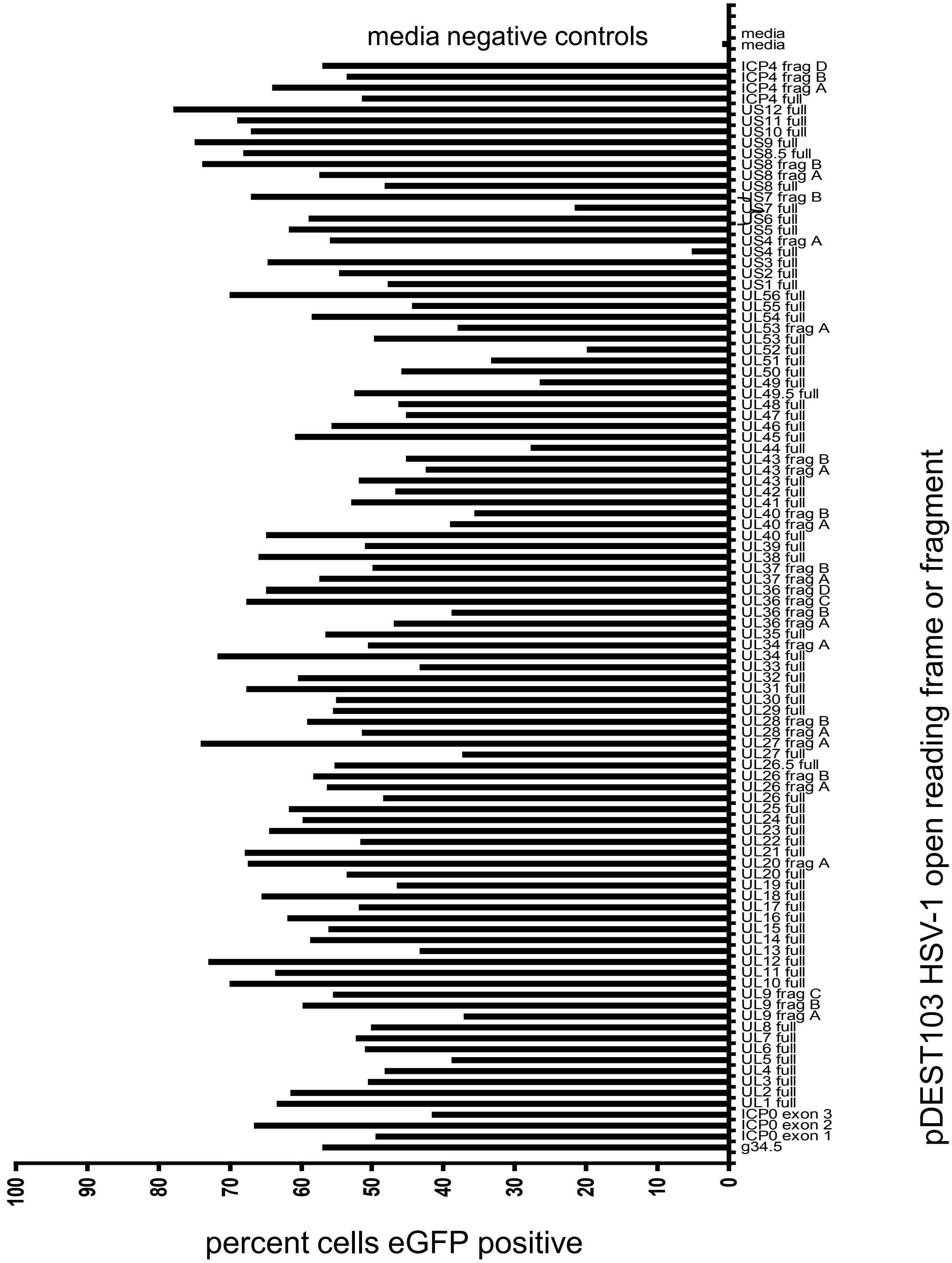
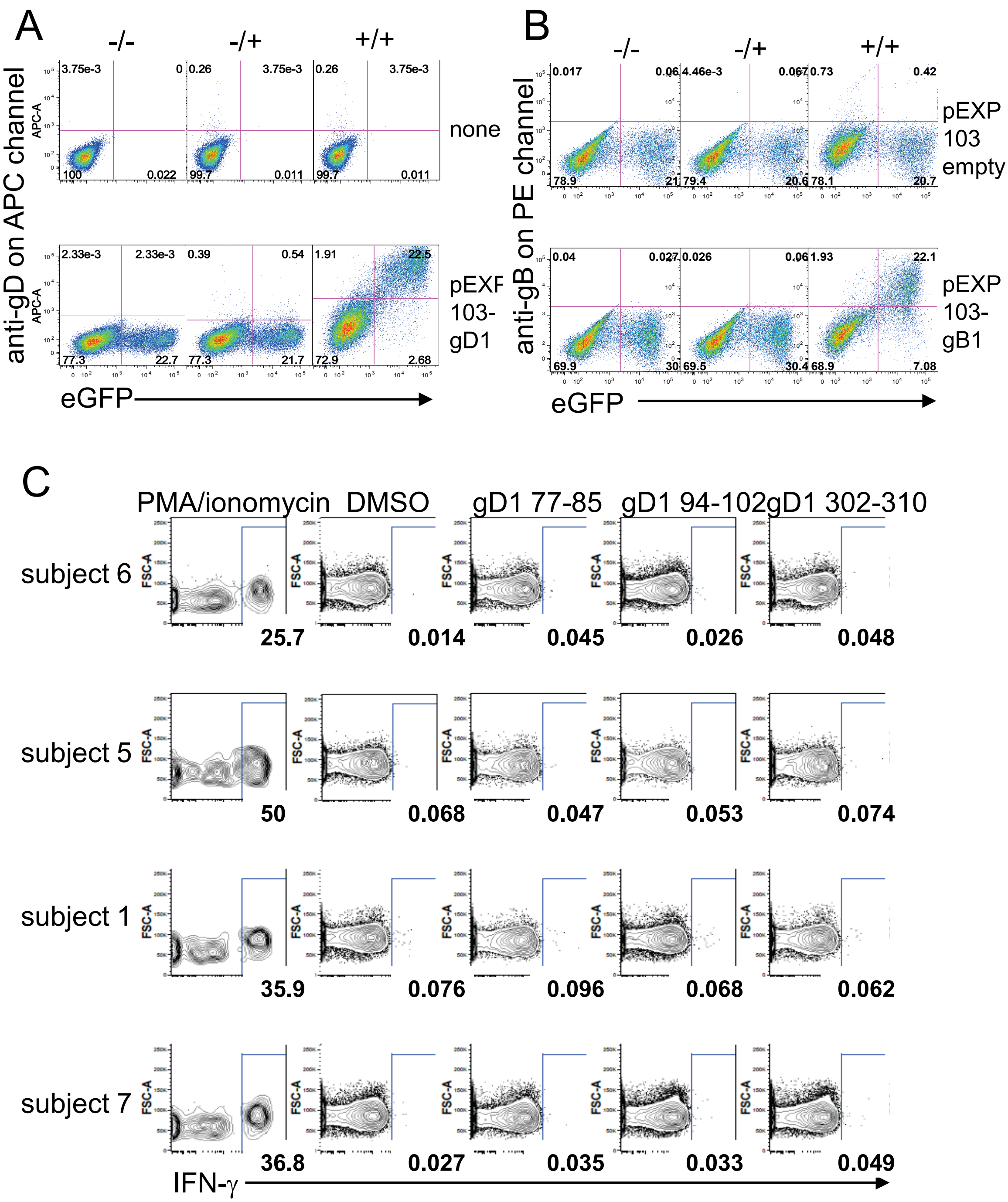
Jing et al. Supplementary Fig. 1 (landscape)

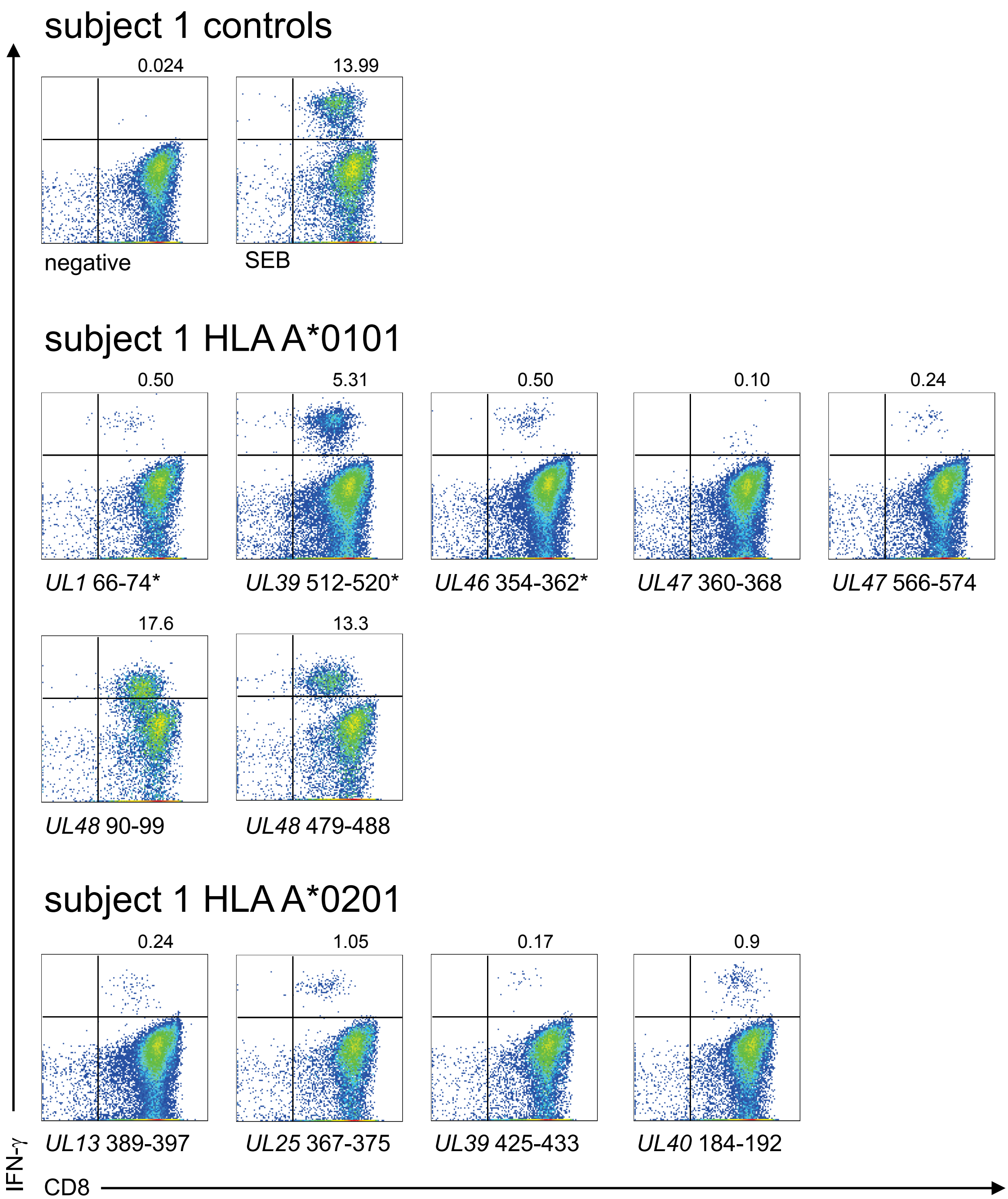


Supplementary Figure 1. Expression of HSV-1 proteins or protein fragments as fusions with EGFP at the N-terminal. HSV-1 clones are arranged with protein names arrayed on the X-axis in their nominal order in the HSV-1 genome per Genbank NC_001806.1. Proteins are full length except those expressed as fragments as detailed in Supplementary Table 1. Cos-7 cells were recovered by trypsinization 48 h after transfection with the indicated plasmid pEXP103-HSV-1 gene DNA as detailed in Materials and Methods, stained with Violet live/dead, washed free of cell culture medium and analyzed by flow cytometry using 488 nm excitation. Live cells in the appropriate forward and side scatter regions were analyzed for EGFP fluorescence and the percent positive indicated with bars. At least 5000 live cells were analyzed per plasmid.

Jing et al. Supplementary Fig. 2

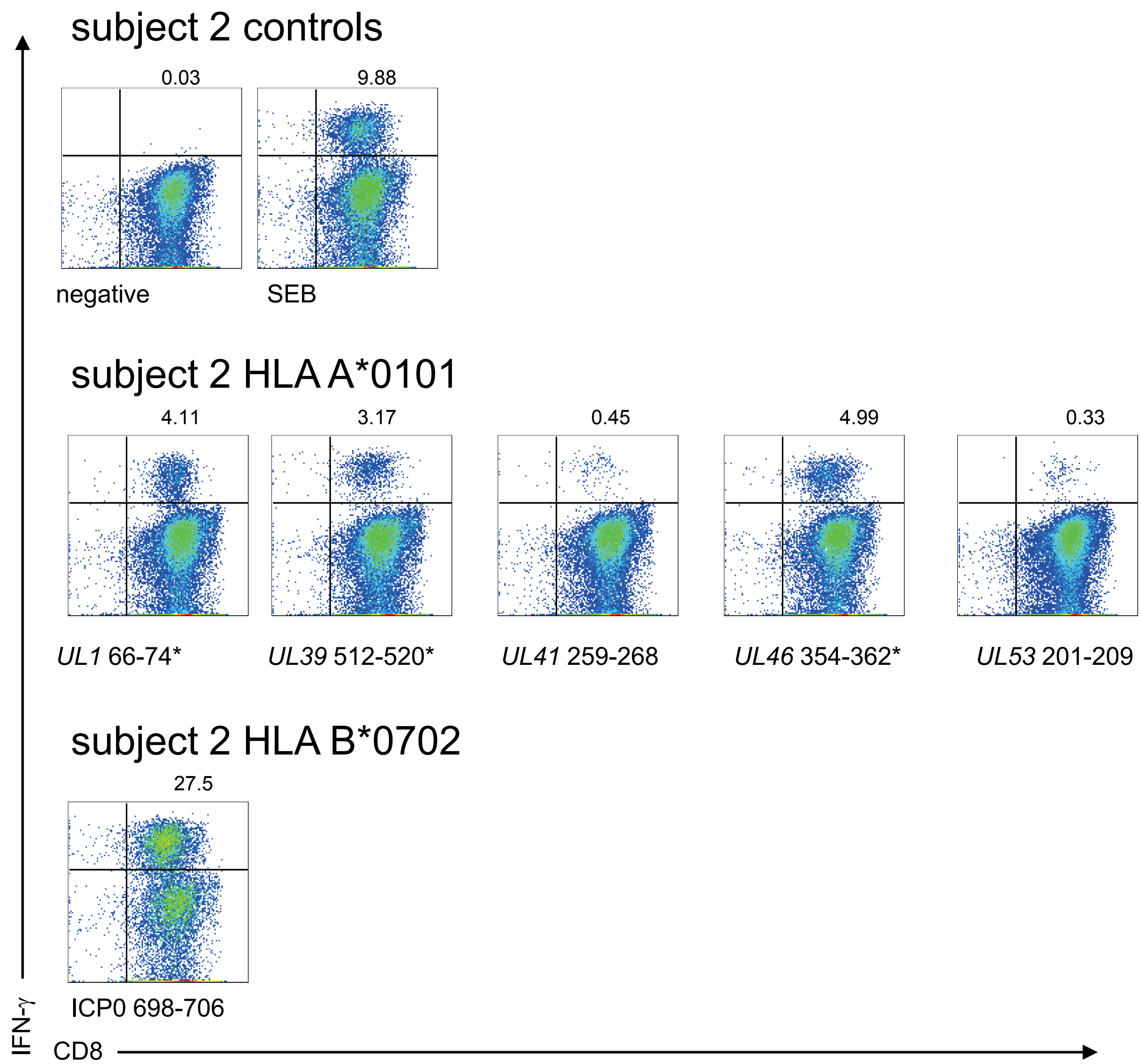


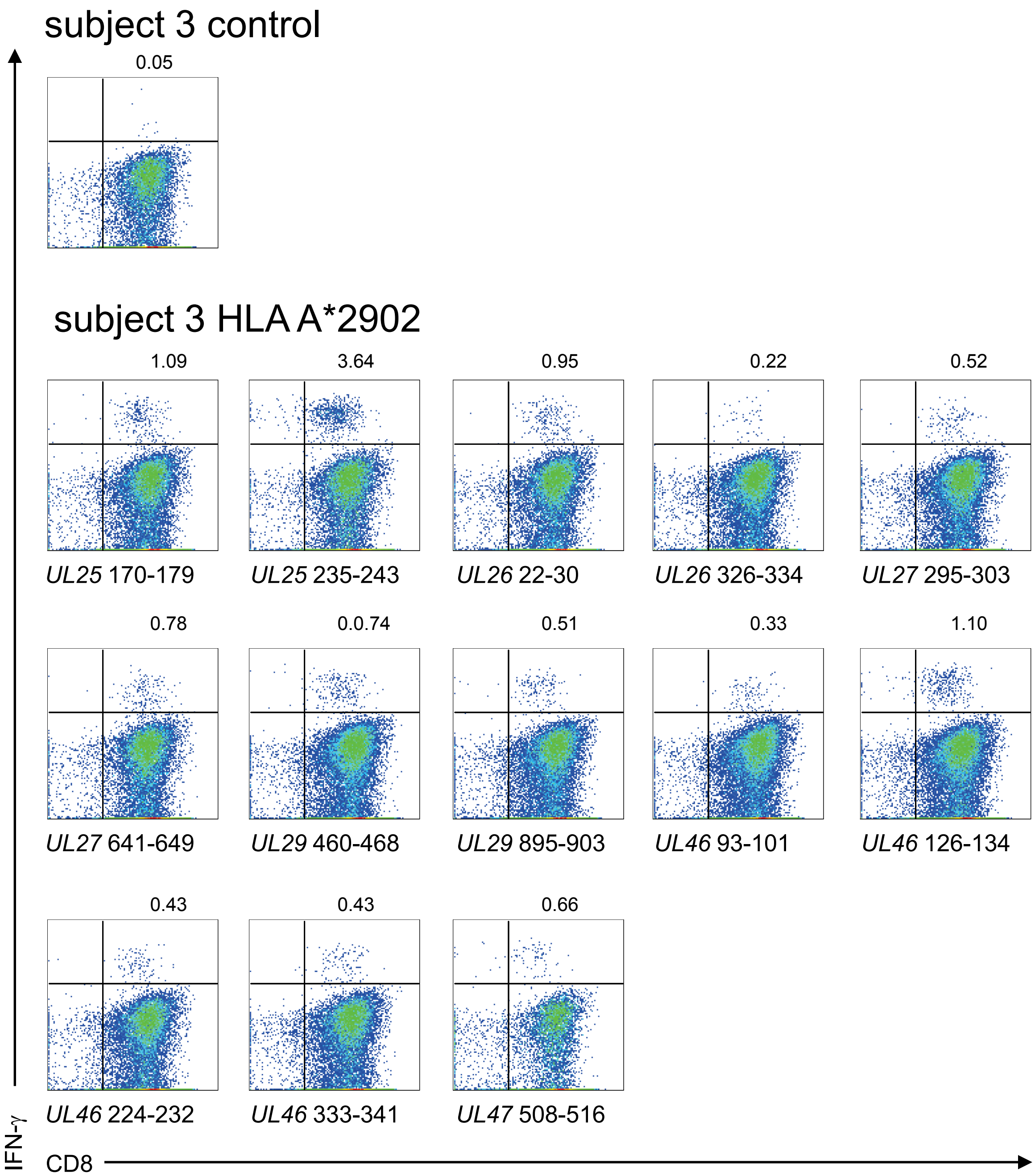
Supplementary Figure 2. Confirmation of expression of selected HSV-1 proteins. A: Expression of HSV-1 envelope glycoprotein gD1, encoded by gene US6, after no transfection (top) or transfection of Cos-7 cells with pEXP103-US6 (bottom). Cells were stained with no antibody (left), secondary APC- labeled anti-mouse antibody only (middle), or primary anti-gD mAb followed by secondary antibody (right) and analyzed for EGFP and APC fluorescence. Numbers are percentages of cells in indicated quadrants. B: Similar data for HSV-1 envelope glycoprotein B1, encoded by gene UL27. Cos-7 were transfected with either empty pEXP103 expressing EGFP (top), or the construct containing the cloned UL27 gene (bottom). Primary antibody was anti-gB, and secondary antibody used PE. C: Polyclonal expanded CD8 cell lines derived from CD3+ CD137^{high} cells show low reactivity with the indicated candidate HLA A*0201-restricted peptides from gD1 at 1 μg/ml. Participants were selected for expression of HLA A*0201 or a related HLA A*02 allele (Table 1). APC were autologous PBMC that are dump-gated for CFSE label (not shown). After gating on live CD3+ CD8+, dot-plots of forward scatter vs. intracellular IFN-γ are shown with numbers indicating percentages of cells in the indicated positive region. Positive control at left followed by DMSO negative control.



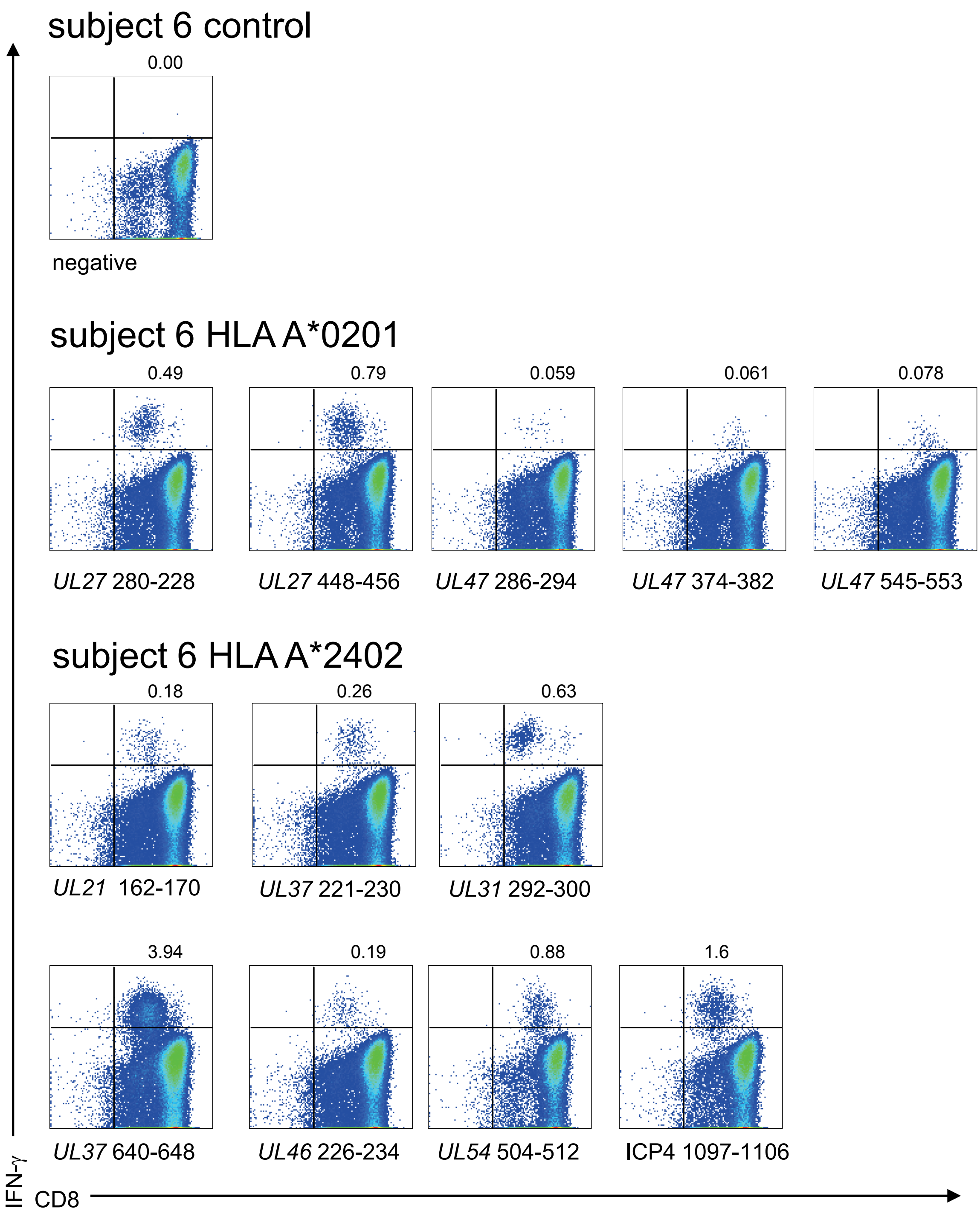
Supplementary Figure 3. Five pages. Reactivity of polyclonal expanded CD8 cell lines derived from CD3+ $CD137^{high}$ cells with synthetic HSV-1 peptides at 1 μg/ml. These data are the basis for Table 4. Autologous PBMC used as APC were CFSE-labeled and dump-gated (not shown). Each page shows results from a distinct participant from Table 1, and begins with negative control DMSO stimulation and positive control SEB stimulation, followed by peptides. Each dot-plot shows expression of CD8 and intracellular IFN-γ. The identity of the peptides is indicated below each dot-plot, with asterisks after three HLA A*0101-restricted peptides studied in both participants 1 and 2. The identity of the HLA allele used to assign restriction is indicated above the relevant dot-plots. The numbers are the percentages of cells in the upper right quadrants of each dot-plot.

Jing et al. supplementary Fig. 3 page 2

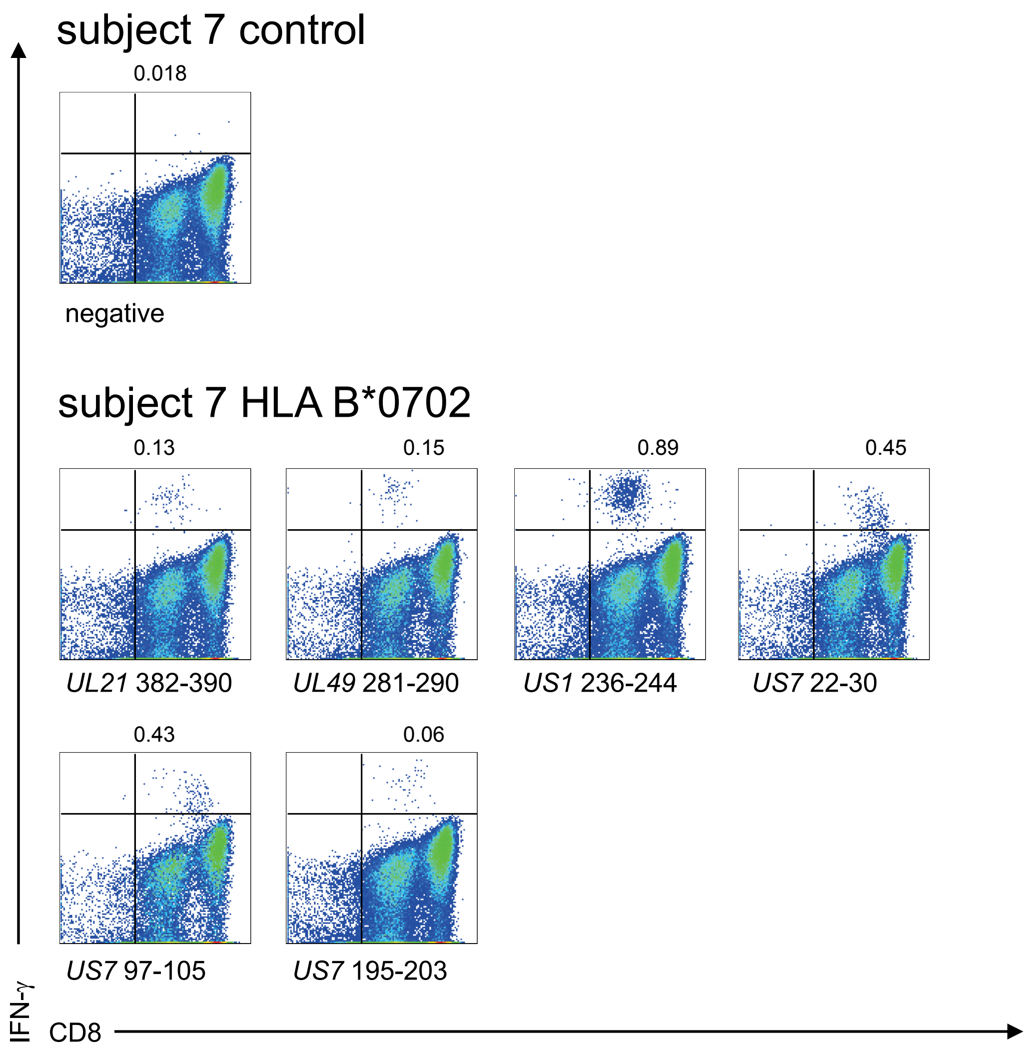



subject 3 control
0.05
subject 3 HLA A*2902
1.09
3.64
0.95
0.22
0.52
UL25 170-179
UL25 235-243
UL26 22-30
UL26 326-334
UL27 295-303
0.78
0.0.74
0.51
0.33
1.10
UL27 641-649
UL29 460-468
UL29 895-903
UL46 93-101
UL46 126-134
0.43
0.43
0.66
UL46 224-232
UL46 333-341
UL47 508-516
IFN-γ
CD8

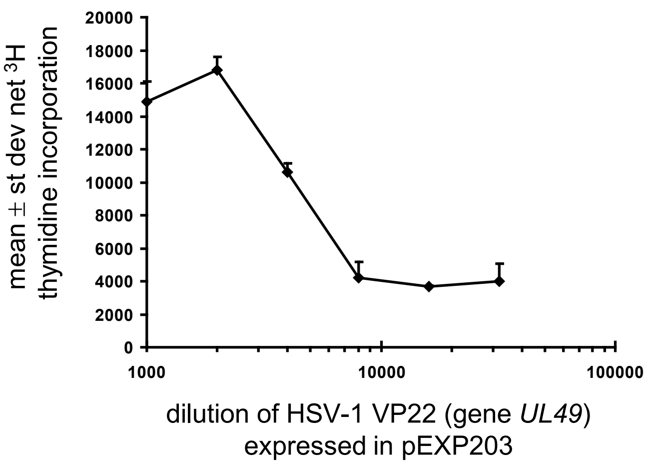
Jing et al. supplementary Fig. 3 page 4



Jing et al. supplementary Fig. 3 page 5



Jing et al. Supplementary Fig. 4



Supplementary Figure 4. Expression of full-length HSV-1 protein VP22 (gene UL49) in the custom pEXP203 vector. Protein derived by in vitro transcription/translation was tested in triplicate ^{3}H thymidine incorporation assays using a CD4 T-cell clone known to be specific for VP22, and autologous irradiated PBMC as APC, as detailed in the text. Y axis is mean ± standard deviation of net CPM ^{3}H thymidine incorporation after subtracting media control.

Supplementary Tables

Supplementary Table 1. Primers used to amplify predicted HSV-1 protein coding regions.

clone name[a]	5' primer[b]	5' primer position[c]	3'primer[b]	3' primer position[c]
*RL*1 (γ34.5) full	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCacgctctctgtctccatggc	*RL*1, (-)15-5	GGGGACCACTTTGTACAAGAAAGCTGGGTCacgttagaccgagttcgccg	*RL*1, 731-747(+)3
*RL*2 (ICP0) frag A	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatggagccccgccccggagcgag	*RL*2, 1-23	GGGGACCACTTTGTACAAGAAAGCTGGGTCgcgcccggcccctcacctcg	*RL*2, 54-57(+)16
*RL*2 (ICP0) frag B	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcccgccccggatgtctgggtg	*RL*2, 58-80	GGGGACCACTTTGTACAAGAAAGCTGGGTCttagtcgtccaggtcgtcgtcatcctcg	*RL*2, 699-723(+)3
*RL*2 (ICP0) frag C	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgcagactacgtaccgcccg	*RL*2, (-)1-724-741	GGGGACCACTTTGTACAAGAAAGCTGGGTCttattgttttccctcgtcccgggtcg	*RL*2, 2303-2328
*UL*1 full	**AAAAAGCAGGCT***ccgcc*atggggattttgggttgggtc	*UL*1, 1-21	**AGAAAGCTGGGT**ctagaggcgccgggagtgg	*UL*1, 657-672
*UL*2 full	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatgaagcgggcctgcagccg	*UL*2, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcaaaccgaccagtcgatgggtgaa	*UL*2, 981-1005
*UL*3 full	**AAAAAGCAGGCT***ccgcc*atggttaaacctctggtctcatac	*UL*3, 1-24	**AGAAAGCTGGGT**ctactcggcccccgaggc	*UL*3, 691-705
*UL*4 full	**AAAAAGCAGGCT***ccgcc*atgtccaatccacagacgacc	*UL*4, 1-21	**AGAAAGCTGGGT**ctaggaccccaaaagtttgtctgc	*UL*4, 577-597
*UL*5 full	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatggcggcggccggcgggga	*UL*5, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCttaatagacaatgaccacgt	*UL*5, 2630-2649
*UL*6 full	**AAAAAGCAGGCT***ccgcc*atgaccgcaccacgctcg	*UL*6, 1-18	**AGAAAGCTGGGT**ctatcgtcggccgtcgcgg	*UL*6, 2013-2028
*UL*7 full	**AAAAAGCAGGCT***ccgcc*atggccgccgcgacgg	*UL*7, 1-16	**AGAAAGCTGGGT**ctaacaaaactgataaaacagcgacg	*UL*7, 866-888
*UL*8 full	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatggacaccgcagatatcgt	*UL*8, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcaggcaaacagaaacgaca	*UL*8, 2234-2253
*UL*9 frag A	**AAAAAGCAGGCT***ccgcc*atgcctttcgtgggggc	*UL*9, 1-18	**AGAAAGCTGGGT**ctacatgtaaatcagtagctcccc	*UL*9, 1180-1200
*UL*9 frag B	**AAAAAGCAGGCT***ccgcc*atggacggctccggggcg	*UL*9, 1201-1215	**AGAAAGCTGGGT**ctatagggtgctaaagttcaccgc	*UL*9, 2533-2553
*UL*9 frag C	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatgaactacggaccggacatggtg	*UL*9, 1114-1137	GGGGACCACTTTGTACAAGAAAGCTGGGTCcagcgtgcatctctcaaagtagtg	*UL*9, 1402-1425
*UL*10 full	**AAAAAGCAGGCT***ccgcc*atgggacgcccggcccc	*UL*10, 1-17	**AGAAAGCTGGGT**ctaccaacggcggacggtg	*UL*10, 1404-1419
*UL*11 full	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatgggcctctcgttctccgg	*UL*11, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCttattcgctatcggacatggggg	*UL*11, 269-291
*UL*12 full	**AAAAAGCAGGCT***ccgcc*atggagtccacggtaggcc	*UL*12, 1-19	**AGAAAGCTGGGT**ctagcgagacgacctccccg	*UL*12, 1862-1878
*UL*13 full	**AAAAAGCAGGCT***ccgcc*atggatgagtcccgcagacag	*UL*13, 1-21	**AGAAAGCTGGGT**tcacgacagcgcgtgccg	*UL*13, 1540-1554
*UL*14 full	**AAAAAGCAGGCT***ccgcc*atggaccgagatgccgcc	*UL*14, 1-18	**AGAAAGCTGGGT**ctattcgccatcgggatagtcc	*UL*14, 639-657
*UL*15 full	**AAAAAGCAGGCT***ccgcc*atgtttggtcagcagctggc	*UL*15, 1-20	**AGAAAGCTGGGT**tcacgagacgcgtgtgatag	*UL*15, 2189-2205
*UL*16 full	**AAAAAGCAGGCT***ccgcc*atggcgcagctgggacc	*UL*16, 1-17	**AGAAAGCTGGGT**ctattcgggatcgcttgaggag	*UL*16, 1101-1119
*UL*17 full	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCatgaacgcgcacttggccaacg	*UL*17, 1-22	GGGGACCACTTTGTACAAGAAAGCTGGGTCctagcgagaccggccgttcc	*UL*17, 2093-2112

*UL*18 full	**AAAAAGCGAGGCT***ccgcc*atgctggcggacggctttg	*UL*18, 1-19	**AGAAAGCTGGGT**ctagggatagcgtataacgggg	*UL*18, 936-954
*UL*19 full	**AAAAAGCGAGGCT***ccgcc*atggccgctcccaaccg	*UL*19, 1-17	**AGAAAGCTGGGT**ctacagagccagtcccttgagc	*UL*19, 4104-4122
*UL*20 full	**AAAAAGCGAGGCT***ccgcc*atgaccatgcgggatgacc	*UL*20, 1-19	**AGAAAGCTGGGT**ctagaacgcgacgggtgcattc	*UL*20, 648-666
*UL*20 frag A	**AAAAAGCGAGGCT***ccgcc*atgaccatgcgggatgacc	*UL*20, 1-19	**AGAAAGCTGGGT**ctagcgctttgaaaagaccggc	*UL*20, 171-189
*UL*21 full	**AAAAAGCGAGGCT***ccgcc*atggagcttagctacgccac	*UL*21, 1-20	**AGAAAGCTGGGT**ctacacagactgtccgtgttgg	*UL*21, 1588-1605
*UL*22 full	**AAAAAGCGAGGCT***ccgcc*atggggaatggtttatggttcg	*UL*22, 1-22	**AGAAAGCTGGGT**ctattcgcgtctccaaaaaaacgg	*UL*22, 2494-2514
*UL*23 full	**AAAAAGCGAGGCT***ccgcc*atggcttcgtacccctgcc	*UL*23, 1-19	**AGAAAGCTGGGT**ctagttagcctcccccatctcc	*UL*23, 1110-1128
*UL*24 full	**AAAAAGCGAGGCT***ccgcc*atggccgcgagaacgcg	*UL*24, 1-17	**AGAAAGCTGGGT**ctattcggaggcggctcggg	*UL*24, 791-807
*UL*25 full	**AAAAAGCGAGGCT***ccgcc*atggacccgtactgcccatttg	*UL*25, 1-22	**AGAAAGCTGGGT**ctaaaccgccgacaggtactgtg	*UL*25, 1721-1740
*UL*26 full	**AAAAAGCGAGGCT***ccgcc*atggcagccgatgcccc	*UL*26, 1-17	**AGAAAGCTGGGT**ctagcgggcccccatcatctg	*UL*26, 1888-1905
*UL*26 frag A	**AAAAAGCGAGGCT***ccgcc*atggcagccgatgcccc	*UL*26, 1-17	**AGAAAGCTGGGT**ctagtaatgggaggccgggatc	*UL*26, 984-1002
*UL*26 frag B	**AAAAAGCGAGGCT***ccgcc*atgaaccagctcgtcgccgg	*UL*26, 1003-1019	**AGAAAGCTGGGT**ctagcgggcccccatcatctg	*UL*26, 1888-1905
*UL*26.5 full	**AAAAAGCGAGGCT***ccgcc*atgaaccccgttccgacatc	*UL*26.5, 1-20	**AGAAAGCTGGGT**ctagcgggcccccatcatctg	*UL*26, 1888-1905
*UL*27 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCcgtagtcccgccatgcgccagg	*UL*27, (-)12-10	GGGGACCACTTTGTACAAGAAAGCTGGGTCaaaccccccatcacaggtcgtcc	*UL*27, 2703-2715 (+)10
*UL*27 frag A	**AAAAAGCGAGGCT***ccgcc*atgcggctgcagagcaaccc	*UL*27, 2398-2414	**AGAAAGCTGGGT**ctacaggtcgtcctcgtcgg	*UL*27, 2696-2712
*UL*28 frag A	**AAAAAGCGAGGCT***ccgcc*atggccgccccggtgtc	*UL*28, 1-17	**AGAAAGCTGGGT**ctacgccagcgcggtcagg	*UL*28, 995-1011
*UL*28 frag B	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCgacgtgtttcaggccaccacgc	*UL*28, 886-907	GGGGACCACTTTGTACAAGAAAGCTGGGTCctggcgcatggcgggactac	*UL*28, 2355-2358(+)16
*UL*29 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggagacaaagcccaagac	*UL*29, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcacagcatatccaacgtca	*UL*29, 3572-3591
*UL*30 full	**AAAAAGCGAGGCT***ccgcc*atgttttccggtggcggcg	*UL*30, 1-19	**AGAAAGCTGGGT**tcatgctagagtatcaaaggctctatg	*UL*30, 3681-3705
*UL*31 full	**AAAAAGCGAGGCT***ccgcc*atgtatgacaccgacccccatc	*UL*31, 1-22	**AGAAAGCTGGGT**ctacggcggaggaaactcgtc	*UL*31, 901-918
*UL*32 full	**AAAAAGCGAGGCT***ccgcc*atggcaacttcgcccccc	*UL*32, 1-18	**AGAAAGCTGGGT**tcatacataggtacacagggtgtgc	*UL*32, 1767-1788
*UL*33 full	**AAAAAGCGAGGCT***ccgcc*atggctgggcgggagggg	*UL*33, 1-18	**AGAAAGCTGGGT**tcagccccgcagaatctggtg	*UL*33, 373-390
*UL*34 full	**AAAAAGCGAGGCT***ccgcc*atggcgggactgggcaag	*UL*34, 1-18	**AGAAAGCTGGGT**ctataggcgcgcgccagcac	*UL*34, 809-825
*UL*34 frag A	**AAAAAGCGAGGCT***ccgcc*atggcgggactgggcaag	*UL*34, 1-18	**AGAAAGCTGGGT**ctaccgtaggtgcttaagaccc	*UL*34, 723-741
*UL*35 full	**AAAAAGCGAGGCT***ccgcc*atggccgtcccgcaatttc	*UL*35, 1-19	**AGAAAGCTGGGT**ctacggggtcccgggcgtc	*UL*35, 321-336
*UL*36 frag A	**AAAAAGCGAGGCT***ccgcc*atgggtggcggaaacaacac	*UL*36, 1-20	**AGAAAGCTGGGT**ctattcctcggccatgcgcg	*UL*36, 2984-3000
*UL*36 frag B	**AAAAAGCGAGGCT***ccgcc*atggcgctgcggcaggcg	*UL*36. 3001-3015	**AGAAAGCTGGGT**ctagaagcagagcgcgtactgc	*UL*36, 5983-6000
*UL*36 frag C	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCcaagaggccgacccgcagatgctgc	*UL*36, 5833-5857	GGGGACCACTTTGTACAAGAAAGCTGGGTCggtggcgcgcgccagggagcgtg	*UL*36, 8063-8085
*UL*36 frag D	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCgttcctgcgcccggcgcgtcgc	*UL*36, 2851-2873	GGGGACCACTTTGTACAAGAAAGCTGGGTCcaagaacttctcccgggcgtcgc	*UL*36, 3065-3087
*UL*37 frag A	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcagaccgcggtctcccgtc	*UL*37, 1-23	GGGGACCACTTTGTACAAGAAAGCTGGGTCgacccatgatacgcgccagcgtc	*UL*37, 1533-1555
*UL*37 frag B	**AAAAAGCGAGGCT***ccgcc*atggcggtcggcctgtcgg	*UL*37, 1501-1516	**AGAAAGCTGGGT**ctattggtaactagttaacggcaag	*UL*37, 3348-3369
*UL*38 full	**AAAAAGCGAGGCT***ccgcc*atgaagaccaatccgctaccc	*UL*38, 1-21	**AGAAAGCTGGGT**ctacgcgcatgcccgccac	*UL*38, 1381-1395

*UL*39 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCtctgttgaaatggccagccgc	*UL*39, (-)9-12	GGGGACCACTTTGTACAAGAAAGCTGGGTCtttgtcggtcacagcgcgca	*UL*39, 3403-3414(+)7
*UL*40 full	**AAAAAGCGAGGCT***ccgcc*atggattccgcggccccag	*UL*40, 1-19	**AGAAAGCTGGGT**tcacagatcgttgacgaccg	*UL*40, 1004-1020
*UL*40 frag A	**AAAAAGCGAGGCT***ccgcc*atggattccgcggccccag	*UL*40, 1-19	**AGAAAGCTGGGT**ctacttttccggaacggaggcg	*UL*40, 519-537
*UL*40 frag B	**AAAAAGCGAGGCT***ccgcc*atgaccaacaaccttctgcggg	*UL*40, 607-625	**AGAAAGCTGGGT**tcacagatcgttgacgaccg	*UL*40, 1004-1020
*UL*41 full	**AAAAAGCGAGGCT***ccgcc*atgggtttgttcgggatgatg	*UL*41, 1-21	**AGAAAGCTGGGT**ctactcgtcccagaatttggcc	*UL*41, 1449-1467
*UL*42 full	**AAAAAGCGAGGCT***ccgcc*atgacggattcccctggcg	*UL*42, 1-19	**AGAAAGCTGGGT**ctaggggaatccaaaaccatacgg	*UL*42, 1444-1464
*UL*43 full	**AAAAAGCGAGGCT***ccgcc*atgtggggcgtgacggaac	*UL*43, 1-19	**AGAAAGCTGGGT**ctaatcgcccgaccgcccg	*UL*43, 1287-1302
*UL*43 frag A	**AAAAAGCGAGGCT***ccgcc*atgtggggcgtgacggaac	*UL*43, 1-19	**AGAAAGCTGGGT**ctacccgcgcgacataacgac	*UL*43, 205-222
*UL*43 frag B	**AAAAAGCGAGGCT***ccgcc*atggccagggactgcttttcc	*UL*43, 643-660	**AGAAAGCTGGGT**ctaaacctcggaaaaccgaaacac	*UL*43, 1075-1095
*UL*44 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggccccggggcgggtgggcct	*UL*44, 1-23	GGGGACCACTTTGTACAAGAAAGCTGGGTCttaccgccgatgacgctgcc	*UL*44, 1517-1536
*UL*45 full	**AAAAAGCGAGGCT***ccgcc*atgcctctgcgggcatcg	*UL*45, 1-18	**AGAAAGCTGGGT**ctacggcagccccagcgc	*UL*45, 502-516
*UL*46 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCgtcaccatgcagcgccggac	*UL*46, (-)6-14	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcaccggctccggcgtcctt	*UL*46, 2144-2163
*UL*47 full	**AAAAAGCGAGGCT***ccgcc*atgtcggctcgcgaaccc	*UL*47, 1-18	**AGAAAGCTGGGT**ctatgggcgtggcgggcc	*UL*47, 2065-2079
*UL*48 full	**AAAAAGCGAGGCT***ccgcc*atggacctcttggtcgacg	*UL*48, 1-19	**AGAAAGCTGGGT**ctacccaccgtactcgtcaattc	*UL*48, 1451-1470
*UL*49 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatgacctctcgccgctccgt	*UL*49, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtttcactcgacgggccgtct	*UL*49, 889-906(+)2
*UL*49.5 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatgggccccccagaagggt	*UL*49A, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCacagggcgggttcaggcgtg	*UL*49A, 268-276(+)11
*UL*50 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCaacaggaagatgagtcagtgg	*UL*50, (-)9-12	GGGGACCACTTTGTACAAGAAAGCTGGGTCctaaataccggtagaaccaa	*UL*50, 1097-1116
*UL*51 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcttctcttctcggggc	*UL*51, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCttattgacccaaaacacacg	*UL*51, 716-735
*UL*52 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggggcaggaagacgggaa	*UL*52, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcaagacgacggttgagagg	*UL*52, 3158-3177
*UL*53 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatgctcgccgtccgttccct	*UL*53, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcatacatcaaacaggcgcc	*UL*53, 998-1017
*UL*53 frag A	**AAAAAGCGAGGCT***ccgcc*atgccgctgcaccgatgtatttac	*UL*53, 97-117	**AGAAAGCTGGGT**ctaccgtgtgtaccatagggtc	*UL*53, 348-366
*UL*54 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcgactgacattgatat	*UL*54, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCctaaaacagggagttgcaat	*UL*54, 1520-1539
*UL*55 full	**AAAAAGCGAGGCT***ccgcc*atgacagcgaccccccctc	*UL*55, 1-18	**AGAAAGCTGGGT**ctacgccttaattttaatcttgacgc	*UL*55, 536-558
*UL*56 full	**AAAAAGCGAGGCT***ccgcc*atggcttcggaggcggc	*UL*56, 1-17	**AGAAAGCTGGGT**ctaccgccacaggaataccag	*UL*56, 685-702
*US*1 full	**AAAAAGCGAGGCT***ccgcc*atggccgacatttccccag	*US*1, 1-19	**AGAAAGCTGGGT**ctacggccggagaaacgtgtc	*US*1, 1243-1260
*US*2 full	**AAAAAGCGAGGCT***ccgcc*atgggcgttgttgtcgtcaac	*US*2, 1-21	**AGAAAGCTGGGT**ctaaagggtggtaaccggatagc	*US*2, 854-873
*US*3 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcctgtcgtaagttttg	*US*3, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCtcatttctgttgaaacagcg	*US*3, 1427-1446
*US*4 full	**AAAAAGCGAGGCT***ccgcc*atgtcgcagggcgccatg	*US*4, 1-18	**AGAAAGCTGGGT**ctacccgcgttcggacggc	*US*4, 699-714
*US*4 frag A	**AAAAAGCGAGGCT***ccgcc*atgtcgcagggcgccatg	*US*4, 1-18	**AGAAAGCTGGGT**ctaggtgtccagggcgggg	*US*4, 555-570
*US*5 full	**AAAAAGCGAGGCT***ccgcc*atgtctctgcgcgcagtc	*US*5, 1-18	**AGAAAGCTGGGT**ctatacgacaactgggtccatgtag	*US*5, 255-276
*US*6 full	**AAAAAGCGAGGCT***ccgcc*atgggggggctgccg	*US*6, 1-16	**AGAAAGCTGGGT**ctagtaaaacaagggctggtgcg	*US*6, 1163-1182
*US*7 full	**AAAAAGCGAGGCT***ccgcc*atgccgtgccgcccgttg	*US*7, 1-18	**AGAAAGCTGGGT**ctataccaacaggggaggcgttg	*US*7, 1151-1170

US7 frag B	**AAAAAGCGAGGCT***ccgcc*atgcacagatgtcaacgccgc	*US7*, 889-906	**AGAAAGCTGGGT**ctataccaacaggggaggcgttg	*US7*, 1151-1170
*US*8 full	**AAAAAGCGAGGCT***ccgcc*atggatcgcggggcgg	*US*8, 1-16	**AGAAAGCTGGGT**ctaccagaagacggacgaatcg	*US*8, 1632-1650
*US*8 frag A	**AAAAAGCGAGGCT***ccgcc*atggatcgcggggcgg	*US*8, 1-16	**AGAAAGCTGGGT**ctaccctaaccgcagggcgc	*US*8, 1247-1263
*US*8 frag B	**AAAAAGCGAGGCT***ccgcc*atgcgcaggcgtgcctggc	*US*8, 1333-1348	**AGAAAGCTGGGT**ctaccagaagacggacgaatcg	*US*8, 1632-1650
*US*8.5 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggatccggctttgagatc	*US*8A, 1-20	GGGGACCACTTTGTACAAGAAAGCTGGGTCttatgcgcctcgggcaattg	*US*8A, 461-480
*US*9 full	**AAAAAGCGAGGCT***ccgcc*atgacgtcccggctctcc	*US*9, 1-18	**AGAAAGCTGGGT**ctagcggagcagccacatcag	*US*9, 253-270
*US*10 full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatgatcaagcggcggggcaa	*US*10, 20	GGGGACCACTTTGTACAAGAAAGCTGGGTCctagcacaggggtggggtta	*US*10, 940-939
*US*11 full	**AAAAAGCGAGGCT***ccgcc*atgagccagacccaacccc	*US*11, 1-19	**AGAAAGCTGGGT**ctatacagacccgcgagccg	*US*11, 467-483
*US*12 full	**AAAAAGCGAGGCT***ccgcc*atgtcgtgggccctggaaatg	*US*12, 1-21	**AGAAAGCTGGGT**ctaacgggttaccggattacgg	*US*12, 252-264
*RS*1 (ICP4) full	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcgtcggagaacaagcagc	*RS*1, 1-23	GGGGACCACTTTGTACAAGAAAGCTGGGTCttacagcaccccgtccccctcg	*RS*1, 3876-3897
*RS*1 (ICP4) frag A	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcgtcggagaacaagcagc	*RS*1, 1-23	GGGGACCACTTTGTACAAGAAAGCTGGGTCgctgacgtacccgacgcgatag	*RS*1, 915-936
*RS*1 (ICP4) frag B	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCgtcgagctggacgccgacgcgac	*RS*1, 871-893	GGGGACCACTTTGTACAAGAAAGCTGGGTCcaggcgcatgagcaccagcgcgtc	*RS*1, 1904-1926
*RS*1 (ICP4) frag D	GGGGACAAGTTTGTACAAAAAAGCGAGGCTTCatggcggcctggatgcgccagatc	*RS*1, 2743-2767	GGGGACCACTTTGTACAAGAAAGCTGGGTCttacagcaccccgtccccctcg	*RS*1, 3876-3897

[a] Name of molecular clone. Full indicates full length clone. Frag indicates clone has a portion of the full length ORF. ORF names and characteristics from Genbank NC_001806.

[b] Nucleotide sequences of primers. Primers starting with bolded regions are from the Haas lab. Bolded regions have *att* homology for Gateway™ cloning, adjacent italic regions are *ccgcc* linkers in 5' primers only, and regular font regions are from the Genbank NC_001806 HSV-1 genome. Primers without bolding are from the Koelle lab. These have capitalized *att* homology regions followed by lower case regions from the HSV-1 genome.

[c] Name of HSV-1 ORF to be amplified from Genbank NC_001806, followed by nucleotides within the ORF coding region included in the primer. Integers refer to the nominal isomer of the HSV-1 genome and diploid HSV-1 gene nucleotide numbers correspond to first (leftward) allele along the linear genome of the nominal isomer. Minus or plus signs in parentheses refer the number of nucleotides offset 5’ or 3’ to the canonical ATG start or last coding nucleotide, respectively.

Supplementary Table 2. HSV-1 ORFs scoring positive for HLA class I-restricted IFN-γ responses for responder cells created by cross-presentation of HSV-1-infected cells by moDC to CD8+ T-cells, sort-enrichment of CD137^{high}, and non-specific expansion.

gene[a]	protein[a]	kinetics[b]	E/NE[b]	virion[c]	function[b]
UL1	gL	γ	E	Y	Modulates gH, fusion
UL9		β	E	N	Helicase/ATPase, DNA binding/synthesis
UL10	gM	γ2	NE	Y	Membrane domains, complexes with UL49.5
UL12		β	NE	N	Alkaline nuclease
UL13		γ	NE	Y	Tegument, protein kinase
UL15	terminase	γ	E	N	DNA cleavage and packaging
UL16		γ1	E	Y	Unknown
UL17		γ	NE	Y	Tegument, DNA cleavage and packaging
UL18	VP23	γ1	E	Y	Capsid
UL19	VP5/ICP5	γ	E	Y	Capsid
UL21		γ	NE	Y	Tegument, microtubule binding
UL23	TK	β	NE	Y	Thymidine kinase, neurovirulence
UL25		γ2	E	Y	Capsid
UL27	gB	γ1	E	Y	Major envelope glycoprotein, entry/fusion
UL29	ICP8	β	E	N	ssDNA binding
UL30		β	E	N	DNA polymerase
UL31		γ	E/NE	N	Nuclear phosphoprotein, binds lamins
UL34		γ1	E	N	Nuclear egress
UL37	ICP32	γ1	E	Y	Tegument
UL38	VP19C	γ2	E	Y	Capsid
UL39	ICP6/10	β	NE	N	Ribonucleotide reductase
UL40		β	U	N	Ribonucleotide reductase
UL41	vhs	γ1	NE	Y	Tegument, RNAse, reduces host protein synthesis
UL46	VP11/12	γ1	NE	Y	Tegument
UL47	VP13/14	γ1	NE	Y	Tegument
UL48	VP16/ICP25	γ	E	Y	Tegument, pre-formed transactivator
UL49	VP22	γ?	NE/E	Y	Tegument

UL50		β	NE	Y	dUTPase
UL52		β	E	N	Helicase/primase subunit
UL53	gK	γ	NE	N	Virion exocytosis, syncytia
UL54	ICP27	α	E	N	RNA processing
US1/1.5	ICP22	α	NE	N	Cell cycle
US3		γ1	NE	Y	Serine threonine kinase
US6	gD	γ	E	Y	Major envelope glycoprotein, binding/entry
US7	gI	γ1	NE	Y	Component of viral Fc receptor
US8	gE	γ1	NE	Y	Component of viral Fc receptor
US9		γ	NE	Y	Unknown
RL2	ICP0	α	NE	Y	E3 ligase, IFN evasion, multiple functions
RL1	ICP γfs34.5	γ1	NE	Y	Evasion of type I IFN response
RS1	ICP4	α	E	Y	Repressor/transactivator

[a] Gene and protein names from [1] and Genbank NC_001806. Not all gene products have separate names.

[b] Expression kinetics (pre-α=hypothetical synthesis during latency, α=immediate early expression dependent on UL48 transactivation, β=early expression but after α proteins, γ1=some expression prior to DNA replication, γ2=expression only after DNA replication, γ=differentiation into γ1 or γ2 not reported; requirement for replication *in vitro* (E=essential, NE=not essential, E/NE=cell type dependent, U=unknown); brief functional summary [1].

[c] Presence of absence in highly purified virions [2]; Y = yes, N= no.

References: Supplementary Tables

[1] Roizman B, Knipe, D.M., Whitley, R.J. Herpes simplex viruses. In: Knipe DM, Howley, P.M., editor. Fields Virology. Fifth ed. Philadelphia: Lippincott, Williams, and Wilkins, 2007: 2501-602.

[2] Loret S, Guay G, Lippe R. Comprehensive characterization of extracellular herpes simplex virus type 1 virions. J Virol 2008 Sep;82(17):8605-18.