

1 **Supplementary Figure 1.** ClustalW alignment of the amino acid sequences of  
2 alphaherpes virus  $\alpha$ 22 homologs. The source of the sequences is described in Table 1.

3

1 **Supplementary Figure 1**

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4	HSV-1	MADISPGAFAPCVKARRPALR-SPPLGTRKRRKRRPSRPLSSESEVESDTELESEVESETAS	59
5	HSV-2	MADIPPDPPALNTTPANHAPP-SPPPGSRKRRRPVLPSSSESESEKPDTESESE---SSTES	56
6	SA8	---MPTDTSAFASASANPSPPPSPVLNGSRRCFRRLPSLSDSDSEGSSGAVVLGGGEAGL	57
7	VZV	-----MFCTSPATRGDS-----SES-----	15
8	GaHV-2	-----	
9	DEV	---MATASRRPSGQACEQVTVTVSYVQGLSNPSTSTALWSSPPATLTKPSIE-----	49
10			
11			
12	HSV-1	DSTESGDQDEAPRIGRRRAPRRLGGRFFLDMSAESTTGTET-----	100
13	HSV-2	SEDEAGD----LRGRRRSPRELGGRYFLDLSAESTTGTES-----	93
14	SA8	ESGGATD----QRSRVRGGLRVAGGMYFIDDEAEEASELESEPETDTDFESVSEADLESV	113
15	VZV	-----	
16	GaHV-2	-----	
17	DEV	-----	
18			
19			
20	HSV-1	-DAS--VSDDPDDTSD-WSYDDIPPRPKRARVNLRLTSSPDRRDGVIFFPKMGR-VRSTRE	155
21	HSV-2	-EGTGPSDDDDDDASDGWLVDTPPRKSKRPRINLRLTSSPDRRAGVVFPEVWRSRPIRA	152
22	SA8	SEVTSGLGSDSDSDSDGSADEPRAGRQPPIRINIRLVSSPDRRAGVVFPEVWRSRPIRA	169
23	VZV	-----KPGASVDVNGKMEYGSAPGLNG-----	38
24	GaHV-2	-----MSRDRDRARPDTLSSSDNESDDEDYQLPHS-----	31
25	DEV	-----SPRRQLDPRTPVKPRQQMSPAGGDMWDLHKS----ITV	83
26			
27			
28	HSV-1	TQPRAPTSPASPNAMLRRSVRQAQRSSARWTPDLGYMRQCINQLFRVLRVARD-PHGS	214
29	HSV-2	AQPQAP-ASLPGIAHAHRRSARQAQMRSGAAWTLDLHYIRQCVNQLFRILRAAPN-PPGS	210
30	SA8	SPGTET-PPSERPDGSEERRATRASEGHHPEWSPDLPYLRRSINGMFRLLRRGIN-PRGA	227
31	VZV	-----RDTSRGPGAFCTPGWEIHPARLVEDINRVFLCIAQSSGRVTRD	81
32	GaHV-2	-----HPEYGSDDSDQDFELNNVGFKFCPLPWKPDVARLCADTNKLFRCFIRCLNSGPF	85
33	DEV	DHKEYGPPVPPDEARSGMDPKMGPGAFASFWLPDATTRLGDVNVLFKAIIRASGSTGRY	143
34		* . : * :*	
35			
36	HSV-1	ANRLRHLIRDCYLMGYCRARLAPRTWCRLQVSGGTWGMHLRNTIREVEARFDATAEPCV	274
37	HSV-2	ANRLRHLVRDCYLMGYCRTLGPRTWGRLQISGGTWDVRLRNAIREVEAHFEPAAEPCV	270
38	SA8	ADRLRRLVRDCYLLGYTRHRLPEGMWPRMLQVGGG-QAARLRNVIENVVLRAGDAGE-IL	285
39	VZV	SRRLRRLICLDFYLMGRTRQRPTLACWEELLQLQPT-QTQCLRATLMEVSHRPPRGEDGFI	140
40	GaHV-2	HDALRRALFDIHMIGRMGYRLKQAEWETIMNLTTPR-QLHLRRTLRDADSR---SAHPIS	141
41	DEV	CRAFRRSLLEFYLIIGRYGPRLPREGWEATLQLSPN-QSGPLRAVLREADGRIVNNTGYME	202
42		*: : ::* * * : : ** . : . :	
43			
44	HSV-1	KLPCLETRRYGPECDSLNLIEHLSATS--DDEISDATDLEAAGSDHTLASQSDTEDAPSP	332
45	HSV-2	ELPCLNARRYGPECVGNLETNGGSTS--DDEISDATD-----SDDTLASHSDTEGGPSP	323
46	SA8	PMPPSPREHHGVACDRSD-ASDAASDD--DSRLGPGDDDTPDSDATLESASDDERAAAP	342
47	VZV	EAPNVPLHRSALECDVSD---DGGEDD--SDDDGSTPSDVIEFRSDAESSDGEDFIVEE	195
48	GaHV-2	DIYASDSIFHPIAASSGTISSDCDVKG--MNDLS-----VDSKLH-----	179
49	DEV	GPFPGTEAPYGAECEVDGGCYSDDERSECESDLSEGDMNFVLSDDTESERGYDSDASVRS	262
50		. . . . *	
51			
52	HSV-1	VTLE---TPE--PRGSLAVRLEDEFGEFDWTPQEGSQPWLSAVVADTSSVERPGPSDGA	387
53	HSV-2	AGRE---NPESASGGAIARLECEFGTFDWTSEEGSQPWLSAVVADTSSAERSGLPAGA	380
54	SA8	PGAASGGPPEENAPGSVASRLRREFFVAFDWTPEEGSQPWLSVAVDTSSEARRRGDSGPG	402
55	VZV	ESEE---STDSCEPDGVPDCYRDGDGNCNTPSPKRPQ----RAIERYAGAETAETAAKA	248
56	GaHV-2	-----	
57	DEV	VTSSSHSNCDDVDYDPLGDLSEEEEMTSSVSTSDSESEVIEVIGTKRKRPTTRSMSALAG	322
58			
59			
60	HSV-1	GRAAEDRKCLDGCCKMRFSTACPYPCSDTFLRP	420
61	HSV-2	CRATEAPEREDGCRKMRFPAAACPYPCGHTFLRP	413
62	SA8	CRERETG----GCRMRRFSTTCPYPCGRTFRLM	431
63	VZV	LTALGEGGVWDKRRRHEAPRRHDIPPPFGV---	278
64	GaHV-2	-----	
65	DEV	TTKRPKS-----	329
66			