leu Pro Asn Asp His His Tyr Ala Leu Lys
1 5 10

<210> SEQ ID NO 429
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 429

Gly Gly Gly Ser Thr Ala Ala Ala Ala Ala Val Gly His Ala Gly Ala
1 5 10 15

Gly Gln Gln Ala Arg
20

<210> SEQ ID NO 430
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 430

Thr Ala Gln Thr Tyr Thr Thr Gly Thr Leu Thr Arg
1 5 10

<210> SEQ ID NO 431
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 431

Leu Leu Pro Leu Phe Ile Val Pro Asp Ala Tyr Arg
1 5 10

<210> SEQ ID NO 432
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 432

Thr Pro Val Leu Ser Pro Glu His Gly Gly Glu Val Arg
1 5 10

<210> SEQ ID NO 433
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

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<400> SEQUENCE: 433

Thr Thr Tyr Ser Asp Ala Asp Asp Gln Ser Val Arg
1 5 10

<210> SEQ ID NO 434
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 434

Gly Gly Gly Gln Val Trp Ser Val Val Pro Ser Leu Val Phe Phe Gln
1 5 10 15

Gln Lys

<210> SEQ ID NO 435
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 435

Gly Gly Gly Ala Val Glu Pro Ala Val Arg
1 5 10

<210> SEQ ID NO 436
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 436

Asp Leu Asp Asp Ser Phe Asp Tyr Leu Val Glu Arg
1 5 10

<210> SEQ ID NO 437
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 437

Glu Thr Met Asn Asn Leu Gly Val Ser Asp His Ala Val Leu Ser Arg
1 5 10 15

<210> SEQ ID NO 438
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 438

Gly Leu Glu Thr Leu Leu Leu Arg
1 5

<210> SEQ ID NO 439
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 439

Asp Phe Phe Leu Leu Glu Leu Gln Lys
1 5

<210> SEQ ID NO 440
<211> LENGTH: 16

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<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 440

Thr Thr Glu Asp Pro Pro Glu Asn His Val Val Ala Asp Val Ala Arg
1 5 10 15

<210> SEQ ID NO 441
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 441

Leu Ile Glu Thr Pro Asp Glu Asn Phe Leu Leu Val Thr Asn Val Ile
1 5 10 15

Pro Arg

<210> SEQ ID NO 442
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 442

Ala Ala Val Gln Gln Glu Leu Gln Arg
1 5

<210> SEQ ID NO 443
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 443

Gln Leu Gln Ser Gly Asn Val Asp Asp Ala Leu Asp Ser Leu Thr Glu
1 5 10 15

Leu Lys

<210> SEQ ID NO 444
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 444

Leu Cys Gly Ser Gly Cys Gly Gly Asn Asp Ser Ser Ser Gly Ser His
1 5 10 15

Arg

<210> SEQ ID NO 445
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 445

Ile Ser Gln Arg Pro Pro Thr Pro Gly Thr Lys
1 5 10

<210> SEQ ID NO 446
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 446

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Leu Pro Trp Thr Thr Val Phe Ala Ala Phe Arg
1 5 10

<210> SEQ ID NO 447
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 447

Ser Leu Glu Glu Gly Ser Thr Ile Ser Ser Arg
1 5 10

<210> SEQ ID NO 448
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 448

Gly Phe Gln Val Pro Thr Asp Gly Thr Val Ile Tyr Val Pro Pro Gly
1 5 10 15

Ile Gln Glu Thr Arg
20

<210> SEQ ID NO 449
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 449

Ser His Ala Leu Val Ala Glu Gln Gln Leu Phe Gln Trp Leu Lys
1 5 10 15

<210> SEQ ID NO 450
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 450

Val Ala Asn Thr Ile Thr Glu Phe Phe Arg
1 5 10

<210> SEQ ID NO 451
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 451

Phe Asp Pro His Glu Gly Ala Trp Glu Arg
1 5 10

<210> SEQ ID NO 452
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 452

Glu Pro Leu Thr Pro Leu Gly Tyr Ala Val Ile Leu Leu Pro Glu Pro
1 5 10 15

Arg

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<210> SEQ ID NO 453
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Human cytomegalovirus

<400> SEQUENCE: 453

Asp Gly Val Leu Asp Ala Val Trp Arg
1 5

<210> SEQ ID NO 454
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 454

Asp His Phe Pro Leu Leu Thr Thr Lys
1 5

<210> SEQ ID NO 455
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 455

Glu Gly Asp Leu Gly Pro Val Tyr Gly Phe Gln Trp Arg
1 5 10

<210> SEQ ID NO 456
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 456

Ser Val Ser Ser Met Glu Glu Phe Thr Pro Asp Asp Phe Arg
1 5 10

<210> SEQ ID NO 457
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 457

Glu Ala Ile Val Phe His Asn Thr His Leu Phe Gln Pro Ile Phe Gln
1 5 10 15

Gly Lys

<210> SEQ ID NO 458
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 458

Leu Ala Ser Met Gly Ile Ser Glu Gly Gly Asp Ala Leu Arg
1 5 10

<210> SEQ ID NO 459
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 459

His Val Ile Met Thr Pro Leu Val Asp Arg

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1 5 10

<210> SEQ ID NO 460
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 460

Gly Ile Val Ile Asp Val Ser Glu Trp Gly Pro Arg
1 5 10

<210> SEQ ID NO 461
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 461

Ile Cys Gln Ile Val Phe Val Glu Arg
1 5

<210> SEQ ID NO 462
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 462

Gly Glu Ile Gln Val Ile Leu Leu Asn Lys
1 5 10

<210> SEQ ID NO 463
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 463

Leu Ala Ser Ser Val Phe Asp Leu Glu Thr Met Phe Arg
1 5 10

<210> SEQ ID NO 464
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 464

Asn Ile Leu Leu Gly Met His Gln Leu Gln Gln Glu Glu Arg
1 5 10

<210> SEQ ID NO 465
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 465

Leu Pro Asp Ala Pro Glu Phe Glu Lys
1 5

<210> SEQ ID NO 466
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 466

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Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys
1 5 10

<210> SEQ ID NO 467
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 467

His Phe Ala Ser Phe Tyr Val Leu Ser Ala Met Glu Lys
1 5 10

<210> SEQ ID NO 468
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 468

Ala Gly Pro Ser Ser Leu Val Asp Ile Leu Pro Gln Gly Leu Pro Gly
1 5 10 15

Gly Gly Tyr Gly Ser Met Gly Val Ile Arg
20 25

<210> SEQ ID NO 469
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 469

Ala Tyr Ala Ala Val Asn Thr Arg
1 5

<210> SEQ ID NO 470
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 470

Asp Ser Glu Glu Ser Val Asp Glu Ala Ala Gly Tyr Lys
1 5 10

<210> SEQ ID NO 471
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 471

Val Thr Val Leu Pro Tyr Arg
1 5

<210> SEQ ID NO 472
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 472

Asp Gly Ser Ser Gly Asp Glu Pro Asp Gly Gly Pro Asn Asp Arg
1 5 10 15

<210> SEQ ID NO 473
<211> LENGTH: 9
<212> TYPE: PRT

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<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 473

Ala Leu Tyr Ala Ala Asn Asn Thr Arg
1 5

<210> SEQ ID NO 474
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 474

Gly Pro His Ile Ser Gln Gln Leu Pro Thr Arg
1 5 10

<210> SEQ ID NO 475
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 475

Gln Leu Gln Gln Ala Leu Glu Glu Lys
1 5

<210> SEQ ID NO 476
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 476

Glu Gln Ile Ile Phe Leu Arg
1 5

<210> SEQ ID NO 477
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 477

Val Ser Pro Val Ala Glu Asn Gly Arg
1 5

<210> SEQ ID NO 478
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 478

Val Pro Phe Ser Ala Thr Thr Thr Thr Thr Arg
1 5 10

<210> SEQ ID NO 479
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 479

Asp Ala His Tyr Asn Ala Glu Ile Arg
1 5

<210> SEQ ID NO 480
<211> LENGTH: 17

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<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 480

Gly Val Glu Ser Pro Ala Ile Gln Ser Thr Glu Thr Trp Val Val Asn
1 5 10 15

Lys

<210> SEQ ID NO 481
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 481

His Ala Pro Pro Val Phe Ile Leu Lys
1 5

<210> SEQ ID NO 482
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 482

Gly Leu Val Asp Thr Val Leu Ala Val Lys
1 5 10

<210> SEQ ID NO 483
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 483

Thr Val Met Leu Pro Leu Asp Leu Ser Thr Val Ala Pro Gly Arg
1 5 10 15

<210> SEQ ID NO 484
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 484

Gln Ser Phe Leu Gln Pro Gly Leu Leu Tyr Ala Asn Leu Val Leu Lys
1 5 10 15

<210> SEQ ID NO 485
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 485

Ala Leu His Leu Gly Glu Thr Ala Leu Arg
1 5 10

<210> SEQ ID NO 486
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 486

Val Val Ser Ser Tyr Leu Gly Gln Ser Gly Gln Ser Leu Asp Leu Glu
1 5 10 15

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Arg

<210> SEQ ID NO 487
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 487

Gln Val Leu Gln Phe Leu Val Val Thr Pro Lys
1 5 10

<210> SEQ ID NO 488
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 488

Ala Cys Thr Ser Asp Val Thr Ala Val Tyr Trp Ala Gly Gln Gly Gly
1 5 10 15

Arg

<210> SEQ ID NO 489
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 489

Tyr Leu Thr Phe Thr Gln Thr Gly Glu Arg
1 5 10

<210> SEQ ID NO 490
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 490

Phe Val Ser Phe Pro Ala Val Leu Leu Pro Gly Lys
1 5 10

<210> SEQ ID NO 491
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 491

Ile Val Ala Pro Gly Val Ile Asn Asn Phe Ser Glu Pro Ile Gly Ile
1 5 10 15

Trp Val Arg

<210> SEQ ID NO 492
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 492

Ile Leu Pro Thr Val Val Glu Ser Ser Ser Ser Val Leu Ile Phe Arg
1 5 10 15

<210> SEQ ID NO 493
<211> LENGTH: 19
<212> TYPE: PRT

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<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 493

Gly Glu Pro Val Trp Asp Ser Val Ile His Pro Ser His Ile Val Ile
1 5 10 15

Ser Asn Arg

<210> SEQ ID NO 494
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 494

Ala Tyr Pro Asn Phe Thr Phe Asp Asn Thr His Arg
1 5 10

<210> SEQ ID NO 495
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 495

Ala Ile Asp Ala Ser Phe Ile Arg
1 5

<210> SEQ ID NO 496
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 496

Asn Pro Tyr Asp Pro Trp Tyr Tyr Ser Pro Gln Leu Pro Gly Tyr Arg
1 5 10 15

<210> SEQ ID NO 497
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 497

Gly Ala Glu Asp Asp Glu Gly His Leu Phe Pro Gly Glu Glu Pro Ala
1 5 10 15

Tyr His Lys

<210> SEQ ID NO 498
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 498

Gly Met Leu Leu Glu Gln Ser Gln Ser Pro Tyr Pro Ala Leu Lys
1 5 10 15

<210> SEQ ID NO 499
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 499

Val Ile Phe His Gly Gly Gln Asp Ala Leu Lys
1 5 10

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<210> SEQ ID NO 500
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 500

Phe Pro Ser Val Thr His Gly Tyr Pro Ile Gln Gly Phe Ser Leu Thr
1 5 10 15

Tyr Lys

<210> SEQ ID NO 501
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 501

Cys Val Leu Glu Asp Ile Asp Asp Pro Asn Asn Ser Asn Pro Gly Arg
1 5 10 15

<210> SEQ ID NO 502
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 502

Gln Ser Thr Ala Ser Ser Gly Ser Glu Asp Val Val Arg
1 5 10

<210> SEQ ID NO 503
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 503

Ala His Thr Pro Lys Pro Val Ala Val Val Ala Gly Arg
1 5 10

<210> SEQ ID NO 504
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 504

Met Leu Pro Ile Glu Gly Ala Pro Arg
1 5

<210> SEQ ID NO 505
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 505

Ile Met Ala Pro Leu Glu Ile Met Thr Lys
1 5 10

<210> SEQ ID NO 506
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 506

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Gly Gln Leu Ala Pro Glu Asn Phe Tyr Ser Ile Thr Gly Ser Ala Glu
1 5 10 15

Lys

<210> SEQ ID NO 507
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 507

Asp Ser Thr Ala Ala Ala Thr Ala Ala Glu Ala Thr Thr Pro Lys
1 5 10 15

<210> SEQ ID NO 508
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 508

Ile Ser Gln Leu Thr Val Glu Asn Arg
1 5

<210> SEQ ID NO 509
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 509

Glu Ala Gln Leu Thr Ala Thr Val Gly Ala Leu Ser Ala Ala Ala Ala
1 5 10 15

Lys

<210> SEQ ID NO 510
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 510

Gln Val Asp Asp Ala Leu Lys
1 5

<210> SEQ ID NO 511
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 511

Phe Asp Asp Ser Ile Ile Pro Arg
1 5

<210> SEQ ID NO 512
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 512

Leu Pro Ala Ser Met Ile Ile Asp Gly Glu Ser Pro Arg
1 5 10

<210> SEQ ID NO 513

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<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 513

Gly Thr Gln Ser Ala Gln Gly Ile Pro Pro Pro Leu Gly Arg
1 5 10

<210> SEQ ID NO 514
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 514

Thr Thr Ile Ser Tyr Gly Asp Asn Leu Thr Ser Thr Val His Lys
1 5 10 15

<210> SEQ ID NO 515
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 515

Ser Val Asp Val Gly Val Val His Thr Asp Ala Leu Ser Arg
1 5 10

<210> SEQ ID NO 516
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 516

Val Pro Asp Ser Ile Pro Asp Ser Arg
1 5

<210> SEQ ID NO 517
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 517

Glu Leu Gly Leu Gln Glu Trp Ala Arg
1 5

<210> SEQ ID NO 518
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 518

Ala Leu Pro Gln Glu Leu Leu Pro Val Pro Ala Trp Arg
1 5 10

<210> SEQ ID NO 519
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 519

Trp Ala Val Asn Leu Glu Thr Asn Val Ser Lys
1 5 10

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<210> SEQ ID NO 520
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 520

Ala Tyr Asp Thr Gln Gln Tyr Ala Val Gln Lys
1 5 10

<210> SEQ ID NO 521
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 521

Leu Leu Thr Val Trp Leu Ala Lys
1 5

<210> SEQ ID NO 522
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 522

Ser Ser Gln Val Leu Asp Leu Ile Leu Arg
1 5 10

<210> SEQ ID NO 523
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 523

Thr Met Gly Thr Glu Pro Val Tyr Glu Ser Val Ala Gln Met Phe Met
1 5 10 15

Arg

<210> SEQ ID NO 524
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 524

Leu Trp Tyr Leu Phe Asp Pro Ala Thr Ala Pro Asn Leu Ile Lys
1 5 10 15

<210> SEQ ID NO 525
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 525

Ala Pro Phe Val Asp Gln Ser Gln Ser Met Ser Phe Phe Leu Lys
1 5 10 15

<210> SEQ ID NO 526
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 526

Leu Asp His Asp Tyr Ala His His Pro Leu Val Ala Arg

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1 5 10

<210> SEQ ID NO 527
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 527

Met Asn Thr Leu Asp Gln Gly Asn Met Ser Gln Ala Glu Tyr Leu Val
1 5 10 15

Gln Lys

<210> SEQ ID NO 528
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 528

Thr Pro Val Thr Val Asp Tyr Arg
1 5

<210> SEQ ID NO 529
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 529

Leu Gln Phe Ile Val Ala Asp Ala Asp Lys
1 5 10

<210> SEQ ID NO 530
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 530

Leu Ser Ala Thr Asp Asp Asp Ser Gly Asp Tyr Ala Pro Met Asp Arg
1 5 10 15

<210> SEQ ID NO 531
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 531

Gly Leu Ala Ser Glu Ala Ser Ala Trp Ile Arg
1 5 10

<210> SEQ ID NO 532
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 532

Gly Pro Leu Gln Val Leu Thr Gly Leu Leu Arg
1 5 10

<210> SEQ ID NO 533
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

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<400> SEQUENCE: 533

Leu Ser Phe Asn Pro Val Asn Ala Asp Val Pro Ala Thr Trp Arg
1 5 10 15

<210> SEQ ID NO 534
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 534

Leu Asp Leu Leu Ile Thr Gln Leu Lys
1 5

<210> SEQ ID NO 535
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 535

Leu Asn Leu Val Ser Leu Leu Gly Pro Lys
1 5 10

<210> SEQ ID NO 536
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 536

Phe Gln Pro Gly Ala Leu Pro Asp Pro Asn Ala Pro Met Leu Lys
1 5 10 15

<210> SEQ ID NO 537
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 537

Ser Ala Thr Gln Leu Ile Asn Gly Arg
1 5

<210> SEQ ID NO 538
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 538

Leu Val Leu Gly Asp Ile Phe Ala Ser Lys
1 5 10

<210> SEQ ID NO 539
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 539

Ser Ser Gln Glu Thr Val Leu Ala Met Val Gln Leu Gly Ala Arg
1 5 10 15

<210> SEQ ID NO 540
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

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<400> SEQUENCE: 540

Leu Gly Ser Trp Ala Ser Gln Glu Asn Leu Arg
1 5 10

<210> SEQ ID NO 541
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 541

Leu Leu Trp Tyr Leu Gln Arg
1 5

<210> SEQ ID NO 542
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 542

Thr Gly Asp Ile Thr Val Glu Thr Cys Val Asn Gly Phe Asn Leu Arg
1 5 10 15

<210> SEQ ID NO 543
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 543

Phe Leu Met Ser Ser Trp Val Lys
1 5

<210> SEQ ID NO 544
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 544

Thr Pro Thr Val His Gln Lys Pro Pro Pro Leu Pro Ala Lys
1 5 10

<210> SEQ ID NO 545
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 545

Asp Ile Ser Thr Pro Ala Pro Arg
1 5

<210> SEQ ID NO 546
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 546

Val Thr Gln Ser Ser Ile Glu Gln Leu Gln Arg
1 5 10

<210> SEQ ID NO 547
<211> LENGTH: 12
<212> TYPE: PRT

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<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 547

Gly Gln Tyr Ser Ser Leu Ser Gln Ser Ala Phe Arg
1 5 10

<210> SEQ ID NO 548
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 548

Thr Leu Glu Tyr Asn Leu Asp Ile Ser Pro Glu Leu Met Asp Tyr Ile
1 5 10 15

Asp Arg

<210> SEQ ID NO 549
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 549

Ala Asp Ile Val Ser Val Thr Trp Gln Lys
1 5 10

<210> SEQ ID NO 550
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 550

Gln Leu Pro Gly Pro Val Asn Val Ala Thr Tyr Ser His Ser Tyr Gly
1 5 10 15

Val Val Val Gln Thr Gln Tyr Arg
20

<210> SEQ ID NO 551
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 551

Leu Met Gln Gln Leu Pro Val Thr Ala Arg
1 5 10

<210> SEQ ID NO 552
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 552

Phe His Ser Thr Thr Gly Ile Asn Gln Leu Gly Leu Ser Met Leu Gln
1 5 10 15

Val Ser Gly Asp Gly Asn Met Asn Trp Gly Arg
20 25

<210> SEQ ID NO 553
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

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<400> SEQUENCE: 553

Leu Tyr Ile Thr Gly Leu Met Arg
1 5

<210> SEQ ID NO 554
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 554

Thr Leu Glu Thr Pro Pro Pro Gly Ala His Phe Leu Ala Ser Ser Leu
1 5 10 15

Asp Ala Ala Leu Gly Leu Ala Arg
20

<210> SEQ ID NO 555
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 555

Glu Ala Leu Thr Gly Pro Trp Pro Val Arg
1 5 10

<210> SEQ ID NO 556
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 556

Tyr Ser Thr Leu Pro Asp Leu Trp Arg
1 5

<210> SEQ ID NO 557
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 557

Phe Gly Thr Pro Asp Ser Ser Thr Leu Pro Leu Tyr Ala Ala Arg
1 5 10 15

<210> SEQ ID NO 558
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 558

Leu Ala Ile Thr Ser Asp Gln Ser Tyr Thr Asn Phe Lys
1 5 10

<210> SEQ ID NO 559
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 559

Asp Leu Val Gly Phe Gln Leu Ala Leu Asn Gln Leu Val Ser Arg
1 5 10 15

<210> SEQ ID NO 560

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<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 560

Thr Leu Gly Ser Ser Thr Val Ser Asp Met Leu Glu Pro Thr Lys
1 5 10 15

<210> SEQ ID NO 561
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 561

Asn Ala Asn Phe Ile Ser Phe Val Ala Thr Thr Gly His Arg
1 5 10

<210> SEQ ID NO 562
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 562

Asp Tyr Gly Leu Phe Ile Ser Gln Pro Arg
1 5 10

<210> SEQ ID NO 563
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 563

Asp Ala Phe Leu Ser Asp Gly Ile Val Asp Met Ala Arg
1 5 10

<210> SEQ ID NO 564
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 564

Leu Pro Tyr Thr Val Pro Ile Ile Asn Thr Thr Phe Gly Arg
1 5 10

<210> SEQ ID NO 565
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 565

Thr Leu Gly Pro Gln Ala Gly Ser His Ala Pro Pro Thr Val Gly Ile
1 5 10 15

Ala Thr Gln Glu Pro Tyr Arg
20

<210> SEQ ID NO 566
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 566

Phe Pro Tyr Ile Ala Pro Pro Pro Ser Arg

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1 5 10

<210> SEQ ID NO 567
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 567

Asn Phe Leu Gly Leu Leu Phe Asp Pro Ile Val Gln Ser Arg
1 5 10

<210> SEQ ID NO 568
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 568

Ala Pro Trp Val Leu Leu Arg
1 5

<210> SEQ ID NO 569
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 569

Gly Thr Gln Tyr Ile Thr Gly Asn Val Gln Thr Gln Arg
1 5 10

<210> SEQ ID NO 570
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 570

Asp Leu Leu Ser Phe Val Asn His Ala Leu Lys
1 5 10

<210> SEQ ID NO 571
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 571

Glu Ala Glu Leu Gly Thr Leu Val Arg
1 5

<210> SEQ ID NO 572
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 572

Phe Gly Gly Ser Ser Ala Val Phe Glu Lys
1 5 10

<210> SEQ ID NO 573
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 573

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Trp Thr Asn Leu Val Val Thr Ser Asn Leu Gly Phe Lys
1 5 10

<210> SEQ ID NO 574
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 574

Ala Thr Ser Ser Gln Ser Leu Asn Pro Val Trp Asp Ala Leu Arg
1 5 10 15

<210> SEQ ID NO 575
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 575

Ile Phe Ser Pro Trp Pro Ile Thr Asn Asn His Phe Val Ala Gly Pro
1 5 10 15

Leu Ala Phe Gly Leu Arg
20

<210> SEQ ID NO 576
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 576

Ala Asn Leu Phe Val Asn Val Arg
1 5

<210> SEQ ID NO 577
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 577

Asp Leu Ala Ile Trp Glu Leu Ala Leu Arg
1 5 10

<210> SEQ ID NO 578
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 578

Thr Ala Ser Leu Pro Val Val Leu Ile Met Thr Val Gly Arg
1 5 10

<210> SEQ ID NO 579
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 579

Asn Asn Ala Leu Val Gly Ser Asn Thr Pro Lys
1 5 10

<210> SEQ ID NO 580
<211> LENGTH: 8
<212> TYPE: PRT

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<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 580

Ala Thr Pro Leu Val Met Phe Lys
1 5

<210> SEQ ID NO 581
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 581

Asn Pro Gly Val Phe Phe Arg
1 5

<210> SEQ ID NO 582
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 582

Glu Leu Leu Asn Leu Leu Met Lys
1 5

<210> SEQ ID NO 583
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 583

Gly Pro Gly Ser Val Asn Leu Leu Thr Ala Asn Thr Phe Gln Ser Leu
1 5 10 15

Gly Arg

<210> SEQ ID NO 584
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 584

Thr Pro Leu Ile Asn Ala Gln Lys
1 5

<210> SEQ ID NO 585
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 585

His Leu Val Leu Thr Ala Gln His Pro Ser Pro Leu Ala Ser Leu Gly
1 5 10 15

Gly Arg

<210> SEQ ID NO 586
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 586

Ala Gln Ile Val Ala Phe Gly Thr Thr Ser Gly Phe Val Lys
1 5 10

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<210> SEQ ID NO 587
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 587

Ala Asn Leu Ala Tyr Ser Leu Gln Gln Leu Tyr Lys
1 5 10

<210> SEQ ID NO 588
<211> LENGTH: 36
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 588

Leu Ala Thr Ala Met Ala Ser Asp Asp Ser Val Ile Trp Ala Ser Glu
1 5 10 15

Ile Ser His Ser Leu Ser Glu Pro Thr Ser Val Leu Pro Leu Thr Pro
20 25 30

Ala Val Thr Arg
35

<210> SEQ ID NO 589
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 589

Ile Pro Ala Gly Cys Gln Glu Thr Val Lys
1 5 10

<210> SEQ ID NO 590
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 590

Leu Gly Asp Pro Leu Glu Gly Cys Pro Glu Arg
1 5 10

<210> SEQ ID NO 591
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 591

Asp Thr Ala Ser Leu Leu Ala Thr Ile Ser Gln Gln Val Pro His Leu
1 5 10 15

Arg

<210> SEQ ID NO 592
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 592

Ile Phe Tyr His Asp Leu Ser Leu Ser Leu Pro Thr Leu Lys
1 5 10

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<210> SEQ ID NO 593
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 593

Ser Ile Glu Asp Trp Leu His Ser Ala Val Trp Asp Lys
1 5 10

<210> SEQ ID NO 594
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 594

Ala Leu Ala Phe Phe Val Pro Pro Ala Pro Ile Asn Thr Leu Gln Arg
1 5 10 15

<210> SEQ ID NO 595
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 595

Ser Leu Ile Gln Ala Phe Asn Ala Glu Gly Ile Arg
1 5 10

<210> SEQ ID NO 596
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 596

Leu Ala Leu Ser Val Ala Gly Pro Val Pro Gly Arg
1 5 10

<210> SEQ ID NO 597
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 597

Leu Pro Pro Thr Ala Pro Thr Pro Ala Thr Ala Ala Leu Glu Thr Lys
1 5 10 15

<210> SEQ ID NO 598
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 598

Ala Val Leu Ala Asn Asn Ala Ala Leu Ala Ile Arg
1 5 10

<210> SEQ ID NO 599
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 599

Gly Phe Gln Gly Asn Met Pro Ser Trp Ala Arg
1 5 10

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<210> SEQ ID NO 600
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 600

Ile Leu Gly Ile Ser Asn Leu Gln Phe Leu Lys
1 5 10

<210> SEQ ID NO 601
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 601

Leu Ile Ala Ser Asp Met Ser Glu Leu Lys
1 5 10

<210> SEQ ID NO 602
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 602

Val Val Ser Glu Asp Val Leu Phe Arg
1 5

<210> SEQ ID NO 603
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 603

Gly Phe Ala Glu Val Val Ala Met Ile Lys
1 5 10

<210> SEQ ID NO 604
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 604

Leu Phe Ala Asp Glu Leu Ala Ala Leu Gln Ser Lys
1 5 10

<210> SEQ ID NO 605
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 605

Glu Thr Ser Pro Asp Tyr Ile Gln Ile Met Gln Tyr Leu Ser Lys
1 5 10 15

<210> SEQ ID NO 606
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 606

Ser Glu Ser Pro Gly Glu Gly Pro Ser Gly Thr Gly Gly Ser Ala Ala
1 5 10 15

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Ala Gly Asp Ile Thr Arg
            20


<210> SEQ ID NO 607
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 607

Ile His Phe Pro Leu Ala Thr Tyr Ala Pro Val Ile Ser Ala Glu Lys
1               5                   10                  15


<210> SEQ ID NO 608
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 608

Thr Ile Gly Gly Gly Asp Asp Ser Phe Asn Thr Phe Phe Ser Glu Thr
1               5                   10                  15

Gly Ala Gly Lys
            20


<210> SEQ ID NO 609
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Kaposi?s Sarcoma herpesvirus

<400> SEQUENCE: 609

Glu Asp Met Ala Ala Leu Glu Lys
1               5
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1. An assay, comprising:

obtaining a sample comprising:

a cell or tissue infected with a herpesvirus,

an extract from a cell or tissue infected with a herpesvirus, or

a protein preparation from a cell or tissue infected with a herpesvirus; and determining abundance level of a plurality of herpesvirus proteins in the sample using parallel reaction monitoring (PRM) to quantify signature peptide(s) corresponding to the herpesvirus proteins;

wherein the herpesvirus is HSV-1 and the signature peptides comprise a sequence selected from one of SEQ ID NOs: 1-21; or the herpesvirus is HCMV and the signature peptides comprise a sequence selected from one of SEQ ID NOs: 220-453; or the herpesvirus is KSHV and the signature peptides comprise a sequence selected from one of SEQ ID NOs: 454-606.

2. The assay of claim **1**, wherein for at least one herpesvirus protein for which the abundance level is determined, at least two signature peptides are quantified.

3. The assay of claim **1**, wherein determining the abundance level of the plurality of herpesvirus proteins using PRM comprises subjecting the sample to liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS).

4. The assay of claim **1**, wherein:

the plurality of herpesvirus proteins comprises at least one herpesvirus protein from each temporal class of viral replication for that herpesvirus; and/or

the cell or tissue infected with the herpesvirus is a human cell or human tissue.

5. (canceled)

6. The assay of claim **1**, wherein the plurality of herpesvirus proteins constitutes approximately 30-70% of the predicted viral proteome, or 50-80% of the predicted viral proteome.

7. A time course assay, comprising:

repeating the assay of claim **1** a plurality of times, where for each repetition the sample is obtained at a different timepoint in a time course.

8. The time course assay of claim **7**, where the different timepoints are:

different times post infection of the cell or tissue with the herpesvirus;

different times post exposure of the cell or tissue to a compound variable; or

different times post exposure of the cell or tissue to an environmental variable.

9. The time course assay of claim **8**, wherein the different times after infection of the cell or tissue with the herpesvirus include at least one time from each state of a replication cycle of the herpesvirus.

10. (canceled)

11. An exposure or dosage course assay, comprising:

repeating the assay of claim **1** a plurality of times, where for each repetition the sample is obtained from a cell or

tissue that has been exposed to a different compound or condition or a different dosage of a compound or a condition.

12. The exposure or dosage course assay of claim **11**, wherein the different compounds comprise one or more of known antiviral compounds, proposed antiviral compounds, test compounds, small molecule drugs or drug candidates, or siRNAs or other biologically active non-coding RNAs.

13. The exposure or dosage course assay of claim **12**, wherein the known antiviral compounds comprise one or more of acyclovir, ganciclovir, another nucleoside, penciclovir, famciclovir, valacyclovir, valganciclovir, cidofovir, another nucleotide phosphonate, fomivirsen, foscarnet, or honokiol.

14. (canceled)

15. The exposure or dosage course assay of claim **11**, wherein the different exposures comprise one or more of genetic modification of the cell or tissue, genetic modification of the herpesvirus, environmental conditions, or cell or tissue growth or harvesting conditions.

16. (canceled)

17. A method for quantification of herpesvirus proteins from multiple temporal classes of viral replication, comprising:

subjecting a cell sample or cell extract from a cell infected with a herpesvirus to parallel reaction monitoring (PRM) to generate abundance data;

analyzing the abundance data to quantify signature peptide(s) corresponding to at least one herpesvirus protein from each of at least two temporal classes of viral replication; and

providing the quantified peptide(s) results from the analyzing to a database, a computer memory, a display, a printer, or another output device;

wherein the herpesvirus is HSV-1 and one or more of the signature peptides comprise a sequence selected from one of SEQ ID NOs: 1-219; or the herpesvirus is HCMV and one or more of the signature peptides comprise a sequence selected from one of SEQ ID NOs: 220-453; or the herpesvirus is KSHV and one or more of the signature peptides comprise a sequence selected from one of SEQ ID NOs: 454-606.

18. Use of the assay of claim **1**, to:

screen a drug candidate as a modulator of viral infection;

analyze a stage of infection at which a test compound acts;

determine what functional family(s) of viral proteins are affected by a drug or drug candidate;

characterize viral and/or host responses to viral infection;

characterize viral and/or host responses to drug treatment; or

characterize viral and/or host responses to genetic manipulation of either the viral genome or the host genome.

19. A kit for use with the assay of claim **1**, comprising:

parameters for performing the assay for a target herpesvirus;

a set of heavy isotope-labeled peptides for use as controls; and

a USB drive or other non-transitory computer readable medium containing software for assay analysis and/or standardized report generation.

20-24. (canceled)

25. A non-naturally occurring, labeled peptide having an amino acid sequence selected from SEQ ID NOs: 1-606.

26. The non-naturally occurring, labeled peptide of claim **25**, wherein the label enables the peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

27. A plurality of the non-naturally occurring, labeled peptides of claim **25**, which plurality is specific for HSV-1, comprising:

at least one peptide, at least two peptides, or at least three peptides each of the 60 proteins listed in Table 1, the peptides comprising a sequence selected from SEQ ID NOs: 1-4, 5-8, 9-12, 13-17, 18-21, 22-27, 28-31, 32-37, 38-42, 43-46, 47-50, 51-54, 55-58, 59-62, 63-66, 67-70, 71-76, 77-79, 80-83, 84-87, 88-92, 93-96, 97, 98-101, 102-103, 104-107, 108-109, 110-115, 116-118, 119-123, 124-126, 127-130, 131, 132-136, 137-141, 142, 143-145, 146-150, 151-156, 157, 158, 159-160, 161-165, 166-171, 172, 173-178, 179, 180-184, 185-189, 190-191, 192-193, 194-195, 196-198, 199-203, 204, 205-207, 208-211, 212, 213-217, 218, or 219;

at least one peptide from at least one protein from each temporal stage of HSV-viral replication, where the peptides from the Intermediate Early (IE) temporal stage are selected from SEQ ID NOs: 13-27, 59-62, and 212; the peptides from the Early (E) temporal stage are selected from SEQ ID NOs: 1-4, 28-37, 43-50, 63-70, 80-83, 108-109, 124-130, 146-150, 192-198, 205-207, and 218-219; and the peptides from the Late (L) temporal stage are selected from SEQ ID NOs: 5-12, 38-42, 51-58, 71-79, 84-107, 110-123, 131-145, 151-191, 199-204, 208-211, and 213-217;

at least 17 peptides comprising sequences selected from SEQ ID NOs: 1-219;

more than 17 peptides each of which comprises a sequence selected from SEQ ID NOs: 1-219;

at least 30 peptides each of which comprises a sequence selected from SEQ ID NOs: 1-219;

at least 50 peptides each of which comprises a sequence selected from SEQ ID NOs: 1-219;

at least 60 peptides each of which comprises a sequence selected from SEQ ID NOs: 1-219;

219 peptides each of which has a sequence of one of SEQ ID NOs: 1-219;

wherein each peptide comprises a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

28. A plurality of the non-naturally occurring, labeled peptides of claim **25**, which plurality is specific for HCMV, comprising:

at least one peptide, at least two peptides, or at least three peptides from each of the 90 proteins listed in Table 2, the peptides comprising a sequence selected from SEQ ID NOs: 220-225, 226-231, 232-234, 235-237, 238-239, 240-242, 243-244, 245-247, 248-250, 251-252, 253-254, 255-257, 258-260, 261-263, 264-266, 267-268, 269-271, 272-274, 275-277, 278-280, 281-283, 284-286, 287-289, 290-291, 292-294, 295-297, 298-300, 301, 302-303, 304-306, 307-309, 310-312, 313-314, 315-317, 318-320, 321-323, 324-326, 327-329, 330-332, 333-335, 336-338, 339-341, 342-344, 345-347, 348-350, 351-353, 354-356, 357-359, 360-362, 363-365, 366-368, 369-371, 372-374, 375-377, 378-

380, 381-383, 384-386, 387-389, 390, 391-393, 394-397, 398-400, 401-402, 403-405, 406, 407-409, 410-412, 413-414, 415, 416-418, 419-420, 421-423, 424, 425-427, 428, 429, 430-432, 433-435, 436, 437-438, 439, 440-441, 442-443, 444-445, 446, 447, 448, 449, 450-452, or 453;

at least one peptide from at least one protein from each temporal stage of HCMV-viral replication, where the peptides from the Intermediate Early (IE) temporal stage are selected from SEQ ID NOs: 245-247, 267-268, 290-297, and 324-329; the peptides from the Late (L) temporal stage are selected from SEQ ID NOs: 226-231, 238-244, 248-250, 261-263, 278-280, 284-286, 301, 304-306, 310-314, 333-335, 345-347, 357-362, 369-374, 401-402, 407-412, 415, 424, 433-435, 437-439, and 444-445; and the peptides from the Late Late (LL) temporal stage are selected from SEQ ID NOs: 220-225, 264-266, 269-274, 298-300, 302-303, 339-341, 351-353, 363-365, 394-397, 406, 428-432, and 448;

at least 90 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453;

more than 90 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453;

at least 30 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453;

at least 50 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453;

at least 100 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453;

at least 150 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453;

at least 200 peptides each of which comprises a sequence selected from SEQ ID NOs: 220-453; or

233 peptides each of which has a sequence of one of SEQ ID NOs: 220-253;

wherein each peptide in the collection comprises a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

29. A plurality of the non-naturally occurring, labeled peptides of claim **25**, which plurality is specific for KSHV, comprising:

at least one peptide, at least two peptides, or at least three peptides from each of the 62 proteins listed in Table 3, the peptides comprising a sequence selected from SEQ ID NOs: 454-456, 457-459, 460-462, 463-464, 465-467, 468-470, 471-473, 474-476, 477-479, 480-482, 483-485, 486-488, 489-491, 492-494, 495-497, 498, 499-501, 502-504, 505-507, 508-510, 511-513, 514-516, 517-519, 520-522, 523-525, 526-527, 528-530, 531-533, 534-536, 537-539, 540-542, 543-545, 546-548, 549-550, 551, 552-553, 554-555, 556, 557-558, 559-561, 562-564, 565, 566-568, 569-570, 571-572, 573, 574-576, 577-578, 579-580, 581-583, 584-585, 586, 587, 588-590, 591-593, 594, 595-597, 598-599, 600-602, 603, 604-605, or 606;

at least one peptide from at least one protein from each temporal stage of KSHV-viral replication, where the peptides from the Intermediate Early (IE) temporal stage are selected from SEQ ID NOs: 474-476, 502-507, 511-513, 552-553, and 586; the peptides from the Delayed Early (DE) temporal stage are selected from SEQ ID NOs: 454-462, 465-473, 483-497, 514-516, 520-525, 528-530, 546-551, 554-555, 573-578, 584-585, 587, 591-593, 598-599, and 606; and the peptides from the Late (L) temporal stage are selected from SEQ ID NOs: 463-464, 477-482, 498, 499-501, 508-510, 517-519, 526-527, 531-545, 556-572, 579-583, 588-590, 594-597, and 600-605;

at least 62 peptides each of which comprising a sequence selected from SEQ ID NOs: 454-606;

more than 62 peptides each of which comprises a sequence selected from SEQ ID NOs: 454-606;

at least 30 peptides each of which comprises a sequence selected from SEQ ID NOs: 454-606;

at least 50 peptides each of which comprises a sequence selected from SEQ ID NOs: 454-606;

at least 75 peptides each of which comprises a sequence selected from SEQ ID NOs: 454-606;

at least 100 peptides each of which comprises a sequence selected from SEQ ID NOs: 454-606;

at least 150 peptides each of which comprises a sequence selected from SEQ ID NOs: 454-606;

151 peptides each of which has a sequence of one of SEQ ID NOs: 454-606;

wherein each peptide comprises a label that enables the labeled peptide to be distinguished from an unlabeled peptide with the same amino acid sequence in liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analysis.

30. (canceled)

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