

Figure S1A. Unrooted NJ tree of **SIVsmE660** stock (black) and variants at ramp-up from animal **CG7V** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CG7V sequences inside the orange rectangle.

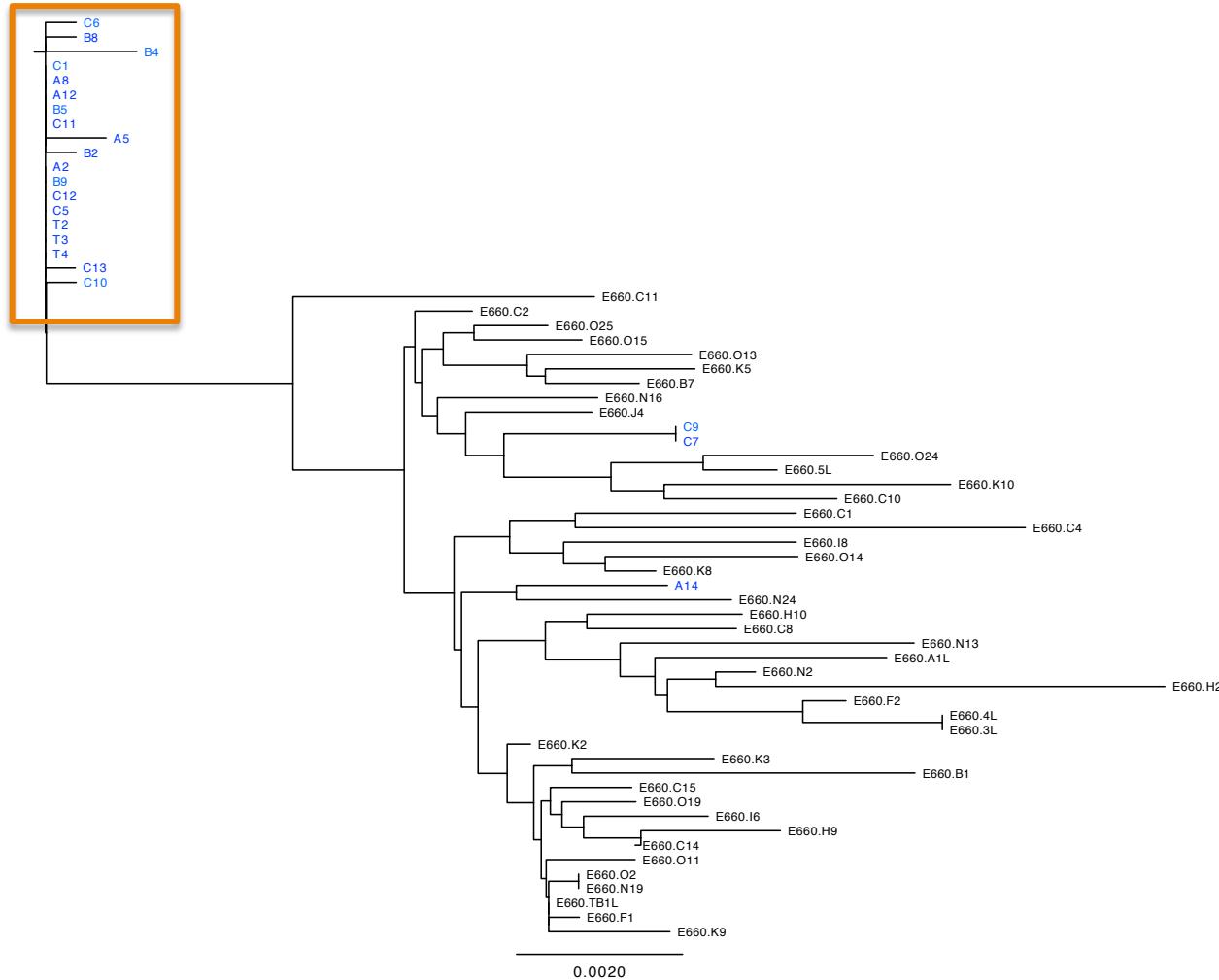


Figure S1B. Unrooted NJ tree of **SIVsmE660** stock (black) and variants at ramp-up from animal **CP3C** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CP3C sequences inside the orange rectangle.

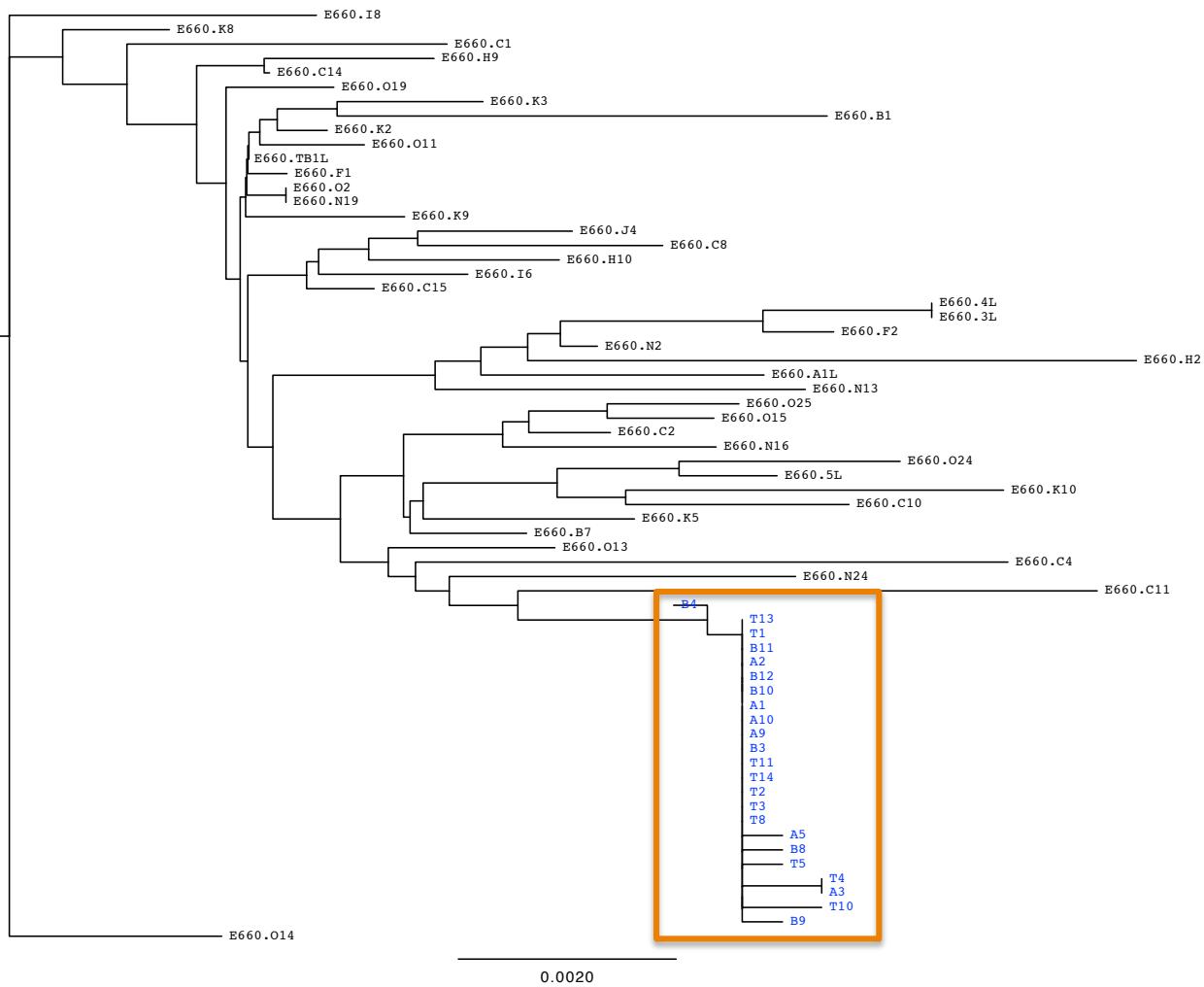


Figure S1C. Unrooted NJ tree of **SIVsmE660** stock (black) and variants at ramp-up from animal **CG87** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CG87 sequences inside the orange rectangle.

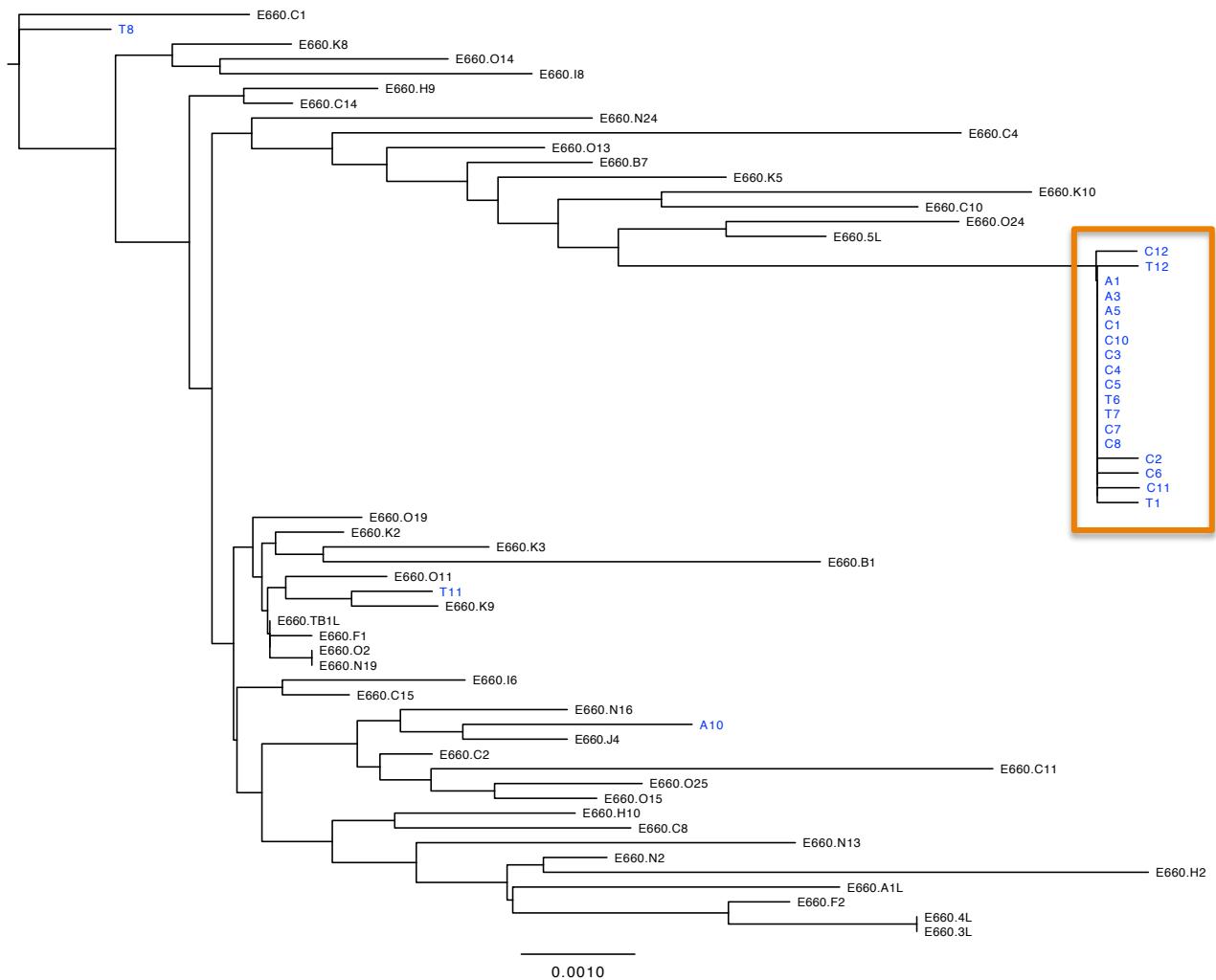


Figure S1D. Unrooted NJ tree of **SIVsmE660** stock (black) and variants at ramp-up from animal **CG7G** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CG7G sequences inside the orange rectangle.

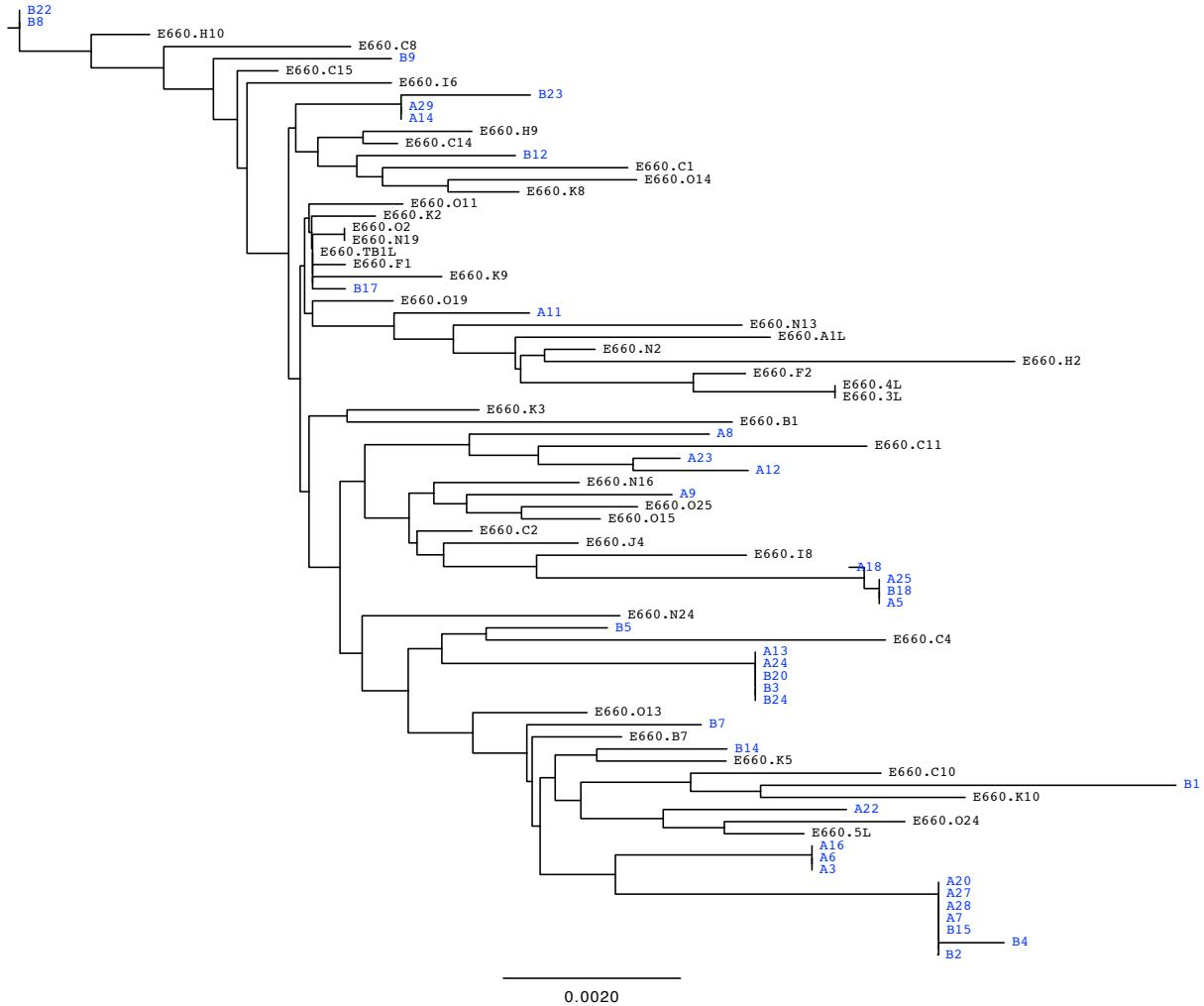


Figure S1E. Unrooted NJ tree of **SIVsmE660** stock (black) and variants at ramp-up from animal **CP37** (blue). A single predominant lineage could not be clearly identified and thus animal CP37 was discarded from the present study.

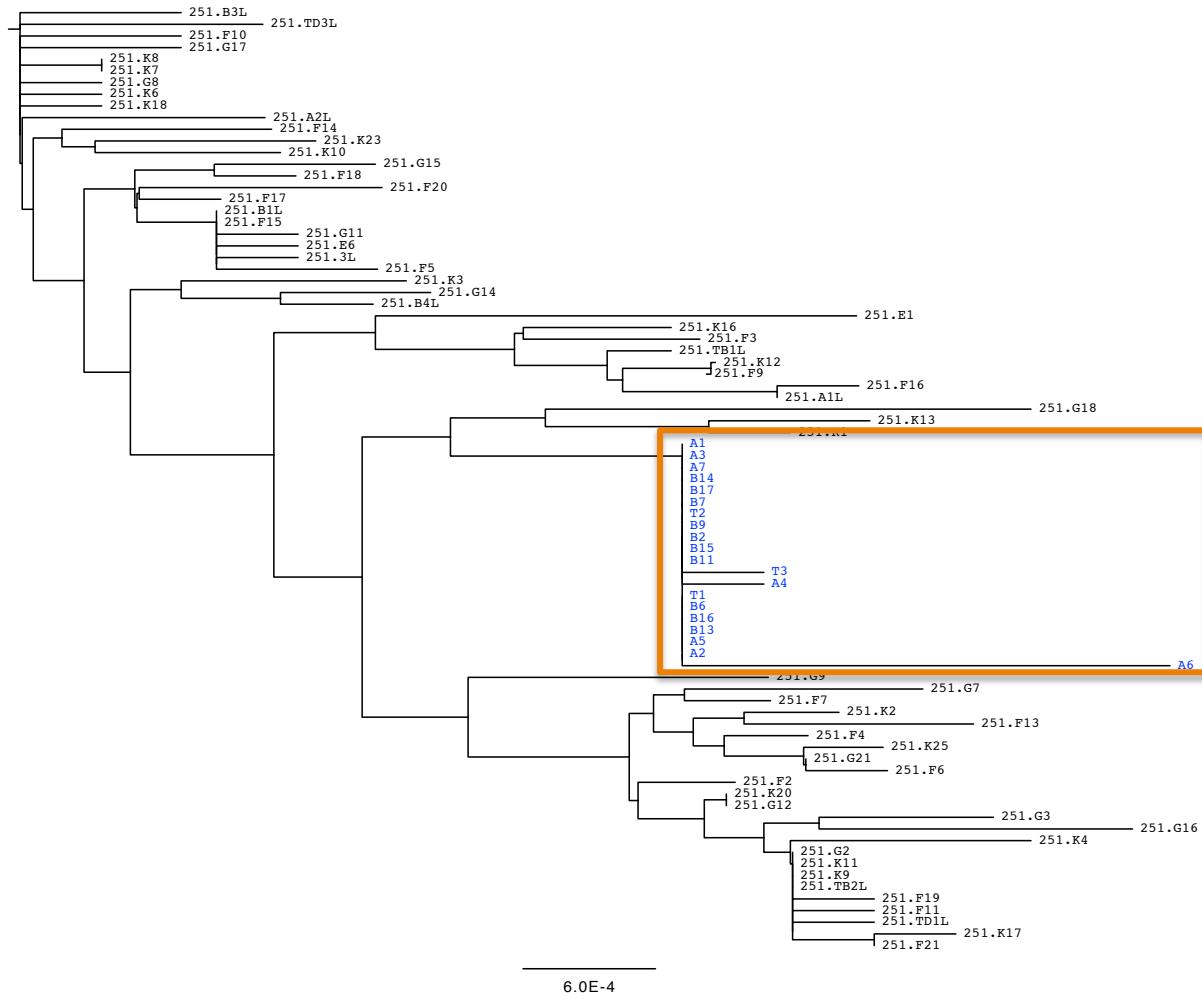


Figure S2A. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **AV66** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the AV66 sequences inside the orange rectangle.

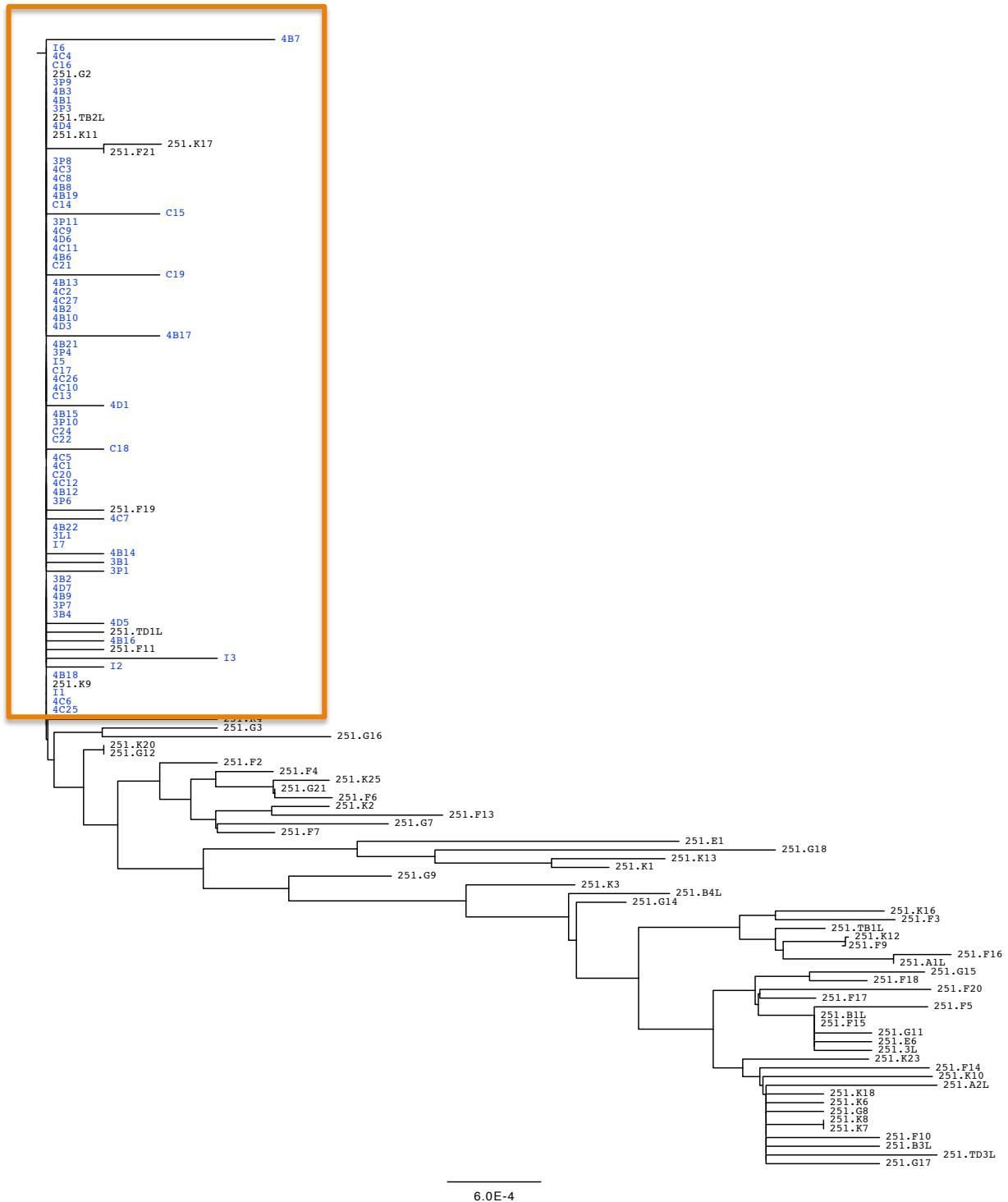


Figure S2B. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **CP1W** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CP1W sequences inside the orange rectangle.

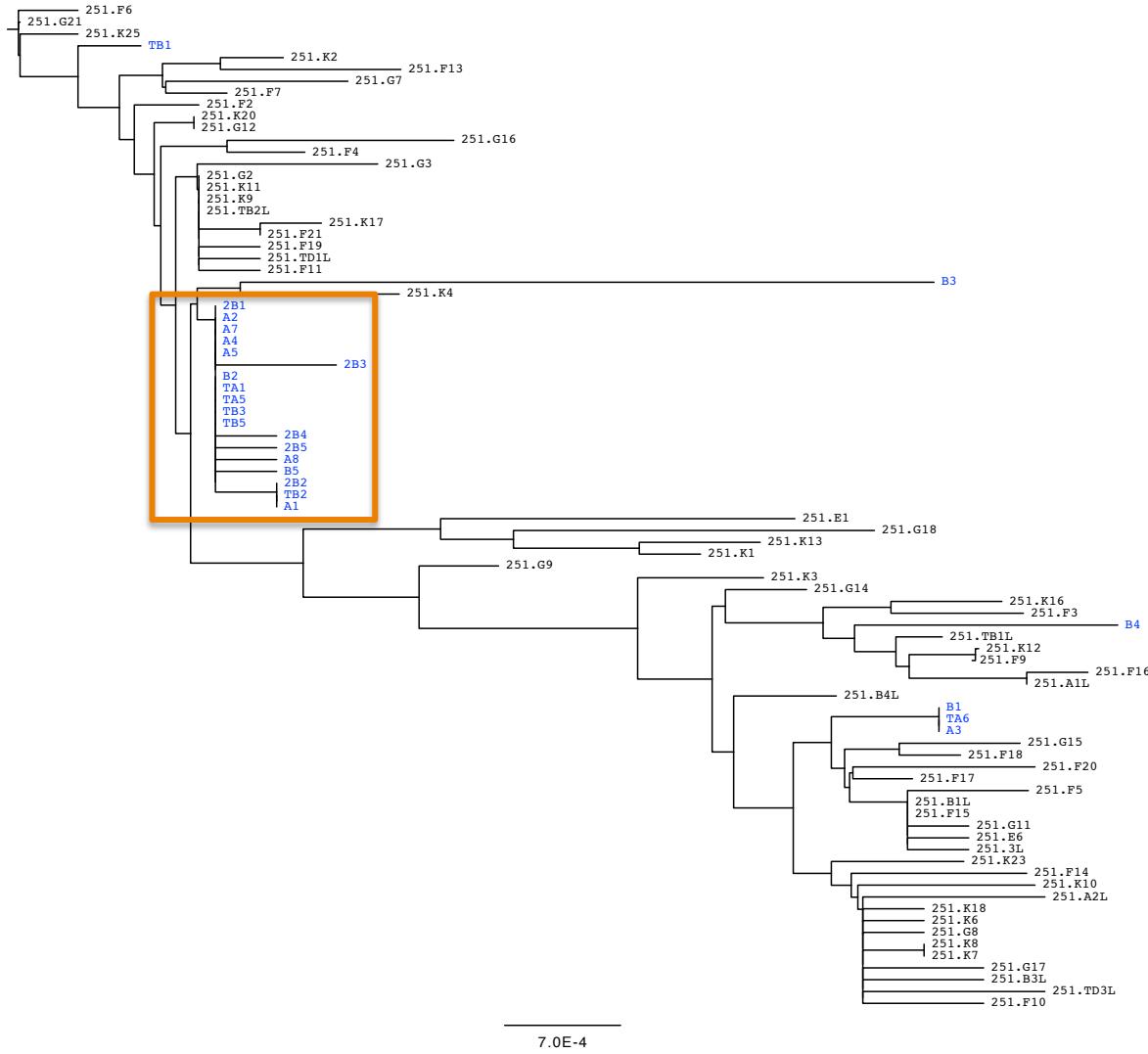


Figure S2C. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **CT76** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CT76 sequences inside the orange rectangle.

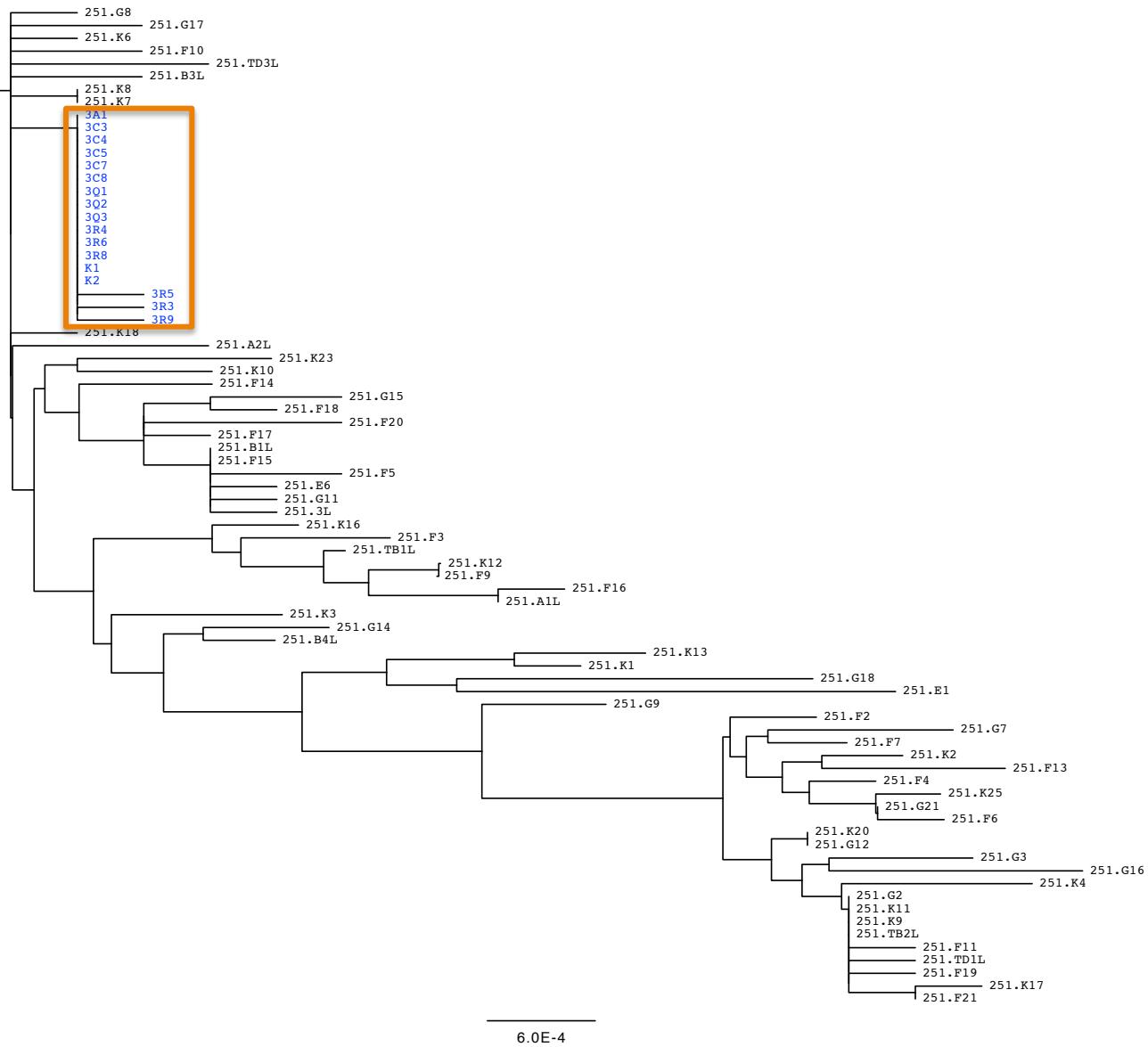


Figure S2D. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **PBE** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the PBE sequences inside the orange rectangle.

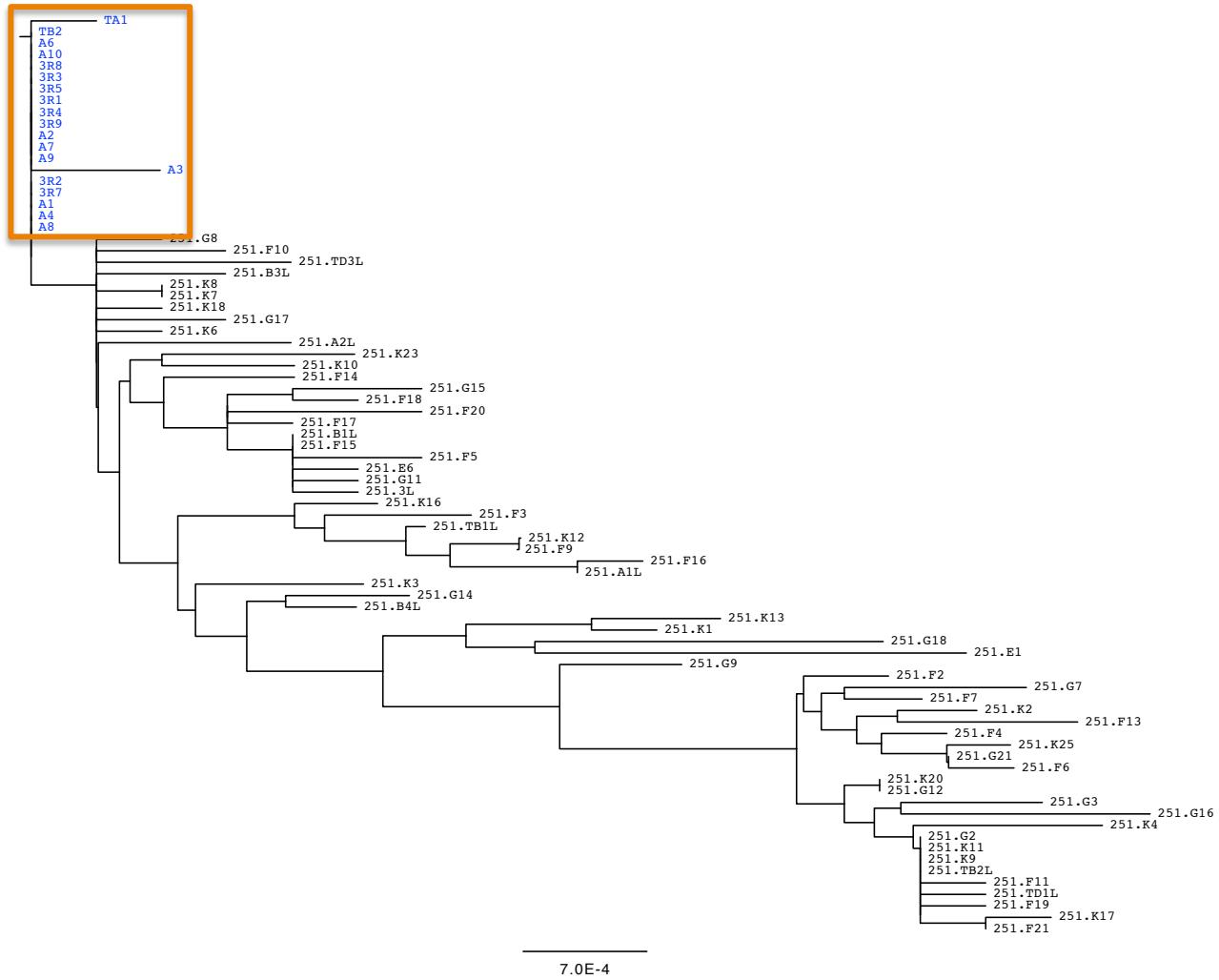


Figure S2E. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **CR2A** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CR2A sequences inside the orange rectangle.

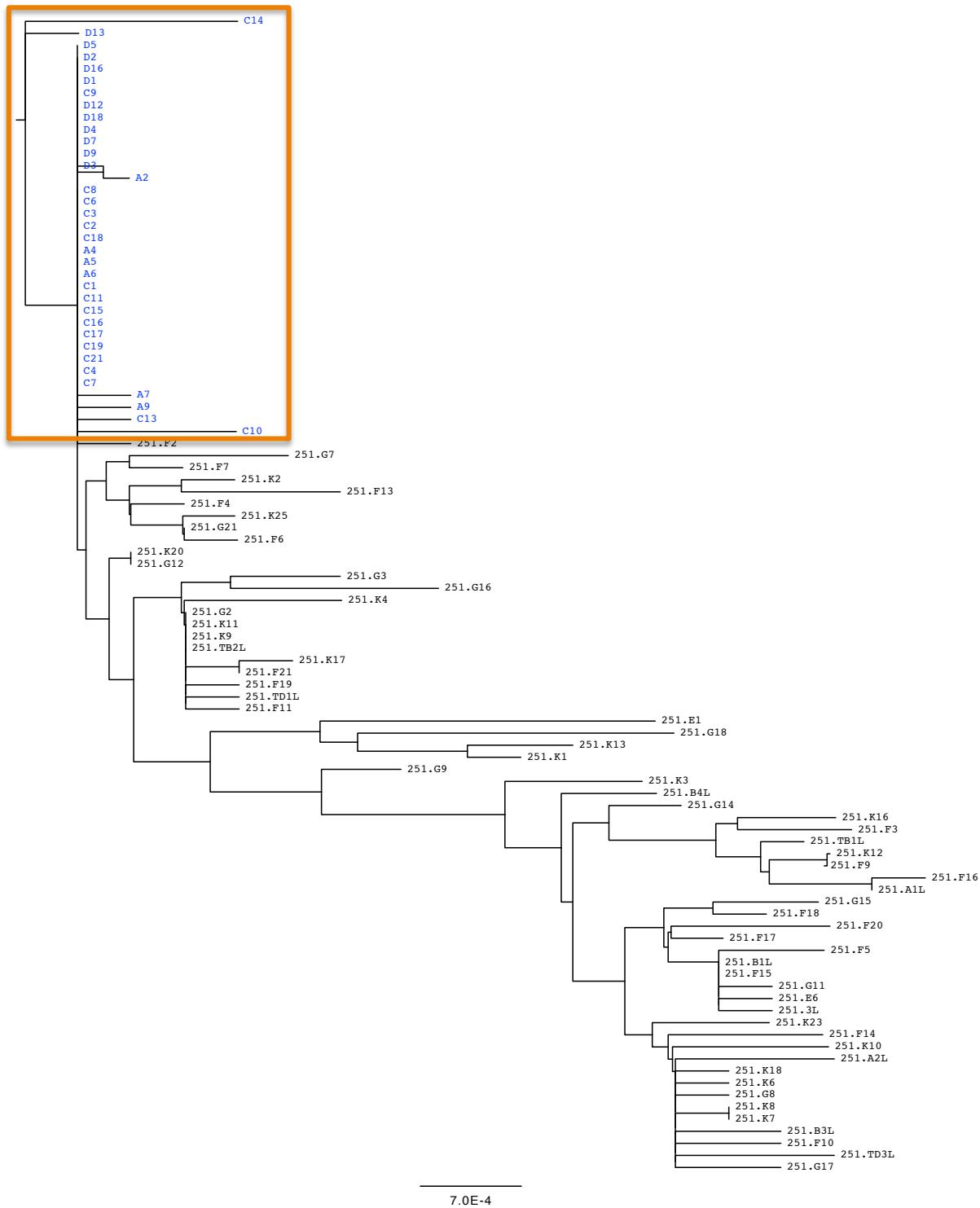


Figure S2F. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **AV74** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the AV74 sequences inside the orange rectangle.

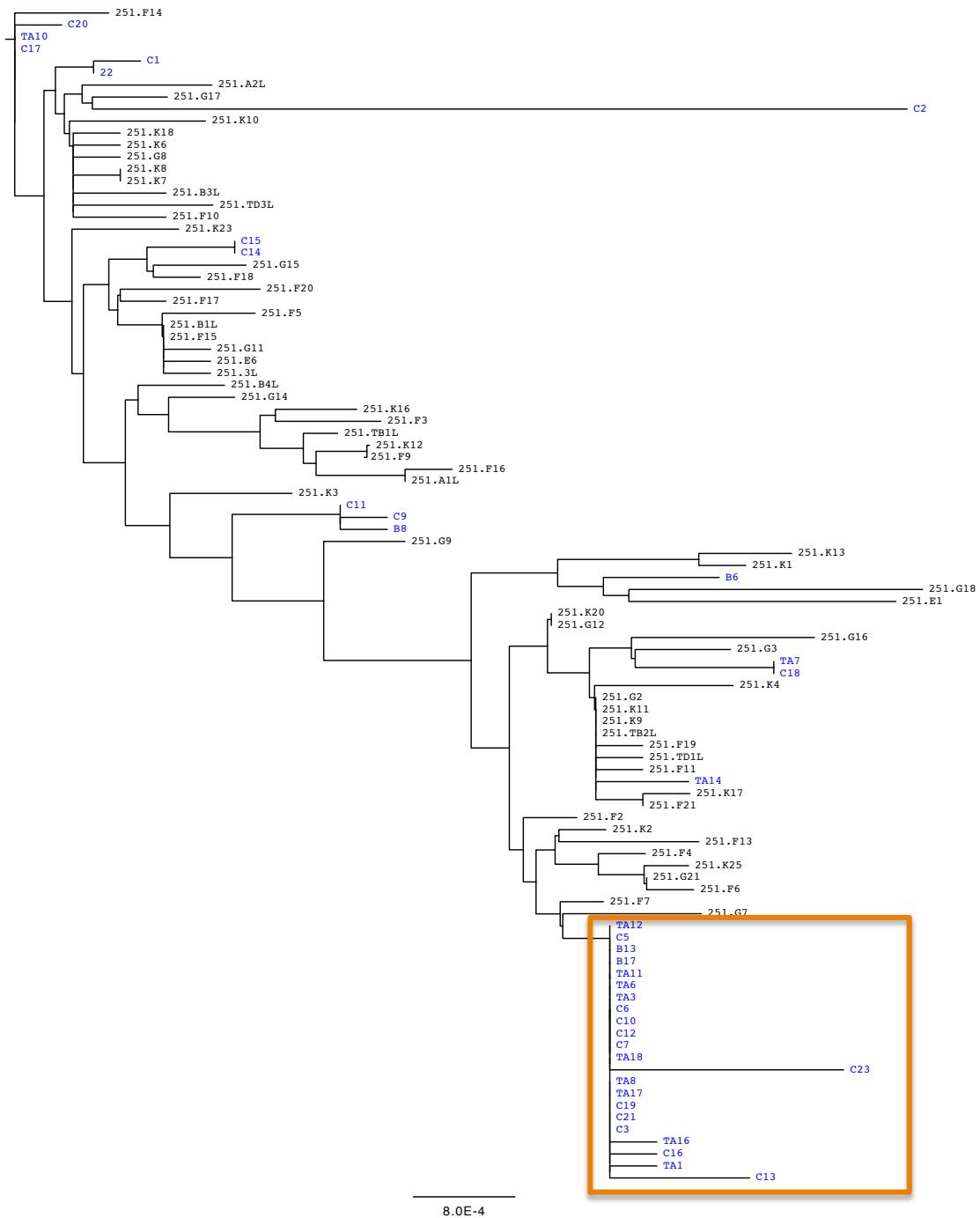


Figure S2G. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **CG71** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CG71 sequences inside the orange rectangle.

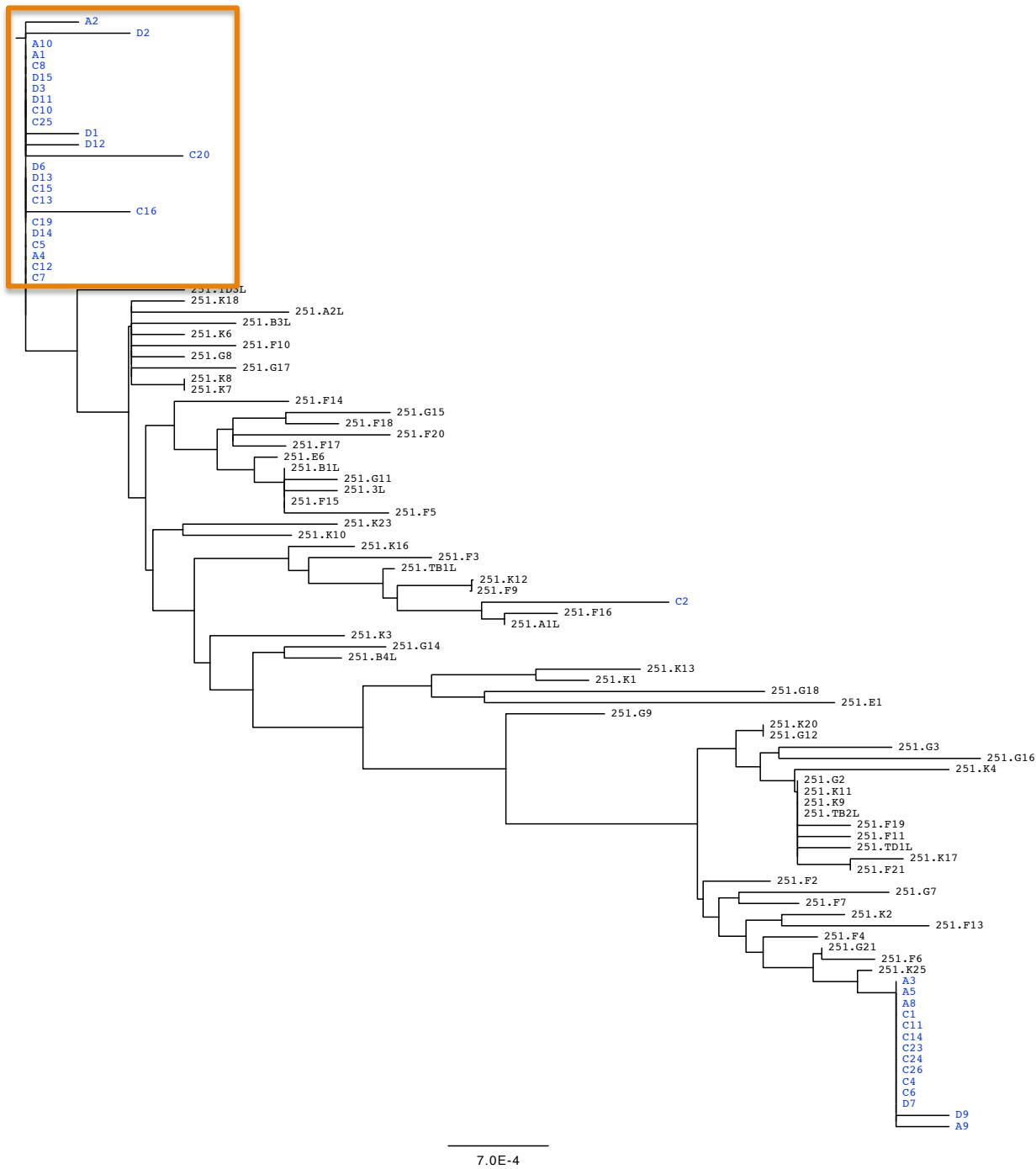


Figure S2H. Unrooted NJ tree of **SIVmac251** stock (black) and variants at ramp-up from animal **CG5G** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the CG5G sequences inside the orange rectangle.



Figure S3A. Unrooted NJ tree of **SHIVBaL** stock (black) and variants at ramp-up from animal **R557**(blue). Predominant lineage chosen to deduce the T/F consensus consists of the R557 sequences inside the orange rectangle.



Figure S3B. Unrooted NJ tree of **SHIVBaL** stock (black) and variants at ramp-up from animal **HJ38** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the HJ38 sequences inside the orange rectangle.



Figure S3C. Unrooted NJ tree of **SHIVBaL** stock (black) and variants at ramp-up from animal **HL02** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the HL02 sequences inside the orange rectangle.

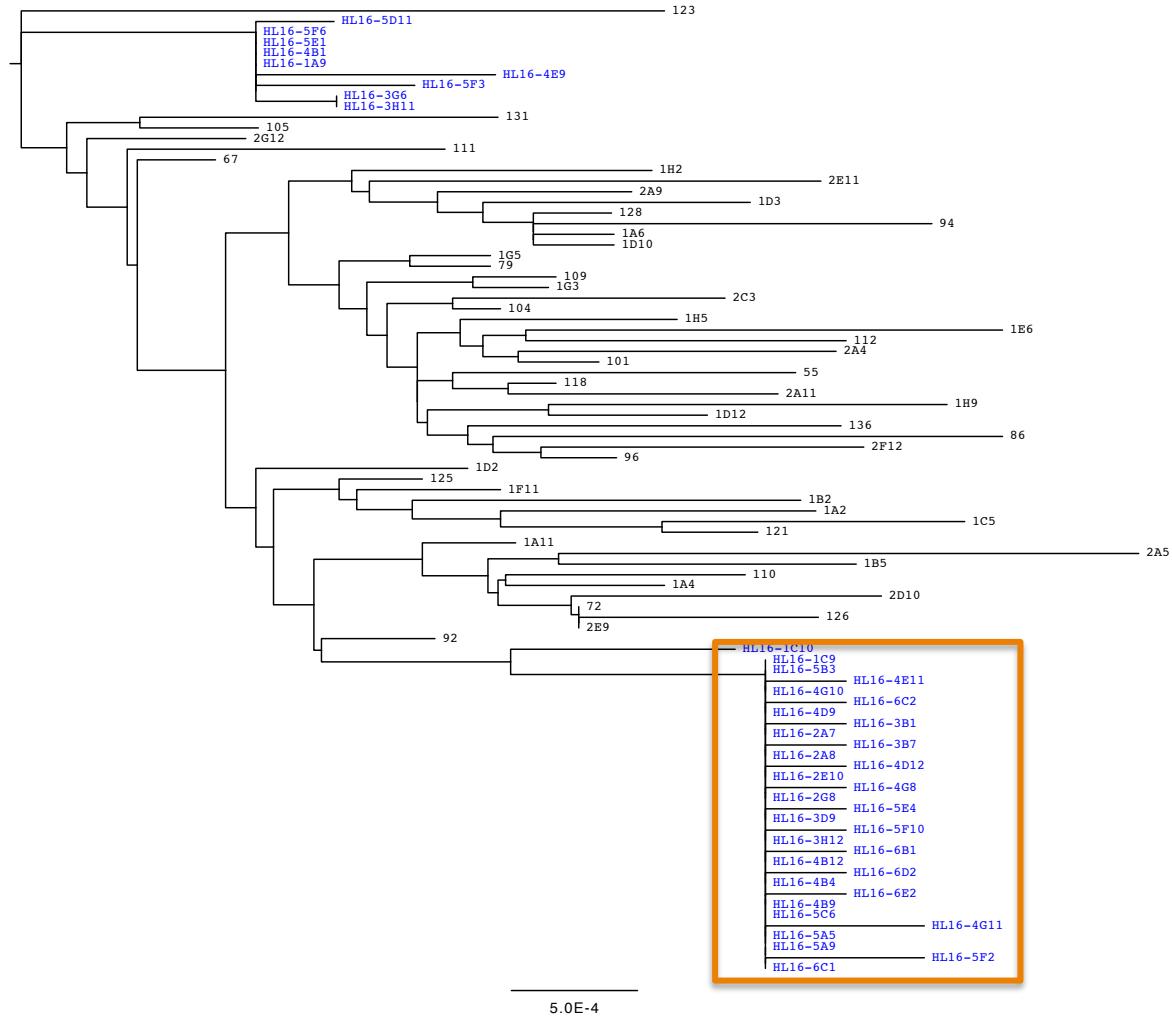


Figure S3D. Unrooted NJ tree of **SHIVBaL** stock (black) and variants at ramp-up from animal **HL16** (blue). Predominant lineage chosen to deduce the T/F consensus consists of the HL16 sequences inside the orange rectangle.

Figure S4:

Please refer to ftp://ftp.ncbi.nlm.nih.gov/pub/gonzale3/gonzalez_JVI03235-14_S4/ to access the gene and protein sequences examined by the present study.

		6	9															33
KeeleE660 stock	M S S	T E E	E L R K R	L R L I	H F I L H Q T S K M G C L G N Q L L I A L	L L V S A L E I Y C	V Q Y V											
KeeleE660 f.	.	.	.	R	I	.	.	
Keelemac251 stock	.	.	H G R	.	K	.	.	L	.	Y	.	.	I	.	L	V Y G	.	T
S Keelemac251 f.	.	.	H E R	.	K	.	.	L	I	.	L	V Y G	.	T
I RoedE660 stock	V	.	.	
V RoedE660 control f.	V	.	.		
RoedE660 gag f.	V	.	.		
RoedE660 mosEnv f.	I	.	.		
RoedE660 m239Env f.	I	.	.		
HXB2 1906385	M R V K E	K	Y Q H L W R W G		W R W . T M	.	G M L	M I C S A T E	K L W V									
KleinSHIV stock	.	T E I R K S	.	W	.	.	I	.	.	I	.	N	.	E	.	.	.	
KleinSHIV f.	.	T	K S	.	W	.	I	.	I	.	N	.	E	
pSF257-SHIV f.	N	.	R G	K N	W	W G	.	G I	.	M	.	Y	N	.	G	Q	.	
S Step placebo f.	.	G	K N	A	
H Step vaccine f.	E	A E D S G	N E S R G S		G R I I S T	.	I	Q	.	.	.	
I Gnanakaran orig. FS2	.	K N W	G M M	.	.	A	.	N L	.	G	.	
V Gnanakaran orig. FS3	.	G	K N	.	.	.	K	.	I	.	.	Q	
Gnanakaran orig. FS4	.	T	R N W	.	.	.	K	.	.	.	A	Q	
Gnanakaran orig. FS5	.	G	K N	.	.	G D	I	.	.	.	A	E	G Q	
H Gnanakaran orig. FS6	K	.	K N C P C	.	.	.	G	L	.	.	A	Q	
I Gnanakaran orig. FSC	.	G	R N	.	G	G T M R L	.	S L I M	.	M	.	A K	Q	E Q	.	.	.	
V Gnanakaran hold. FS2	.	K N	.	.	G I M L	L	.	I	.	M	.	A	E	Q	.	.	.	
Gnanakaran hold. FS3	.	R N W	.	.	.	K	A	Q	
Gnanakaran hold. FS4	.	G	K N	.	.	G I M L L	K	.	I	.	I	.	G G	
Gnanakaran hold. FS5	.	G	K N	.	.	.	I	.	.	I	.	A	.	N	.	.	.	
Gnanakaran hold. FS6	.	G	K N C	.	.	.	G	I L	.	.	.	N K E N	
Gnanakaran hold. FSC	.	G	K N	.	.	G G I L N L	.	G	.	M	.	AA	E	Q	.	.	*	
55																		
KeeleE660 stock	T V F Y G V P A W K N A T I P L F C	T			T R	N R D T W G T T Q C L P D N D D Y S E L A I		S I										
KeeleE660 f.	A	.	K	N	.	N	.	N	.	
S Keelemac251 stock	.	.	.	R	A	.	K	.	.	G	.	N	.	N	V	N	V	
I RoedE660 stock	T	R	.	.	.	G	.	L	N	V	.	S	.	
V RoedE660 control f.	T	R	.	.	.	G	.	S	.	S	.	S	.	
RoedE660 gag f.	T	R	.	.	.	G	.	S	.	S	.	S	.	
RoedE660 mosEnv f.	.	.	A	T	A	K	.	.	L	.	N	.	N	.	N	.		
RoedE660 m239Env f.	A	.	A	.	K	N	.	N	.	N	.		*
HXB2 1906385	T V Y Y G V P V W K E A T T L F C	A	S D A K A Y D T E V H N V W A T H A C V P T D P N P Q E V V L V N V															
KleinSHIV stock	.	.	.	A	.	E	E	K	.		.		
KleinSHIV f.	.	.	.	A	.	E	E	.	K	N	.	.		
pSF257-SHIV f.	.	.	.	A	.	E	.	.	.	E	.	E	.	N	.	.		
S Step placebo f.	.	.	.	A	.	E	.	.	E	.	E	.	E	N	.	.		
H Step vaccine f.	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
I Gnanakaran orig. FS2	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
V Gnanakaran orig. FS3	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran orig. FS4	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran orig. FS5	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
H Gnanakaran orig. FS6	.	D	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
I Gnanakaran orig. FSC	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
V Gnanakaran hold. FS2	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran hold. FS3	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran hold. FS4	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran hold. FS5	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran hold. FS6	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		
Gnanakaran hold. FSC	.	.	A	.	E	.	E	.	E	.	E	.	E	N	.	.		*

Figure S6:

Alternative alignment to that shown on Fig. 2. This alignment was built using individual Gnanakaran-HIV sequences from Fiebig stages 2-5 rather than a consensus of all acute sequences, as shown on Fig.2. Note that Gnanakaran et al.'s signature site H12 (in orange) corresponds to HXB2 site H9 in this alignment. In this alternative alignment, the signature residue on the signal peptide falls on position 6 rather than on site 9. Asterisks mark sites with complete conservation across all datasets.