

A

DH840.K_UCA	EIVMTQSPAT	LSLSPGERAT	LSCRASQSVS	SRLAWYQQKP	GQAPRLLIYD	50
DH840.1L	..MV.....	..V.....R	N.I.....	..S.....	
DH840.K_UCA	ASSRATGIPD	RFSGSGSGTE	FTLTISSLEP	EDVAVYFCQQ	ESNWLTFGGG	100
DH840.1L	..I..P....	.L.....N....	S.....L	.A.....	
DH840.K_UCA	TKVEIK....	115			
DH840.1L				

B

DH842.L_UCA	QPVLTOPTSL	SASPGASARL	TCTLRSGISV	GSYRIFWYQQ	KPGSPPRYLL	50
DH842.L	.A.....A.	AD.....	R.....	
DH842.L_UCA	NYHTSDSKHQ	GSGVPSRFSG	SKDASANAGI	LLISGLQSED	EADYYCMIWH	100
DH842.L	..R....H..D...T.F	.V.....H...R.	
DH842.L_UCA	NNAYIFGAGT	RLTVL	115			
DH842.L	.T.....G..	...L.				

C

DH845.K_UCA	DIQMTQSPSA	LSASVGDRVT	ISCRASQNIY	SGLAWYQQKP	GKAPKLLIYA	50
DH845.1L	A..L.....N.....FG	
DH845.2L	A..L.....S.....V....	
DH845.3L	A..L.....N.....FG	
DH845.4L	A..L.....N.....FG	
DH845.K_UCA	ASRLQSGIPS	RFSGSGSGTD	FTLTISLQP	EDSAAYYCQQ	VYSNFYSPGQ	100
DH845.1LT....	
DH845.2L	
DH845.3LT....	
DH845.4LT....	
DH845.K_UCA	GTKVEIK...	115			
DH845.1L				
DH845.2L				
DH845.3L				
DH845.4L				

D

DH846.K_UCA	EIVMTQSPAT	LSLSPGERAT	LSCRASQSVS	SRLAWYQQKP	GQAPRLLIYD	50
DH846.1L	
DH846.2LF.....	T.....	
DH846.K_UCA	ASSRATGIPD	RFSGSGSGTE	FTLTISSLEP	EDVAVYFCQQ	ESNWSTFGQG	100
DH846.1L	..N.....G...E	DH.....	
DH846.2L	..I.....F.....	DN.....	
DH846.K_UCA	TKVEIK....	115			
DH846.1L				
DH846.2L				

S9 Fig. Amino acid alignments of light chain variable regions for each CON-S autologous neutralizing antibody clonal lineages. Amino acids for (A) DH840, (B) DH842, (C) DH845, and (D) DH846 lineages are shown. Periods indicate the presence of identical amino acids at that position. UCAs were inferred with Cloanlyst using the 2017 macaque reference library.