Global variation in the HIV-1 V3 region

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Introduction

Due to the immunogenicity and functional importance of the V3 loop, there has been a great deal of interest in the V3 region of the envelope protein, resulting in a large international effort to obtain V3 region sequences. This section, which includes sequences taken from more than 2500 individuals, with complete references, provides an overview of the variation of sequences that span this region.

Sequences

To best summarize the spectrum of international HIV-1 variants, only one representative viral sequence was included per infected individual. A complete set of references accompanies the sequence alignments, and nomenclature was preserved from the original papers so individuals and isolates can be clearly identified. HIV-1 was deleted from the sequence names in this section, as all sequences included here are HIV-1. Included with the references, when available, are brief descriptions of critical features of the sequences. This includes the health status of the individual from whom the virus was derived, whether or not the virus was cultured, and the year the blood sample was taken, if known.

All sequences are prefaced by a subtype association (see phylogenetic clustering below) and a two letter country code to identify the country in which the individual resided at the time that the blood sample was taken. If the person was a recent immigrant and this information was available, we included the country of origin in the references. The two letter code was developed for Internet (Copyright 1992, Lawrence H. Landwater and the Internet Society), and incorporated here based on a suggestion made by Dr. Francine McCutchan. The key to the country codes follows this introduction. Note that this key was updated for 1998, with several country codes for eastern European nations added since 1995.

Sometimes only one viral sequence was available from a person: a clone from an isolate, or a direct sequence of PCR amplified peripheral blood DNA. For other individuals, up to 80 viral sequences from PCR amplified DNA or RNA from blood samples were available. Consequently, over 11,000 sequences are represented by the 2588 included in this section. When two sequences were available from a person, one of the two was randomly selected. When three or more sequences were generated from a person, all available sequences were aligned (without regard to different time points of sampling) and either one representative sequence was chosen, or a consensus of the most common base found in each position in the alignment was generated. If there was a tie (e.g., 10 As, 10 Ts), the top base or amino acid in the alignment was used. If a set of sequences from two or more individuals was epidemiologically linked, and genetically very similar, only one sequence from the set was included, preferably the most recently infected. In the sequence description and references section, the short hand “PCR-direct, peripheral blood DNA” is used to signify that viral DNA was amplified from PBMCs, without culturing, and a single “direct” sequence was obtained from the amplification reaction products. The short hand “Consensus, PCR-clones, peripheral blood DNA” signifies that viral DNA was amplified from PBMCs and a set of clones was generated and sequenced from the PCR amplification products. The cloned sequences were aligned and a consensus was generated. In a handful of cases, a particular gp160 clone from an isolate was shown to be expressed and functional using a vaccinia virus T7 expression system. In these cases, the clone rather than the consensus of all sequences from a particular individual is included.

Phylogenetic clustering

Sequences have been organized according to the phylogenetic subtype association (A–J) of their envelope V3 regions only. The original sequence subtype (A–H) designations were defined based on the phylogenetic relationships determined by using both gag and env genes (when possible), are

approximately genetically equidistant in envelope, and have multiple members. The phylogenetic subtype designations and associations have generally been adopted by the HIV research community, and are now often presented with the publication of new sequences. We have either determined the subtype designations here, if not specified in the original manuscript, or else confirmed the subtype designations of the original manuscripts, and then used the subtypes to organize this section. Generally, confirmations were done by aligning a set HIV-1 V3 region sequences with longer env gene sequences (Part IIIC) that have clear subtype associations, and then using parsimony or neighbor joining trees to determine associations. Some of the shorter gene fragments from this region were given a subtype designation based on Hamming distances, using the similarity function of the MASE program (Faulkner DV, and Jurka *J. TIBS* **13**:321–322 (1988)); these sequences have ".sh" appended to their name to indicate that they were too short for phylogenetic analysis. Parsimony trees were generated using PAUP (David Swofford, Illinois Natural History Survey), and neighbor-joining trees were generated with Kimura distances and a transition to transversion ratio of 1.3 using PHYLIP (Joseph Felsenstein, University of Washington). All available nucleotide sequence information was used for phylogenetic analysis; longer protein sequences were trimmed to be approximately the same length as the majority of the PCR fragments in this region, for the purposes of presentation. Some sequences were difficult to classify, and are included in the "U", or unclassified, section. In addition, recombination between HIV-1 strains occurs when an individual is infected with more than one strain. A meeting was held in Santa Fe, New Mexico in October, 1995 to discuss the implications of recombination and methods for detecting recombinant sequences. Because intersubtype as well as intrasubtype recombination is known to occur, the subtype designations reported in this section should be interpreted only as pertaining to the V3 region of the envelope gene. For example HIV-1 MAL from Zaire, is known to be recombinant between subtypes A and D, with the V3 loop of env resembling subtype D. D_ZR-MAL is still listed with other subtype D sequences in this study, but may be moved to the U (uncertain) group in the future. In the V3 region MAL is strongly associated with the D subtype.

The set of sequences used to help resolve subtype associations included at least two sequences from each subtype (A–J), plus a simian immunodeficiency virus (chimpanzee) outgroup sequence. The sequences were selected based on being "typical" of the subtype they represent based on phylogenetic analysis. The set has changed as more sequences have accumulated. Thus not all subtype designations were based on the same reference set.

Limitations of phylogenetic analyses

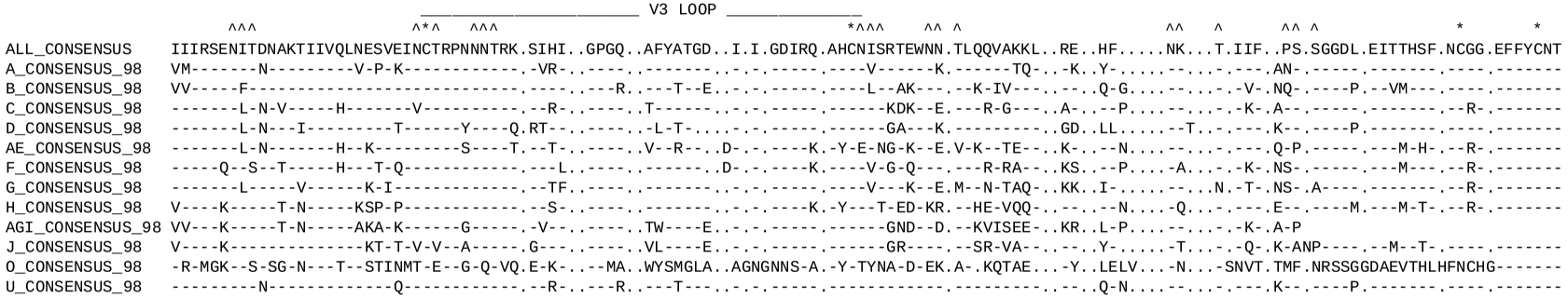
Most of the PCR derived sequences contain a sub-optimal length for phylogenetic analyses, given the level of variability in this region – typically on the order of 250 to 300 nucleotides. Due to this limitation, some of the classifications in this section are uncertain and are our best estimate given the available information. Control studies were performed to compare the phylogenetic clustering of the V3 region using available longer sequences, however, and these studies indicate that our subtype designations based on the V3 region are generally reliable. For 146 sequences, we had an approximately 700 base region of env available representing all of the subtypes A–H. (The limitation in length was due to including the H subtype sequences, which did not cover all of gp120.) After removing positions in the alignment which included gaps, 519 bases were left. When a 298 base V3 region fragment was excised from this set, and neighbor joining trees were constructed using both the 519 base and 298 base long sequences, the phylogenetic subtype designations were consistent in each case. Further, when a subset of longer gp120 sequences was analyzed (92 of the 146), including 935 bases after removing positions in the alignment which included gaps, the subtype designations were again clear in neighbor-joining trees. This indicates that the limited V3 region PCR fragments, which include more than the V3-loop, are generally able to serve as a reliable basis for subtype determination, given the limitation that the V3 loop sequence may be embedded in a recombinant genome.

Without detailed analysis, genetic recombination between subtypes may obscure phylogenetic relationships between sequences. A characteristic of recombination is an indeterminate place in phylogenetic analyses, and some of the "Uncertain" category sequences may prove to be recombinant genomes upon further inspection. Also, while a subtype designation based on a gene or gene fragment may be correct, recombination events outside the region examined may have occurred. Therefore,

care should be taken to not overinterpret the subtype designations. If one is to discuss the subtype designations of viral isolates based on the data presented here, they should refer to the designation as "B-like over the V3 loop region," rather than as "subtype B".

Limitations of V3 amino acid consensus sequences

The V3 amino acid consensus sequences generated for each subtype have interesting features; however, one should be wary about assuming that any of the consensus sequences may broadly represent their subtype. Certainly many V3 loop variants in each of the subtypes are extremely divergent from the consensus sequences. These divergent forms may have very different biological and immunological characteristics from viruses which are similar to the consensus. Additionally, because of the relatively small sample size of most of the subtypes, consensus sequences can be dominated by a small group of highly similar sequences, which may in turn be a sampling artifact. Hence, these consensus sequences are "evolving" as new sequences from each subtype become available.



Subtype consensus sequences. This V3 region alignment shows a consensus sequence generated for each of the eleven subtypes or circulating recombinant forms. The subtype consensus sequences indicate the most common amino acid found in each position among the sequences associated with each subtype. The sequences are aligned to a consensus based on the most common amino acid in the subtype consensus sequences, which approximates a “global” consensus. It was generated in this way (rather than by using all 2588 sequences) to avoid over-representation of the B subtype, which has by far the largest number of available sequences. As is the convention in this compendium, a dash (-) indicates concurrence with the top sequence in the alignment; a period (.) indicates a deletion. The carets show where the N-linked glycosylation sites are found in the consensus. The V3 loop is set off from the surrounding sequence by a space on either side to facilitate viewing. Interesting features of the consensus alignment are: 1) Only in the B subtype is GPGR the most common tip of the V3 loop; globally, GPGQ is more prevalent. 2) A highly conserved N-linked glycosylation site is constitutively absent in the C subtype, proximal to the first cysteine (C) in loop. 3) The D subtype consensus has 33 amino acids from cysteine (C) to cysteine (C) rather than the more common 35; at the point where the deletion occurs, it is not uncommon to find insertions of 2 to 4 amino acids, as can be observed in the sequence alignments. 4) A higher degree of variation is seen in the region just downstream of the V3 loop than within it. This difference is also observed internally among the sequences of the different subtypes. 5) The A, C, G and H consensus sequences have very similar V3 loop sequences.

V3 Loop Amino Acids

The following pages present amino acid alignments of the V3 loop, arranged by phylogenetic subtype. For each subtype, the number of sequences used to construct the alignment is indicated. The top line in each alignment represents the consensus sequence for that subtype, where consensus simply means the most common amino acid found in each position among the sequences of the given subtype. The subscripts record the frequency with which that amino acid is observed at that location among members of the subtype. An amino acid which is conserved 100% is shown with no subscript. Directly beneath the most common amino acid in each position are the other amino acids observed in that position, listed from most common to least common. An asterisk (*) subscript means less than 0.5% of the sequences had the indicated amino acid at that location. A dash (-) indicates a gap inserted to maintain the alignment. Percentages were rounded to the nearest whole number.

For this year's alignment, the HMMER (version 1.8) hidden Markov model software

http://hmmer.wustl.edu/

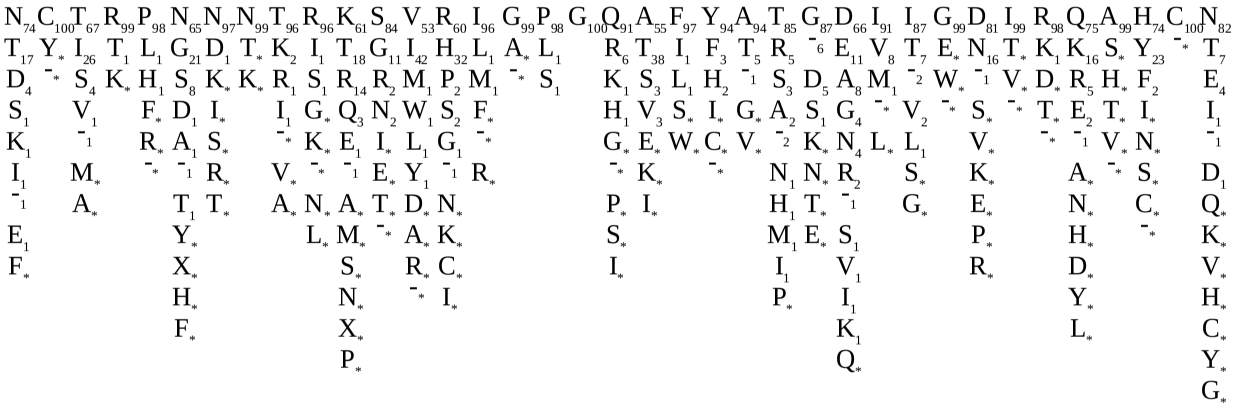
(Sean Eddy, Dept. of Genetics, Washington U. School of Medicine, St. Louis, MO 63110) was used to align all 2588 sequences objectively. The frequency counts are derived from this alignment. Because each subtype required different numbers and positions of gaps in order to create the full multiple sequence alignment, some sequences with unusual insertions were trimmed from the HMMER alignment, and a few positions were adjusted by hand, using MASE, prior to printing the full alignment which appears following the country codes description. The sequences which were culled from the alignment after counting frequencies, are appended.

Both the untouched HMMER alignment, and the edited version, will be available via ftp from the LANL HIV database.

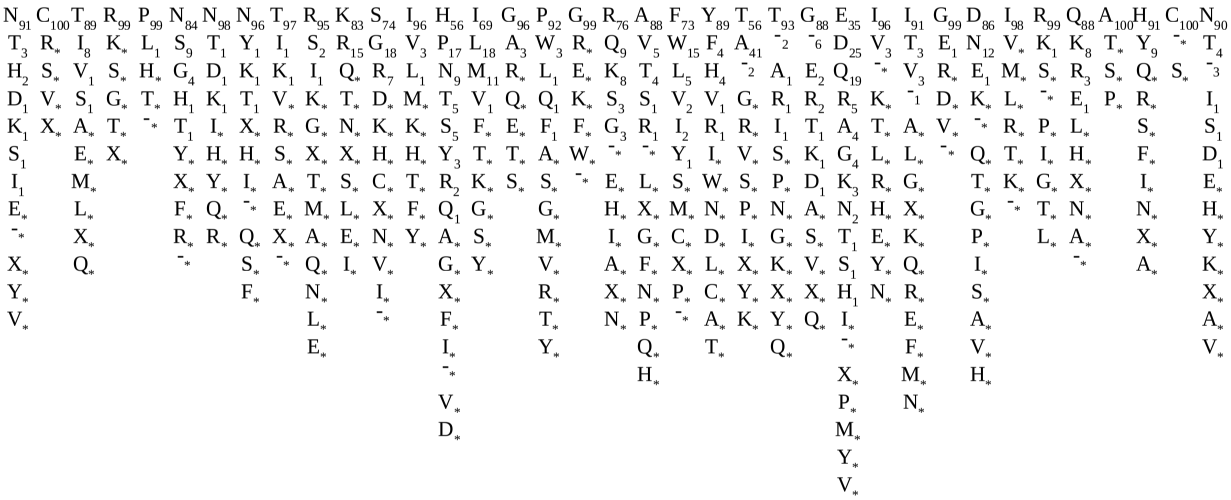
http://hiv-web.lanl.gov

Questions about these alignments should be directed to email: btf@t10.lanl.gov, phone: 505-665-1970.

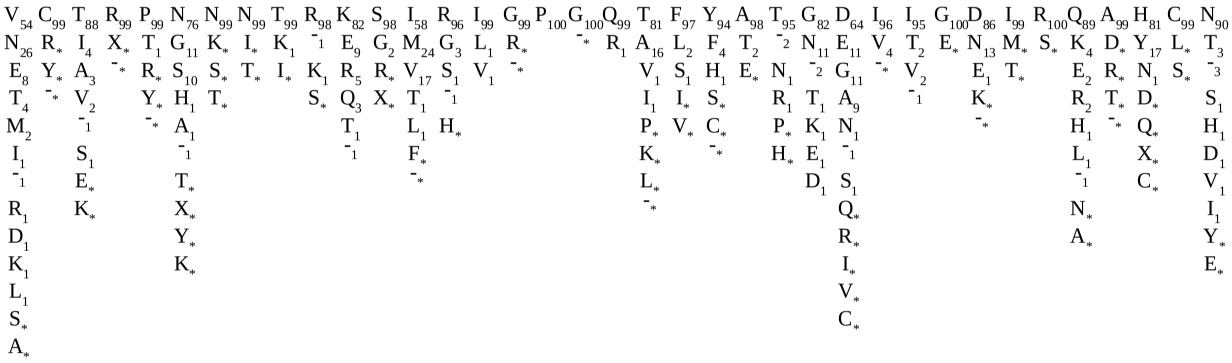
A subtype (417 sequences)



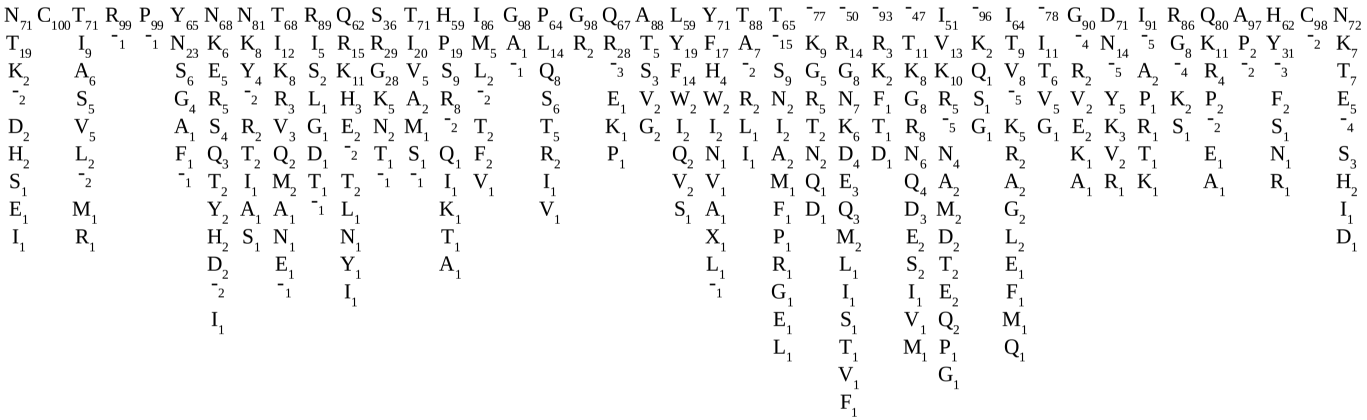
B subtype (1289 sequences)



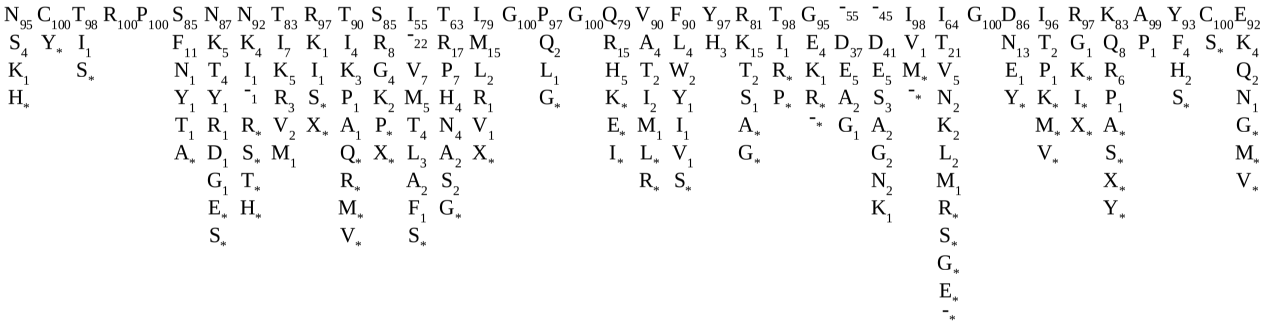
C subtype (339 sequences)



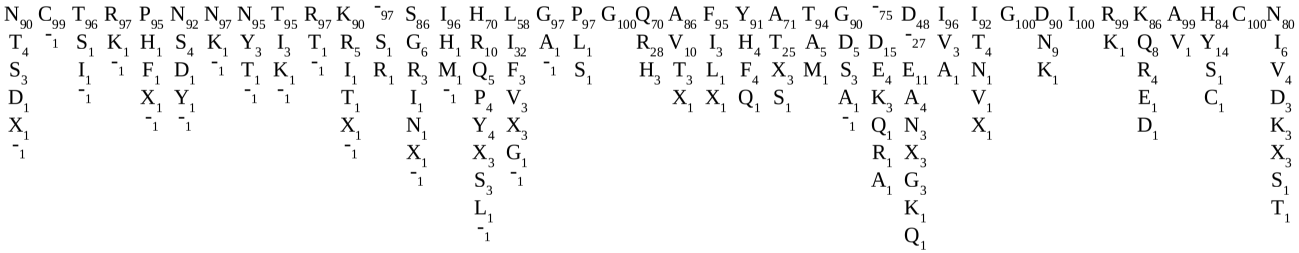
D subtype (133 sequences)



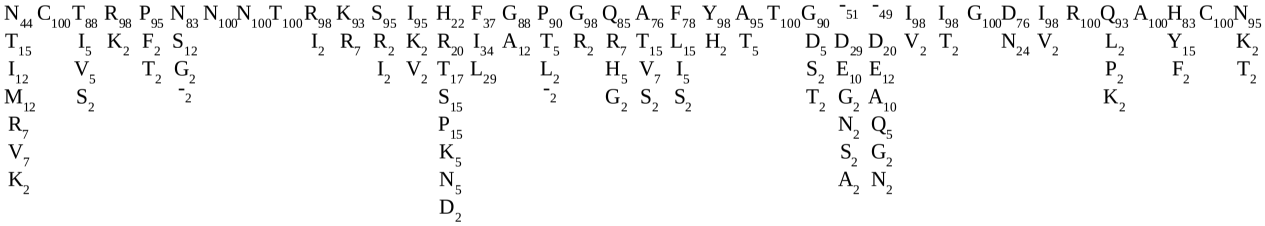
E subtype (227 sequences)



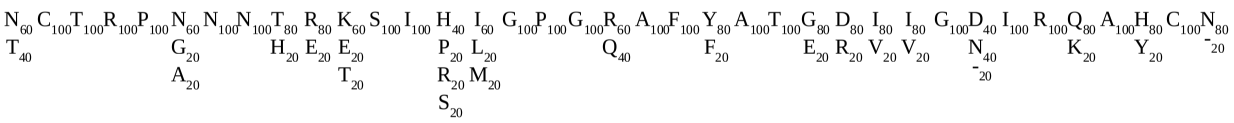
F subtype (79 sequences)



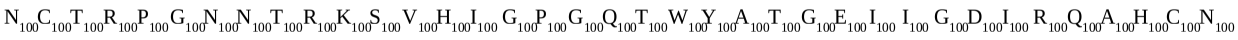
G subtype (41 sequences)



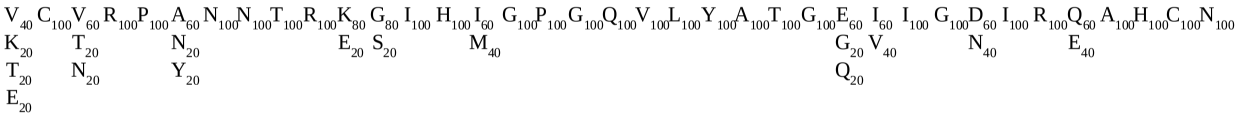
H subtype (5 sequences)



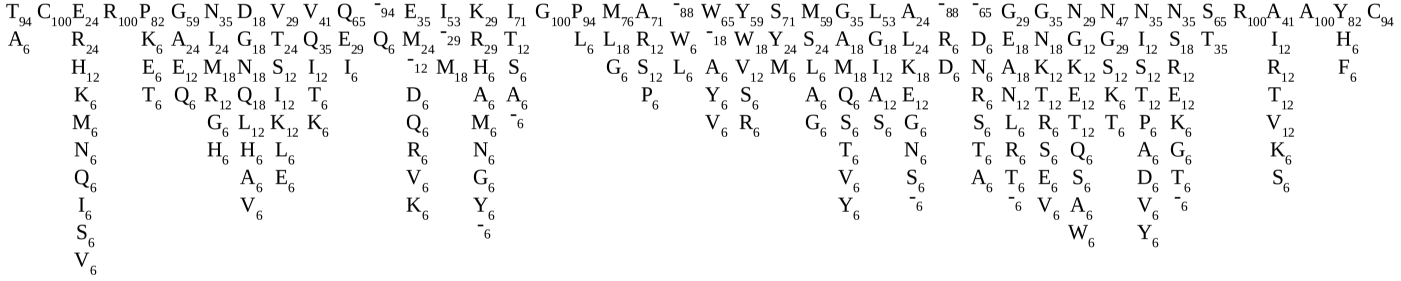
I subtype (1 sequence)



J subtype (5 sequences)



O subtype (17 sequences)



U subtype (28 sequences)

N 86	C 100	T 89	R 100	P 100	N 68	N 89	N 82	T 79	R 89	K 61	- 96	S 75	V 43	H 46	I 50	- 89	- 96	G 96	P 86	G 96	Q 64	A 79	F 86	Y 89	A 57	T 75	G 64	D 57	I 75	I 79	G 96	D 79	I 79	R 89	Q 79	A 93	H 46	C 96	N 46
K 4		I 4			G 11	K 4	I 4	L 11	K 7	R 18	R 4	R 7	I 36	R 32	L 25	I 7	R 4					T 11	L 7	F 11	T 36	N 11	E 11	V 11	T 7	R 4	N 14	V 14	N 4	K 14	P 4	F 21	I 11		
S 4		S 4			S 11	S 4	K 4	K 7	N 4	I 7		G 7	T 11	T 7	F 11	R 4			S 4			V 11	I 4		- 4	R 7	G 7	M 7	K 4		K 4	- 4	G 4	P 4	- 4	Y 18	S 7	Q 4	S 4	
T 4		A 4			Y 7	T 4	D 4	R 4		Q 4		Q 4	R 4	P 4	H 7				T 4			Y 4				S 4	S 4	K 4	N 7	E 4	G 4			- 4		Q 4	- 4	K 4	- 4
V 4					A 4		T 4			E 4		T 4	M 4	M 4	M 7													R 4	- 4	V 4									
							Y 4			T 4		X 4	Q 4	S 4															V 4										
										X 4				N 4															X 4										
																												- 4										

Summary of variations in the tetrameric tip of the V3 loop. This table is a tally of the different tetramers observed in the 2588 individuals analyzed. This tip is thought to form a turn, and is the focal point of the potent neutralizing antibody epitopes that have been mapped to the V3 loop, as well as of T cell epitopes. Each column shows the number of occurrences of a given tetramer in either the entire 2588 sequences (combined), or in subsets consisting of subtypes A–O, and the unclassified sequences (U). Underneath the column heading is the number of sequences in each category. The most common form found in each subtype is highlighted in bold lettering. In the B subtype, GPGR is the predominant form, however globally GPGQ is more common.

	Combined	A	B	C	D	E	F	G	H	I	J	O	U
Totals	2588	418	1290	339	136	227	80	41	6	1	5	17	28
GPGQ	**1151**	**374**	116	**333**	**46**	**178**	**53**	**29**	2	1	**5**		**14**
GPGR	1067	17	**838**	4	32	30	20	1	**3**				7
GPGK	115	6	106		1	1							1
GWGR	42		42										
GPGS	34	1	33										
GPGG	32	2	29					1					
APGR	29	1	28										
GLGR	25	4	17		1	1	1						1
GLGQ	18				17								1
GPGH	15	1	1			10	2	1					
GQGR	12		9		1	2							
GPMA	11											**11**	
GSGQ	11	2			7		1						1
GQGQ	10		1		8	1							
GSGR	4	1	3										
xPGQ	1	1											
GLGH	3	2											
GPGx	6	2	2		2								
APGQ	6	1					1	4					
AGGR	2		2										
SPGR	1		1										
RPRR	1		1										
RPGQ	2			1									1
xPxQ	1			1									
GYGR	1		1										
GAGR	2		2										
GFGR	8		8										
TPGR	3		3										
AWGR	1		1										
APWG	1		1										
AGGK	1		1										
APGS	3		3										
GTGG	1		1										
GVGR	4		2		1		1						
GMGR	2		2										
GSGx	1				1								
GLGK	1		1										
GRGR	1		1										
EPGR	3		3										
GARR	1		1										
GPGX	1		1										

	Combined	A	B	C	D	E	F	G	H	I	J	O	U
Totals	2588	418	1290	339	136	227	80	41	6	1	5	17	28
GPEK	1		1										
GPGN	1		1										
GPRR	3		3										
GPGE	3		2			1							
APGE	1				1								
GIGR	1				1								
GPG-	3		2		1								
GPFR	2		2										
GPGA	1		1										
GPER	1		1										
GLGS	1		1										
APGG	2		2										
RPGR	3		3										
GPKR	2		2										
GPxR	1		1										
QPGR	3		3										
GPWG	1		1										
GRGQ	5	1			3				1				
GTGQ	6				6								
AQGR	1				1								
GLRQ	1				1								
GPGI	2	1	1										
GPGP	2	1			1								
GPRQ	2				1			1					
GGGQ	1					1							
GQGI	1					1							
*PGR	1						1						
GTGR	3							2					1
GPMR	1											1	
GPLS	1											1	
GPMS	1											1	
GPLR	1											1	
GGGR	2		2										
GIGQ	1				1								
GGRA	1				1								
AxGQ	1							1					
GLGH	1							1					
GLGP	1											1	
GPLA	1											1	
GPLA	1												1

COUNTRY CODES

It is becoming increasingly useful to name viral isolates and samples with a country code. The following code was captured from Internet files:

`ftp://ftp.ripe.net/iso3166-countrycodes`

for ISO two-letter codes and for ITU three-letter codes.

This is a list based on the International Organization for Standardization (ISO) 3166:1993 standard, updated from a list prepared by Mark Horton. Note that the original standard has this same information sorted into about 6 different orders, both in English and French, therefore this is an abbreviated version not to be taken as the entire standard. While it has been checked against the standard, it may possibly contain errors; the standard and registration newsletters should be verified for any critical application.

This copy has been updated in 1998 from the version that was originally downloaded in 1995. Of particular note, is that we are delaying the change of "Zaire : ZR : ZAR : 180" to "Congo, Democratic Republic of : CD : COD : 180" until next year, to give people time to get used to the change.

Table of Country Codes from ISO 3166

Country	A 2	A 3	Number
AFGHANISTAN	AF	AFG	004
ALBANIA	AL	ALB	008
ALGERIA	DZ	DZA	012
AMERICAN SAMOA	AS	ASM	016
ANDORRA	AD	AND	020
ANGOLA, REPUBLIC OF	AO	AGO	024
ANGUILLA	AI	AIA	660
ANTARCTICA	AQ	ATA	010
ANTIGUA AND BARBUDA	AG	ATG	028
ARGENTINA	AR	ARG	032
ARUBA	AW	ABW	533
AUSTRALIA	AU	AUS	036
AUSTRIA	AT	AUT	040
AZERBAIJAN	AZ	AZE	031
BAHAMAS	BS	BHS	044
BAHRAIN	BH	BHR	048
BANGLADESH	BD	BGD	050
BARBADOS	BB	BRB	052
BELGIUM	BE	BEL	056
BELIZE	BZ	BLZ	084
BENIN	BJ	BEN	204
BERMUDA	BM	BMU	060
BHUTAN	BT	BTN	064
BOLIVIA	BO	BOL	068
BOTSWANA	BW	BWA	072
BOUVET ISLAND	BV	BVT	074
BOSNIA AND HERZEGOWINA	BA	BIH	070
BRAZIL	BR	BRA	076
BRITISH INDIAN OCEAN TERRITORY	IO	IOT	086
BRUNEI DARUSSALAM	BN	BRN	096
BULGARIA	BG	BGR	100
BURKINA FASO	BF	BFA	854
BURUNDI	BI	BDI	108

BYELORUSSIAN SSR	BY	BYS	112
CAMBODIA	KH	KHM	116
CAMEROON	CM	CMR	120
CANADA	CA	CAN	124
CAPE VERDE	CV	CPV	132
CAYMAN ISLANDS	KY	CYM	136
CENTRAL AFRICAN REPUBLIC	CF	CAF	140
CHAD	TD	TCD	148
CHILE	CL	CHL	152
CHINA	CN	CHN	156
CHRISTMAS ISLAND	CX	CXR	162
COCOS (KEELING) ISLANDS	CC	CCK	166
COLOMBIA	CO	COL	170
COMOROS	KM	COM	174
CONGO	CG	COG	178
CONGO, DEMOCRATIC REPUBLIC OF	see ZAIRE		180
COOK ISLANDS	CK	COK	184
COSTA RICA	CR	CRI	188
COTE D'IVOIRE	CI	CIV	384
CROATIA	HR	HRV	191
CUBA	CU	CUB	192
CYPRUS	CY	CYP	196
CZECH REPUBLIC	CZ	CZE	203
DENMARK	DK	DNK	208
DJIBOUTI	DJ	DJI	262
DOMINICA	DM	DMA	212
DOMINICAN REPUBLIC	DO	DOM	214
EAST TIMOR	TP	TMP	626
ECUADOR	EC	ECU	218
EGYPT	EG	EGY	818
EL SALVADOR	SV	SLV	222
EQUATORIAL GUINEA	GQ	GNQ	226
ERITREA	ER	ERI	232
ESTONIA	EE	EST	233
ETHIOPIA	ET	ETH	231
FALKLAND ISLANDS (MALVINAS)	FK	FLK	238
FAROE ISLANDS	FO	FRO	234
FIJI	FJ	FJI	242
FINLAND	FI	FIN	246
FRANCE	FR	FRA	250
FRANCE, METROPOLITAN	FX		249
FRENCH GUIANA	GF	GUF	254
FRENCH POLYNESIA	PF	PYF	258
FRENCH SOUTHERN TERRITORIES	TF	ATF	260
GABON	GA	GAB	266
GAMBIA	GM	GMB	270
GEORGIA	GE	GEO	268
GERMANY	DE	DEU	276
GHANA	GH	GHA	288
GIBRALTAR	GI	GIB	292
GREECE	GR	GRC	300
GREENLAND	GL	GRL	304
GRENADA	GD	GRD	308
GUADELOUPE	GP	GLP	312

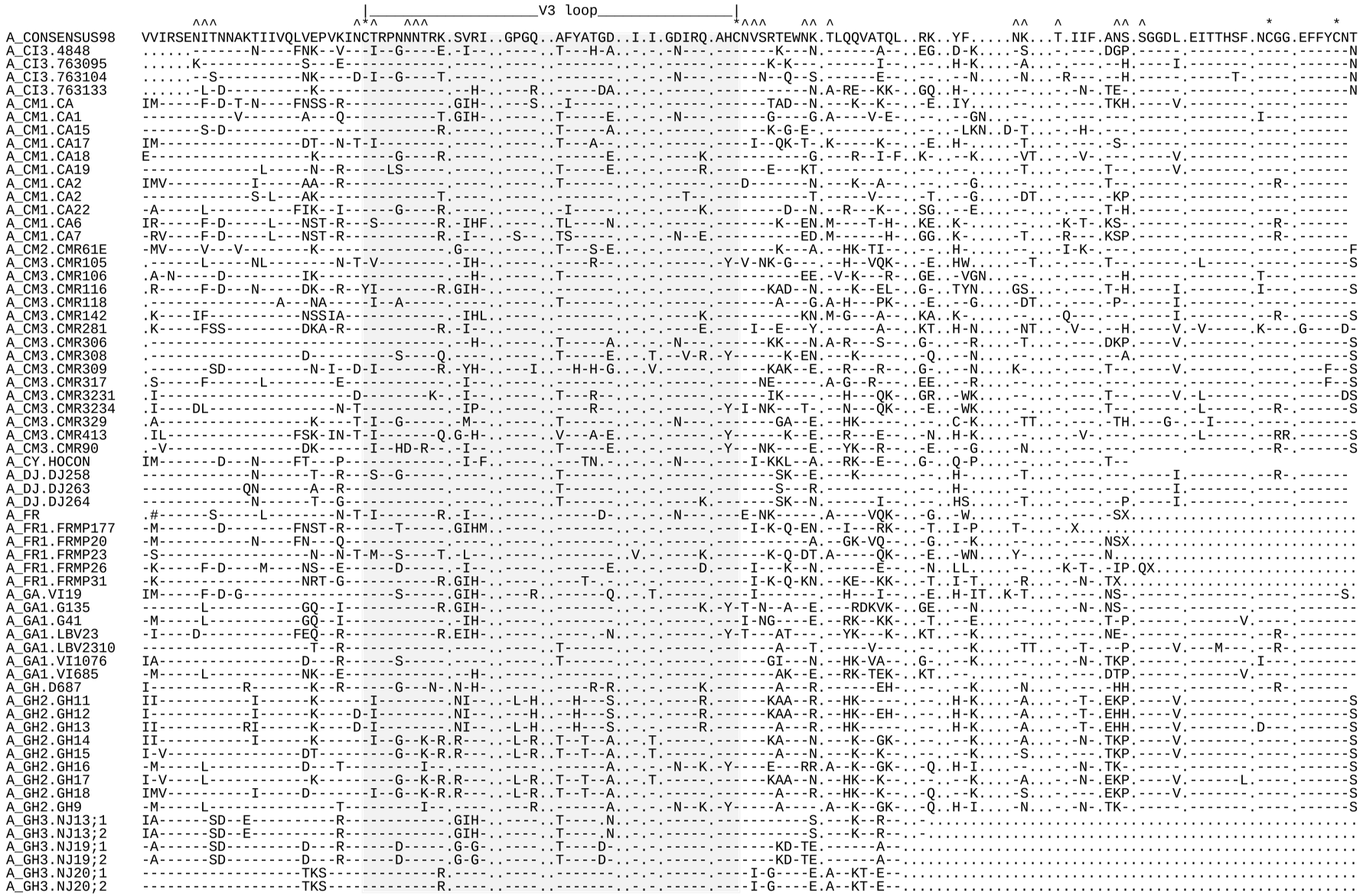
GUAM	GU	GUM	316
GUATEMALA	GT	GTM	320
GUINEA	GN	GIN	324
GUINEA-BISSAU	GW	GNB	624
GUYANA	GY	GUY	328
HAITI	HT	HTI	332
HEARD AND MCDONALD ISLANDS	HM	HMD	334
HONDURAS	HN	HND	340
HONG KONG	HK	HKG	344
HUNGARY	HU	HUN	348
ICELAND	IS	ISL	352
INDIA	IN	IND	356
INDONESIA	ID	IDN	360
IRAN (ISLAMIC REPUBLIC OF)	IR	IRN	364
IRAQ	IQ	IRQ	368
IRELAND	IE	IRL	372
ISRAEL	IL	ISR	376
ITALY	IT	ITA	380
JAMAICA	JM	JAM	388
JAPAN	JP	JPN	392
JORDAN	JO	JOR	400
KAZAKHSTAN	KZ	KAZ	398
KENYA	KE	KEN	404
KIRIBATI	KI	KIR	296
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF	KP	PRK	408
KOREA, REPUBLIC OF	KR	KOR	410
KUWAIT	KW	KWT	414
KYRGYZSTAN	KG	KGZ	417
LAO PEOPLE'S DEMOCRATIC REPUBLIC	LA	LAO	418
LATVIA	LV	LVA	428
LEBANON	LB	LBN	422
LESOTHO	LS	LSO	426
LIBERIA	LR	LBR	430
LIBYAN ARAB JAMAHIRIYA	LY	LBY	434
LIECHTENSTEIN	LI	LIE	438
LITHUANIA	LT	LTU	440
LUXEMBOURG	LU	LUX	442
MACAU	MO	MAC	446
MACEDONIA, FORMER YUGOSLAV REPUBLIC OF	MK	MKD	807
MADAGASCAR, REPUBLIC OF	MG	MDG	450
MALAWI	MW	MWI	454
MALAYSIA	MY	MYS	458
MALDIVES	MV	MDV	462
MALI	ML	MLI	466
MALTA	MT	MLT	470
MARSHALL ISLANDS	MH	MHL	584
MARTINIQUE	MQ	MTQ	474
MAURITANIA	MR	MRT	478
MAURITIUS	MU	MUS	480
MAYOTTE	YT	MYT	175
MEXICO	MX	MEX	484
MICRONESIA	FM	FSM	583
MOLDOVA	MD	MDA	498
MONACO	MC	MCO	492

MONGOLIA	MN	MNG	496
MONTSERRAT	MS	MSR	500
MOROCCO	MA	MAR	504
MOZAMBIQUE	MZ	MOZ	508
MYANMAR	MM	MMR	104
NAMIBIA	NA	NAM	516
NAURU	NR	NRU	520
NEPAL	NP	NPL	524
NETHERLANDS	NL	NLD	528
NETHERLANDS ANTILLES	AN	ANT	530
NEUTRAL ZONE	NT	NTZ	536
NEW CALEDONIA	NC	NCL	540
NEW ZEALAND	NZ	NZL	554
NICARAGUA	NI	NIC	558
NIGER	NE	NER	562
NIGERIA	NG	NGA	566
NIUE	NU	NIU	570
NORFOLK ISLAND	NF	NFK	574
NORTHERN MARIANA ISLANDS	MP	MNP	580
NORWAY	NO	NOR	578
OMAN	OM	OMN	512
PAKISTAN	PK	PAK	586
PALAU	PW	PLW	585
PANAMA	PA	PAN	590
PAPUA NEW GUINEA	PG	PNG	598
PARAGUAY	PY	PRY	600
PERU	PE	PER	604
PHILIPPINES	PH	PHL	608
PITCAIRN	PN	PCN	612
POLAND	PL	POL	616
PORTUGAL	PT	PRT	620
PUERTO RICO	PR	PRI	630
QATAR	QA	QAT	634
REUNION	RE	REU	638
ROMANIA	RO	ROM	642
RUSSIAN FEDERATION	RU	RUS	643
RWANDA	RW	RWA	646
ST. HELENA	SH	SHN	654
SAINT KITTS AND NEVIS	KN	KNA	659
SAINT LUCIA	LC	LCA	662
ST. PIERRE AND MIQUELON	PM	SPM	666
SAINT VINCENT AND THE GRENADINES	VC	VCT	670
SAMOA	WS	WSM	882
SAN MARINO	SM	SMR	674
SAO TOME AND PRINCIPE	ST	STP	678
SAUDI ARABIA	SA	SAU	682
SENEGAL	SN	SEN	686
SEYCHELLES	SC	SYC	690
SIERRA LEONE	SL	SLE	694
SINGAPORE	SG	SGP	702
SLOVAKIA	SK	SVK	703
SLOVENIA	SI	SVN	705
SOLOMON ISLANDS	SB	SLB	090
SOMALIA	SO	SOM	706

SOUTH AFRICA	ZA	ZAF	710
SOUTH GEORGIA AND THE SOUTH SANDWICH ILANDS	GS		239
SPAIN	ES	ESP	724
SRI LANKA	LK	LKA	144
SUDAN	SD	SDN	736
SURINAME	SR	SUR	740
SVALBARD AND JAN MAYEN ISLANDS	SJ	SJM	744
SWAZILAND	SZ	SWZ	748
SWEDEN	SE	SWE	752
SWITZERLAND	CH	CHE	756
SYRIAN ARAB REPUBLIC	SY	SYR	760
TAIWAN, PROVINCE OF CHINA	TW	TWN	158
TAJIKISTAN	TJ	TJK	762
TANZANIA, UNITED REPUBLIC OF	TZ	TZA	834
THAILAND	TH	THA	764
TOGO	TG	TGO	768
TOKELAU	TK	TKL	772
TONGA	TO	TON	776
TRINIDAD AND TOBAGO	TT	TTO	780
TUNISIA	TN	TUN	788
TURKEY	TR	TUR	792
TURKMENISTAN	TM	TKM	795
TURKS AND CAICOS ISLANDS	TC	TCA	796
TUVALU	TV	TUV	798
UGANDA	UG	UGA	800
UKRAINE	UA	UKR	804
UNITED ARAB EMIRATES	AE	ARE	784
UNITED KINGDOM	GB	GBR	826
UNITED STATES	US	USA	840
UNITED STATES MINOR OUTLYING ISLANDS	UM	UMI	581
URUGUAY	UY	URY	858
UZBEKISTAN	UZ	UZB	860
VANUATU	VU	VUT	548
VATICAN CITY STATE (HOLY SEE)	VA	VAT	336
VENEZUELA	VE	VEN	862
VIET NAM	VN	VNM	704
VIRGIN ISLANDS (BRITISH)	VG	VGB	092
VIRGIN ISLANDS (U.S.)	VI	VIR	850
WALLIS AND FUTUNA ISLANDS	WF	WLF	876
WESTERN SAHARA	EH	ESH	732
YEMEN	YE	YEM	887
YUGOSLAVIA	YU	YUG	891
ZAIRE	ZR	ZAR	180
ZAMBIA	ZM	ZMB	894
ZIMBABWE	ZW	ZWE	716

V3 Region Alignment

III-135
DEC 98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A_CI3.763095
A_CI3.763104
A_CI3.763133
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A_CM1.CA1
A_CM1.CA15
A_CM1.CA17
A_CM1.CA18
A_CM1.CA19
A_CM1.CA2
A_CM1.CA2
A_CM1.CA22
A_CM1.CA6
A_CM1.CA7
A_CM2.CMR61E
A_CM3.CMR105
A_CM3.CMR106
A_CM3.CMR116
A_CM3.CMR118
A_CM3.CMR142
A_CM3.CMR281
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A_CM3.CMR308
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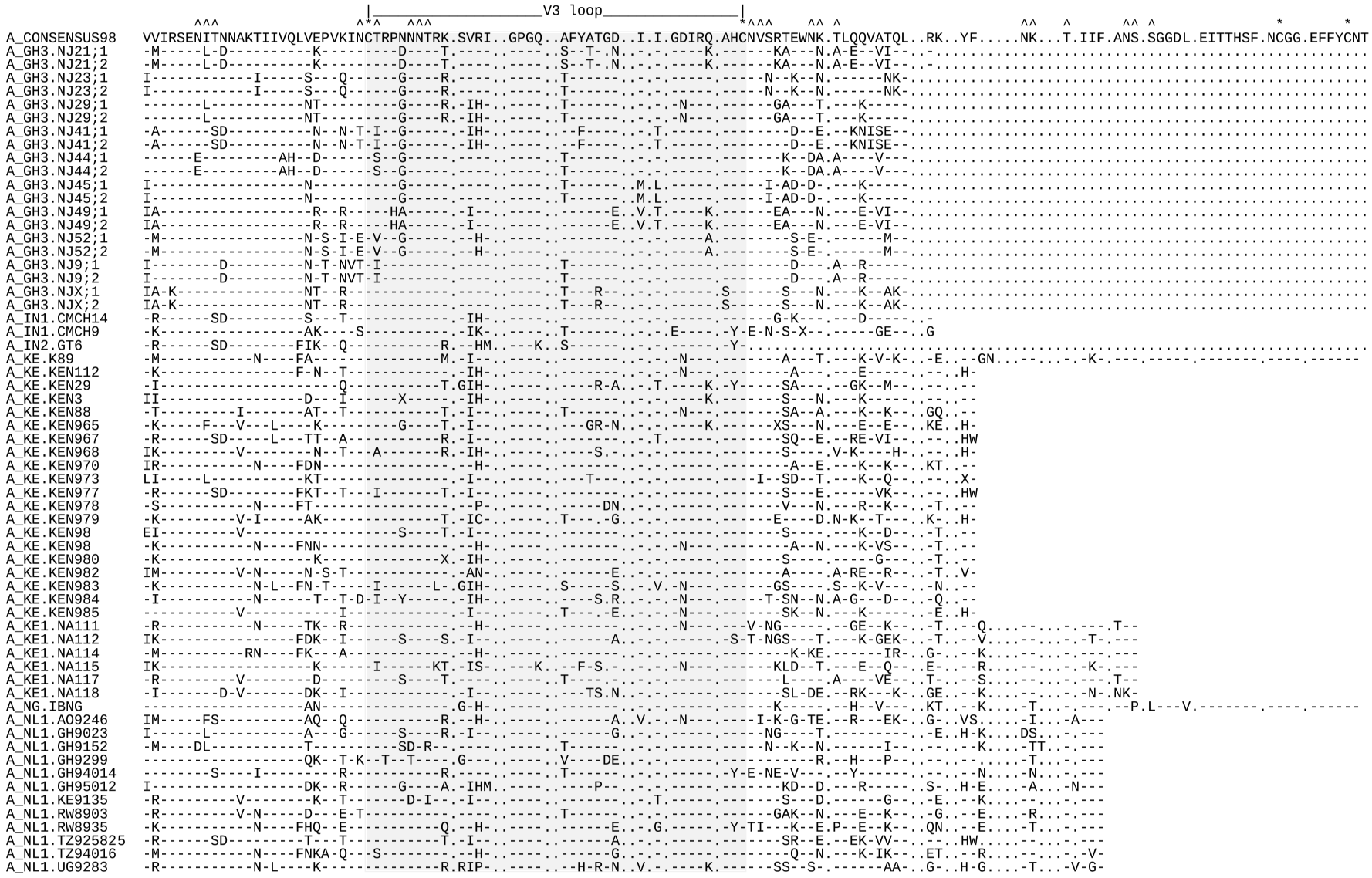
A_CM3.CMR3231
A_CM3.CMR3234
A_CM3.CMR329
A_CM3.CMR413
A_CM3.CMR90
A_CY.HOCON
A_DJ.DJ258
A_DJ.DJ263
A_DJ.DJ264
A_FR
A_FR1.FRMP177
A_FR1.FRMP20
A_FR1.FRMP23
A_FR1.FRMP26
A_FR1.FRMP31
A_GA.VI19
A_GA1.G135
A_GA1.G41
A_GA1.LBV23
A_GA1.LBV2310
A_GA1.VI1076
A_GA1.VI685
A_GH.D687
A_GH2.GH11
A_GH2.GH12
A_GH2.GH13
A_GH2.GH14
A_GH2.GH15
A_GH2.GH16
A_GH2.GH17
A_GH2.GH18
A_GH2.GH9
A_GH3.NJ13;1
A_GH3.NJ13;2
A_GH3.NJ19;1
A_GH3.NJ19;2
A_GH3.NJ20;1
A_GH3.NJ20;2


V3 loop
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A_GH3.NJ21;1
A_GH3.NJ21;2
A_GH3.NJ23;1
A_GH3.NJ23;2
A_GH3.NJ29;1
A_GH3.NJ29;2
A_GH3.NJ41;1
A_GH3.NJ41;2
A_GH3.NJ44;1
A_GH3.NJ44;2
A_GH3.NJ45;1
A_GH3.NJ45;2
A_GH3.NJ49;1
A_GH3.NJ49;2
A_GH3.NJ52;1
A_GH3.NJ52;2
A_GH3.NJ9;1
A_GH3.NJ9;2
A_GH3.NJX;1
A_GH3.NJX;2
A_IN1.CMCH14
A_IN1.CMCH9
A_IN2.GT6
A_KE.K89
A_KE.KEN112
A_KE.KEN29
A_KE.KEN3
A_KE.KEN88
A_KE.KEN965
A_KE.KEN967
A_KE.KEN968
A_KE.KEN970
A_KE.KEN973
A_KE.KEN977
A_KE.KEN978
A_KE.KEN979
A_KE.KEN98
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A_KE1.NA118
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A_NL1.GH95012
A_NL1.KE9135
A_NL1.RW8903
A_NL1.RW8935
A_NL1.TZ925825
A_NL1.TZ94016
A_NL1.UG9283

Analyses

V3 Region Alignment

```
                                      |___________________V3 loop_______________|
       ^^^                         ^*^   ^^^                                      *^^^    ^^ ^                     ^^   ^      ^^ ^             *       *
A_CONSENSUS98   VVIRSENITNNAKTIIVQLVEPVKINCTRPNNNTRK.SVRI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTEWNK.TLQQVATQL..RK..YF.....NK...T.IIF.ANS.SGGDL.EITTHSF.NCGG.EFFYCNT
A_NL1.ZR93033   -AV---------------FT---R---S--------.-I--..----..T-----G..-.-.-----.-------MD---.----------..YS..--N....-P...-.MV
A_RU1.GAN1             --------N--E---S--------.GIH-..----..-------..-.-.-----.----I---R--Q.---
A_RU1.IVA6             -------N-T--------G-----.----..----..T-----A..-.-.-----.-----T--N--N.---
A_RU1.MLY10     -I---K--SE-TNN-----KT--H---I-LA-----.-IH-..-----..-I-TN.-..-.-.-----.----I-EGL--D.--YEI----.--..H-N....--...-.---.KP-.T---I.-------.----.-------
A_RU1.SHL9         K---E-TNN-----KT--Q------G-----.-IH-..-----..-I-.--E..-.-.-N--R.----I-AGL--E.--YE-----.--..H-N....--...-.-S-.KP-.T---I.--A-
A_RU3.2728B     ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.323       ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.6525B     ...------D-G-I-----T---N-T-I--G----T.-I--..---P..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.7517      ...------D-S-I-----T---N-T-I--S----T.-I--..-----..T-----E..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.7624B     ...------D-S-I-----T---N-T-I--G----T.-I--..-----..T------..V.T.----K.-Y---R-AA--S.---KI.............................................................
A_RU3.8722B     ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.9022      ...------D-G-IT----T---N-T-I--G----T.-IG-..-----..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.936       ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.947       ...------D-G-I-----T---N-T-I--G--A-T.-I--..-----..T------..V.-----K.-Y----AV--S.---KI.............................................................
A_RU3.9536      ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----K.-Y----AA--S.---KI.............................................................
A_RU3.9611      ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----N.-Y----AA--S.---KI.............................................................
A_RU3.97048     ...------D-G-I-----T---N-T-I--G----T.-I--..-----..T------..V.-----K.TY----AA--N.---KI.............................................................
A_RW.564C       -R--A----D-----M-H-NT--Q------------.----..-----..T-----E..-.-.-N---.-Y--LN--A--Q.---K-V---..G-..--G....-T...-N-R-.T-
A_RW.SF1703     -K-----------------NKT-E------------.----..-----..-------..-.-.-----.-Y-----AD---.---G--N--..KS..--S....--...-.---.-S-.-----.-------.----.-----D
A_RW1.W2RW008        -----V--------K-------------T.-I--..-----..S-H----..-.-.-----.-------S---E.A-R--VE--..-G..H-G....--...-.M--.T--.-
A_RW1.W2RW016        -------------DKA-N-T-I--------.--P-..---R..-------..-.-.-N---.--------------.--EK--K--..GE..H-R....--...-.---.--
A_RW1.W2RW02         -------------DKA--------------.----..-----..-------..-.-.-----.-------AK--D.--RG--KK-..-E..H-K....--...-.---.EK-.-
A_RW1.W2RW024        -L-----I-L---RK--------------T.----..-----..T------..-.-.----R.-Y-TIN-----N.------N--..G-..H-GK...--...-.---.TK
A_RW1.W2RW025        -------N------K------V-------T.----..-----..T-----E..-.-.----R.-F-T-NES---E.--R------..G-..H-E....--...-.-K-.T
A_RW1.W2RW026        --------------S--------------R.-I--..-----..-------..-.-.----K.-------S---N.-----V---..S-..--E....--...-.---.NS-.-
A_RW2.1613WCONS -K-------D---------DKA-Q------G-----.----..-----..-------..-.-.----K.---T-NG----N.--HK------..E-..H-R....--...-.-N-.TK-.----
A_RW2.1613CON   IK---K-L-D---------T-A-----S--------.--H-..-----..-----DA..-.-.-N---.-------A---N.---K--Q--..-E..--V....--...-.---.NS-.-----.---
A_RW2.1701CONS  -R-----------S----FXK--R------------T.-M--..-----..------G..-.-.----K.-----T-S---R.------K---..-E..--.....-R...-.---.NS-.-----.---
A_RW2.1831WCONS -M-------D---------K-N-T-T-I--G-----.-I--..-----..----S--..-.-.-N---.-------AD---.--XE--I--..S-..--G....--...-.---.T-.----
A_RW2.1831CONS  -M-------D---------K-N-T-T-I--G-----.-I--..-----..T------..-.-.-----.-------AD---.--IE-----..S-..--K....--...-.---.-K-.----
A_RW2.561ACONS  IK-------D---------DKA-N-T-I--------.--H-..-----..-------..-.-.-N---.-N-TI--AD--E.--RK--I--..-T..--E....-TT..-.---.NK-.----
A_RW2.561WCONS  -K-------D---------DKA-N-T-I--------.----..-----..--F---G..-.-.-----.-------AD--E.--XK--K--..-T..--N....-TT..-.---.NK-.----
A_RW2.R2235     -M-----------------TK-------------T.-IH-..-----..-------..-.-.----K.-Y-E-NK---TE.A-K--SG--..T-..--V....--...-.-K-.DKA.--
A_RW2.R2235W    -M--------------A--TK-------------T.-IH-..-----..-------..-.-.----K.-Y-E-NK---TE.A-K--SG--..T-..--V....--...-.-K-.DKA.-----.-
A_RW3.PVP       -Q-----------------FTKA---------KT---.G---..-----..-W--R-N..M.-.----K.-Y--------Q.---K------..G-..H-....--...-.-T-.TK-.-----.-------.----.-------
A_RW3.PVP2          -D-------H-NKT-N-T-I-------E.-I--..-----..T---A-A..-.-.-----.----I-SS--K
A_RW3.PVP3          -----------AQ--E------------.--S-..-----..-------..-.-.-----.-----G-AKRK
A_RW3.PVP4          -D---------N-S-V------------.-IP-..---G..-------..-.-.-N---.-Y--I--AK--
A_RW3.PVP5           --V-------AKS-Q-K-I-------R.-I--..-----..----S.-..-.-.-S---.----IT-LQ--
A_RW4.074       -QV----------M-----DKA---E----------.--H-..-----..-------..-.-.----K.-F-I-N-----Q.--DK--R--..-R..H-K....--...-.-T-.-K
A_RW4.081CONS   -R-----------------NQ--E------------.--S-..-----..-------..-.-.-N---.-------AK--E.--RK------..G-..--K....--...-.---.DS
A_RW4.082CONS   -K--------------I--T----------------.--S-..-----..-------..-.-.-----.------KE----.--G--VM--..--..H-.....D-...-.---.--
A_RW4.226       -K-------D-T-I-----NKS-E-I----------.--H-..-----..------G..-.-.-N---.-----NG-GX-Q.A--E-VKK-..-E..H-....--...-.-K-.NS
A_RW4.439CONS   IR-----------N-L----K----D-S--------.----..-----..T---S.-..-.-.-----.-------S---E.--KEI-----..--..--E....--...-.-S-.DK
A_RW4.538CONS   -K--C--------------D-A--------------.--H-..-----..-------..-.-.-----.--------A--R.---K--M--..KS..LL....--T..-.---.--
A_RW4.564CONS   -R--A----D-----M-H-NTS-Q------------.----..-----..T-----E..-.-.-----.-Y--L---A--Q.---K-V---..G-..--G....-T...-K-R-.T-
A_RW4.566CONS   IMV-F----D---S----FDKA-E------------.GIH-..-----..----A-E..-.-.----K.-Y-T-NK---T-.---K--EK-..KR..H-K....--...-.---.--
A_RW4.618CONS   -R---------V---L----K--------------T.-I--..-----..--F---G..-.-.----K.---T-N-S---N.-----V----..--..--G....--...-.---.--
A_RW4.730CONS   -Q-----------------FN-T-R-----------.--H-..-----..----I--..V.-.-P-KK.-Y-D--GI--ER.--KE--K--..G-..H-I....--...-.-N-.TK
A_TZ.TAN142     -R-----------N----FA-------I--------.--H-..-----..-------..-.-.-----.-------AP-RE.A
A_TZ.TAN15CON   -K-----------N-----T---E---I--------.--H-..-----..TS-----..-.-.-----.--------K--T.---K-VK--..KQ..--G....--...-.---.T-
A_TZ.TAN8       -M-----------N----FIK---------------.--H-..-----..-------..-.-.-----.-------A----.-----VQ--..-T..H-G....--...-.-T-.-R
A_TZ.TAN9CON    -R-----------N----FSR--------------R.--H-..-----..-------..-.-.----R.-------A---T.--KE--D--..-I..--E....--...-.---.--
A_TZ2.016       -M---------V-N-----FT-------S-------.----..-----..-------..-.-.-----.-------AR---.---K-VN--..-T..--G....--...-.---.-K-.A----.-------.---
A_TZ2.017       -M---------V-N-----T---Q-----S------.----..-----..-------..-.-.-----.-------AG---.---E--K--..ST..H-E....--...-.---.T---.-------.----.S
A_TZ3.1574           -----V---L---TQ--E------------.-I--..-----..-------..-.-.-----.--------Q--N.--K--VD--..-T..--K....-A...-.---.PE-.-----.---S---.----.-------
A_TZ3.1576           -----HQEH----N---E------------.--H-..-----..-------..-.-.-----.-------AK--E.A--K-V---..-T..--G....--...-.---.T----.-------.----.-------
A_TZ3.1577           -------N-L--FAK----D----F----T.--H-..-----..--F---A..-.-.----K.-------S---N.--L---D--..--..H-N....--...-.---.--P.-----.-------.----.G------
A_TZ3.1584           -----V-------D---E------------.-IH-..-----..-------..-.-.-----.------KSK--N.----------..-N..--G....--...-.---.A----.-------.--M-.-----D-
A_UG.1033        M-----------N----FT---T------------.-IHL..---R..-------..-.-.-----.-------AD---.--KE-VK-
A_UG.92UG037    -M---------V-N-----N-S-T-----------R.----..-----..T------..-.-.-----.------GSQ---.--H--VE--..--..-WN....-N...-.---.NS-.-----.-------.--A-.-------
A_UG.964        -T--A--------N----FAR--R-----------E.----..-----..-------..-.-.-----.------KE---N.---E--K--..Q-..ELGN...--...-.---.-----.-------.----G-------
A_UG.UG06       -K------SD---------TK--T------YKKV-R.RIH-..---R..S--TSN...L..-.-.----.-Y---GSQ---.-----V-K-..-E..-W.....-T...-.-N-.SKP.-----.-------.--V-.------
A_UG1.W2UG03         --S----------HT--N-S-I--------.----..-----..-------..-.-.-N---.---T-K-S----.--T--VKE-..--..-W....--...-.---.T--.-
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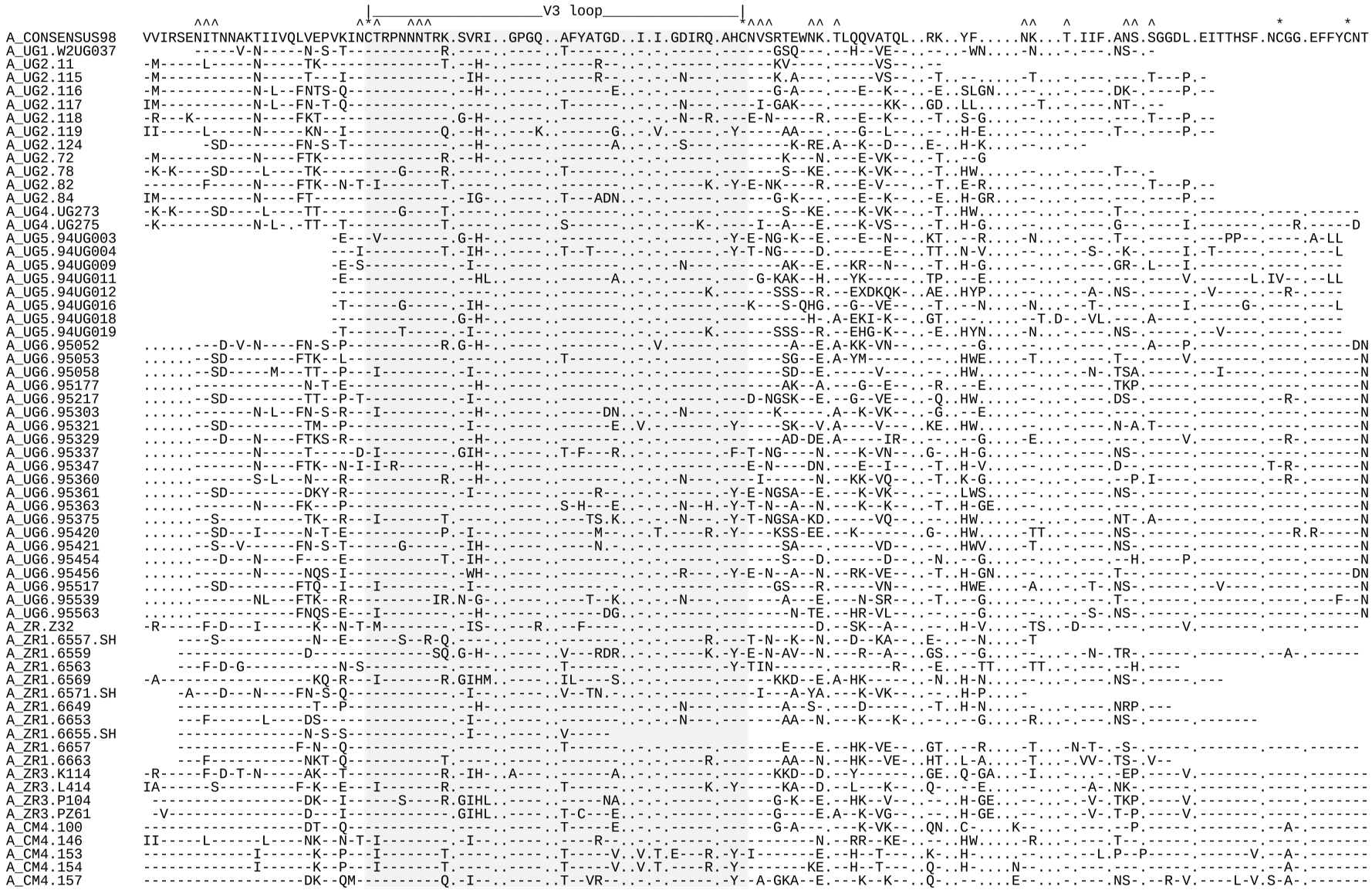
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A_UG2.82
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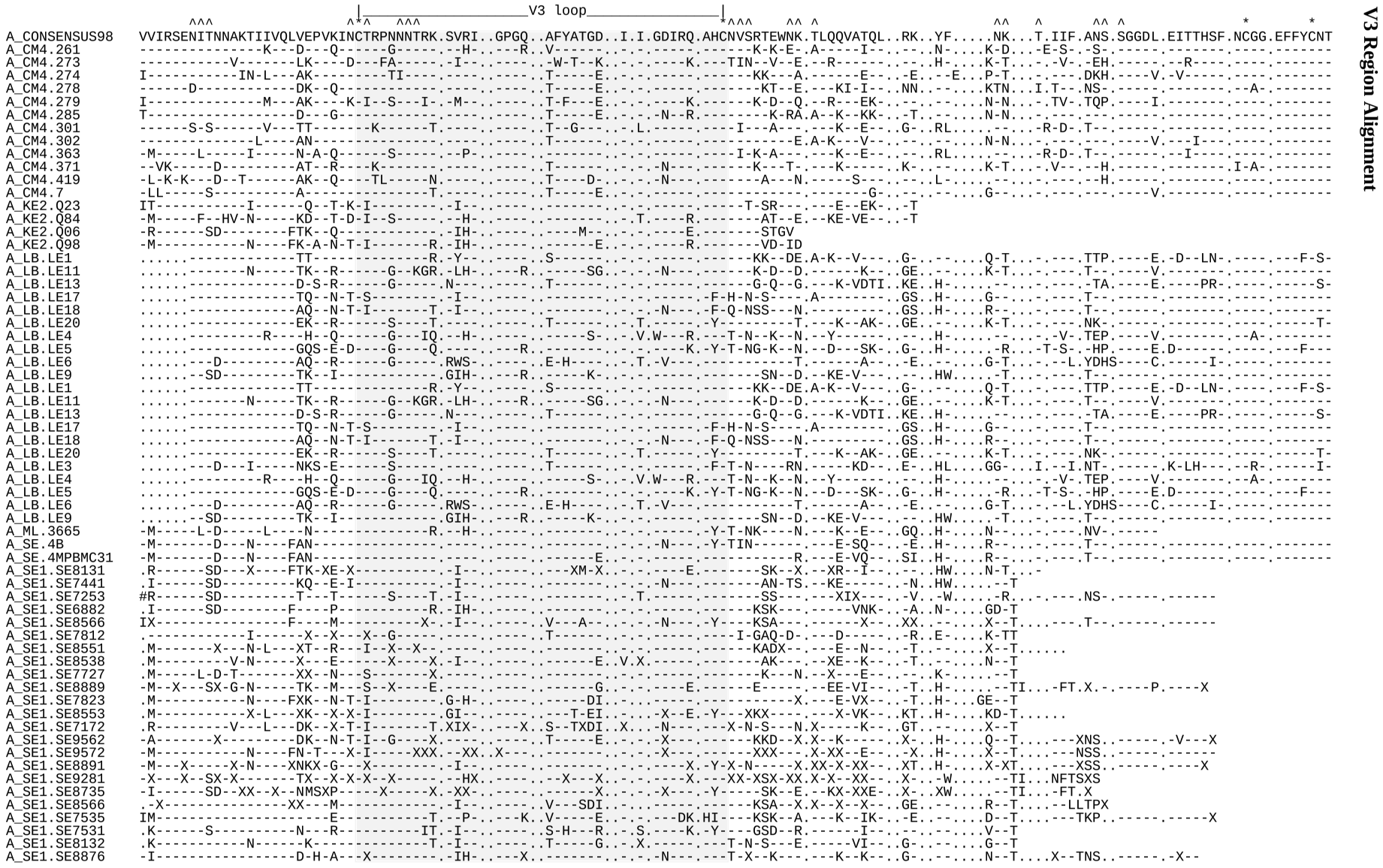
A_CM4.153
A_CM4.154
A_CM4.157

Analyses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A_CM4.302
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A_CM4.371
A_CM4.419
A_CM4.7
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A_KE2.Q84
A_KE2.Q06
A_KE2.Q98
A_LB.LE1
A_LB.LE11
A_LB.LE13
A_LB.LE17
A_LB.LE18
A_LB.LE20
A_LB.LE4
A_LB.LE5
A_LB.LE6
A_LB.LE9
A_ML.3665
A_SE.4B
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A_SE1.SE7441
A_SE1.SE7253
A_SE1.SE6882
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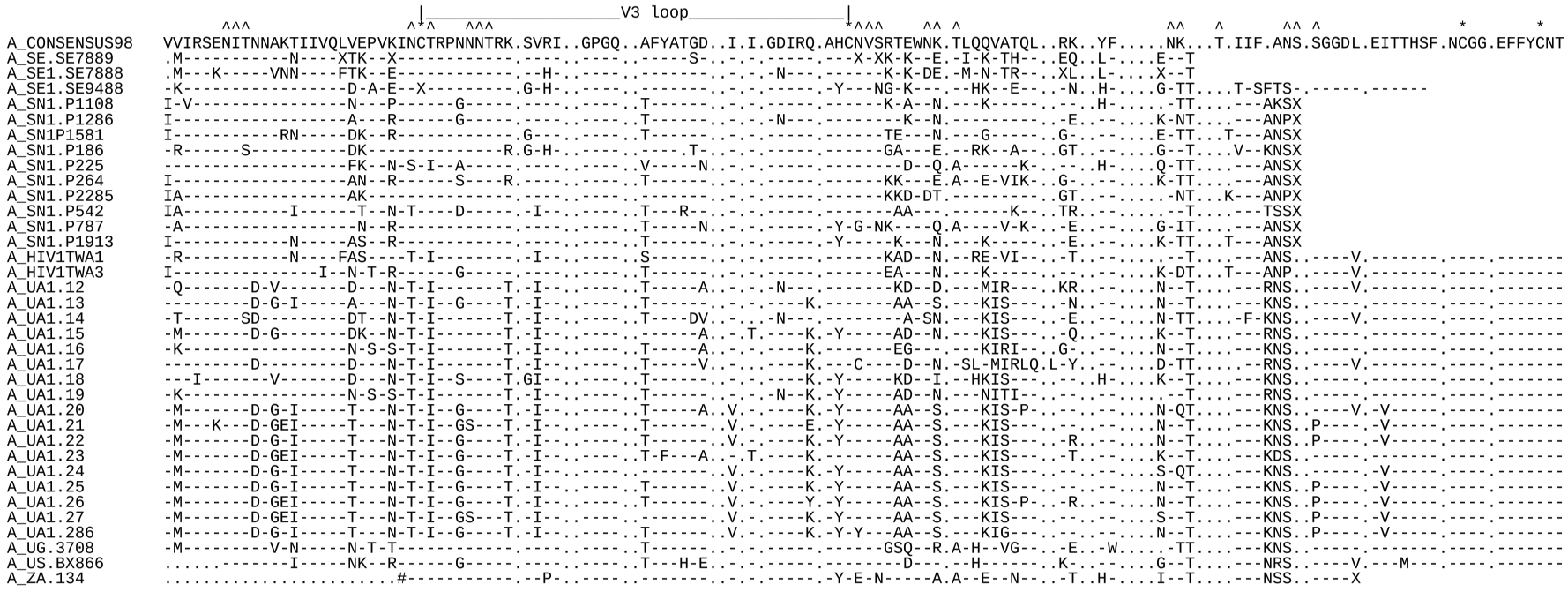
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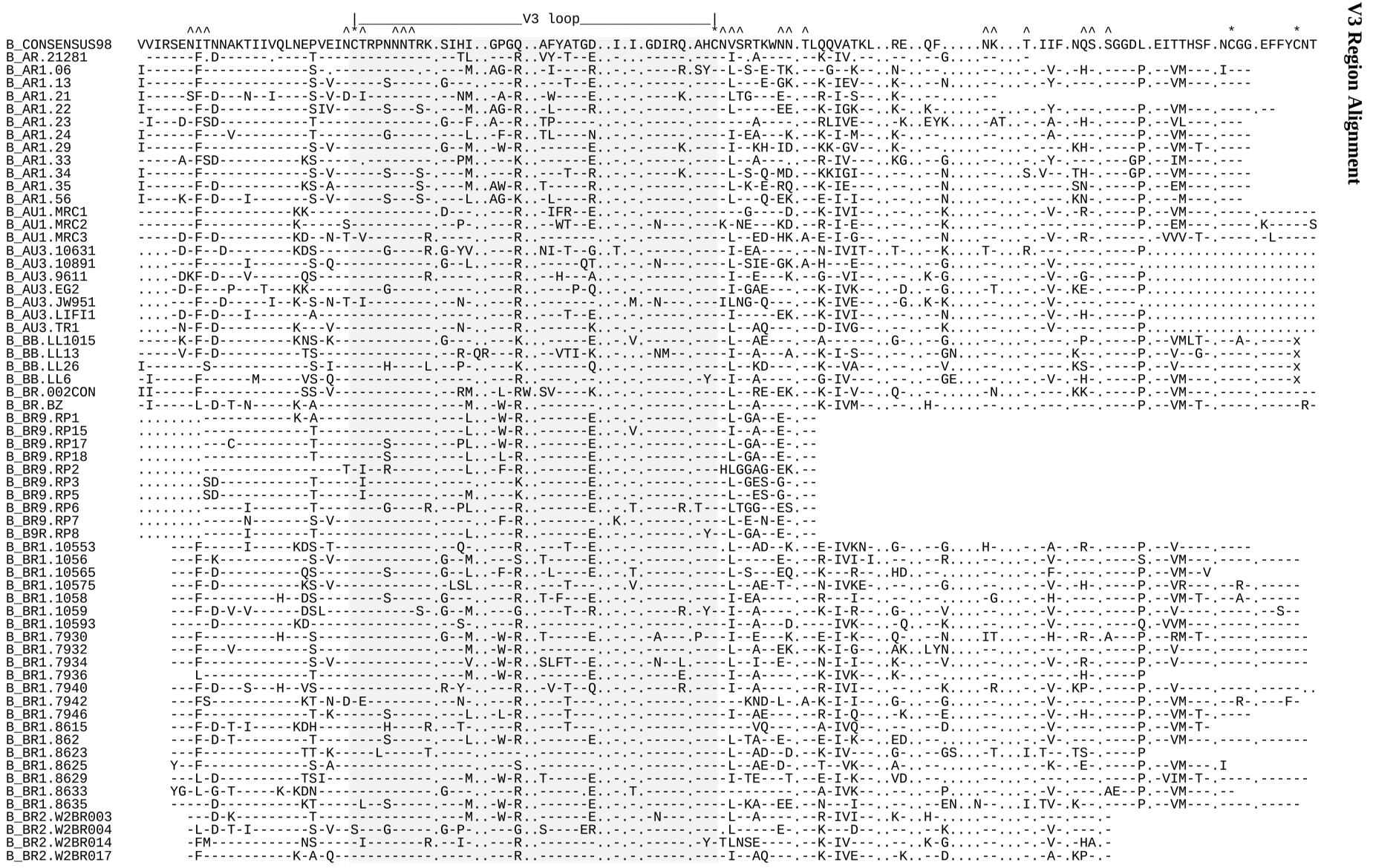
A_SE.SE7889 .M----------N----XTK--X-----------.----.----..-----S-..-.-.-----.---X-XK-K--E.-I-K-TH---.EQ..L-....E--T
A_SE1.SE7888 .M---K-----VNN----FTK--E----------.--H-..----..-------..-.-.-N---.------K-K-DE.-M-N-TR--..XL..L-....X--T
A_SE1.SE9488 -K----------------D-A-E--X---------.G-H-..----..-------..-.-.-----.-Y---NG-K---.--HK--E--..-N..H-....G-TT....T-SFTS-.-----.------
A_SN1.P1108 I-V----------------N---P------G-----.----..-----..T------..-.-.-----.------K-A--N.---K-----..--..H-.....-TT.......AKSX
A_SN1.P1286 I----------------A---R------G-----.----..-----..T------..-.-.-N---.--------K--N.----------..-E..----..K-NT...---ANPX
A_SN1P1581 I----------RN-----DK--R----------.G---..-----..T------..-.-.-----.------TE---N.---G------..G-..----..E-TT...T---ANSX
A_SN1.P186 -R------S----------DK-------------R.G-H-..----..-----.T-..-.-----.------GA---E.--RK--A--..GT..----..G--T....V--KNSX
A_SN1.P225 ----------------FK--N-S-I--A-----.----..-----..V-----N..-.-.-----.--------D--Q.A------K-..---..H-....Q-TT.......ANSX
A_SN1.P264 I----------------AN--R------S----R.----..-----..T------..-.-.-----.------KK---E.A--E-VIK-..G-..----..K-TT.....---ANSX
A_SN1.P2285 IA---------------AK-------------.----..-----..-------..-.-.-----.------KKD-DT.----------..GT..---.....-NT...K---ANPX
A_SN1.P542 IA----------I------T--N-T----D-----.I--..-----..T---R--..-.-.-----.-------AA---.------K---..TR..---.....--T.......TSSX
A_SN1.P787 -A----------------N--R------------.----..-----..T-----N..-.-.------.-Y-G-NK----Q.A----V-K-..-E..----..G-IT.....---ANSX
A_SN1.P1913 I----------N-----AS--R------------.----..-----..T------..-.-.-----.-Y-----K---N.---K------..-E..----..K-TT...T---ANSX
A_HIV1TWA1 -R----------N----FAS----T-I--------.I--..-----..S------..-.-.-----.------KAD--N.--RE-VI---..-T..---.....--T.....---ANS..----V.-------.----.-------
A_HIV1TWA3 I---------------I--N-T-R------G-----.----..-----..T------..-.-.-----.------EA---N.---K-----..--..--....K-DT...T---ANP..----V.-------.----.-------
A_UA1.12 -Q------D-V-------D---N-T-I-------T.-I--..-----..T-----A..-.-.-N---.-------KD--D.---MIR----.KR..---....N--T.......RNS..----V.-------.----.-------
A_UA1.13 ---------D-G-I-----A---N-T-I--G----T.-I--..-----..T------..-.-.----K.-------AA--S.---KIS----..-N..---...N--T.......KNS..-----.-------.----.-------
A_UA1.14 -T------SD---------DT--N-T-I-------T.-I--..-----..T----DV..-..-N---.--------A-SN.---KIS----..-E..---...N-TT.....F-KNS..----V.-------.----.-------
A_UA1.15 -M-------D-G-------DK--N-T-I-------T.-I--..-----..------A...T.----K.-Y-----AD--N.---KIS----..-Q..---...K--T.......RNS..-----.-------.----.-------
A_UA1.16 -K----------------N-S-S-T-I-------T.-I--..-----..T-----A..-.-.----K.-------EG---.---KIRI---.G-..---...N--T.......KNS..-----.-------.----.-------
A_UA1.17 ---------D---------D---N-T-I-------T.-I--..-----..T-----V..-.-.----K.---C----D--N.-SL-MIRLQ.L-Y..---...D-TT.....--RNS..----V.-------.----.-------
A_UA1.18 ---I-------V-------D---N-T-I--S----T.GI--..-----..T------..-.-.----K.-Y-----KD--I.--HKIS---..---..H-....K--T.......KNS..-----.-------.----.-------
A_UA1.19 -K----------------N-S-S-T-I-------T.-I--..-----..T------..-.-.-N--K.-Y-----AD--N.---NITI-..--..--.....--T.......RNS..-----.-------.----.-------
A_UA1.20 -M-------D-G-I-----T---N-T-I--G----T.-I--..-----..T-----A..V.-.----K.-Y-----AA--S.---KIS-P-..---..---...N-QT.....---KNS..----V.-V-----.----.-------
A_UA1.21 -M---K---D-GEI-----T---N-T-I--GS---T.-I--..-----..T-------.V.-.----E.-Y-----AA--S.---KIS---..--..---...N--T.......KNS..P-----.-V-----.----.-------
A_UA1.22 -M-------D-G-I-----T---N-T-I--G----T.-I--..-----..T-------.V.-.----K.-Y-----AA--S.---KIS----..-R..---...N--T.......KNS..P-----.-V-----.----.-------
A_UA1.23 -M-------D-GEI-----T---N-T-I--G----T.-I--..-----..T-F---A..-.T.----K.-------AA--S.---KIS----..-T..---...K--T.......KDS..-----.-------.----.-------
A_UA1.24 -M-------D-G-I-----T---N-T-I--G----T.-I--..-----..--------.V.-.----K.-Y-----AA--S.---KIS---..--..---...S-QT.....---KNS..------.-V-----.----.-------
A_UA1.25 -M-------D-G-I-----T---N-T-I--G----T.-I--..-----..T-------.V.-.----K.-Y-----AA--S.---KIS---..--..---...N--T.......KNS..P-----.-V-----.----.-------
A_UA1.26 -M-------D-GEI-----T---N-T-I--G----T.-I--..-----..T-------.V.-.----Y.-Y-----AA--S.---KIS-P-..-R..---...N--T.......KNS..P-----.-V-----.----.-------
A_UA1.27 -M-------D-GEI-----T---N-T-I--GS---T.-I--..-----..--------.V.-.----K.-Y-----AA--S.---KIS---..--..---...S--T.......KNS..P-----.-V-----.----.-------
A_UA1.286 -M-------D-G-I-----T---N-T-I--G----T.-I--..-----..T-------.V.-.----K.-Y-Y---AA--S.---KIG---..--..---...N--T.......KNS..P-----.-V-----.----.-------
A_UG.3708 -M---------V-N-----N-T-T------------.----..-----..T------..-.-.-----.------GSQ--R.A-H--VG---..-E..-W.....-TT.......KNS..-----.-------.----.-------
A_US.BX866 .....--------I-----NK--R------G-----.----..-----..T---H-E..-.-.-----.--------D----.--H-------.K-..---...G--T.......NRS..----V.---M---.----.-------
A_ZA.134 ....#----------.--P-..----..-------..-.-.------.-Y-E-N-----A.A--E--N---.-T..H-....I--T.......NSS..----X

Analyses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B_AR.21281
B_AR1.06
B_AR1.13
B_AR1.21
B_AR1.22
B_AR1.23
B_AR1.24
B_AR1.29
B_AR1.33
B_AR1.34
B_AR1.35
B_AR1.56
B_AU1.MRC1
B_AU1.MRC2
B_AU1.MRC3
B_AU3.10631
B_AU3.10891
B_AU3.9611
B_AU3.EG2
B_AU3.JW951
B_AU3.LIFI1
B_AU3.TR1
B_BB.LL1015
B_BB.LL13
B_BB.LL26
B_BB.LL6
B_BR.002CON
B_BR.BZ
B_BR9.RP1
B_BR9.RP15
B_BR9.RP17
B_BR9.RP18
B_BR9.RP2
B_BR9.RP3
B_BR9.RP5
B_BR9.RP6
B_BR9.RP7
B_B9R.RP8
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B_BR1.1056
B_BR1.10565
B_BR1.10575
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B_BR1.1059
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B_BR1.7934
B_BR1.7936
B_BR1.7940
B_BR1.7942
B_BR1.7946
B_BR1.8615
B_BR1.862
B_BR1.8623
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B_BR1.8633
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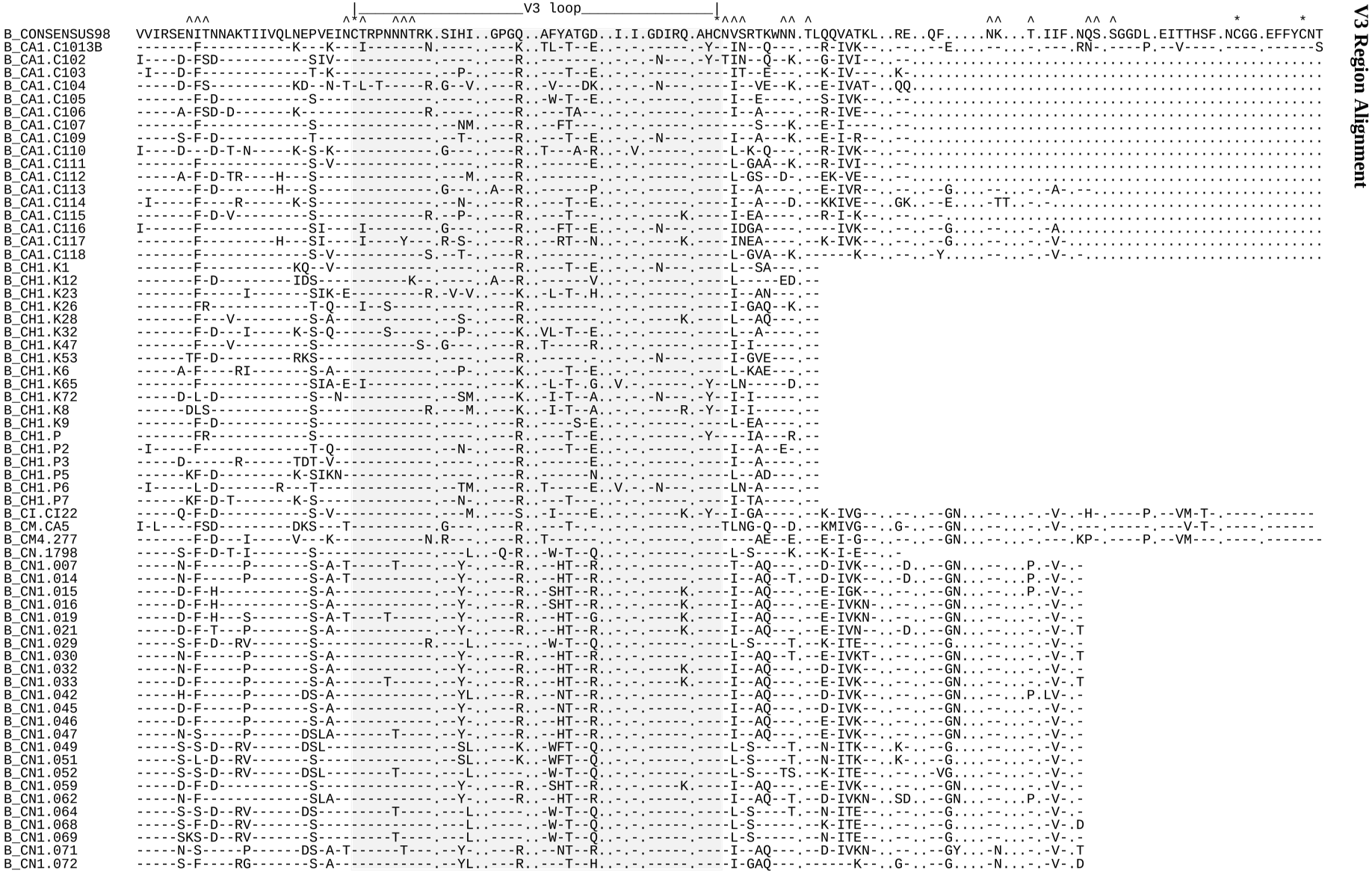
V3 Region Alignment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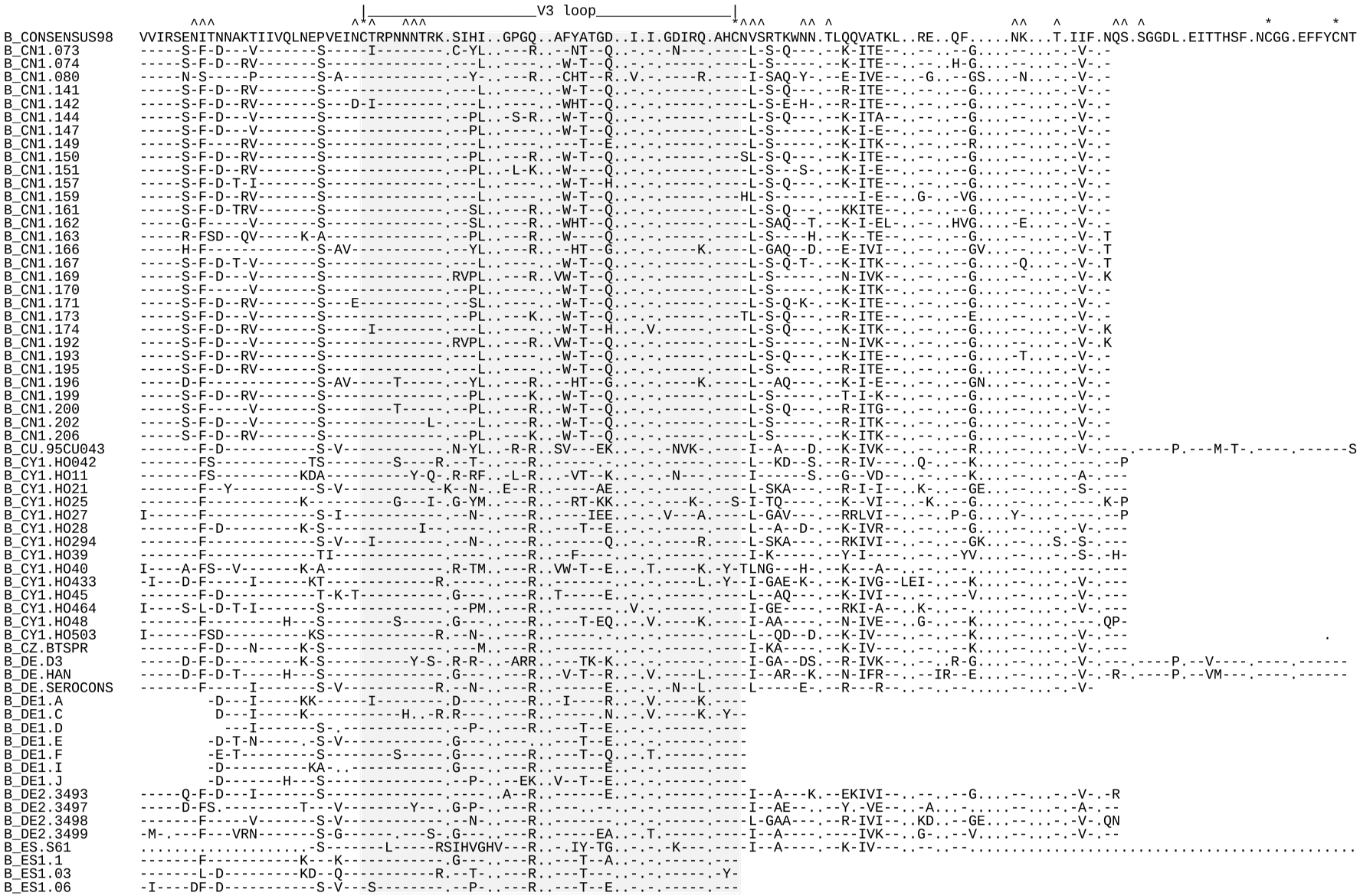
B_CA1.C1013B -------F----------K---K---I-------N.----.---K..TL-T--E..-.-.-----.-Y--IN--Q---.--R-IVK--..--.---E....---...----.RN-.----P.--V----.----.------S
B_CA1.C102 I----D-FSD----------SIV----------.----.---R..--------..-.-.-N---.-Y-TIN--Q--K.--G-IVI--..--.....
B_CA1.C103 -I---D-F----------T-K----------.--P-.---R.---T--E..-.-.-----.----IT--E---.--K-IV----..K-.....
B_CA1.C104 -----D-FS----------KD--N-T-L-T-----R.G--V.---R..-V---DK..-.-.-N---.----I--VE--K.--E-IVAT-..QQ.....
B_CA1.C105 -------F-D----------S----------.----.---R..-W-T--E..-.-.-----.----I--E----.--S-IVK--..--.....
B_CA1.C106 -----A-FSD-D-------K----------R.----.---R.----TA--..-.-.-----.----I--A----.--R-IVE--..--.....
B_CA1.C107 -------F----------S----------.--NM.---R..-FT---..-.-.-----.-------S---K.--E-I----..--.....
B_CA1.C109 -----S-F-D----------T----------.--T-.---R.---T--E..-.-.N---.----I--A---K.--E-I-R--..--.....
B_CA1.C110 I----D---D-T-N-----K-S-K----------.G---.---R..T---A-R..-.V.-----.----L-K-Q---.--R-IVK--..--.....
B_CA1.C111 -------F----------S-V----------.----.---R..-------E..-.-.-----.----L-GAA--K.--R-IVI--..--.....
B_CA1.C112 -----A-F-D-TR----H---S----------.---M.---R..-------..-.-.-----.----L-GS--D-.--EK-VE--..--.....
B_CA1.C113 -------F-D-------H---S----------.G----.A--R..------P..-.-.-----.----I--A----.--E-IVR--..--.--G...--...-A-..--.....
B_CA1.C114 -I-----F----R------K-S----------.--N-.---R.---T--E..-.-.-----.----I--A---D.--KKIVE---.GK.--E....-TT..-.-.....
B_CA1.C115 -------F-D-V---------S----------R.--P-.---R.---T----..-.----K.----I-EA----.--R-I-K--..--.---.....
B_CA1.C116 I------F----------SI----I---------.G---.---R..-FT--E..-.-.N---.----IDGA----.----IVK--..--.--G...--...-.A.....
B_CA1.C117 -------F---------H---SI----I----Y---.R-S-.---R..--RT--N..-.-.----K.----INEA----.--K-IVK--..--.--G...--...-.V-.....
B_CA1.C118 -------F----------S-V----------S.--T-.---R.-------..-.-.-----.----L-GVA--K.------K--..--..-Y....--...-.V-.-.....
B_CH1.K1 -------F----------KQ--V----------.----.---R..---T--E..-.-.N---.----L--SA---.--
B_CH1.K12 -------F-D---------IDS----------K--.----..A--R..------V..-.-.-----.----L-----ED.--
B_CH1.K23 -------F-----I-------SIK-E---------R.-V-V.---K..-L-T-.H..-.-.-----.----I--AN---.--
B_CH1.K26 -------FR----------T-Q---I--S----.----.---R..---------..-.-.-----.----I-GAQ--K.--
B_CH1.K28 -------F---V---------S-A----------.--S-.---R..-------..-.-.----K.----L--AQ---.--
B_CH1.K32 -------F-D---I-----K-S-Q------S-----.--P-.---K..VL-T--E..-.-.-----.----L--A----.--
B_CH1.K47 -------F---V---------S----------S-.G---.---R..T-----R..-.-.-----.----I-I-----.--
B_CH1.K53 ------TF-D---------RKS----------.----.---R..------.-..-.-N---.----I-GVE---.--
B_CH1.K6 -----A-F----RI-------S-A----------.--P-.---K.---T--E..-.-.-----.----L-KAE---.--
B_CH1.K65 -------F----------SIA-E-I--------.----.---K..-L-T-.G..V.-.-----.-Y--LN-----D.--
B_CH1.K72 -----D-L-D----------S--N----------.--SM.---K..-I-T--A..-.-.N---.-Y--I-I-----.--
B_CH1.K8 ------DLS----------S----------R.---M.---K..-I-T--A..-.-.----R.-Y--I-I-----.--
B_CH1.K9 -------F-D----------S----------.----.---R.-----S-E..-.-.-----.----L-EA----.--
B_CH1.P -------FR----------S----------.----.---R.----T--E..-.-.------.-Y----IA---R.--
B_CH1.P2 -I-----F----------T-Q----------.--N-.---R.----T--E..-.-.-----.----I--A--E-.--
B_CH1.P3 -----D------R------TDT-V----------.----.---R.-------E..-.-.-----.----I--A----.--
B_CH1.P5 ------KF-D---------K-SIKN---------.----.---R.-------N..-.-.-----.----L--AD---.--
B_CH1.P6 -I-----L-D-------R---T----------.--TM.---R..T-----E..V.-.N---.----LN-A----.--
B_CH1.P7 ------KF-D-T-------K-S----------.--N-.---R.---T---..-.-.-----.----I-TA----.--
B_CI.CI22 -----Q-F-D----------S-V----------.---M.---S..-I----E..-.-.----K.-Y--I-GA-----.--K-IVG---..--.---GN...--...-.-V-.-H-.----P.--VM-T-.----.------
B_CM.CA5 I-L----FSD---------DKS---T----------.G---.---R.---T-.-..-.-----.---TLNG-Q--D.--KMIVG---..G-.---GN...--...-.-V-.---.-----.---V-T-.----.------
B_CM4.277 -------F-D---I-----V---K----------N.R---.---R..T-----..-.-----.-------AE--E.--E-I-G---..--.---GN...--...-.---.KP-.----P.--VM---.----.-------
B_CN.1798 -----S-F-D-T-I------S----------.---L..-Q-R.-W-T--Q..-.-.-----.----L-S----K.--K-I-E---..-
B_CN1.007 -----N-F-----P-------S-A-T-----T----.--Y-.---R.--HT--R..-.-.-----.----T--AQ---.--D-IVK---.-D.---GN...---...P.-V-.-
B_CN1.014 -----N-F-----P-------S-A-T----------.--Y-.---R.--HT--R..-.-.-----.----I--AQ--T.--D-IVK---.-D.---GN...---...P.-V-.-
B_CN1.015 -----D-F-H----------S-A----------.--Y-.---R..-SHT--R..-.-.----K.----I--AQ---.--E-IGK---..--.---GN...---...P.-V-.-
B_CN1.016 -----D-F-H----------S-A----------.--Y-.---R..-SHT--R..-.-.----K.----I--AQ---.--E-IVKN-..--.---GN...---...-.-V-.-
B_CN1.019 -----D-F-H---S-------S-A-T----T----.--Y-.---R.--HT--G..-.-.----K.----I--AQ---.--E-IVKN-..--.---GN...---...-.-V-.-
B_CN1.021 -----D-F-T---P-------S-A----------.--Y-.---R.--HT--R..-.-.----K.----I--AQ---.--E-IVN---.-D.---GN...---...-.-V-.T
B_CN1.029 -----S-F-D--RV------S----------R.---L.-----..-W-T--Q..-.-.-----.----L-S----T.--K-ITE---..---.-G...---...-.V-.-
B_CN1.030 -----N-F-----P-------S-A----------.--Y-.---R.--HT--R..-.-.-----.----I--AQ--T.--E-IVKT-..--.---GN...---...-.V-.T
B_CN1.032 -----N-F-----P-------S-A----------.--Y-.---R.--HT--R..-.-.----K.----I--AQ---.--D-IVK---..--.---GN...---...-.V-.-
B_CN1.033 -----D-F-----P-------S-A------T----.--Y-.---R.--HT--R..-.-.----K.----I--AQ---.--E-IVK---..--.---GN...---...-.V-.T
B_CN1.042 -----H-F-----P------DS-A----------.--YL.---R.--NT--R..-.-.-----.----I--AQ---.--D-IVK---..--.---GN...---...P.LV-.-
B_CN1.045 -----D-F-----P-------S-A----------.--Y-.---R.--NT--R..-.-.-----.----I--AQ---.--D-IVK---..--.---GN...---...-.V-.-
B_CN1.046 -----D-F-----P-------S-A----------.--Y-.---R.--HT--R..-.-.-----.----I--AQ---.--E-IVK---..--.---GN...---...-.V-.-
B_CN1.047 -----N-S-----P------DSLA-------T----.--Y-.---R.--HT--R..-.-.-----.----I--AQ---.--E-IVK---..--.---GN...---...-.V-.-
B_CN1.049 -----S-S-D--RV------DSL----------.--SL.---K..-WFT--Q..-.-.-----.----L-S----T.--N-ITK---..K-.---G...---...-.V-.-
B_CN1.051 -----S-L-D--RV------S----------.--SL.---K..-WFT--Q..-.-.-----.----L-S----T.--N-ITK---..K-.---G...---...-.V-.-
B_CN1.052 -----S-S-D--RV------DSL--------T----.---L.-----..-W-T--Q..-.-.-----.----L-S---TS.--K-ITE---..---..VG...---...-.V-.-
B_CN1.059 -----D-F-D----------S----------.--Y-.---R.--SHT--R..-.-.----K.----I--AQ---.--E-IVK---..--.---GN...---...-.V-.-
B_CN1.062 -----N-F----------SLA----------.--Y-.---R.---HT--R..-.-.-----.----I--AQ--T.--D-IVKN-..SD.---GN...---...P.-V-.-
B_CN1.064 -----S-S-D--RV------DS---------T----.---L.-----..-W-T--Q..-.-.-----.----L-S----T.--N-ITE---..--.---G...---...-.V-.-
B_CN1.068 -----S-F-D--RV------S----------.----.---L.-----..-W-T--Q..-.-.-----.----L-S------.--K-ITE---..--.---G...---...-.V-.D
B_CN1.069 -----SKS-D--RV------S---------T----.---L.-----..-W-T--Q..-.-.-----.----L-S------.--N-ITE---..--.---G...---...-.V-.-
B_CN1.071 -----N-S-----P------DS-A-T------T----.--Y-.---R.---NT--R..-.-.-----.----I--AQ---.--D-IVKN-..--.---GY...-N...-.V-.T
B_CN1.072 -----S-F----RG------S-A----------.--YL.---R.---T--H..-.-.-----.----I-GAQ---.------K---.G-.---G....-N...-.V-.D



V3 Region Alignment

Analyses

V3 Region Alignment

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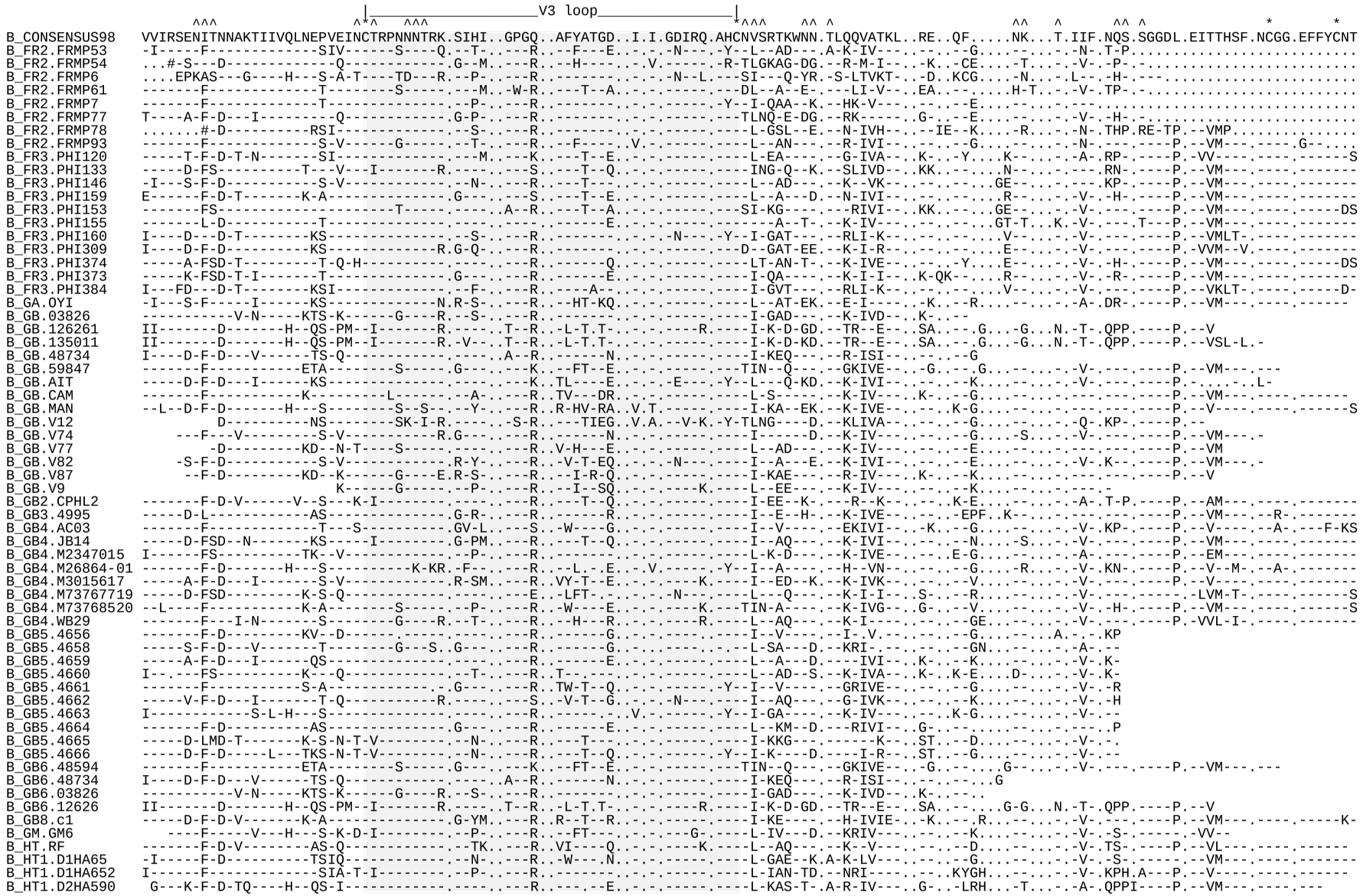
                                                  |____________________V3 loop________________|
                   ^^^                          ^*^    ^^^                                       *^^^    ^^ ^                     ^^   ^      ^^ ^               *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_ES1.07        -----D-FSD-T--------KSI-------------.--P-..---R..-------.-.-.-----.---
B_ES1.09        -------F-D----------T---------------.--P-..---R..---T--E..-.-.-----.---
B_ES1.10        I----D-F-D-T---------AIK------------.--P-..---R..------E..-.-.-----.---
B_ES1.106       I--------D-------H---SI-------------.----..---R..------E..-.-.-N---.---
B_ES1.108       I------F-D-------H---SIQ------------.G---..---N..---T-.E..-.T.-----.---
B_ES1.13        I------F-D----------T--------------R.--T-..---S..V--.--E..-.-.-N---.---
B_ES1.14        -----A-F-D-------H---S-------------R.----..---K..V--.--..-.-.-----.---
B_ES1.15        -----D-F---V-------K----------------.--P-..---R..---T--E..-.-.-----.---
B_ES1.17        -------F--HI-------K---Q-----------R.----..---K..--.---..-.-.-N---.---
B_ES1.18        --V-A----D-T-------K-AIQ------------.--T-..---R..---T--E..-.-.-----.---
B_ES1.20        --V--A-FSD-T-------K--I-----------S-.G---..---R..T----.N..-.-.-----.---
B_ES1.26        -------F--HV-------KD-IA------------.G---..---R..------..-.-.-----.---
B_ES1.D17       -I-----F-------------S--------------.RVS-..---R..-WRT--Q..-.-.----K.-Y-
B_ES1.I1        ---------D-T---------TI---------Y---.RVS-..---R..--RTA-S..-.-.-----.---
B_ES1.III       -----V-F-D----------TT-T------------.G-P-..---R..-----AS..-.-.-V-T-.---
B_ES1.IV        I------F-------------S--------------.G---..---R..-L-T-.E..-.-.-----.---
B_ES1.P12       -----D-F-D---S-------T-----S--------.G--L..---G..---T--A..-.-.-----.---
B_ES1.P13       II-----FSD----------QTI--T-M--H----R.---L..---S..-------..-.-.-----.---
B_ES1.P14       -------F-D-V---------S-V-------KKVER.R---..---R..-----.-..-T-.-----.---
B_ES1.P17       -------F-D-----------S-P-K-I-------R.G-N-..---R..-----.-..-.-.-N--E.---
B_ES1.P18       I------F-D-L-N---------Q-K-I--------.G---..---K..-----R..-.-.-----.---
B_ES1.P19       -----D-F-----------K-------I--------.G---..---R..V----.G..-.-.-----.---
B_ES1.P20       -----D-F-D---V------TSI---------IT---.---M..---R..TVH-I-R..-.-.-----.---
B_ES1.P21       -------FS---R--------TIQ------------.----..---R..---TS.E..-.-.-----.---
B_ES1.P6        I----D-F-D-V---------SI-------S-----.----..---R..---T--E..-.-.-----.---
B_ES1.P9        -------FKE-I-P-------S-----I--------.----..---R..--HT--A..-.-.-----.---
B_ES1.R1        -------F-----------K-SIK-----------R.GV--..--RR..G--T-.E..-.-.-N---.---
B_ES1.S1        -----D-F-----------K-AI-------------.--P-..---R..---TI--..-.-.--L--.---
B_ES1.THF13A    I----A-F-D----------ASI------------R.G---..---R..---G-..-.T.-N---.---
B_ES1.THF17     -------F---------H---SI-------------.----..---S..---T--R..-.-.-----.---
B_ES1.V         -------F-D---N-----K-S--------------.G---..---R..-------..-.-.-----.---
B_ES1.VI        -------F-D-V--------KS--------------.--AL..---G..-V----E..-.-.-----.---
B_ES1.VIII      I------F-------------SIA------------.G--L..---G..--F--N..-.-.-----.---
B_FR.120        -----T-F-D-T-N-------SI-------------.---M..---K..---T--E..-.-.------.----L-EA----.--G-IVA--..K-..-YK.........-A-.RP-.----P.-VV----.----.------S
B_FR.133        -----D-FS----------T---V---I-------R.----..---S..---T--Q..-.-.------.----ING-Q--K.--SLIVD--..KK..--N.............RN-.----P.--VM---.----.-------
B_FR.146        -I---S-F-D-----------S-V------------.--N-..---R..---T---..-.-.------.----L--AD---.--K--VK--.......--GE.............KP-.----P.--VM---.----.-------
B_FR.153        -------FS--------------------T------.----..A--R..---T--A..-.-.------.---SI-KG----.---RIVI--..KK..--GE.........-V-.--------P.--VM---.----.-----DS
B_FR.155        -------L-D-----------T--------------.----..----..------E..-.-.------.--------A--T-.--K-IV---.......--GT...-T...K.-V-.----.T---P.--VM---.----.-------
B_FR.159        E------F-D-T-------K-A--------------.G---..---S..---T--E..-.-.------.----L--A---D.--N-IVI--.......--R.........-V-.-H-.----P.--VM---.----.-------
B_FR.160        I----D---D-T--------KS--------------.--S-..---R..-------..-.-.N---.-Y--I-GAT---.--RLI-K--.......--V.........-V-.--------P.--VMLT-.----.-------
B_FR.309        I----D-F-D----------KS-------------R.G-Q-..---R..-------..-.-.------.---D--GAT-EE.--K-I-R--.......--E.........-V-.--------P.-VVM--V.----.-------
B_FR.373        -----K-FSD-T-I-------T--------------.G---..---R..------E..-.-.------.----I-QA----.--K-I-I--..K-QK--R.........-V-.-R-.----P.--VM---.----.-------
B_FR.374        -----A-FSD-T---------T-Q-H----------.----..---R..------Q..-.-.------.----LT-AN-T-.--K-IVE--.......-YE.........-V-.-H-.----P.--VM---.----.-----DS
B_FR.384        I---FD---D-T--------KSI-------------.--F-..---R..----A--..-.-.------.----I-GVT---.--RLI-K--.......--V.........-V-.--------P.--VKLT-.----.-----D-
B_FR.CA         ---------------V----K-S------------R.R-T-..---R..VY-T--A..-.-.----K.----I--A----.--K-IVK--.......--E.........-V-.--------P.-
B_FR.CB         ------K------S-------T--------------.G---..---R..-------..-.-.N---.----I--A---D.--R-I-I--..G-..--K.........-V-.--------P.-
B_FR.CC         I----D-F-D----------QS-V------------.D---..---R..------E..-.-.------.----L--VQ---.--R-------..........--K..-.VV-.K--.----P.-
B_FR.CD         -------FA----------K---K------------.--P-..---K..-------..-.-.------.----L--A---D.--K-IVN--..G-..--K.........-S-..--.----P.-
B_FR.J6          ----D-FSD-----------T--------------.----..---R..------E..-.-.------.----I--A----.--K-IVR--.......-YE.........-V-.K--.----P.--VM---.I---.------S
B_FR.J91         ----D-FSD-----------T--------------.----..---R..------E..-.-.------.----I--A----.--K-IVR--..K-..-YK.........-V-.K--.----P.--VM---.T---.------S
B_FR.LAI        -----A-F-D----------QS--------------.--R-QR--R..--VTI-K....-.NM--.----I--A---A.--K-I-S--.......--GN.............K--.----P.--V----.----.------
B_FR2.FRMP122   .------F-D---S-------S-I-----------R.--S-..-L-RYNRV-T--M..-.-.--RLRK-Y--I-EE----.--KKIVE--..Q-..K-G.........................................
B_FR2.FRMP159   -------F-D-T---------T-K-----G------.----..---R..------G..-.T.------.----L--A---D.--K-IV---.......--E....A....-V-.----.LR....................
B_FR2.FRMP27    IM---A-FSD---------K----------------.--Y-..---K..--HT-DR..-.-.------.----I-EG----.--KLIVD--.......K-G.............-H-.-......................
B_FR2.FRMP29    I--------D---V-----K--I---I---------.R-S-..---R..-V-T--Q..-.-.------.----I--G---G.----I-K--.......--V.........-V-.-P-.-......................
B_FR2.FRMP291   -------F-----------KKS-Q-----------R.--S-..---R..---.---..-.-.------.----L--KD--D.--G--VK--.......--G..........................................
B_FR2.FRMP32    ---I-K---D-T-------K---------------R.G---..---R..-----.-..-.-.------.-Y--I-KAR--T.----IVD--..-G..--G.........-V-.---.L.......................
B_FR2.FRMP329   .-V----F-----I------KT-V-----L------.----..---R..-------..-.-.----K.----I--ED--T.---R--A--..KG.............-V-.-H-.----P.-.................
B_FR2.FRMP36    -------F-------------T--------S-----.G--M..-W-R..---T--A..-.-.------.----I-EGA--K.---E-GK--..N-..H-F.........-S-.AP........................
B_FR2.FRMP45    ..#--A-L-D---I---------Q------------.G-PM..---R..------E..-.-.----K.---AL-T-Q-D-.---EI-I--..G-..--G...-T....-V-.TH-.----P.--VM---............
B_FR2.FRMP47    ----AK--S---G----H---S-T-----------L.--S-..---R..------A..-.-.------.----I-E-Q-KR.--KLTVE--.......K-G.............-H-.V.......................
B_FR2.FRMP51    -------FS----------T---Q------------.R-PM..---R..---T--E..V.-.----R.---TL--AS--G.--REIVK--.......--G.........-V-.YSL.......................
B_FR2.FRMP52    .........#---I---------Q------------.G---..---R..-C-T--G..-.V.--L-K.---TLNK---EG.--REI-I--..G-..--K.........-V-.--------P.--VM...............
```


V3 loop
B_CONSENSUS98
B_FR2.FRMP53
B_FR2.FRMP54
B_FR2.FRMP6
B_FR2.FRMP61
B_FR2.FRMP7
B_FR2.FRMP77
B_FR2.FRMP78
B_FR2.FRMP93
B_FR3.PHI120
B_FR3.PHI133
B_FR3.PHI146
B_FR3.PHI159
B_FR3.PHI153
B_FR3.PHI155
B_FR3.PHI160
B_FR3.PHI309
B_FR3.PHI374
B_FR3.PHI373
B_FR3.PHI384
B_GA.OYI
B_GB.03826
B_GB.126261
B_GB.135011
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B_GB.59847
B_GB.AIT
B_GB.CAM
B_GB.MAN
B_GB.V12
B_GB.V74
B_GB.V77
B_GB.V82
B_GB.V87
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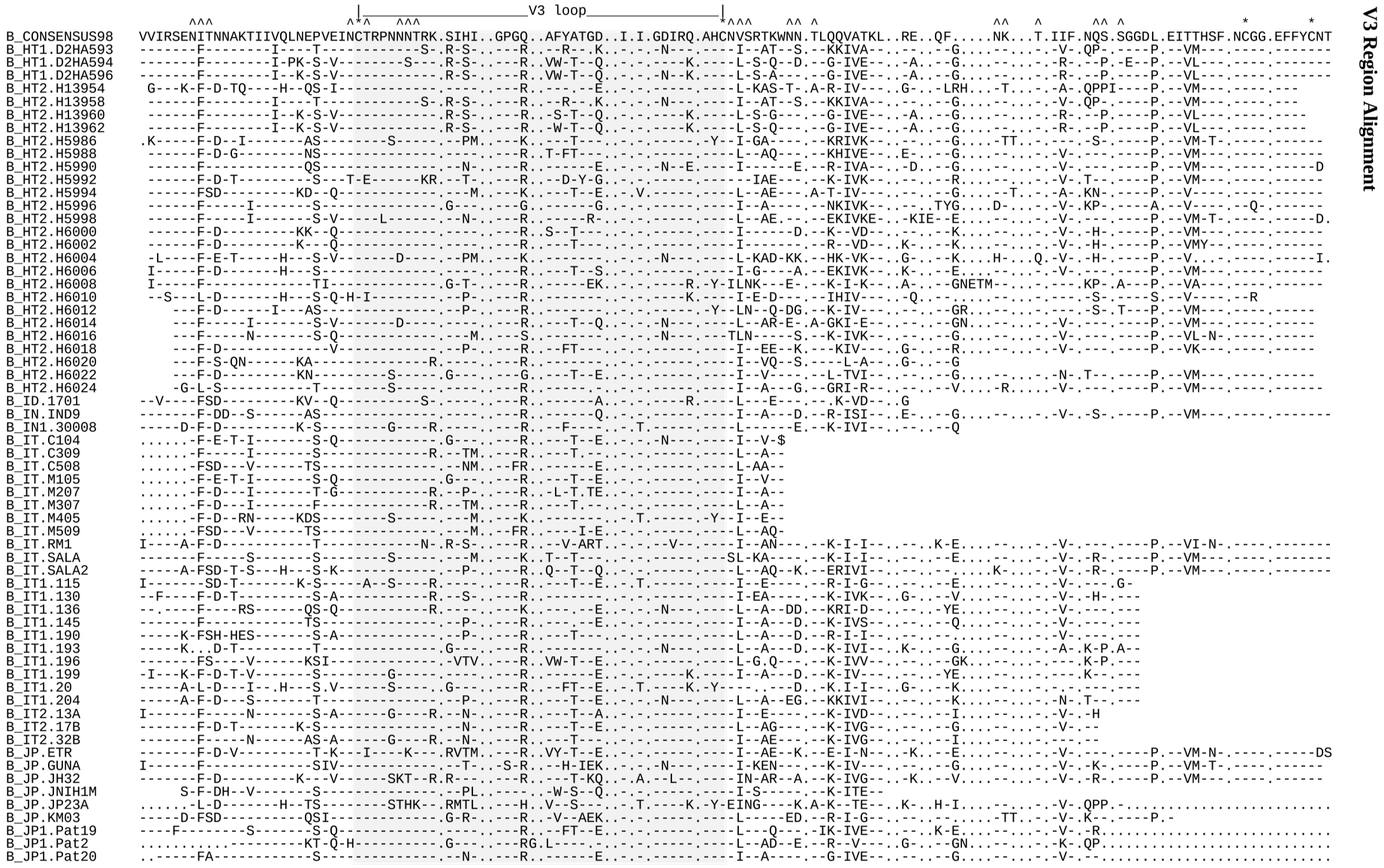
B_GB5.4665
B_GB5.4666
B_GB6.48594
B_GB6.48734
B_GB6.03826
B_GB6.12626
B_GB8.c1
B_GM.GM6
B_HT.RF
B_HT1.D1HA65
B_HT1.D1HA652
B_HT1.D2HA590

Analyses


V3 loop
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B_HT1.D2HA593
B_HT1.D2HA594
B_HT1.D2HA596
B_HT2.H13954
B_HT2.H13958
B_HT2.H13960
B_HT2.H13962
B_HT2.H5986
B_HT2.H5988
B_HT2.H5990
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B_HT2.H5994
B_HT2.H5996
B_HT2.H5998
B_HT2.H6000
B_HT2.H6002
B_HT2.H6004
B_HT2.H6006
B_HT2.H6008
B_HT2.H6010
B_HT2.H6012
B_HT2.H6014
B_HT2.H6016
B_HT2.H6018
B_HT2.H6020
B_HT2.H6022
B_HT2.H6024
B_ID.1701
B_IN.IND9
B_IN1.30008
B_IT.C104
B_IT.C309
B_IT.C508
B_IT.M105
B_IT.M207
B_IT.M307
B_IT.M405
B_IT.M509
B_IT.RM1
B_IT.SALA
B_IT.SALA2
B_IT1.115
B_IT1.130
B_IT1.136
B_IT1.145
B_IT1.190
B_IT1.193
B_IT1.196
B_IT1.199
B_IT1.20
B_IT1.204
B_IT2.13A
B_IT2.17B
B_IT2.32B
B_JP.ETR
B_JP.GUNA
B_JP.JH32
B_JP.JNIH1M
B_JP.JP23A
B_JP.KM03
B_JP1.Pat19
B_JP1.Pat2
B_JP1.Pat20

V3 Region Alignment

V3 Region Alignment

```
                                          |____________________V3 loop________________|
                   ^^^                  ^*^    ^^^                                     *^^^    ^^ ^                     ^^   ^      ^^ ^              *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_NL.c73C-S     I------FS-----------QS---------------.G---.---R..---TRDR..-.-.--L--.----I-GA---D.--K--VI--..SK..--..K.--..-.-V-.-P-.----P.--VL
B_NL.c79A-F     -I---D-FS-----------KA-K------S-----.----.---R..------E..-.T.-----.----I--AD---.--K-IVI--..--..--..K.--..-.-A-.K--.----P.--VM
B_NL.c79B-S     -------F-----------K--IN-T-I--S-----.--P-.----K..-------..-.-.-----.---ILNG----D.--K-IVI--..--..--..K.--..-.-V-.-P-.----P.--VK
B_NL.c92A-F     -------L-D---I-----KD---------------.G---..A-WG..S------..-.-.-----.-Y--I-NA---D.--R--VE--..KG..K-.GK.--..-.---.-H-.----P.--VM
B_NL.c92B-S     -I-----L-D---I-----KD---------S----R.G---..A--R..----A---..-.-.-----.-Y--I-SA----.--GK-VE--..K-..K-.GK.--..-.---.-H-.----P.--VM
B_NL.c92C-S     -I-----L-D---I-----KD--V------S-----.----..A--R..-------..-.-.-----.---TIN--T--D.--G--VK--..--QL--..G.--..-.---.-H-.----P.--VM
B_NL.h159       -----N-F-D-----------SIA------------.----.---R..---T---..-.-.-N---.----L-----E-.--K-I-K--..--..--G...--..-.-V-.-H
B_NL.wolfscon   -----D-F-D-----------S-V------------.----.---R..---T--E..-.-.-----.---
B_NL1.A         I----D---D---------K-A-Q------------.----.---K..------E..-.-.-----.----L--VD-ED.--K-I-E--..--..--R...--..-.-V-.--
B_NL1.A10       -----A-F-D-----------S--------------.----.---S..---T---..-.-.-----.----I-----------IVK--..--..--N...--..-.-V-.--
B_NL1.A13       -I---A-F-------------KS-------------.RVTM.---R..VW-T--E..-.-.-N-K-.----L--AE-E-.--K---E--..-G..--GN...--..-.-A-.--
B_NL1.A2        -------F-------M---K---V------------.G--L.---G..T-----E..-.-.-----.----L-S----D.--R-IV--..--..--V...--..-.-V-.-R
B_NL1.A3        -A---S-F-D-----------S-----I--------.--N-.---R..---T--E..-.-.-----.----I-GA---S.--KMIVE--..--..--G...--..-.-N-.--
B_NL1.A4        I------F-D---------K-S-------------R.G---..-L-R..R--TR.K..-.-.-----.----I--A----.--R-IVD--..--..--G...--..-.---.--
B_NL1.A5        -------F-------------S-V-----H------.----.---R..---T--E..-.-.-----.----L-SV----.--R-IVR--..K-..--G...--..-.-V-.--
B_NL1.A7        -------F-------------T--------G----R.--P-.---K..--FT-.E..-.-.-----.----I-KG----.M-K--VI--..--..--GE..--..K.-V-.--
B_NL1.A9        -----A-F-D-----------S--------------.----..-L-R..---T---..-.-.-----.----I-G-----------IVK--..--..--N...--..-.-V-.--
B_NL10.BR8914   --V----F--------I----S-A-S----------.---L..-L-R..------E..V.-.----K.-Y-ELNG-----.--K-I-R--..K-..--G...--..-.-E-
B_NL10.GF921953 -------F-------------TS-------------.VP-.---R..---T-.E..-.-.-N---.----L--AT--A.A-NKTVE--..--..--GK..--..-.-T-
B_NL10.GQ93013  --L--D-F-D---------K-S--------S-----.--P-.---R..---T---..-.-.-----.----I-G----D.A-K-I-Q--..--..--G...--..-.-V-
B_NL10.MA9136   -----K-F-D-T--------K-------------M-.----.---R..---T---..-.-.-----.----I--AE--D.--K-I-G--..--..--GV..--..-.-V-
B_NL10.SR9038   I----A-LS----------K---Q-----------R.--P-.---K..V-------..-.-.-----.----L-----E.--K-IVG--..--..--G...--..-.-V-
B_NL10.SR9115   -----K-F-D---S-------S-V-----------R.--PM.---R..V-------..-.-.-----.----I-------.A-K-IVI--..G-..--G...--..-.-A-
B_NL10.SR9235   I----K---D---------K--I-------------.--PM.---R..---T--Q..-.-.-----.----L-IE---D.--K-I-D--..--..KVGN..--..-.---
B_NL10.SR925752 -------F-------------VS-------------.--N-.---R..---T--Q..-.-.-----.----I--E----.--K--V---..K-..--GK..--..-.---
B_NL10.SR9269   -----D-FS----N-------T--------------.----.---R..---T--E..-.-.----R.-Y--IN--------.--E-I-R--..K-..--......--T..-.VV-
B_NL10.SR93047  -----V-F-DTG-N-------S-V-----------R.---F.---A..R-----E..-.-.-----.----I-GAQ----.--KWIVMR-..--..--G...--..-.-V-
B_NL10.UM893272 -------F-D-----------T-------------R.--P-.---R..-W-T---..-.-.-----.----L--AQ--K.--E-I-M--..--..--K...--..-.-V-
B_NL10.UM94030  -------F-D-----------KS-V-----------.----.---R..-------..-.-.-----.----L--A---E.--K--V---..A..--R....R..-.-S-
B_NL10.UM94038  -------F-D-VR--------T--------------.----.---R..-------..-.-.-N---.----L--A--EK.--E-IVI--..G-..--G...--..-.-V-
B_NL11.patFcon  -------L-D-----------S-V------S-----.--PL.---R..-------..-.-.-----.----I---E----.--K-IV--..--..--K...--..-.-V-.-H-.----P.--VM
B_NL11.patNcon  -----A-F-----V-------S--------G-----.R-SL.---R..VY-T--Q..-.-.-----.----I--A----.--R-I-G--..K-..--G...--..E.-V-.TH-.----P.--A
B_NL12.0008     -----D-F-D---------K-S--------------.--X-.---R..---T--E..-.-.-----.----L-----D-.--K-I-R--..--..--G...--..-.-V-.--
B_NL12.0157     -----D-F-D---I-----K----------------.--N-.---R..---T--E..-.-.-----.----I-S----D.X-R-IVR--..--..--G...--..-.-G-.-R
B_NL12.0211     -------F----R--------S-----I--------.----.---R..---T--E..-.-.-----.----L-S----D.--K-IVK--..--..--G...--..-.-V-.--
B_NL12.0230     --L--D-F-D---------A-S--------------.----.---R..---T--G..-.-.-----.----L-KA----.A-E-I-K--..G..--E...--..-.-V-.--
B_NL12.0337     -----D-F-D---------K-S---X-X--------.----.---R..---T--E..-.-.-----.---TI--AN-T-.A---IVK--..--..E-K...--..-.-V-.--
B_NL12.0583     -------F-----------K-S-------------X.--N-.---R..---T--E..-.-.-----.----L-SL---D.--R-IVV--..--..--G...--..-.-V-.-K
B_NL12.0617     -------F-----------K-S--------------.--N-.---R..---T--E..-.-.-----.----L-----D-.--E-IVK--..--..--K...--..-.-V-.--
B_NL2.Wolfsh     ----D---D---------KKA-Q-I----------.--P-.---R..------E..-.-.-----.----L--VN-EI.--H-I-E--..--..--R...--..-.-A-.--
B_NL2.Wolfsh495  ----D-F-D---I--------S-------------.--P-.---R..---T--E..-.-.-----.----I--A----.--G-IVK--..--..--R...--..-.---.--
B_NL3.NET       -------F-D-T---------KS-------------.----.---R..---T--E..-.-.-N---.----I--A----.--K-I-V--..--..--K...--..-.-V-.-H
B_NL3.NET2      -------F-----------K---R-----------R.--G-.---R..-I---DR..V.-N---.----L-KAE--R.--E-IVK--..--..--R...--..-.-V-.--
B_NL3.NET3      -----D-FSD---------KD--N-T-I--------.--S-.---R..------E..-.-.-N---.----L-G-E---.A-K---E--..SK..--G...--..-.-V-.K-
B_NL3.NET4      -------L-D-----------VS-------------.G---.---R..-----ER..-.-.-N---.----I-SE----.--KL-V---..--..K-GN..--..-.-V-.--
B_NL3.NET5      -------FS----------K---K-----------R.G---.---R..-V-T--K..-.-.-----.----I------D.----IVI--..K-..--G...--..-.-V-.--
B_NL3.NET6      --M----F-----S-------S--------S----R.----.---R..---T--Q..-.T.-N---.---SL--A----.--K-IVI--..-K..--E....R..-.-V-.--
B_NL4.B63_84     ----D-F-D---I-----K----------------.--Q-.---R..---T--E..-.-.-N---.----I--A----.----IVI--..--..--G...--..-.-V-.---
B_NL4.BA1_84     ----A-F-----------K----------------.----.---R..---T---..-.-.-----.----L-SS--YD.--R---K--..--..--G...--..-.-V-.---
B_NL4.BA206_84   ----D-F-D---------X-S-V------------.----.---R..---T--E..-.-.-----.----L--A---D.--E--VX--..--..--G    S-...-.-V-.---
B_NL4.BA65_85    ----D-F-D---------KA--V------------.G---.---R..---T--E..-.-.-----.----L---Q--D.P---I-I--..--..--K...--..-.-V-.---
B_NL4.BN130_85   ----D-F-D-----------S--------------.----.---R..------E..-.-.-----.----L-KA--E-.--E-IVK--..--..--K....ET..-.-V-.---
B_NL4.BN132_84   ----V-FAD-----------GS-------------.RMTL.---K..V--T--E..-.-.-----.----L--A--D-.--K-I----..--..--V...--..-.-V-.-R-
B_NL4.BN142_84   ------F-----I-------S-----I--------.----.---R..---T--E..-.-.-----.----I-KAR----.--E-IVK--..--..--G...--..-.-V-.---
B_NL4.BN152_84   ----D-F----N------K-S--------------.----.---R..---T--E..-.-.-----.----L--E--D-.A-E-IDG--..--..--S...--..-.-V-.---
B_NL4.BN18_84    ----D-FSD-----------AS-------------.----.---R..------E..V.-.-----.----L-----D-.I-E-I-KN-..--..--R...--..-.-V-.-H-
B_NL4.BN29_85    ----D-F-D--R--------AS-V-----------.G---.---R..---T---..-.-.-----.----L---E-D-.--K-I----..--..--G...--..-.---.---
B_NL4.BN90_85   I-----F-D-----------T--------------.----.---R..---T--E..-.-.-----.----I--E-----.M---IVI--..--..--E....R..-.-V-.KR-
B_NL4.BN93_85    ------F-----I-------S-----I--------.----.---R..---T--E..-.-.-----.----I-KA----.--K-IVK--..--..--V...--..-.-V-.---
B_NL4.H1091_90   ------F-D-V---M-----S--------------.--P-.---R..---T---..-.-.-N---.----L-----D-.----IVQ--..--..--G...--..-.-V-.---
B_NL4.H1112_90  M-----F-D------------SIK-D-I-------R.--P-..-L-S..---T-.E..-.-.-----.----INS---D-.--K-IV---..K-..--G...--..-.-V-.---
B_NL4.H135_90    ------F--------------S-V-----------.---M.---K..T--T---..-.-.-----.----I--E----.--N-IVK--..--..--G...--..-.-V-.---
B_NL4.H153_82    ------F-D------------SIA-----------.----.---R..---T--Q..-.-.-----.-Y--L--E--D-.--E-XV---..K-..--G...--..-.---.--P
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                                       |___________________V3 loop_______________|
                   ^^^                ^*^   ^^^                                   *^^^    ^^ ^                  ^^   ^     ^^ ^                *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_NL4.H164_90    ------FSD-----------S--------------.--P-..---R..---T--E..-.-.---S-.---TIN-A---D.--K-IVG--..-D..--G.....--...P.-V-.---
B_NL4.H169_85      A--F-D---------K-A-R-------------.----..---R..-------.-.-.-----.----I-KAE---.--R-IV---..K-..--G.....--....-.-V-.-R-
B_NL4.H17_82     ------F-----I-------S--------------.----..---R..------E..-.-.-----.----I--A---D.--E-I----..--..--R....I-...P.-A-.X--
B_NL4.H186_85    ----D-F-----------KT--N-T-I--G-----.--P-..---R..-------.-.-.-----.----L--AD---.--KEI-K--..--..K-.....--....-.-A-.---
B_NL4.H187_90    ------F-D-G---------S-------------.G-R-..---R..--I-ATK..-.-.-----.----I-GE----.--K-IV---..--..--G.....--....-.-V-.-R-
B_NL4.H188_90    ------F--SG--------VS--------------.--P-..---R..---T---..-.-.-----.----I--A---D.--K-IVM--..--..--G.....--....-.-V-.---
B_NL4.H1_85      ----D---D---------K-A-Q------------.----..---K..------E..-.-.-----.----L--VD-ED.--K-I-E--..--..--R.....--....-.-V-.---
B_NL4.H228_90    ------F------------KSI------------.G---..---R..-----EA..-.-.----K.-Y----AA---.----LV---..--..--G.....--....-.-V-.-R-
B_NL4.H23_82     ----D-F-----I-----K-S-------------.G---..---K..---T--E..-.-.-----.----L--A--G-.--KEI-R--..--..--E.....--....-.-V-.---
B_NL4.H293_85    -F--D--SD---------K-A--------------.----..---R..---T--E..-.-.-----.----L--A----.--K-IVIE-..-K..--G.....--....-.-----.---
B_NL4.H29_82     ---A--L-D---------K-S--------------.--N-..---R..---T--G..L.-.-----.----I------D.--K-I----..K-..--A.....--....-.-V-.---
B_NL4.H339_82    ----D-F-D---------K-S--------------.----..---R..---T--E..-.-.-----.----L--A---E.A-K-IVG--..-K..--E.....--....-.-V-.K--
B_NL4.H35_80     ----D-F-----------K-S--------------.----..---R..---T--E..-.-.-----.----L--A--DG.--R-IVK--..--..--G.....--....-.-----.---
B_NL4.H36_82     ----D-F-----------K-S--------------.----..---R..---T--E..-.-.-----.----L--E--D-.S-E-I-R--..--..--R.....--....-.-V-.---
B_NL4.H434_85    ----D-F-------------SI------------.----..---G..------E..-.-.-----.----I--G--V-.--K-IV---..K-..-YG....-I...-.-V-.IS-
B_NL4.H43_90     ------FSD----------QS-----------R.G---..---R..---T--Q..-.-.-N---.----I-GE----.--K-IVV--..--..--GK....--....-.-V-.K--
B_NL4.H450_85    I-----F-------------T-------------.G---..---R..-------.-.-.-----.----L-I-----.--K-I-E--..--..--V.....--....-.-V-.-H-
B_NL4.H457_85    ----D-F-D-T---------S-K-D-IS-------.----..---R..---T--E..-.-.-----.----L-KAQ--K.--T-IVI--..--..--E.....--....-.-V-.---
B_NL4.H466_82    ----D-F-D---------K-S--------------.----..---R..---T---..-.-.-----.----I--A----.--K-LVL--..--..--R.....--....-.-V-.---
B_NL4.H490_85    -L----F---V-------K----------------.---L..---K..-V-T--E..-.-.-----.----L-EA---D.--E-IVR--..--..--E    S-...-....-.-S-
B_NL4.H495_85    ----D-F-D---I-------S--------------.--P-..---R..---T--E..-.-.-----.----I--A----.--G-IVE--..--..--R....D-....-.-R-
B_NL4.H552_90    ----A-L-D-----------S--------------.----..---R..------E..-.-.-----.----I-GA----.----I-R--..--..--E.....--....-.-V-.---
B_NL4.H557_82    ----D-F-D---I------GS--------------.----..---R..---T--E..-.-.-N---.----L-KA--ED.--K-IV---..G-..--E.....--....-.-V-.---
B_NL4.H594_85    ------F--------H---S---------------.----..---R..-------.-.-.-----.----I--A----.--K-IVR--..--..--G....DTE..-....K--
B_NL4.H724_8     ----D-F-D---------K-S--------------.----..---R..---T---..-.-.-----.----I--A----.--N-IVM--..--..--R.....--....-.-V-.---
B_NL4.H748_90    ----K-F-D-TE------K-S--------------.--N-..---R..------E..-.-.-----.----L--A----.--N--V---..--..L-Q....V-...-.-A-.---
B_NL4.I1020_86   ----D-F-D-----------S--------------.----..---R..------E..-.-.-----.----L--A--E-.--E-IVI--..--..--R.....-E...-SVV-.-H-
B_NL4.I1025_89   ----A-F-D---I-------T-----------R.--P-..---R..------N..-.-.-----.----I-GA----.--KRL-R--..--..--R.....--....-.-V-.QP-
B_NL4.I1035_87   ----A-F-D-T-I-------S-Q------------.--N-..---R..---T--E..-.-.---S-.----L--A---D.--K-IVK--..--..--K.....--....-.-V-.---
B_NL4.I1057_87   ------F-D-----------S-V-----F------.--P-..---R..---T---..-.-.-----.----L--A---E.--K-IVI--..--..--K.....--....-.-V-.---
B_NL4.I1083_87   ----D-F-D-----------T-----------R.----..---R..---T--G..-.-.-----.----L--A---D.--K-IV-Y-..--..--G.....--....-.-V-.I--
B_NL4.I1164_90   ------F------------GS-V------------.----..---R..---T---..-.-.-----.----L--A---E.--K-IV---..--..--K....-R...-.-V-.---
B_NL4.I117_90    ----D-F-D-----------S-----------I.G---..---R..------E..-.-.-----.----I--A-------I-M--..--..--V.....--....-.-V-.---
B_NL4.I138_89    ----A-FSDST---------T--------------.--NT..---R..---T---..-.-.-----.----L--AQ---.--K-IVK--..GD..--R.....--....-.-A-.T--
B_NL4.I141_9     ----A-F-D-T-S-------S-K-----S-----.G-Q-..---R..---T--Q..-.T.-----.----L--A--D-.--K-IVI--..--..--K.....--....-.-V-.-P-
B_NL4.I142_87    ----D-F-----I-M-----S---K----------.G---..---R..------E..-.-.-N---.----I--A---E.--KRIVM--..G-..--K.....--....-.-V-.---
B_NL4.I221_90    ----A-F-D-T-S------KS--------------.--T-..---R..---T--E..-.-.-----.----L-KAE---.--R-IVI--..Q-..--K.....--....-.-V-.---
B_NL4.I257_9     ----A-F-D---I-------S--------------.----..---R..---T--E..-.-.-----.----L--A---D.--K-IV---..--..--G....D-...-.VV-.-R-
B_NL4.I3007_86   ----D-F-D---I------A---------------.----..---R..---T--E..-.-.-----.----L--A---D.--K-IVI--..--..--K....-S...-.-V-.---
B_NL4.I3008_88   ------F-----N-------S--------------.----..---R..------E..-.-.-----.----L--A---D.--KRIVI--..G-..--K.....--....-.-V-.K--
B_NL4.I3048_89   -.-T--HF-----V------S---T----------.----..---R..---T--E..-.-.-N---.----I-G----D.--KKIVV--..KD..--G.....--....-.-V-.-H-
B_NL4.I3057_9    ------F-D----------KSIA---------R.G---..---R..-V-T--E..-.-.-N---.----IT-KE--E.--T--VN--..--..--K.....--....-.-V-.T--
B_NL4.I3064_90   ----A-FSD---I-------T--------------.----..---R..-------.-.-.-----.----I--A--DD.--RRIVI--..--..--G.....--....-.-V-.---
B_NL4.I3072_90   ----N-FSD-T-S-------S-V------------.--N-..---R..--FT--K..-.-.-----.----L--A---D.--K-IVI--..--..--K.....--....-.-A-.SP-
B_NL4.I3077_9    ----A-F-----I----------------S-----.X---..---R..------E..-.-.-----.----L--A---D.--ENIVI--..--..--K.....--....-.-A-.---
B_NL4.I3084_90   ------F-----I-------S-----------S-.G---..---R..---T---..-.-.-----.----L------D.--KR-VV--..--..--R.....--....-.-V-.---
B_NL4.I3091_9    ----N-F-D---I-------S--------------.G---..---R..------E..-.-.-----.----L--A----.--K-I-I--..--..--G....-I...-.-V-.---
B_NL4.I33_90     ----A-F-----I-------S-V-----G---SR.G---..---R..---T-XK..-.-.-----.----I--AQ---.--K-IVI--..--..--K.....--....-.-V-.---
B_NL4.I4004_88   ------F-D---S------VS--------------.--PM..---R..---T---..-.-.-N---.----L--A---D.--R-IVI--..--..--......--....-.-V-.---
B_NL4.I4008_86   ----D-F-D---I-------S-Q-----H------.--P-..---R..---T--E..-.-.-----.----I--EN-E-.--KKIVI--..--..--K....T-...K.-V-.---
B_NL4.I5020_89   -.-TA-F-D-----------S--------------.G---..---R..---T--E..-.-.-N---.----L--AD--D.A-K--VI--..--..--D.....--....-.-V-.---
B_NL4.I5032_87   ------F-D---N------AS--------------.----..A--R..------E..-.-.-----.----L-I----E.--K-IVI--..--..--R.....--....-.----.KH-
B_NL4.I5037_89   ------L-D---I---H---S--------------.--X-..---R..------E..-.-.-----.----L--AT--A.--KRIVI--..K-..--G....-R...-.-V-.---
B_NL4.I5038_89   ----N-FSD-T-S-------S-V------------.--N-..---R..---T--E..-.-.-----.----L--A---D.--K-IVI--..--..--K.....--....-.-A-.SP-
B_NL4.I7025_9    ------F-----I-------S--------------.--P-..---R..---T--Q..-.-.-----.----I--A--TD.--KKIVI--..--..--G....-N...I.S--.---
B_NL4.I70_88     ---A--F-D-T--------KSI-------------.G---..---K..------E..-.-.-N---.-Y--L--SD--E.A-K--VN--..--..--E.....--....-.-V-.---
B_NL4.I90_89     ----A-FS----V-------S--------------.G---..---S..------E..-.-.-----.----L--AQ--D.--KRIVI--..-D..--E.....--....-.-V-.-H-
B_NL4.K999_86    ----D-F-----I-M-----S--------------.----..---R..---T--E..-.-.-----.----L--A---D.--KRIVI--..--..--E.....--....-.-V-.---
B_NL5.pt10con   -------F-----------KDA--V-----------.----..---R..--FT---..-.-.-----.----I--A---S.--K-IVK--..E-..--K.....--....-.-V-.--
B_NL5.pt11con   -------F-----------K-S-N-.-I------R.G---..---R..-------.-.-.----K.-Y-ILNS-----.--S--VD--..--..--K.....--....-.-V-.-H
B_NL5.pt13con   -----D-F-----I-M-----S-Q-----------.G---..---R..------E..-.-.-N---.----I------D.--KKIVI--..--..--K.....--K..-.-V-.T-
B_NL5.pt14con   II-----F-D-------H--KSII---I------R.----..---R..----R--..-.-.-----.---KLN--E---.--R-IV---..--..--E.....--....-.-V-.K-
B_NL5.pt15con   ---------D-T-----H---S-K---I-------.G---..---...------K..-.-.-----.----I--A----.--GKIVI--..K-..K-G....-TT..-.-V-.--
B_NL5.pt16con   -------F------------KS-K------S---R.----..---R..------E..-.T.-----.----I-GAE---.--E-IVK--..--..--G.....--T..-.-V-.K-
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Analyses

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                                                       |___________________V3 loop________________|
                   ^^^                     ^*^   ^^^                                               *^^^    ^^ ^                  ^^   ^     ^^ ^              *        *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_NL5.pt17con   -------F------------KSIV----------R.--NM..---R..------Q..-.-.-----.----L--VE---.--K-IV---..-D..--G....--...-.-V-.--
B_NL5.pt19con   -------F-----I-------S------------R.----..---S..-------..-.-.-----.----I-KE--D-.--K-I-I--..--..--E....--...-.-R-.--
B_NL5.pt1con    -----D-F-D-----------S-----------------.----..---K..---T--E..-.-.-----.----L--A--DY.----IVI--..--..--K....--...-.-V-.--
B_NL5.pt2con    -------F-----------K---K-H----H----R.----..---R..-------..-.-.-----.----L-K-D--K.--E-IVK--..--..--E....--...-.-V-.--
B_NL5.pt3con    -I---Q-F-------------SIQ--------------.--N-..---R..------A..-.-.-----.----L--AQ---.--K-IV---..K-..--G....--...-.-V-.--
B_NL5.pt4con    -----D-FSD-----------KS-T-------------.G-N-..---R..---T--E..-.-.-----.----L--A---D.--K-I-I--..--..--K....--...-.-V-.--
B_NL5.pt5con    -----A-F-----I-----K-S----------------.--P-..---R..-L-T--E..-.-.-----.----I--------.----I-K--..--..--K....--...-.-V-.--
B_NL5.pt6con    ---------D-I-----H--AS----------------.--P-..---R..---T--E..-.-.-----.----I-KE---E.--G-IVI--..--..--R....--...-.-V-.K-
B_NL5.pt7con    -----A-FSD---------K---I--------------.--PM..---K..-------..-.-.-----K.-Y-ELNG-Q---.----IVK--..--IE--K....--...-.-V-.-H
B_NL5.pt8con    -----S-F-D-----------KS---H-----------.R---..---R..-V-T--E..-.-.-----.----L--AA--D.--KEIVI--..--..--G....--...-.-V-.--
B_NL5.pt9con    -------F-------------S----------------.--N-..---R..------E..-.-.----E.----L--E--EK.--K-IV---..--..--K....--...-.-V-.-H
B_NL6.16        -----D-F-D-----------S-V--------------.G---..---R..-V-T--R..-.-.-----.----I-GV---K.--E-IV---..--..--R....--...-.-V-.---.----P.--VM---.----.------
B_NL6.320       -----A-FS--------H---S-A--------------.G--M..---K..------Q..-.-.-----.----L--A----.--K-IVS--..-K..--G....--...-.-V-.S-P.L---P.--VM---.----.------
B_NL7.NE1058con I----D-FSD-----------T----------------.--P-..---R..---T--E..-.-.-----.----I--------.--N-I-K--..--..-L......--T.-.-V-.---.----P.--V----.----.-------
B_NL7.NE537con  -----A-F-D--R--------S-V----------R.--N-..---R..--WT-.-..-.-.-----.----L-IA----.--K-IV---..--..--GN...--...-.-V-.---.----P.--IM-H-.----.-------
B_NL8.594       -------F---------H---S----------------.----..---R..-------..-.-.-----.----I--A----.--K-IVR--..-D..--GD...T-...-.---.K--.----P.--VM---.----.-------
B_NL8.672       -----D-F-D-----------S----------------.---M..---K..---T-.G..-.-.-----.-Y--I--A---D.--R-IV---..K-..K-G....--...-.-V-.---.----P.--VM---.----.------S
B_NL9.H239      -------F-D-----------TI---------------.----..---K..------G..-.-.-----.----L--A---D.--K-IV---..KD..--G....--...-.-V-.--
B_NL9.h1054     I------L-D-----------AS---------------.G---..---R..------E..-.T.-----.----I--E----.--E--VI--..--..K-GN....--...-.-A-.--
B_NL9.h1081     -------F-D-----------S-V-----L--------.--N-..---R..------E..-.-.-N---.--------F-E-E-.--ER-VR--..--..--R....--...-.-V-.--
B_NL9.h1082     I------F---------H---SI-------S----R.----..---R..------K..-.-.-----.----I-GD-----.--K-IVI--..K-..--G....--...-.-V-.--
B_NL9.h1110     -------------I---H---S----------------.----..---R..---T--E..-.-.-----.----I--A---D.--EKIVI--..K-..K-E....-T...-K-V-.--
B_NL9.h1135     -------F-D-----------T-Q--------------.--P-..---R..---T--E..-.-.-----.----L--AR--D.--K-IVI--..--..K-GN....--...-.-V-.--
B_NL9.h1140     -------F--S----------S-V-----H--------.----..---R..---T--E..-.-.-----.----L-SV----.--R-IVR--..K-..--G....--...-.-V-.--
B_NL9.h1145     -----D-F-----------K-S----------------.----..---R..------E..-.-.-----.----L--A----.A-G-IVK--..--..--GN....--...-.-V-.--
B_NL9.h159      -----N-F-D-----------SIA--------------.----..---R..---T---..-.-.-N---.----L-----E-.--K-I-K--..--..--G....--...-.-V-.-H
B_NL9.h39       -------F-D-----------S------------R.--S-..---R..---T--E..-.-.-N---.----I--A----.----IVN--..--..K-E....--...-.-V-.--
B_NL9.h411      -----D-F-D-T---------S----------------.----..---R..---T--E..-.-.-----.----I-K---D-.--K-IV---..--..--R....--...-.-V-.-R
B_NL9.h412      -------F-D-----------SIV--------------.----..---R..---T---..-.-.-N---.----L-----E-.--K-IVE--..-K..--G....--...-.-V-.--
B_NL9.h424      ---------D---------K-A----------------.----..---R..---T--E..-.-.-Q---.----I--A----.----IVR--..--..--E....--...-.-V-.-H
B_NL9.h526      -------F-D---------K------------------.----..---R..---T--E..-.-.-N---.----L--AQ---.--K-IVI--..--..--R....--...-.-V-.--
B_NL9.h569      -------F-D---------K------------------.----..---R..---T--E..-.-.-----.----L--A---D.--N-IVK--..--..--K....--...-.-V-.--
B_NL9.h57       I------FS------------QS---------------.--N-..---R..---T--E..-.-.-----.----I-GA---D.--K-IVI--..--..--G....--...-.-V-.--
B_NL9.h571      -------F------------TDS---------------.--T-..---R..---T--E..-.-.-----.----I--------.--EKIVK--..--..--G....--...-.-V-.-H
B_NL9.h709      -----A-F-----V-------S----------------.----..---R..---T--A..-.-.-E---.----I-KE--E-.--K-I-----..--..--K....--...-.-A-.--
B_NL9.h716      -------F-------------S----------------.---L..---K..---T--E..-.-.-----.-Y--I--A----.--K-IVR--..--..--G....--...-.-V-.-S
B_NO1.10          --A-F--------------S----------------.G-N-..---R..------E..-.-.-----.----I--A----.--K-I-I--..G-..--K....--...-
B_NO1.11          --D-F-D------------S-A---I----------.G--L..---K..-I-T--E..-.-.-----.----I--V----.--G-IVA--..K-..E-K....--...-
B_NO1.12          --A-F-D--R---------S----------------.----..---R..---T--E..-.-.-----.-Y--I--A----.--K-I-I--..--..--K....--...-
B_NO1.15          ----F--------------S-V------S----R.G---..---K..V---.-E..-.-.-----.----L--ER-D-.--K-IVI--..--..--K....--...-.-
B_NO1.16          ----F-D------------S-L--------------.----..---R..------E..-.-.-N---.-F-TLNK----D.--R--VE--..-K..--E....--...-
B_NO1.20          --A-F----RN-------AS--------T---I-.G--M..---R..---T--A..-.-.-----.----L--A--ED.--KKI-I--..--..--.........-.-
B_NO1.21          ----F-----I-------KS----------------.----..---R..---T--E..-.-.-----.----L--AQ--E.--R-IVI--..G-..--K....--...-
B_NO1.22          --A-F-D------------S-D-H-I----------.----..---R..---T--E..-.-.---I-.----I--AN-T-.--R-I-I--..--..--G....--...-
B_NO1.23          ----F-D-----------GS-----V------R.----..---R..-W------..-.-.-----.---EL-G----D.--R-IVI--..Q-..--V....--...-
B_NO1.24          --A-F-D------------S---H-I----------.--Q-..---R..------E..-.-.-----.----I--A----.--K-I-I--..--..--A....--...-
B_NO1.25          ----F-D--R-------K-S----------------.--P-..---R..---T--E..-.-.-----.----I--A---T.--K-I----..--..--K....-T...-
B_NO1.26          ----F-D-----------AS----------------.----..---R..------E..-.-.-----.-Y--I--AQ---.--KLIVR--..--..--K....--...-
B_NO1.27          --D-F-D------------S---H-I----------.----..---R..---T--E..-.-.-----.----I--AN-T-.--K-I-I--..G-..--A....--...-
B_NO1.29          --D-F-D---S-L----K-S-----I----------.--P-..---R..------A..-.-.-----.----I--------.--S-IVK--..--..--K....--...-
B_NO1.30          ----F-D---I-------KS----------------.----..---R..---T--E..-.-.-----.----L---Q--T.--E-IRI--..--..--R....-N...-
B_NO1.31          --S-FS-----------K-A--------------R.--T-..---R..------G..-.-.-----.----I--E----.--K-IVK--..T-..--E....--...-
B_NO1.32          --D---D-T--------K------------------.G---..---R..-------..-.-.-----.----I-G-----.--NLIVK--..--..-LG....--...-
B_NO1.34          --D-F-D------L-H---S-T--------------.----..---R..---T--E..V.-.-----.----L--AQ--K.--G-IV---..--..--P....--...-
B_NO1.35          ----F--------------S--------S---I-.G---..---R..---T--Y..-.T.-----.----L-S------.--K-IV---..-K..--G....--...-
B_NO1.36          --A-F-D------------S-K-H-I----------.----..---R..---T--K..-.-.-----.----I-KA--T-.--R-I-I--..G-..--V....--...-
B_NO1.37          --S-F-D----------K-S----------------.--P-..---R..---T---..-.-.-----.----L--A---D.--S-IV---..-A..--G....-N...-
B_NO1.38          --A-LSD--R---------SI--H-I----------.--N-..---R..---T--E..-.-.-----.----I--AN-T-.--K-I-I--..--..E-A....-R...-
B_NO1.39          --A---D--R---------S----------------.G---..---R..-------..-.-.-----.----I--A----.--K-I-I--..G-..--K....--...I
B_NO1.40          --A-F-D------------S-A-H-I----------.--P-..---R..---T---..-.-.-----.----I--AN-T-.--EKIVI--..--..--K....-T...-
B_NO1.41          --D-F-----I-----KD--V---------------.--N-..---R..---T--E..-.-.-N---.----I-AAE---.----IV---..-D..--.....--...-                                    ...S
B_NO1.42          --V-F--------------S----------------.----..---R..---T--E..-.-.-----.----I--E----.--K-I-I--..--..--P....--...-
B_NO1.43          --S-F-D------------S-V--------------.G---..---R..---T--Q..-.-.-----.----I--E---K.--G-I----..--..--G....--...-
B_NO1.44          --A-L-D-T----------S---H------------.--P-..---R..---T-.E..-.-.-----.----I--A----.--K-I-I--..G-..--K....--...-.-
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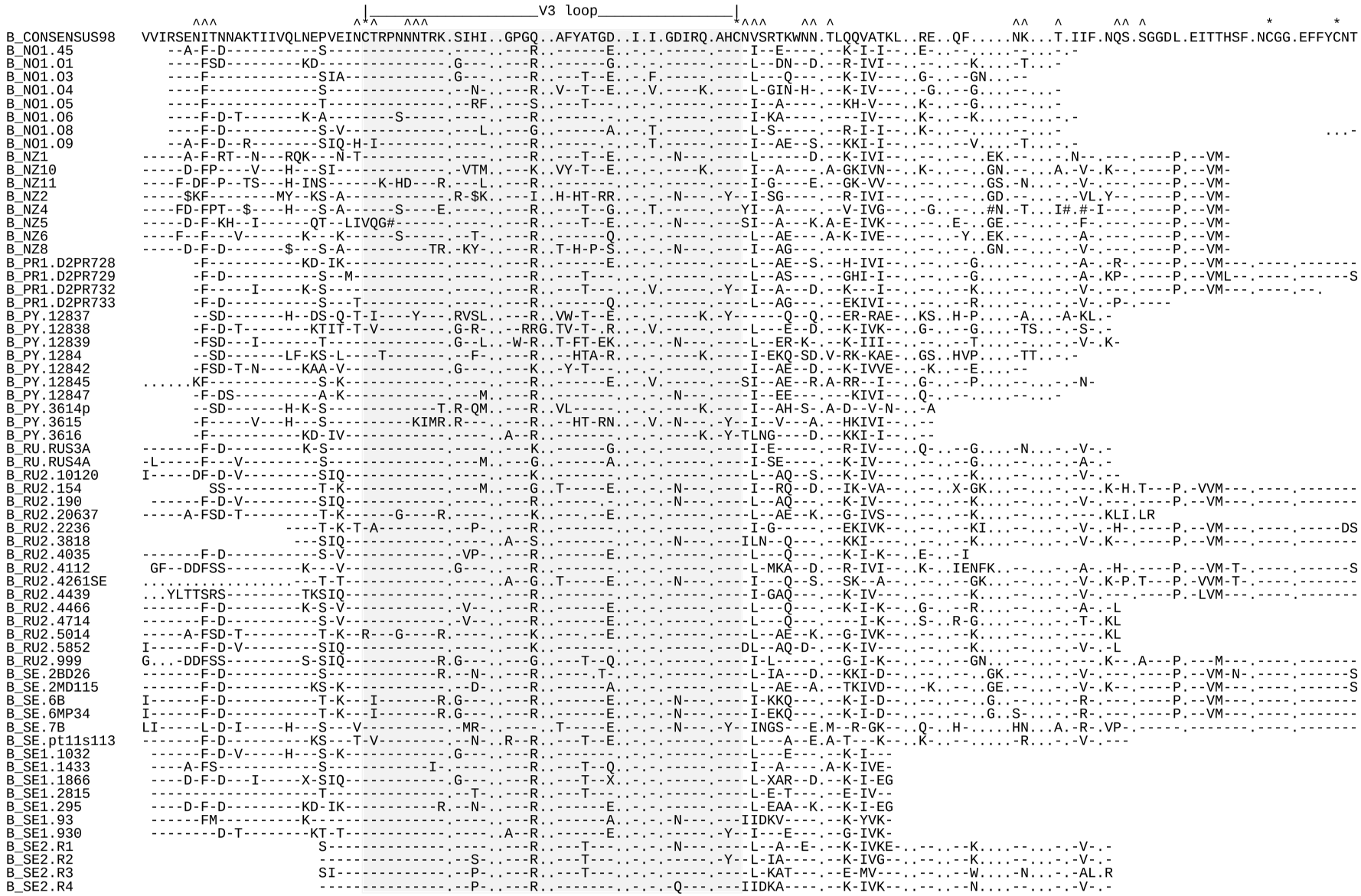

V3 Region Alignment

Analyses

V3 Region Alignment

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                                                            |___________________V3 loop_______________|
                    ^^^                        ^*^   ^^^                                                *^^^    ^^ ^                     ^^   ^      ^^ ^               *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_SE2.R5                            S---I-V---------.--T-..---R..---T--E..-.-.-N---.-Y--L--AA--E.--R---K--..K-..--.....-R...-.-V-.--
B_SE3.AJ2195    ..............-------S-V------------.--P-..---R..---T--E..-.-.-N---.----I--A---D.--K...........................................................
B_SE3.BJ562     ..............-----K-S--------H-----.----..---R..---T--E..-.-.-----.-------A-----.---......................................................
B_SE3.CJ669     ..............-----K-S-V-------X---.G---..---R..------E..-.-.-----.----I-GV----.--K...........................................................
B_SE3.DJ1874    ..............-------S-----------I-.----..---R..---T--Q..-.-.-N---.----I--A----.--K...........................................................
B_SE3.EJ2090    ..............-----K-----------X---.--T-..---K..--F---G..-.-.-----.----L--A---D.--K...........................................................
B_SE4.SE7898    .------F-----I-------S-----------------.----..--xR..------E..-.-.---K-.----I--A----.--K--VN--..--..--......--...-
B_SE4.SE7901    .----A-F-x---I------KSI-------x-x---.----..---R..x-----G..x.x.-----.----I--AE--D.--K-I-G--..--..--..G..--...-
B_SE4.SE8613    --V--N-FS----I-------S-G----------R.G---..---x..FYATGEI..-.G.D.---.----L-GEQ-HR.--K-I-I--..--..--..K..--....-IVLINP-
B_SE4.SE8875    -------xxx---x----x-KSx-------------.--x-..---x..---T--E..-.-.-----.----L--AD--x.--K-x-x--..x-..--..G..--...-.-A-.---.---x
B_SG1.86001     -----A-F-D-T--------KS-----I-------R.----..---R..-LF-A--..-.-.-----.----I-K----A.----IVE--..K-..IYG......................
B_SG1.89001     .......F-----S-----K---K------------.G---..---R..---T--G..-.-.-----.----L--KD---.--REI-KQ-..QV..--.......................
B_SG1.90003     I----A-LSD----------KT-N-T-I--S----T.----..---R..T-H---A..-.-.-----.----I--EE---.--K-I-I--..G-..--GN...--...-.-V-.-H-
B_SG1.90004     -----S-FSD---V-------T--------------.---L..-----..-W---Q..-.-.-----.----T-S-----.--R-I-K--..--..--G....-#................
B_SG1.91003     -M-----F-D-V---------S--------------.G---..---R..------Q..-.-.-N---.-YSTL-G-----.--K-IV---..--..--G.....................
B_SG1.91004     -------F-----------K-A--------------.--P-..---R..---T---..-.-.-----.----L-KA---A.--K-IVI--..--..--E....-#................
B_SG1.92001     -------F-----------KD--K------G-----.G---..---R..---T--Q..-.T.-----.----I--AHR--.--D-IVK--..E-..--G....-#................
B_SG1.92002     I-V--Q-F-D-------H---SIQ------------.R-TL..---R..VL-T--Q..-.-.--V--.----L-A---EH.--R--V---..--..--..K..--...-.-V-#...
B_SG1.92004     ...............#----S---------------.---L..---R..-W-T--Q..-.-.-----.----L-S-----.--R-I-E--..#.........................
B_SG1.93002     -IVK-D-F-D---R------K--I-T----S-----.G-QM..---R..---T--E..-.-.-----.----L--ND---.---EI-KE-..-V..H-G...-.................
B_SG1.93005     -----D-F-----------K-A-Q----------R.--NM..---R..---------..-.-.-----.----I-GAE--Y.--I-IVR--..--..--GN...--...-.-V-.K-..
B_SG1.93007     .................--K-S-K-S-A------G-.----..---R..--HT--R..-.-.-----.-------#$AKW-N--K-I-K--..S-..--.....................
B_SG1.93008     ............#-------T-------------R.--N-..---R..---T--E..-.-.-#---.---II-GA----.--KRIVS--..--..--RN#...............
B_SG1.93009     ............#------AS-Q-----------R#---..---R..-----.TE..-.-.-----.----I---Q---.--G-IVM--..--..#.....................
B_SG1.94001     -----A-LS--------H---S--------S-----.----..A--R..------H..-.-.-----.----I-EV----.--R---A--..Q-..V-#T....-T..-.-V#....
B_SG1.94002     -------F-----------KD--K------G-----.----..---R..---T--E..-.T.-----.----I--AH-T-.--N-IVK--..E-..--G....--...-.-#.....
B_SG1.94003     --T--D-F-D-----------S-V------S-----.---L..---G..--------..-.-.-N---.----I--G----.--G-IV---..K-..K-NTE...-KI#....
B_SG1.94005     -------FSD--G------K----------------.--N-..---R..--LT---..-.-.-----.----I-K----D.--G-I#$-I..--..--G....-#................
B_SG1.94007     -------F-D---N-------T--------H-----.----.Q--R..---T--E..V.-.----K.----I-GE--D-.M-R-IVI--..G-..--.....K................
B_SG1.94008     I----D-F-D-V-P------KS-----I--------.G---..---R..------E..-.-.----R.-Y--I--AQ-GE.--E-IVA--..-..........................
B_SG1.94009     -----D-F-----------K-S-R-T-A------A-.----..---K..--HT--R..-.-.-----.----I-------.--E-IV---..--..--G.....................
B_SG1.94010     ................#---AS--------S-----.----..---K..--HT--A..-.-.-----.-Y--I-------.--H--VR--..Q-..--GN...--...-.-A-.K--
B_SG1.94013     .................--KKA-V------------.G---..---R..---T---..-.-.-E---.----I--AA--D.--R-I-I-$..EK..#-G...--...#............
B_SG1.94014     ...........#-------T-AIK------------.--P-..---R..---T--G..-.-.-----.---TING-----.--S-IYK--..--..--#.....................
B_SG1.94015     ............-------KDS-K-------T---R.----..---R..---T.--..-.V.-----.----L-K-E---.--V-IVK-F..--..H-GN...--...-.-N-....
B_SG1.95001     ...........#-------KD--K-------TI-RRR---..---R..---T.-S..-.-.-N---.----L-K-D---.--TRIVK-F..--..--G....-#................
B_SK1.BTS11     -----D-L-D-T-------KDS-K------------.G---..---K..------E..-.-.-N---.----I--AE-EK.A-N-TSI--..S-..H-K...--...-.-A-.---
B_SK1.BTS12     -------F------------NSIA-E----S-----.G--M..---K...-F---E..-.-.-----.----I-E-D-E-.A-K---I--..S-..H-P...--...-.---.---
B_SK1.BTS18     -----D-F-D---------K-S--------------.----..---R..---T--E..-.-.-N---.---TI-K---YS.--N-TVI--..--..--G...--...-.-V-.---
B_SK1.BTS20     -----A-F-D---------S-S-K----------R.---L..---K..-------..-.-.-----.----L--AD--K.--N-IV---..--..--GN...-R...-.---.---
B_SK1.BTS22     -----A-F-D------E---YS-T------------.--R-..---S..T-----E..-.T.-----.----L--EE---.--N-IVK--..K-..--G...--...-.-V-.---
B_SK1.BTS23     -------FAD-----------S-----I-------R.----..---R..---T--E..-.-.--V-R.----I--E----.--K-I-I--..S-..R-N...--...-.-V-.---
B_SK1.BTS28     -------F-----------K----------G---R.--N-..---R..---T--A..-.-.-----.-------KE----.--N-IVK--..--..--G....-R...-.--.-H-
B_SK1.BTS9      -------F-D---------K---V-------------.-V-L..--KR..V-FT--K..-.V.-----.----L---Q---.--E-IVK--..--..--G...--...-.-S-.---
B_TH.93TH067    -----S-F-D--RV-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-G---R-.--E-ITE--..K-..--G...--...-.-V-.---.----P.--VR-T-.----.-------
B_TH.JP23B          -F-------------DS-----S----------.---V..---R..-L-T--E..-.-.-----.----L--AQ--D.--HKIVIT-..--..--G...--...-.-V-.KH-.-
B_TH.T8174        -S-F-D-TRI-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G...--...-.-V-.---.----P.--VM---.----.-------
B_TH1.7787            -D-TRI-------S--------------.---L..---R..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G...--...-.-V-.---.---
B_TH1.864        -V--S-F-D---V-------S--------------.---L..-----..-W---E..-.-.-----.----L-S-----.--R-ITK--..--..--G...--...-.-V-.---.----P.--VM---.----.------
B_TH1.8643       ----S-F-D--RV-------S--------------.---L..-Q--..-W---E..-.-.-----.----L-S---I-.--K-ITE--..-D..--G...--...-.-V-.---.----P.--VM---.----.------
B_TH1.8645       ----S-F-D---V-------S--------------.---L..-----..-W-T--Q..-.-.-----.----L-S-----.--K-ITK--..--..--G...--...-.-V-.--P.----Q.--VM---.----.------
B_TH1.8647       ----S-F-D--RV-------S--------------.--PL..---R..-W---E..-.-.-----.----L-S-----.--R-ITE--..--..--G...--...-.-V-.---.----P.--VM---.----.------
B_TH1.8649           -F-D--RV-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S---S.--K-I-E--..--..--G...--...-.-V-.---.----P.--VM---.----.------
B_TH1.865            -F-D--RV-------S-------------.G--L..-----..-W-T--Q..-.-.-----.----L-S--H-.--E-ITE--..--..--G...--...-.-V-.---.----P.--VM---.----.------
B_TH1.8653       ----S-F-D--RV-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....-T...-.-V-.---.----P.--VM---.----.------
B_TH1.8655        -S-F----RV-------S--------------.--PL..-----..VWFT--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G...--...-.-V-.--P.----P.--VM---.----.------
B_TH1.8669            F-D--RI-------S--------------.---L..-----..-W-T--Q..-.-.-----.----L-S-----.--K-ITK--..--..--G...--...-.-V-.---.-A--P.--VM---.----.------
B_TH12.86       ......-F-D--RI-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S-----.--K-I-K--..--..--G...--...-.-V-.---.----Q.--VM---.----.-------
B_TH12.87       ......-F----RV-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G...--...-.-V-.K--.----Q.-VEM---.----.-------
B_TH12.88       ......-F-D---V-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S-----.A-K-ITE--..--..--K...--...-.-V-.---.----P.--VM---.----.-------
B_TH12.90       ......-F----RV-------S--------------.--PL..-----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G...--...-.-V-.---.----P.--VM---.----.-------
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V3 Region Alignment

V3 Region Alignment

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                                                 |____________________V3 loop________________|
                   ^^^                      ^*^    ^^^                                        *^^^    ^^ ^                    ^^   ^      ^^ ^              *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_TH7.154             -F-D---I-------S--------------.G--..----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.---.-----.--VM---.----.-------
B_TH7.155             -F-D--RV-------T-----------I-.G--L..----..-W-T--Q..-.-.-----.----L-S-----.--K-I-A--..--..--G....--...-.-V-.---.----P.--VM---.T---.-------
B_TH7.156             -F-D--RV-------S--------------.---L..----..-W---Q..-.-.-----.----L-S-----.--K-ITG--..--..--G....--...-.-V-.---.----Q.-VVM---.----.-------
B_TH7.157             -F-----V-------S--------------.--QL..---R..-W---Q..-.-.-----.----L-S---H-.--K-ITE--..--..--G....--...-.-V-.---.----P.--EM-I-.----.-------
B_TH7.158             -F-D-TR----H---S--------------.-VPL..---R..-W-T--Q..-.-.-----.----L-S-----.--G-ITE--..--..--G....--...-.-V-.--P.-----.--QM-I-.----.-------
B_TH7.159             -F----RV-------S--------------.G--L..---R..-W-T--Q..-.-.-----.----L-S---K-.--K-ITE--..--..--G....--...-.-V-.---.----P.-VVM---.S---.-------
B_TH7.160             -F-D--RV-------S--------------.---L..----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.---.----P.-LVM---.----.------S
B_TH7.162             -F----RV-------S--------------.---L..---R..-W-T--Q..-.-.-----.----L-S-----.--R-ITG--..--..--G....--...-.-V-.-H-.----P.--VM---.----.-------
B_TH7.163             -F-D--RV-------S--------------.----..----..-W-T--Q..-.-.-----.----L-S---T-.--K-ITK--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.165             -F-D--RV-------S-------------R.---L..---R..-W--P--..-.-.-----.----L-S-----.--K---E--..--..--G....--...-.-V-.---.----P.--VM---.----.-----D-
B_TH7.166             -FSD-TRV------KS--------------.--PL..----..-WFT--Q..-.-.-----.----L-I-Q---.--E-ITE--..--..R-G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.167             -F-D---V-------S--------------.---L..----..-WFT--Q..-.-.-----.----L-S-Q---.--K-ITE--..--..--G....--...-.-V-.---.----P.--AM---.----.-------
B_TH7.168             -FSD--RV-------S--------------.-V-L..---R..-W-T--Q..-.-.-----.----L-S-----.--N-I-K--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.169             -FSD--RV-------S--------------.--PL..---R..-W-T--Q..-.-.-----.----L-S---S-.--K-ITE--..--..--G....--...-.-V-.---.----Q.--VM---.----.-------
B_TH7.173             -F-D-TRI-------S--------------.--PL..---R..-W---Q..-.T.-----.----L-S---S-.--K-I-A--..--..--G....--...-.-V-.---.-----.--VL---.----.-------
B_TH7.174             -F-D-T-V-------S--------------.--PL..---K..-W-T--Q..-.-.----R.----L-S-----.--K-ITE--..--..--G....--...-.-V-.---.----P.--VM-T-.----.-----D-
B_TH7.176             -F-----V-------S--------------.--PL..-A-R..-W-T--Q..-.-.-----.----L-S-----.M-K-ITE--..--..--G....--...-.-V-.---.----P.--VM---.---R.GI-----
B_TH7.177             -F-D--RV-------S--------------.---L..----..-W-T--Q..-.-.-----.----L-S-----.--R-ITE--..--..--G....--...-.-V-.---.-----.--VM---.----.-------
B_TH7.181             -F----RV-------S-A------------.---L..----..-W-T--Q..-.-.-----.----L-S-Q---.--KRITE--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.182             -F-D--RV-------S--------------.--PL..----..-WFT--Q..-.-.-----.----L-S-----.--R-ITE--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.183             -F-D--RI-------S--------------.---L..-Q-R..-W---Q..-.-.-----.----L-S---H-.--K-ITE--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.184             -F----RV-------S--------------.--N-..---R..-W---Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.-R-.-----.--EM---.----.-------
B_TH7.82              -FMD--RI-------S--------------.--PL..----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.---.----P.--VM-N-.----.-------
B_TH7.85              -F-D--RV-------S--------------.--PL..----..-W-T--E..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.-H-.----P.--VM---.----.-------
B_TH7.86              -F-D--RI-------S--------------.--PL..----..-W-T--Q..-.-.-----.----L-S-----.--K-I-K--..--..--G....--...-.-V-.---.----Q.--VM---.----.-------
B_TH7.87              -F----RV-------S--------------.--PL..----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.K--.----Q.-VEM---.----.-------
B_TH7.88              -F-D---V-------S--------------.--PL..----..-W-T--Q..-.-.-----.----L-S-----.A-K-ITE--..--..--K....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.90              -F----RV-------S--------------.--PL..----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.91              -F-----------K-S--------------.-----.A--R..------E..-.-.-----.----I-AE----.--G--VA--..K-..-YGS...-T....VV-.D-P.AE---.V-VM---.T---.-------
B_TH7.92              -F-D--RV-------S--------------.--PL..----..-WFT--Q..-.-.-----.----L-S-----.--K-I-E--..--..--GS...-T....VV-.---.----P.--VL---.----.------S
B_TH7.93              -FSD---V-------T--------------.--PL..---R..-W-T--Q..-.-.-----.----L-S-----.--R-ITA--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH7.94              -F-D---V-------S--------------.--PL..----..-W-T--Q..-.-.-----.----L-S-----.--R-I-K--..--..--G....--...-.-V-.---.----P.--VM-T-.----.-------
B_TH7.96              -F-D-T-------T-S-K-D-I--------.--NL..-L-R..-W---Q..-.-.-----.----L-S-E---.--KKITE--..--..-YG....-TK..-.-V-.---.----P.--VM---.V---.-------
B_TH7.99              -FSD---V-------S--------------.---L..----..-W-T--Q..-.-.-----.----L-S---G-.--R-I-E--..--..--G....--...-.-V-.---.----P.--VR--V.----.-----D-
B_TH8.27        ......-F-----V-------S--------------.--N-..----..-W---Q..-.-.-----.----L-S---H-.--K-ITE--..--..--E....--...-.-V-.---.----P.--VM---.----.-------
B_TH8.30B       ......-F-D--RV-------S--------------.---L..----..-W-T--Q..-.-.-----.----L-S-----.--R-ITK--..--..--G....--...-.-V-.---.----P.--IM---.----.-------
B_TH8.34        ......-FS---V-------S--------------.--PL..---R..-L-T--Q..-.-.----R.----L-S---H-.--R-ITE--..--..--G....--...-.---.---.----P.--VM---.----.-------
B_TH8.39        ......-F-D---I-------S--------------.---V..----..-W-T--Q..-.-.-N---.----L-S-----.--K-IVK--..--..--G....--...-.-V-.---.AE--P.--VM---.----.-------
B_TH8.41A       ......-F-D--RV-------S--------------.--PL..----..-W-T--Q..-.V.-----.----L-S-----.--K-I-E--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH8.45        ......---D--RV-------S--------------.---L..----..-W-T--Q..-.-.-----.----L-S-----.--R-LTV--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH8.531       ......TML----A-------S--------------.--N-..----..-W---Q..-.-.-----.----L-S---H-.--K-ITE--..--..--K....--...-.-V-.---.----P.--VM---.----.-------
B_TH8.533       ......-F-D---V-------T--------------.--SL..---R..-W-T--Q..-.-.-----.----L-S-R---.--K-IYE--..--..--G...-N...KT-V-.---.----P.--VM---.----.-------
B_TH8.713       ......-F-D---V-------S-V------------.---L..----..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.-H-.----P.--VM---.----.-------
B_TH8.834       ......-F-D---V-------S--------------.---L..---E..-W-T--Q..-.-.-----.----L-S-----.--K-ITK--..--..--G....--...-.-V-.---.----P.--VM---.---E.-------
B_TH8.837       ......-F----RV-------S--------------.---L..-Q-R..-W-T--Q..-.-.-----.----L-S-----.--K-ITE--..--..--G....--...-.-V-.---.----P.--VM---.----.-------
B_TH8.838       ......-F-----I-----K----------------.--SL..---R..-W-T--Q..-.-.----K.----I-S-----.--T---E--..--..--G....--...-.-V-.---.----P.--VM---.----.---F---
B_TT.QZ4589     -------F-------L-----S-V------------.-----.---R..----.--E..-.-.-----.----L------D.--K-IVI--..--..--GE...--...-.-V-.---.----P.--VM---.----.------S
B_TW1.138                 --------KKS-K-------RHI-R.R---..---R..S-V.--N..H.N....-K.----L--SE-DD.--A-IVG-F..-
B_TW1.236          -P--L-D---S-----KN--K------G----R.---M..-L-R..---T--G..-.-.-----.----L---E---.--TEI-K-F..K-
B_TW1.237            D-FSD-T--------KS-K-----------------.-----.---R..---T---..-.-.-----.----L---E--E.--RKIVE--..-K..-
B_TW1.257             -F------------DT-K------------.-V-M..---S..TL---A..-.-.-N---.----L--IN-ED.--KKIVI--..K-..-YK
B_TW1.261        --K---V-----------K-S-I--------TKIR.H---..---R..T---R.E..K.-.-----.----LNK-E---.--VKIVE--..--
B_TW1.358             -F-D-V-N-------S-P---I---------.R-TL..--RR..V--T--E..-.-.----R.----I-EA-XS-.--K-IVN--..K-..--K.....--T..-
B_TW1.366             -F-D---I-M----KS-T--------------.-----.---K..---T-.-.-.-.----K.----I-GAE--H.--KLIVE--..-K..--GE...--...-.-V-.--
B_TW1.382               -D---------RK------------------.-----.---R..------.-..V.-.-----.----I------E.--K-IVK--..--..K-K....--...-
B_TW1.384          --A-F-D---------K-T-N-T-------------.--PM..---K..-------..-.-.-----.----I-K-A---.--K-IVE--..--..--K....--...-.-V-
B_TW1.386                ---I-------S-T--------------.-----.---K..---T-.E..-.-.----R.----INK-T--H.--ELIVE--..--..--GE...--...-
B_TW1.391           ---F-D----------KS-T-H-----------.--S-..---R..---T-.N..-.-.----K.----I--AD--D.--T-IVG--..--..-YGK...-N...S
B_TW1.394          --L-F-----V------QS-V----------R.--P-..---R..---T-.-.-.-.-.----K.----I--KD---.--K-IVG--..--..--G....--...S
B_TW1.646                       -----KS-T-----LHKI---.R-IL..---R..S--T--T.....-.E-K-K.----I---D--H.--KLIVE--..--..-YG
B_TW1.91        -----V-F-D---V------KS-T-I-----KI---.G---..---R..---T--T.....-.E---K.----I---N--H.--K-IVG--..--..-YGE....--...-.-V-
B_US.613.P02    -------L-D-T---------S-V------------.--P-..---R..-------..-.-.-----.----L---T-EK.--K-I-I--..--..--Q....E-...N.-A-.---.----P.--VM---.----.------S
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V3 Region Alignment

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                                                  |____________________V3 loop_______________|
                       ^^^                     ^*^    ^^^                                      *^^^    ^^ ^                       ^^   ^      ^^ ^               *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_US.SF128      -----D-F-------------S-V-------------.--N-..---R..-I-T--A..-.-.-----.---.TLNK-Q-D-.--R-I-I--.--.--K...--...-.-S-.K--.----P.--VMQ--.----.-------
B_US.SF162      -------F-D---------K-S-------------.--T-..---R..-------.-.-.-----.----I-GE----.--K-IV---..QA..--G...--...-.-V-.K--.----P.--VM---.----.------
B_US.SF2        -----D-F-------------S-A-------------.--Y-..---R..--HT--R..-.-.----K.----I--AQ---.--E-IVK--..--..--GN...--...-.-V-.---.----P.--VM---.--R-.------
B_US.SF33       -----D-F-------L----VS-----------R-R.R-TS..---K..VL-T--E..-.-.----K.-Y--I--A---K.--E------..--..--G...--...-.-V-.K--.----P.--VM---.--R-.------
B_US.TN100                -V---------SIQ----------R.--N-..---R..-W-T--E..-.-.-----.----L--AA-K-.--K
B_US.TN1000           -F-D---I-------S-------------.--S-..---R..---T---..-.-.-----.----I-
B_US.TN1002     I------------I-------S-------------.----..---R..-------.-.-.-----.----I-KAT-
B_US.TN1003     -----D---D-T-------K---------S----.----..---R..---T--A..-.-.-----.----I-KA--S
B_US.TN1005     -------F-----I-----K-S-----I--------.----..A--R..-------.-.-.-N---.----I-EE---K
B_US.TN1006     D----A-FSD---N-----KD--------------.--PM..---R..-------.-.-.-----.----L-G-N-
B_US.TN1007     -------F-D-G-------K-S-V-----------.----..---R..---T--E..-.-.-----.----I--E--
B_US.TN1009     -------F-------------SIV----------R.--N-..---R..------Q..-.-.-----.----I-A
B_US.UNC116.694 -------F-------L---K-S-Q------Y-YKK-.K-TT..---R..VL-T-EE..-.-.----R.----I--A---E.--G-I----..--..--.....-R...-.-V-.K
B_US.WM         -------F-----------K---Q---I--------.G---..---K..---T--E..-.-.-N---.----I--VT---.--K--VK--..--..--K...--...-.-V-.K--.----P.--VM---.----.---F--
B_US.WMJ22      I------F-D-------H---S--------Y--V-R.-LS-..---R..--RTR.E..-.-.-I---.----I--A----.--K-IVE--..--..--K...--...-.-V-.-H-.----P.--V----.----.------
B_US.WR27       -----A-F-----------K-S--------G-KI-R.R---..---R..---.-.-..R.V.-----.-Y--I-G---K-.--EKIVA-I..--IK--K...--...-.-V-.-H-.----P.--VM---.----.------S
B_US.YU         I------F-------------S-V-------------.--N-..---R..-L-T--E..-.-.-----.----L-K-Q-E-.--E-I-I--..K-..--GN...--...-.----.KP-.----P.--V----.----.------
B_US.twinABcon  I-SK---FS--V---M---T-SIH------S-----.----..---R..-------.-.-.-----.----I--E---V.---K-VE--..G-..--K...--...-.-V-.---.L---P.--VM-T-.----.------S
B_US1.HC0        ----A-F-D---I------AS-------------.G---..---R..------E..-.-.-----.----I--E----.--R--V---..--..--G...--...-.----.-H-.----P.--VM---.----.------
B_US1.HC05       ------F-----I---H--KT-N-T---------R.--PM..---K..---T-.E..-.-.-N---.----L-KAE---.--R-IVK--..--..--K...--...-.-V-.-H-.----P.--VM--
B_US1.HC06       ----A-F-D-T-I-------S--------S-Y-G-.RLS-..---R..--V--RK..-.-.-----.----I--A---D.--KRIVI--..--..--G...--...-.-V-.D-P.----P.--VK---
B_US1.HC07       ------F-D-T--------TS-T------G-----.--TM..---K..V---.-E..-.-.-----.----L--AA--D.--K-IVG--..Q-..--G...--...-.-V-.-H-.----P.--VM---.VE-N.F
B_US1.HC08       ------F-K---N-----K-S--------------.--PM..---R..---T--E..-.-.----K.-Y-T-NK-----.--AKI-S--..--..--E...--...-.-V-.TP-.----P.--AM-N-.--R-
B_US1.HC09       ----A-FSD----------KS-N-T-V--S----Q.--P-..---K..------E..-.-.----K.----L-EAE---.--T-IVK--..K-..--N...--...-.-V-.---.----P.--VM---.----.K-
B_US1.HC1        ------F-----------K-S-K---I-------R.--NM..---R..---T---..-.-.-----.----I-KAE---.--K-IVQ--..K-..--R...--...-.-V-.---.----P.-VV----
B_US1.HC10       ------F-D---------KNS-G-----------R.-V--..---S..-L-T-..-.-.-----.----L--AN--K.--E-IV---..G-..--GN...--...-.-A-.-S-.----P.--VF---.SF
B_US1.HC12       ------F---S-------K-S-V-----------R.----..---R..-W-T--K..-.T.-----.---TIN-A-X-E.--K-I-I-F..--..--K...GX...-.-V-.-H-.----P.--VM---
B_US1.HC13       ------FSD---------K-S--------------.R-TM..---R..VL-T--Q..-.-.--V-R.----I-GVQ--K.A-K--VA--..K-..--R...--...-.-V-.KPP.----P.--V----
B_US1.HC16       ------F-D-V---------S-Q------------.----..A--R..------E..-.-.-----.----L-SI---D.--R-I-K--..K-..--G...--...-.----.---.----P.--PEI
B_US1.HC18       ------F------------VS-------------.G---..---R..-------.-.-.-----.-Y--I--A----.--K--V---..--..--G...IT...-.MV-.YH-.----P.PVVML
B_US1.HC19       ------F-D---------K----------S-----.G-P-..---R..---T--G..-.-.-----.----L--A---D.--K-IV---..K-..--E...--...-.-V-.---.----P.--VM---.----.--.
B_US1.HC2        ------F-----------K-S-K-----------R.--NM..---R..---T---..-.-.-----.----I-KAD---.--E-IVK--..E-..--K...--...-.-A-.---.----P.-VVM---.----.------
B_US1.HC20                  -------KD--------------.----..A--R..------G..-.-.-----.----I--A----.--G-IVS--..--..H-G...-TT..-.VA-.QS
B_US1.HC22       ----D-F-D----------KS--------S-----.--T-..---R..---T--E..V.-.-----.----I-----D.--K-IVR--..G-..K-G...-E...-K---.EP-.----P.-------.----.D-STVI
B_US1.HC23       ----D-F-D-V---------A-V-----------R.G---..---R..---T--E..-.-.-----.----I--A----.--K-IVV--..-V..--G...--...-.-V-.-H-.----P.--VM---.----.----
B_US1.HC24       ------F-D-----------SI-------------.--P-..---R..-------.-.-.-----.----L--AT---.--K-IV---..--..--G...-R...-.-V-.---.----P.--VM---.----.----
B_US1.HC25       I-----L-D---------K---I-------------.----..---K..--D--.-.-.-----.-----S-E---.--RE-----..KG..L-G...-T...-.VA-.---.----P.D-VI---.----.----
B_US1.HC26                ---I-------T--------------.----..---R..------E..-.-.----K.----I--AQ---.--ERIVI--..G-..--G...KTN..-.-V-.---.----P.--VM--V.----.----
B_US1.HC27               ----I-------S-V-------------.G--M..---R..---T--A..-.-.----E.----I--K--E-.--G-I-S--..--..--K...-TT.T-.LV
B_US1.HC28       ----D-F-D-----------VS-----------R.--T-..---R..-----.-.-.-.-----.----I-G-R---.--E-
B_US1.HC29       ------F-------L----AS-A-----LS-K--R.----..---R..-----.-.-.-.-----.----I--ED---.--K-IVI--..G-..--G...-TT..-.-A-.-K-.----P.--VM---.----.----
B_US1.HC3        ----D-FSD--R--------S-V-----------SR.R-S-..---R..--T-REG..-.-.-----.----I-GAE-ES.--KRIVE--..G-..--K...--...-.-V-.-H-.----P.--VM---.----.----
B_US1.HC30       -------SD-----------S-V-----------R.----..A--R..-------.-.-.-----.-Y-TINK---H-.--K--VE--..--..--N...-T...-.-V-..R-.---
B_US1.HC32       ------F-D-----------QS-----------R.----..---K..------G..-.-.-----.----L---A---.--KLIVD--..--..--G...--...-.-V-.---.----P.--V---A----.----
B_US1.HC33                D----------TS--------------.----..---R..---T---..-.-.-----.----I-----E-.--K-I-----..--..-YGN...-T...-.-V-.---.----P.--V----.----.----
B_US1.HC34       ------F-DT---------KD--------------.----..---R..-------.-.-.-----.----I--A----.--R-IVDIC..-V..--G...--...-.-V-.---.----P.--VM-T-.----.----
B_US1.HC35         --K-F-D------------------------------.----..---R..---T---..-.-.-----.----L--A----.--K-IVV--..--..--G...--...-.-V-.---.----P.--VM-T-.----.----
B_US1.HC36       ----D-F-D---I-------S-V-------------.----..---S..---T---..-.-.-H---.----L--A---D.--K-IVI--..--..--E...-R...-.-V-.K--.----P.--V----.----.----
B_US1.HC37       ------F----R----H---SIV---------G-.---L..A--R..G-H---E..-.-.-N---.----L-AEE-D-.--EKI-K--..G-..R-P...--...-.-N-.TK-.----P.--VM---.----.----
B_US1.HC38       ------S-----N-L---KA-I-------------.G-A-..---R..TV---R..-.-.-----.----L-S---D-.--G-I-I--..--..--G...--...-.-T-.---.----P.--KM---.----.----
B_US1.HC39       ----D-F-D-----------QT-------------.----..---R..------G..-.-.-E---.----L--V--E-.--E-I-I--..--..--K...--...-.-V-.---.----P.--VM---.----.----
B_US1.HC4        ------F-D---------T-----------------.----..A--R..------E..-.-.-----.---TI--A---D.----I-I--..S-..--G...-N...-
B_US1.HC40       ------F-------------S-A-------------.G-P-..---R..---T---..-.-.-----.----L--AD-D-.--KLIV---..--..--G...-E...-.----.---.----P.--VM---.----.----
B_US1.HC42       ----K-F-D-----------S-A--S---------.G---..---R..-------.-.-.-----.----L--AD---.--KLIVEN-..G-..HLG...MQ
B_US1.HC43       ------F-D-L-N-----K----------G---R.----..---R..---T--E..-.-.-N--L.----I--A----.--K-I-D--..--..--E...--...-.-V-.-H-.----P.-FV----.----.----
B_US1.HC44       ------F-------------S-V-------------.--P-..---R..-------.-.-.-----.----L--EA---.--K--VA--..--..--GK..G-...-.----.-H-.----P.--VM-T-.----.----
B_US1.HC45       ------F-------------T--------------.----..---R..---T---..-.-.-----.----L--AQ---.--K-IVE--..--..--K...-S...-.-V-.KP-.----P.--V----.----.----
B_US1.HC46      -.L--D-F-D-----------S-V-------------.G---..---R..------E..-.-.-N---.----I-AAN-T-.--K-I-I--..-K..--G...-N...-.----.-R-.----P.--V----.----.----
B_US10.MA145con          E-H-V-----K----------G-----.--PM..---R..-WF---.-.-.----K.----I--A----.--E--VK--..G-..--E...--...-.----.---.----P.--VM---.----.-------
B_US10.SFPEcon  -------F-D-----------SIA-------------.----..---R..-------.-.-.-N---.----I--KD---.--KLIVK--..--..--KEQLV--...-.-V-.---.----P.--VM---.----.------S
B_US11.074      I-----------------K--------------.--N-..---R..---T--E..-.-.-N---.----ING-----.--K-IVE--..--..--G...--...-.----.---.-----.--VM---.----.------S
B_US11.107      -------F--------I----T-----------R.G-N-..---R..-----.G..-.-.----K.----I-G-----.--K-IVQ--..--..--G...--...-.-V-.---.L---P.--V----.--T-.-------
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V3 Region Alignment

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                                                   |__________________V3 loop_______________|
                      ^^^                      ^*^    ^^^                                    *^^^    ^^ ^                             ^^    ^      ^^ ^                *       *
B_CONSENSUS98    VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_US11.306       I------L-----------K--------------R.G---.----.---T--E..EVT.----R.-Y--I-SA---E.--K-IVIQ-..-K..--G....--....-.-S-.---.T---I.--V----.----.-------
B_US11.333       -------F-----I-------S--------------.----.---R.---T--E..-.-.-----.----L--A--D-.--K-I-I--..-D..--V....--...I.---.---.----P.--VM---.----.-----DS
B_US11.349       -----D-F-D----------VS--------------.-VTM..---R..VW-T--E..-.V.----K.----L---T---.--R--VE--.---..K-R....-AT..-.-V-.-H-.-----.--VM---.T---.-------
B_US11.419       -------F-D-----------S--------------.----.----..-L-----..-.-.-----.----I--A----.--K-IVE--..KV..--G....--....-.---.---.----P.--VM---.----.-------
B_US11.44        -I-----F-D----------ASI-------------.---L..---R..SV-T--K..-.V.-----.----I-GA----.A-K-IVE--..-D..--K....--....-.-V-.-K-.----P.--V----.--A-.-------
B_US11.550       -------F-D---------K-S--------------.----.---R.---T--E..-.-.-----.----L--E--EK.--D-IVA--..S-..--G....--....-
B_US11.552       -------F-----I-------S----I---------.--P-..---R.--F----..-.-.-----.----I--AN---.--K-ITKN-..KD..--R....X-....-.-V-.---.T---P.--VM-N-.-
B_US11.725       -----D-FSD----------T---------------.--P-..---R.---T---..-.-.-----.----I-KDD---.--K-IV-N-..-D..--G....--....-.-V-.-R-.----P.--VM---.----.------S
B_US11.UK        -------FSD---------K-S-K-H-I--------.---M..---K..-Y----..-.-.-----.----I-EAH--R.--G-IV---.---..--G....--...A.-V-.---.----P.--V----.----.------S
B_US12.CHB2A        ---F-----------T--------G-----.--N-..---R..-W---.-.-.-----.----I--A----.----I-K--
B_US12.CHBMOM       ---F-D---I---H---S--------------.R-S-..---R..--RT--N..-.-.-----.----I--A----.--EK--K--
B_US12.LC1A         ---F-A-----------A---K--S-------.----.---R..--D---A..-.-.-----.-Y-TR-G-R---.--EK-VE-I
B_US12.LC2A         ---F-D-----------S-V---------KR.--N-..---R.------E..-.-.-----.----L-T----D.--G-IV
B_US12.LC3A         -D-FSD----------KS--------S-----.G-N-..---R..-V-T--E..K.-.-----.----L--AR--D.--K-IVE--
B_US12.LC4A         ---FAD---------K-R--------------R.---M..---K..---G-.-.-.-----.----L--AA---.--K-IVE--
B_US13.141con    -I-----FSD-----------S-I------S-----.--P-..---R.------E..-.-.-----.-Y--I--KE--K.--R-IVP--..---..-VGV....--....-.---.-S-.----P.--VY---.----.-------
B_US13.144con    -----D-F-D-V-------K-A---------S-----.G--L..---R..-I-T-EQ..-.T.-----.----I--E----.--K-IVG--..---..--G....-AT..-.-V-.---.----P.--V----.----.-------
B_US13.149con    -------FS----N-------S---T-I--G---R.---L..Q--R..---SS-G..-.-.----K.---TINIPQ---.--KL-VD--..-N..--K....-R....-A-.T-PPP---P.-VVMY--.----.-------
B_US14.          --V--A-F-----I-------S-Q---I--------.----.---R..-I----G..-.-.----R.-Y--I--------.--K-ITK--..Q-..--G....K-....-V-.K--.----P.-VVM---.----.-------
B_US14.2         -----V-F----R------R-A---------S-----.----.---R.---T--N..-.-.-----.----I--G----.--K-IVS--..---..--G....--....-.-V-.---.----P.--VM---.----.------S
B_US14.3         -------F-D-----------S--------------.--P-..---R.--------..-.-.-----.-------KA---S.--E-IVK--..G-..--G....-N....-.-V-.---.----P.--VM---.----.------S
B_US14.4         I-L----F-D-----------S----I---------.----.---R.--------..-.-.-----.---YI-KAN-T-.--E-IVE--..---..--GN....--....-.---.-S-.----P.--VF---.----.-------
B_US15.A         -------F-----S-------S----I---------.--NM..---R.---T---..-.-.-----.----I-EA----.--K-IVN--..---..--R....--....-.---.---
B_US15.B         -------F----RI-------S---H---------R.--NM..---R.---T---..-.-.-----.----I--A----.--K-I-N--..---..--E....--....-.---.---
B_US15.C         I----V-L-D---I---H---S--M-----------.----.---R.---T--E..-.-.-----.----L-SA---D.--KNI-I--..---..K-E....--....-.-V-.---
B_US15.D         ---S-A-L-D-------K--DS-VM----S-----.--PM..---R.---T---..-.-.-----.----L--AD---.--KR--I--..---..---....--....-.---.K--
B_US15.E         I----A-FSE-D---------T--M-----------.RMT-..---R..V--T--E..-.-.-----.----L-EA----.--R-I-I--..K-..--E....--....-.-V-.-H-
B_US15.F         -----A-L-D-----------S-A-H-I-------R.--P-..---R.--------..-.-.-----.----L--EE---.--K-IVK--..---..--K....--....-.-V-.---
B_US16.NYRT      -------F-----I---H---S--------------.G---.--WG..T-F---N..-.-.-----.-Y--I--A--D-.--KKIVD--..---..--G....--....-.-V-.---.----P.--VM---.--R-.-------
B_US16.NYRT3     -----A-F-D----------KS--------S---S-.G---.---R.---T-EA..-.T.----R.-Y--I--AA--E.--G-IVE--..---..--E....-R....-.-A-.-K-.-----.--VM---.----.-------
B_US17.CB        -----A-L-D---------K-Y--------------.--S-..---R.---T--E..-.-.-----.----I-G-----.--S-IV---..---..E-K....--....-.---.---.----P.--VM---.----.-----D-
B_US17.CB2       -------FMD-V-------K-S-K------------.G-N-..---R.------E..-.V.-----.----L-SAE--D.A-N-TV---..---..H-K....--....-.-V-.QP-.-----.--V----.----.-------
B_US17.CB3       I------F---V-N-------SI-------H-----.---M..---G..-L---R..-.-.-N---.----I--A----.--EKIVR--..---..K-G....--....-.-N-.T--.----R.--VM---.----.G-L---S
B_US17.CB4       -----D-FSD---------KD--------------I-.G---.---R.------Q..-.V.-----.----I------K.--H-I---..---..--K....-IT..-.-S-.---.----P.--VM---.----.------S
B_US17.CB5       -------F-D----L----K----------------.--N-..---R.---T--Q..-.-.-----.----I--A----.--G-IVK--..---..--R....--....-.-V-.---.----P.--VM---.----.-----S-
B_US17.CB6       -----D-F-D----------KSI------------R.--N-..---R.---T---..-.-.----R.----L------D.--K-I-N--..---..---....-AT..-.-V-.-H-.----P.--V----.----.-----DS
B_US17.CB8       I------F-D-V-----HK--SI-------------.----.---R.---T--Q..V.-.-----.----L-EA----.--K-I-I--..---..--V....--....-.-V-.-K-.----P.--VM---.----.-----DS
B_US17.CB9       -----D-F-------------A--------------.----.---R.------G..-.-.-----.---VLDKA----.--K-IVR--..---..--Q....--....-.-V-.---.----P.--VM---.----.-------
B_US18.LBAcon          -F-D-T-I-------S--------------.--N-..---R.---T---..-.-.-----.----I-EK--F-.--K---G--..---..--K....--....-.-V-.--P
B_US18.LBB             -F-------------T-Q---S--------.G---.---S.------E..-.-.-----.----I--V----.--GYIVK--..---..--G....--....-.-V-.KT-
B_US18.LBBB            -FSD-------H--KS-K----------S-.G---.---G..--FT--R..-.-.-N--H.----I--KE---.--GLITE--..ED..--K....I-....-VT-.-H-
B_US18.LBD             -F---------H---T-N-T-V-------R.----.---R.----A--..-.-.-----.----I-GAE-T-.--KK-V---..Q-..--GN....--....-.---.RP-
B_US18.LBE             -F-------T---T-SIK------T----.----..E--R.---T--E..V.-.-N---.-Y--I-KAD--K.--AK--E--..---..-YK....--....-.-V-.K-P
B_US18.LBF             -F-D-V---------TS-Q------G----.---M..---K..V---.-E..-.-.-----.----I--KE--D.--EK-VN--..-N..-W.....-N....-.---.S
B_US18.LBG             -F-D-----------KT-K-----------.----.---R.--------..-.-.----K.-Y--L---E--T.--G--VE--..---..-
B_US18.LBI             -F-D---------K-A--------S-----.---L..---R..-W-T--E..-.-.-----.----L--A----.--K-IVE--..---..R-E....--....-.-V-.-H-
B_US18.LBJ             -FSD---I-----K----------------.----.---R.---T---..-.-.-----.----I--A----.--S-I-I--..---..--G....--....-.-V-.-K-
B_US18.LBK             -F-D---I------AS--------H-----.----.---R.---T--E..-.-.-----.----L--A---D.--K-IVI--..---..--G....-TT..-.-V-.-R-
B_US18.LBLCN           -F-G-------H---S-Q------S-----.----..E--R.------.-.-.-.-----.----I---H---.--KKIVK--..---..---....--....-.-V-.QP-
B_US18.LBLCT           -F-D---------K--IQ------------.-VP-..---R.------E..-.-.-----.----L-SVT---.--K-IVK--..---..--G....--...S.-A-.---
B_US18.LBM             -F-------------T--------------.----.---R..--FT---..-.-.-----.----I--AR--E.--NRIV---..---..--GN....--....-.-V-.-H-
B_US18.LBO1            -F-D--EI------K-------------SR.---L..---R..TL-T-.E..-.-.-----.----L--A---D.--T-IV---..---..-YG....--....-.-V-.---
B_US18.LBPATH2         -FSD-----VI----S-A------------.G---.---R.---T--E..-.-.-----.----I-LG----.--N-IV---..-G..--G....--....-.-V-.---
B_US18.LBPTCC1         -F-D---------K-S-V------------.----.---R.---T--E..-.-.-----.----L---Q---.--T-IVK--..---..--G....--....-.-V-.-H-
B_US18.LBQ             -F-D---I------KSID------S-----.----.---R.---T---..-.-.-----.----I--A---D.--K-IV---..---..--G....--....-.-V-.---
B_US18.LBSDIR          -F-------------S--------------.--S-..---R.---T---..-.-.-----.----I--A---D.--KRIVI--..-K..-YK....--....-.-V-.---
B_US18.LBV             -FSD-----------KS---H-I---------.R-TL..---R..VY-T--E..-.-.-N---.----I--AN-TD.--K-IV---..K-..--G....--....-.-V-.KP-
B_US18.LBW             -F--------------A-V-----------.G---.---R.--------..-.-.-----.----L-KVA--E.--KK-VE--..---..--K....K-...I.-V-.-S-
B_US18.LBY             -F---I-N--------S---H-I-------.G---..A--R..T-----A..-.-.-----.----L-IAN-T-.--KRIVK--..-D..--GE....--....-.-V-.-H-
B_US18.LBZ             -L-D-------H--KS-V----------I-.--R-..---R..-W-T--E..-.T.-----.----L--AD---.--R--VM--..---..H-K....--....-.-V-.---
B_US19.VA1con                                ------G----R.---M..-----..-L-T--E..V.V.-----.----I--VD---.--K--V---..---..-
B_US19.VA2                                   ------SI-K-R.-VR-..---G..-W-K--Q..V.T.----R.----L--AD--D.--K-IVN--..---..-
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                                        |___________________V3 loop_______________|
                   ^^^                ^*^   ^^^                                   *^^^    ^^ ^                    ^^   ^     ^^ ^               *       *
B_CONSENSUS98   VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_US2.D2US656               ---------S-V-----------.----.----R.-------.-.-.-----.----L---Q---.--K-IVI--.--.--.--GN..--.-.-.-V-.---.----P.--VM---.-
B_US2.D2US657       -F-------------TIK------------.G---.----R.---T--E..V.-.-N---.----I-S-D-GK.--EK-VE--..-K..--GS..--.-.-.-V-.-H-.----P.--VM---.----.------
B_US2.D2US660       -L-D-T-------KN--V------------.--PM.----K..-M----E..-.-.----K.-Y--I---E---.--K-IVK--..EG..--K..-.-.-.-V-.DR-.AD--P.--VL-T-.----.------
B_US2.D2US662       -F-----------K-A--------------.----.----R.---T--E..-.V.-------.----I-S-----.--G-IVK--..-.-.--D....-R..-.-.-V-.DK-.----P.--VMLN-.----.------S
B_US2.D2US664       -F-D---I-V-H--KS-V------------.----.----R.-------.-.-.-----.----L-KAD-EE.A-N-T-R--..K-..-L......-TT..-.-V-.---.----P.--VM---.----.--I---S
B_US2.D2US665       ---D-------H---SI-------------.--PM.----R..---T--E..V.-.-N---.-Y--I-KA---D.--K-IV---.-.-.H-K..-.-.-.-V-.---.----P.--VM---.----.------D-
B_US2.D2US704       -F-------------T-V------------.----.----R..--HT--E..V.-.-----.----I-GE----.--EKIVK--..K-..--R....D-.-.-.-V-.KH-.----P.--VM---.----.--Y---
B_US2.D2US705       -F-----------K-A-K------------.--N-.----R.-------E..-.-.-----.----I---D---.--GKIVE--..-A.--.-.-...-CS..K.-V-.K--.----P.--VM---.----.------
B_US2.D2US706       -F-D-----------SI-------------.--N-.----R..---T--E..-.-.-----.----L-KE--ET.--K-I-E--..-K..-Y..-.-.-.-V-.K--.----P.--VM-
B_US2.D2US714       -FSD---N-L-----S-N-T-I-------R.---M.----R.-------.-.-.-----.----I------E.---RIVK--..G-..-.-.-.-.-P-V-.---.----P.-
B_US2.D2US717       -F-D---------------KMD-I-------R.--N-.----R..---T---..-.-N---.----L--AN-T-.---KI-I--..G-..--Q..-.-.-.-V-.---.----P.---MI--.----.------SS
B_US2.D2US724       -FS---A-------AS-------G-K-IR.--SM.----R..--R.--Q..-.-.-N---.-N-TL--A---E.--R--VK--..SK..--G..-.-.-.-A-.K-P.----P.--V---.----.------
B_US2.D2US725   -------F-D---------K-S--------------.--P-.----R.-------.-.-.-----.----I--A----.--K-IVE--..K-..--G..-.-.-.-V-.---.----P.--
B_US2.D2US726       -F-D----------K--V-----------R.-----.A--R..--H---N..-.-.-----.----L---Q-D-.--H-IV---..-K..--GA...D-.-.-.-V-.---.----P.--VM---.----.------
B_US2.D2US727       -F-------------S-A------S-----.-V--.----R..---T--E..-.-.-----.----I-A-----.--K-IVD--..K-..--G..-.-.-.-V-.K--.----P.--VM---.----.------
B_US20.C1con    -----A-LSD-S-I-------S-VM-------------.--N-.----R..---T--E..-.-.-----.----L--AN--D.--EKIVI--.--.--.--Q..-.-.-.-V-.---.----P.---MI--.----.------S
B_US20.C2con    -------F-----------K---------------R.-----.----S..-L-T--E..-.-.----K.-Y-TIDAA----.--K-IVK--.--.--.--K....-N..-.-VV-.Q-A.----P.--V---.----.------
B_US20.C3con    -------F-----------KDA-K---S--G----R.R-S-.----R..--V--KR..-.-.-----.----I-KKD---.--N--VK--..QG..--.-.-...-T.-.---.QPH.----P.--V----.I--.------
B_US21.P1       -------F-D-V---------SI--------------.--Q-.----R..---T--E..-.-.-----.----L--A--D-.--E-IVR--.--.--.--K..-.-.-.-V-.---.----P.--V---.----.------S
B_US21.P2       -I-----F----R------K---------------.G---.----R..---T--E..-.-.-N---.----I-KA----.--K-IV---.--.--.--G..-.-.-.-V-.---.----P.--VM---.----.------S
B_US21.P3       -----D-FSD---I-------T----------------.----.----R..---T---..-.-.-N---.----I-S-----.--K-IVE--..K-..--G..-.-.-.-V-.---.----P.--VM---.----.------S
B_US21.P4       -----D-F-D-T-------K-S----------------.----.----R..---T---..-.-.-----.----I-KAI--T.--K-IV---.--.--.--E..-.-.-.-V-.---.----P.--VM---.----.------S
B_US21.P5       -------F-D---------K-SI---------------.----.----R..---T---..-.-.-----.----I--A----.--R-IVE--.--.--.--G..-.-.-.-T-.---.----P.--V---.----.------S
B_US21.P6       -----D-F-----------K------------------.----.----R..---T--E..-.-.-----.----I--A----.--K-IVN--.--.--.--K..-.-.-.-V-.---.----P.--VM---.----.------S
B_US22.E0105    -----A-F-------------S--------------.--P-.----R.-------.-.-.-----.----L--A--YD.--K-IV---.--.--.--G..-.-.-.-S-.-R-.----P.--VM---.----.------
B_US22.E0204    -----A-F-----I-------S-I------------.--N-.----R..--V---A..-.-.-----.-Y--I--A---D.--KRIVI--.--.--.--GV..-.-.-.-V-.KH-.----P.--V---.----.------
B_US22.E03A03   I------F-D---------K---V--------------.----.----S.------Q..-.-.-----.----DL--KD---.--E---D--..S-..--P..-.-.-.-.-S-.----P.--V---.----.--Y---
B_US22.E04B03   I------F-D---------EK--I----X---------.----.----R.------Q..-.-.-----.----L--KE--E.--T---A--..K-..--E..-.-...N.-S-.KS-.----P.--V---.----.------
B_US22.E0502    -----A-FSE-T-N-------S-V--------------.----.----R..---T--E..-.-.-----.----I-GK--E-.--K-I----..QG..-Y..-.-.-.-V-.-H-.----P.--V---.----.------
B_US22.E0607    -----A-FSE-T---------KS-V--X-------K-.----.----R..---T--K..-.-.EN---.----I-GK--E-.--K-I----..QG..-Y..-.-.-.-V-.---.----P.--VM---.--R-.------D.
B_US22.E0704    II-----L-D---------K---V-------D-K--.G--M.----G..-M----A..-.-.----K.-Y-TLNA---DD.--K---D--..-G..L-V..-.-.-.-A-.-R-.----P.--VM---.----.------
B_US22.E0803    -------L-D-----------S-K-D-I---------.--P-.----R..V-----R..-.-.-N---.----I--A----.--K-IVD--..-G..--G..-.-.-.-V-.S--.----P.--VM---.----.------
B_US22.E0903    I------FS-----------DS-----I-------R.--P-.----K.-------.-.-.-N---.----I--A----.--SKIVK--.--.--.--M..-.-.-.-A-.-S-.----P.--VM---.----.------
B_US22.E1001    I------L-D-----------S--------------.--N-.----R.-------E..-.-.-----.----I--A----.--K-IVE--.--.--.--V..-.-.-.-A-.-S-.----P.--VM---.----.------
B_US22.E11A06   -----D-F-D---I-------S-A-----------R.--T-.----R.-------E..-.V.-----.----I-G-E---.--RKI-D--..-K..-.-.-RN..-.-V-.---.----P.--V---.----.------
B_US22.E12A03   ----P--F-D-V-V-------S-------------R.-----.----R.------G..-.-.-----.----I---------.--K-T-E--..GK..--E....TG...I.TV-.-R-.----P.--V---.----.------D.
B_US23.201       I---D-F-D-T--------AS-------------R.-VR-.----G..-MFR---.-.-.R---.----I--------.--N-I-R--.--.--.--K..-.-.-.-A-.K--.---
B_US23.303       ------FA----I-------S-V--------------.----.----R.-------.-.-.-----.----I--A---D.---KIVG--.--.--.-LG....H-.-.-.-V-.QP-.---
B_US23.811       I---K-FSD-T--------K-S-K-S-I---------.G---.----R..-I---K..-.-.-----.----L--E---D.A-K-IV---.--.--.-SP..-.-.-.-.-V-.---.---
B_US24.85W3F    -I-----L-D---------K------------------.----.----R..---T---..-.-.-----.----I--A----.--T-IVK--..K-..H-E..-.-.-.-V-.-H-
B_US24.85W6A    -------F-----------K-----------------.--P-.----R.-------E..-.-.----K.-Y-TLNG-----.----IYR--.--.--VG..-.-.-.-.-.-S-
B_US24.8674A    -----A-F-------------S--------------.--N-.----R..-W---.-.-.-.-----.----I--A----.--NKI-K--.--..H-K..-.-.-.-V-.T--
B_US24.87Y3E    -------F-------------S-V-----LS-----.--T-.----R..---T--G..V.-.-----.----L-EA---A.--K---E--.--.--.--G..-.-.-.-V-.---
B_US24.88B4E    -----D---D----------T-S--------S---------.----.----R..-W-T--A..-.-.-----.----I--I----.--N-IVK--.--.--.--K..-.-.-.-V-.H--
B_US26.13A      I------L-D---------K-S-K-------------.--NM.----R..---T--Q..-.-.-----.----I--AQ---.--G-IVE--..-G..K-..-.-.-.-V-.---.----P.--V---.----.------S
B_US26.14B      -------F-----------PKV--K----------IQ.G---.----S..---T--Q..-.-.-----.----L--KD---.--N-IVN--.--.--.--.-.-.-.-.-F-.---.----P.---M---.----.------S
B_US28.10189G   -----A-L-D---I--I--DNS-GM--S----------.--N-.----R..---T--E..-.-.-N---.----I--AH--D.--KRIVI--.--.--.--N..-.-.-.-V-.T--
B_US28.3799a    -------F---G-------K-A---------H----R.--N-.----R..---T---..-.T.-----.----L--A--EA.--K-IVI--..G-..--GR...T-...I.-V-.---.........................
B_US28.861a     -----D-F-D---------K-A---------G-----.--T-.----R..---T--G..-.-.----K.----I--A---S.--G-IVK--.--.--.--N..-.-.-.-V-.---.........................
B_US28.863      -I---K-F-D-T-----H---S----------------.--T-.----R..---T--Q..-.-.-----.----I--AQ---.--E-IVK--.--.--.--G....-N..-.-V-.---.........................
B_US28.868      -------FKD-----------S--------S----R.--T-.----R.-------EE..-.-.-----.----L-S--$--.--K-IVR--..K-..--E..-.-.-.-V-.---.........................
B_US28.86Aa     -----D-FSE-DNI------KT----------------.----.----R.-------E..-.-.----K.-Y--I---A--D.--K-IVK--.--.--YK....I-.-.-.-V-.R--.........................
B_US28.86Na     -----A-L-D---I---K--KS--M-------------.--P-.----R..---T--E..-.-.-----.----L--A--DD.--EKI-I--.--.--.--K..-.-.-.-V-.S-P.........................
B_US28.873a     -----V-F-D-----------S--------S-------.----.----R..---T--G..-.-.-N---.----L------D.--R-IVK--.--.--.--G..-.-.-.-V-.---.........................
B_US28.87Aa     ---------D------I--S-S-T-E-I---------.--N-.----R.-------E..-.-.-----.----LNG----G.--G-IVI--.--IER-R..-.-.-.-.-.EP-.........................
B_US28.87Wa     -----D-FLD-----M-----S-------------R.-----.----R.-------E..-.-.-----.----L--AR-T-.--K--VG--..G-..--K..-.-.-.-V-.---.........................
B_US28.88Qa     ---------------------AS-V-------------.----.----R.-------N..-.-.-----.----I-KEQ-DK.--K-I-R--.--..H-P....K-.-.-.-V-.---.........................
B_US28.896a     -----D-F-------------RS--------S---------.R--R..-W-T--A..-.-.-----.----I---E-T-.--KHI-E--..--IK--E..-.-.-.-V-.---.........................
B_US28.8AWa     -------F-D-----------KS--------S-----.K-N-.----R..-W-T--A..-.-.-----.----I--------.--DKIVK--.--.--.--.-.-.-.-.---.---.........................
B_US28.8BAa     ----YN-PKD---I-------S---------------.G---.----G..---T--E..-.-.-----.----I-K---E-.--K-IVK--.--.--.--.-.-.-.-.-V-.---.........................
B_US29.ME1      II---D-FMD-T--------AS-------------R.-VR-.----G..-MFR---.-.-.-----.----L---Q---.--N-I-Q--.--.--.--T..-.-.-.-A-.K--.----P.--VM---.----.------
B_US3.D1US712   -----A-LSD---I-------S--M--I----------.----.----R..---T---..-.-.----K.----I--A----.--K-I-I--..K-..--E..-.-.-.-V-.---.----P.--M-LM-.----.------S
B_US3.D2US71    -------F-----------K-A-----------------.---L.----R.-------E..-.-.-----.---TLNK----E.A-K-IVM--..-G..--G..-.-.-.-.-.-K-.----P.--EQ---.----.------
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V3 Region Alignment

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                                          |____________________V3 loop_______________|
                  ^^^                 ^*^    ^^^                                      *^^^    ^^ ^                          ^^    ^      ^^ ^              *       *
B_CONSENSUS98    VVIRSENITNNAKTIIVQLNEPVEINCTRPNNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRQ.AHCNVSRTKWNN.TLQQVATKL..RE..QF.....NK...T.IIF.NQS.SGGDL.EITTHSF.NCGG.EFFYCNT
B_US3.D2US715    -----A-LSD----------S-QM----------.----.---R..---T--E..-.-.-----.----L------E.--KRIVI--.---..-YE...--...-.-V-.---.----P.--VML--.----.------S
B_US3.D2US716    I------F----------K-S--M----------.----.---R..---T--Q..-.-.-----.----L--AS---.--ENITI--.---..--G...--...-.-V-.KP-.----P.--VML-L.----.------S
B_US30.A9307     -------F------------S-V-----------.--N-.---R..---T---..-.-.-----.----I-K---S-.-----VK--.---..--GE...--...-.-V-.---.Y.......................
B_US30.B9309     I------F----------K-A-------------.R-SL.---R..VY-T--E..-.-.----K.----L--AQ--E.--K-IS---.---..--R....-E...-.-V-.---.Y.......................
B_US30.C9105     -------F-----I------DS-G----------.G---.---R..-----E..-.-.-----.----I-KA---R.--E-IVK--.---..--GN...--...-.-V-.---.Y.......................
B_US30.D9110     --------SD-L-N-------T-K-----G----.----.---R..---.--E..-.-.-N---.----L-S-Q---.--K-IVKE-.---..--K....--...-.-E-.KP-.Y.......................
B_US30.E9108     -----D-F-D-T-------K---V----------.G---.---S..---T--A..-.-.-----.----I--G----.--N-IVK--.---..--E....--...-.-T-.KH-.Y.......................
B_US30.F9106     -----P-F-D---------K--------------S.RLS-.---R..S--T-RT..-.-.-----.----I--E----.--K-IVK--..-G..--G....-A...-.-V-.---.Y.......................
B_US30.G9004     -------F-D---P-------S-V----S-S---R.--T-.---R..-------..-.-.-----.----I-EG----.--G-IVA--..K-..--G....--...-.-V-.---.Y.......................
B_US30.H9308     -----P-FSD---I------KSI-----S-G----.--SM.---R..VI-T--Q..-.-.-----.----I--AR--E.--K---E--.---..-YK....--...-.---.SPP.Y.......................
B_US30.I9108     -----D-F-D-----L-----S-I---V--------.G---.----.------A..-.-.-----.----L-SAN-T-.--K-IVL--..GK..--E....--...-.-A-.---.Y.......................
B_US30.J9110     -----D---D-T-------K---N-T-V--------.--N-.---R..-------..-.-.-----.----IT-G----.----IV---.---..--KD..K--...-.-V-.---.Y.......................
B_US32.33c11     -----A-LS----------KS-V-----------.--N-.---R..---T.TE..-.-.-N---.----I-K-L-E-.--K---N--.---..--GE...--...-.-V-.---.----P.--
B_US32.45c11     -----A-F-D---------K---------H----.----.A--R..-L---E..-.-.-----.----I--A---D.--R---D--.---..--G....--...-.---.---.----P.--
B_US32.48c11     -IV----FSD----M----RD-------------.-V--.---R..-----E..-.-.-N---.----I------D.--E-IVR--.---..--G....--...-.-V-.---.----P.--
B_US32.52c12     -----A-FSD---------KQNIT-D-I-------Q.--N-.---R..-----A..-.-.-N---.----I-EVQ-K-.--N-TVQ--..--IQ--K....D-...-.-V-.---.----P.--
B_US32.53c11     -------F-----I------KS-T-----------.----.---R..---T---..-.-.-----.----I-G-E---.--K-IVE--.---..--E....--...-.-V-.---.----P.--
B_US32.53c11CVL  -------F-----I------KS-T-----------.----.---R..---T---..-.-.-----.----I-G-E-K-.--K-IVE--.---..--E....--...-.-V-.---.----P.-F
B_US32.54c11     I---T--F-DY--N-----KT--G----------.--P-.---R..-IFT--S..-.-.-E---.----L--RD-D-.--K-IVS--..-N..--KGQHE-Q....-.-V-.-S-.----P.--
B_US32.55c11     I--------D-I-P-----EI--K---S--------.--PL..-Q-R..-I---Q..-.-.-N---.----I-KGN-T-.--R---I--..E-..--R....--...-.-K-.--A.----P.--
B_US32.56c11     -------L-D------I--S-SIV-----------.----.---S..---T--A..-.T.-----.---TL---Q-E-.--R-I-K--..Q-..--G....--...-.-V-.---.----P.--
B_US32.57c11     -----S-F-D---I---H---S-------------.--S-.---R..-------..-.-.-----.----I--E---K.--E-------.---..KY....--...-.-T-.-H-.----P.--
B_US32.57c11CVL  -----S-F-D---I---H---S-------------.--S-.---R..-------..-.-.-----.----I--E---K.--E-------.---..KY....--...-.-T-.-H-.----P.-F
B_US32.59c12     I------L-D-T-----H---SI------------.----.---R..---T--E..-.-.----K.-Y--I-KSQ--K.--KRIEV--..K-..K-EG...--...-.-K-.QN-.----P.--
B_US32.61c12     I--------D-I-P-----EI--K---S--------.--P-.---R..-I---Q..-.-.-N---.----I-KGN-T-.--R---I--..E-..--R....--...-.-A-.--A.A--P.--
B_US32.62c11     -----V-F-D---------K--------------.----.A--R..-L---E..-.-.-----.----I-KA---D.--R--VG--.---..--G....--...-.---.---.----P.--
B_US32.64c11     I----D-FSD-T--------QS---T-V-------R.---M.---K..-------..-.-.----R.-Y--I--VQ---.--R-I-I--.---..--Q....--...-.-V-.---.----P.--
B_US32.65c11     -------L-D-----------SIV-----------.--P-.---S..---T.TE..-.-.----K.----L---E-E-.--R-I----..Q-..--G....--...-.---.---.----P.--
B_US32.66c11     I----A-L-D----------TS--------S-----.G--M.---G..-L---A..-.-.----R.----I--Q----.----I-K--..G-..--E....--...-.-T-.-H-.A--P.--
B_US32.66c11CVL  I----A-F-D----------AS--------S-----.G-RM.---G..-L---A..-.-.-----.----I--Q----.----IVK--..G-..--K....--...-.-T-.K--.----P.--
B_US32.67c12     -------F-----I------KA-K-----------.G---.---R..T--T--E..-.-.-----.----I--EA--K.--K-IFE--..K-..K-.....--...-.-V-.---.----P.--
B_US32.69c12     -I-----F-D-V---------S-V-D---------.--P-.---K..---T---..-.-.-N---.----LNS-Q--D.--KRIVE--.---..--K....--...-.-V-.---.----P.--
B_US32.71c11     -------F-D-V---L-----S-Q-----------.----.---R..---T---..V.-.-----.----I-K-----.--E-IVN--.---..--R....-R...-.---.---.----P.--
B_US32.72c11     -------F-D----------AS-------------.--P-.---R..-CF-----..-.-.-----.----L-S--C-R.-VR-LVE--..K-..--G....-I...-.VV-.-S-.----P.--
B_US32.74c11     I------F-D------I---KS------------S-.G---.---R..---P-RI..-.-.--M--.----L-G-D--K.--AMIV---..-A..--G....--...-.-V-.---.----P.--
B_US32.76c11     I------F-D----------A------I--S---QR.----.---R..---T--A..-.-.-----.----I--KD---.--K---I--.---..--E....--...-.---.-H-.----P.--
B_US32.77c11     -----K-F-E-TA------K-S-N-T---------.----.---K..-----E..-.-.-N---.----L--KD--D.--K-IVG--.---..-YK....--...P.---.TS-.----P.--
B_US32.78c11     -----K-F-----V------QS-------------.G-R-..R-RR..-I--AEK..-.-.-----.----I--AE--K.----IVK--..G-..--K....--...-.-V-.-H-.----P.--
B_US32.79c11     -----A---D-T-I---H---S-GM----------.--PM..--ER..-------..-.-.-----.----I--A---K.--G-IVD--..-K..--V....--...-.-V-.---.----P.--
B_US32.79c11CVL  -----A---D-T-I---H---S-GM----------.--PM.---R..-------..-.-.-----.----I--A---K.--G-IVD--..-K..--V....--...-.-V-.---.----P.--
B_US32.81c11     -----A-F-----------A---------------.--N-.---R..---T--E..-.-.-----.---SL--A---E.--K--VK--..G-..--K....--...-.-V-.K--.----P.--
B_US32.82c11     ---K---F-----------KD---------------.---V.---R..TL-T--E..-.-.-----.----I--A---S.----I-Q--.---..--E....--...-.-V-.---.----P.--
B_US32.83c13     -I---D-F-D--R--------S-------------.G---.---R..---T-DR..-.V.----R.----I-G---S.--R-IVI--.---..--K....--...-.-V-.---.----P.--
B_US32.84c11     -------F-----------K---V-----G-----.----.---R..------N..-.-.-----.----L-IAE--K.A-N-TVS--.---..--K....--...-.-V-.-S-.A--P.--
B_US32.85c11     -------F-----I-------S-T-----S-----.G---.---R..TL---Q..V.-.----R.----I-GI--EK.A-K--VE--.---..K-GE...--...-.-A-.-H-.----P.--
B_US33.112587    -------F-----I------KS-------------.----.---R..---T---..-.-.-----.----I--AE-D-.--K-IVI--.---..H-V....--...-.-V-.-H-.-
B_US33.114287    -------F-----I-------S------K------.----.---R..---T--N..-.-.-----.----I--AE---.--K-IVI--.---..H-G....--...-.-V-.-H-.-
B_US34.HEM012    -----V-F-D-T---------S-V-----------.--P-.---S..---T--E..-.-.-----.----L-KAA-DR.--K-IV---..-D...I
B_US34.HEM017    -------F-----------K-S-A------S----T.--N-.---R..---T---..-.-.-----.----I--AQ---.----IV---..-K..--......G...R
B_US34.HEM027    -----V-FSD-T---------S-V-----------.----.---R..---T--E..-.-.-----.----L-KEA-DR.--K--V---.---..--R....-...
B_US34.HEM048    -------F-----------K---------------.--N-.---R..---T---..-.-.-----.----I-G----S.--KLI-A--.---..--R....-N...
B_US34.sc14.1    ---K-K-F-D----------KS-K----K------.----.----..-L---EA..-.-.EN---.----I-KA-$--.--K-IVK--..KV..--R....--...-.---.---.----P.K-VM---.----.-------
B_US34.sc14.2    ---K-K-F-D----------KS-K----K------.----.----..-L---EA..-.-.EN---.----I-KA-$--.--K-IVK--..KV..--R....--...-.---.---.----P.K-VM---.----.-------
B_US34.sc14.3    -------F-D-----------S-------------.----.----..-L---A..-.-.-----.----I--A----.--K-IVK--..KV..--G....--...-.---.---.----P.--VM---.----.-------
B_US34.sc14.5    -------S-D-----------S-------------.----.----..-L---A..-.-.-----.----I--A----.--K-IVK--..KV..--G....--...-.---.---.----P.--VM---.----.-------
B_US35.85111     -------F-----I-------S-------------.G---.---G..---T.TK..-.-.-----.----I-IA----.--K-IVK--.---..--G....--...-.-V-.---.----P.--V---.----.--L----
B_US35.85214     -----D-F-----------K-A-------------.----.Q--R..---T---..-.-.-----.----L-KAN---.--K-IVI--..-Q..--N....--...-.-V-.-H-.----P.--VM---.----.------S
B_US35.8531      -------F-D---I-------S--S----------.--P-.---R..---T--E..-.-.-E---.----L-----D-.A---I-K--..GK..--G....T-...-.-V-.---.----P.--VM-T-.----.------S
B_US35.8611      -------F--S-----------T----R-------R.--NM.---K..TL-T-DI..-.-.-----.----L--A---D.--K-IVI--.---..--G....--...-.-V-.---.----P.--VM---.----.-------
B_US35.86165     -------F-----------K-SI------------.----.---R..---T--E..-.-.----K-.----L--A---D.--K-IVI--.---..--G....--...-.---.---.----P.--V---.----.------S
B_US35.86171     -------F-D-----------SIA-----------.----.A--R..-VHT--E..-.-.-N---.----I-----TS.--E-IVK--.---..--G....-N...-K---.-H-.----P.--V---.----.-------
B_US35.86182     -------F-----I-----K-S-V---------G-.--N-.---G..---T--K..-.-.-----.-Y--I--AQ---.--K-IVE--.---..--E....--...-.-V-.-H-.----P.--E---.----.-------
B_US35.8629      I-----------------K----------------.----.---R..---T--E..-.-.-----.----I--A---D.--R-I-KQ-.---..--K....--...-.---.---.V--P.--V---.----.------S
B_US35.8641      -----D-F-D---I-----K-A-------------.--N-.---K..-L-T--E..-.-.-----.----I--A----.--K-IV---.---..--G....--...-.-V-.-R-.-----.--V---.----.--L---S
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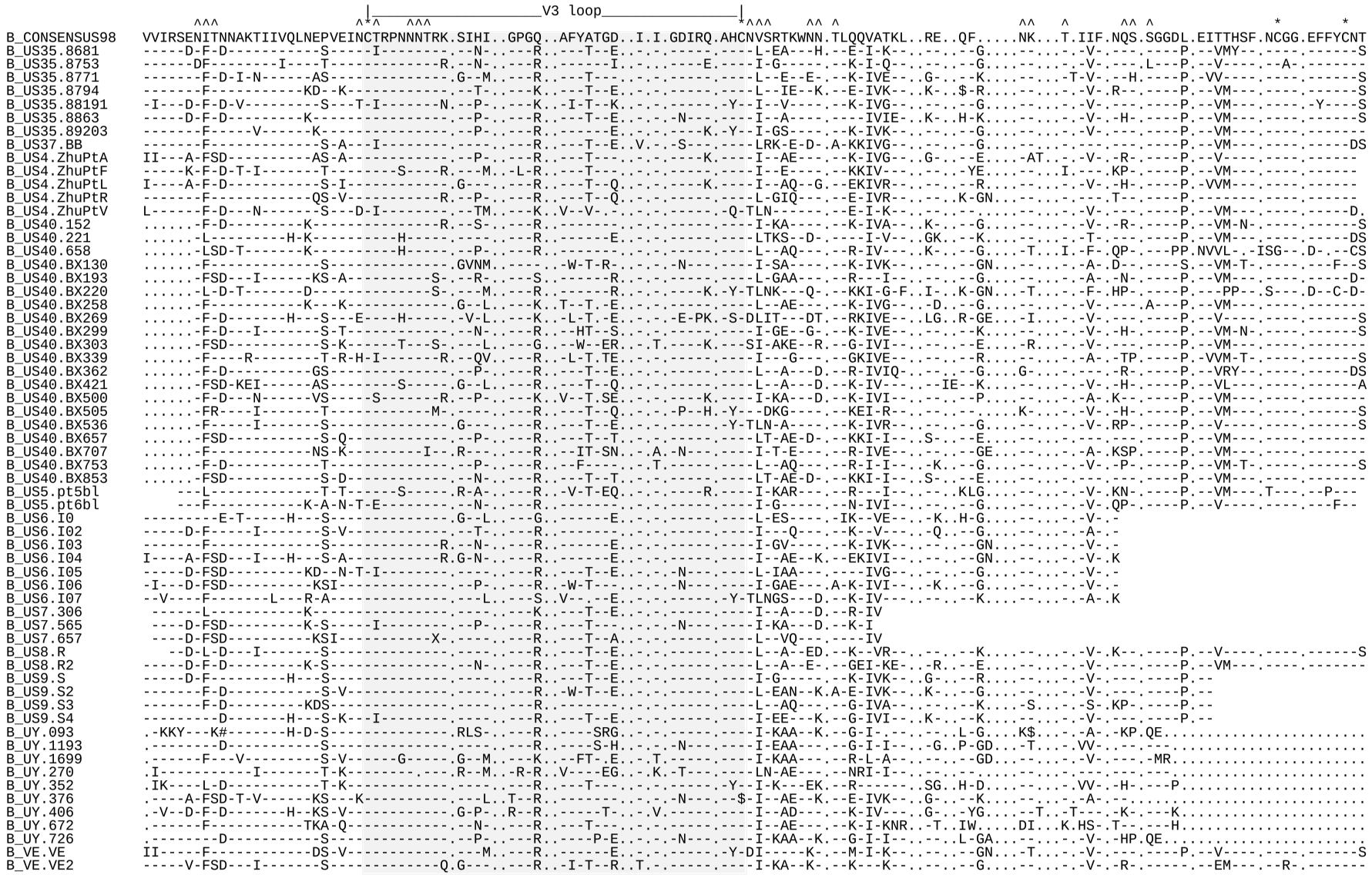
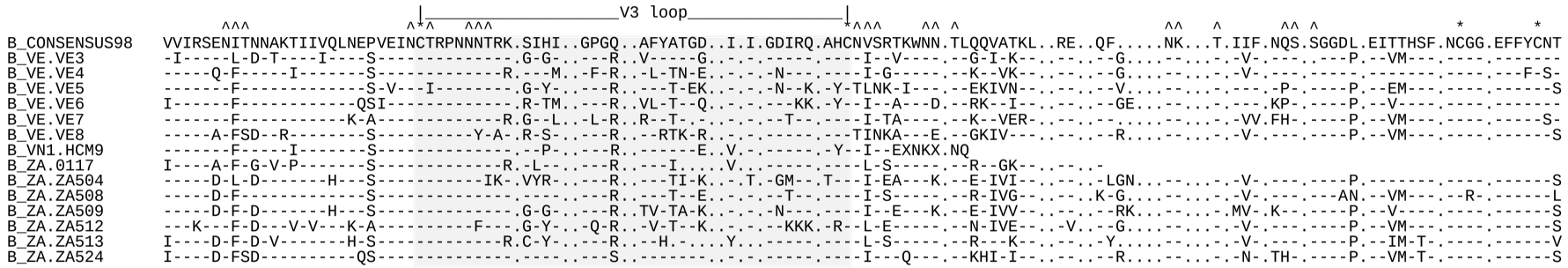
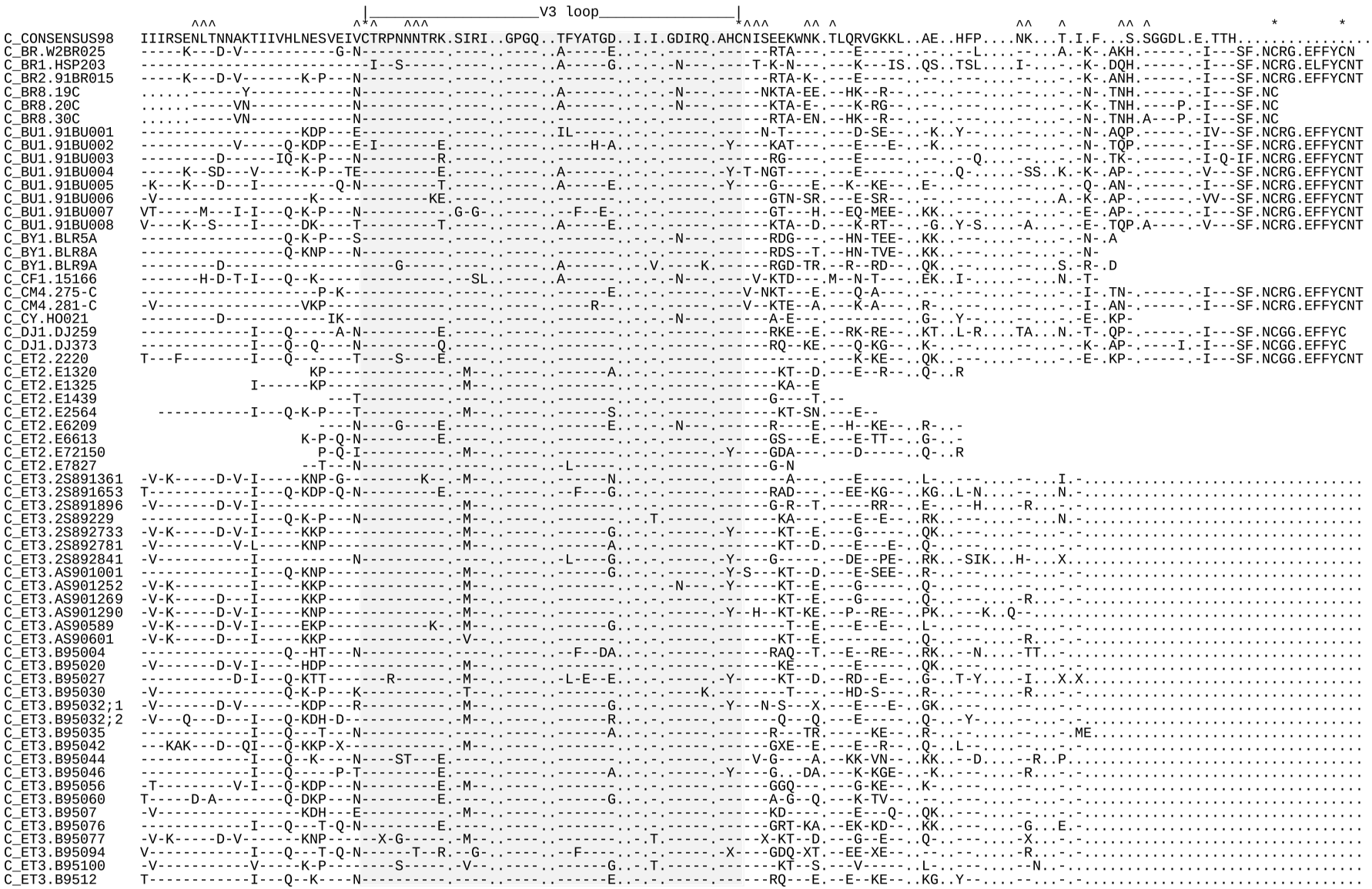


V3 Region Alignment

Analyses



V3 Region Alignment


V3 loop
C_CONSENSUS98 IIIRSENLTNNAKTIIVHLNESVEIVCTRPNNNTRK.SIRI..GPGQ..TFYATGD..I.I.GDIRQ.AHCNISEEKWNK.TLQRVGKKL..AE..HFP....NK...T.I.F...S.SGGDL.E.TTH.
C_BR.W2BR025
C_BR1.HSP203
C_BR2.91BR015
C_BR8.19C
C_BR8.20C
C_BR8.30C
C_BU1.91BU001
C_BU1.91BU002
C_BU1.91BU003
C_BU1.91BU004
C_BU1.91BU005
C_BU1.91BU006
C_BU1.91BU007
C_BU1.91BU008
C_BY1.BLR5A
C_BY1.BLR8A
C_BY1.BLR9A
C_CF1.15166
C_CM4.275-C
C_CM4.281-C
C_CY.HO021
C_DJ1.DJ259
C_DJ1.DJ373
C_ET2.2220
C_ET2.E1320
C_ET2.E1325
C_ET2.E1439
C_ET2.E2564
C_ET2.E6209
C_ET2.E6613
C_ET2.E72150
C_ET2.E7827
C_ET3.2S891361
C_ET3.2S891653
C_ET3.2S891896
C_ET3.2S89229
C_ET3.2S892733
C_ET3.2S892781
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C_ET3.B9507
C_ET3.B95076
C_ET3.B95077
C_ET3.B95094
C_ET3.B95100
C_ET3.B9512

Analyses

V3 Region Alignment

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                                                   |___________________V3 loop_______________|
                  ^^^                       ^*^   ^^^                                         *^^^     ^^ ^                         ^^   ^     ^^ ^               *       *
C_CONSENSUS98    IIIRSENLTNNAKTIIVHLNESVEIVCTRPNNNTRK.SIRI..GPGQ..TFYATGD..I.I.GDIRQ.AHCNISEEKWNK.TLQRVGKKL..AE..HFP....NK...T.I.F...S.SGGDL.E.TTH................
C_ET3.B9516      -V-----------I---Q--Q-------------.-M--.----.------E..-.-.-N---.-Y--N-KA--E.---N-S---.Q-..--T....--...-.-...............................
C_ET3.B9524      -V---------------Q-KKP------------R.-T--.----.-------..-.-.----K.-Q-----T---.--HD-S---.L-..---....--...-.-...............................
C_ET3.B953       -------------I---Q--NPI-----------.-M--.----.A----A..-.-.------.-Y-----T---.---E--EE-.X-..---....-X...S.-...............................
C_ET3.B9545      -V-------D---------K-P----S--------.-M--.----.------E..-.-.------.--I---QT---.---E-----.Q-..-Y-....-T...-.-...............................
C_ET3.B9552      -T--------V-I---Q-KDP---N----------.-M--.----.-------..-.-.------.-----G-T---.---E-KR--.QK..---....--...-.-...............................
C_ET3.B9562      -V-K-------V-------KDP-K-----G-----.-M--.----.------A..V.-.------.-----XD---.---E-----.HD..R--....XR...-.-...............................
C_ET3.B9585      -V-----I---V-------KDP------------.-M--.----.------A..-.-.------.----X-QT--D.---X-----.E-..---....GR...-.-...............................
C_ET3.B9590      -V-K---R---X-X---X-K-H---T----X-----.XM--.----.-------..-.-.------.-----GKT---.---E--R--.Q-..---....--...-.-...............................
C_ET3.B9595      TV-------K-V-I-----KNP-------S-----.-M--.----.------E..-.-.------.------K---N.---D-----.Q-..--L....-R...-.-...............................
C_ET3.B9599      TV-------D-V-I-----KDP-A----------.-M--.----.-------..-.-.------.-----------N.---E-----.Q-..---....--...S.-...............................
C_ET3.KAZS9204   -V-------D-V-I-----KKP------------.-M--.----.-------..-.-.------.-----GKA--E.---G-----.Q-..---....-S...-.-...............................
C_ET3.KAZS92109  T---A--------I---Q---P---N--------E.----.----.------S..-.-.------.-----R---KN.---K-EER-.KK..---....--...-.-...............................
C_ET3.KAZS9239   -----------V-----Q-RNH---N---------.--G-.----.-----DE..-.-.------.------G--ST.V-RK-ER--.Q-..--LMH.S-...................................
C_ET3.KAZS9242   -V-K-----D---I-----K-P------------.-M--.----.-------..-.-.------.------QA---.---G-----.Q-..---....--...-.-...............................
C_ET3.KAZS9249   -----------V-I---X--N-X-----------.-M--.----.-------..-.-.------.-----R-R---.---E-R---.X-..---....--...-.-...............................
C_ET3.KAZS9258   T------------I---Q-------T---------.----.----.-------..-.-.------.----NG----A.---K-RE--.EK..--L....--...-.-...............................
C_ET3.KAZS9258A  -V-K---------I-----K-P------------.-M--.----.-------..-.-.------.------Q----.---E-----.L-..---....--...-.-...............................
C_ET3.KAZS9258B  -V-------D-V-V---Q--KP------------.-VG-.----.-------..-.-.------.-Y----QT--E.---G-----.Q-..---....--...N.-...............................
C_ET3.KAZS9263   -----------V-----Q-MKP---N---------.--G-.----.-------..-.-.-N---.-Y----KA--D.---K--R--.Q-..S--....-R...-.-...............................
C_ET3.KAZS9265   -V---------V-------K-P------------.-V--.----.-------..-.-.-N---.-Y----KA--D.---E--G--.Q-..S--....-R...-.-...............................
C_ET3.KAZS9277   VM-----------I---Q-K-P---N---------.----.----.--F---E..V.-.-N---.-Y--V-RQA--Q.---E-A-Q-.RK..--N....--...-.-...............................
C_ET3.KAZS9294   -------------I---Q---T---N---G-----.----.----.A----E..-.-.----K.------G--RT.V--K-E---.Q-..---....-G...-.-...............................
C_ET3.KP95016    -V---------V------------------R.-M--.----.------A..-.-.------.------G---A.---K-EN--.Q-..---....-R...-.-...............................
C_ET3.KP95036    -----------V-----Q---T---N--------E.----.----.-------..-.-.------.-----R----N.--E--KER-.RK..---....SR...-.-...............................
C_ET3.KP95040    -------------I---Q--Q---N----------.----.----.------A..-.-.------.-----RQQ---.--DK-RT--.K-..---....-T...-.-...............................
C_ET3.KP95043    TV---------V-I---Q-KDP-------S-----.-M--.----.------E..-.-.------.------QN---.---D-SE--.QK..--L....-R...-.-...............................
C_ET3.KS92021    TV---K---D-T-I-----KNP------------.-M--.----.-------..-.-.------.------RA--D.---E--E--.QG..---....--...-.-...............................
C_ET3.KS95006    -------------I---Q-K-P---N---------R.----.----.AL-H--.-.-.-.------.---T-N-TT-HN.---K-----.Q-..---....--...-.-...............................
C_ET3.KS95012    -V----S------I-----TKP-------S-----.-M--.----.-------..-.T.------.------KT--D.---E-----.E-..---....--...S.-...............................
C_ET3.KS95020    -V-K----XD-V-I-----KKP------------.-----.----.-------..-.-.------.------Q---E.---EI-E--.K-..---....--...S.-...............................
C_ET3.KS95024    -------------I---Q-K---X----------.-M--.----.-------..-.-.-N---.-Y----KN--D.---K-----.L-..Y--....--...S.-...............................
C_ET3.KS95029    T---------------Q---T---N---G-----.-M--.----.-------..-.-.------.------G-N---.---K-KE--.G-..L--....--...-.-...............................
C_ET3.KS95030    ----------------Q-K-P---N---G----R.-MG-.---R.--------.V.-.------.-Y---RT----.---E-----.Q-..Q--....--...-.-...............................
C_ET3.KS95036    -V-K---------I-----KNP------------R.-M--.----.-------..-.-.------.-Y--N-ST---.---E-A---.Q-..---....I-.........QQ......................
C_ET3.KS95038    ----------------Q---T-Q-N---S-----.---L.-----.A----G..-.-.-E---.------RD----.--EK-KE--.KR..---....-G...-V...............................
C_ET3.KS95047    -V-------D---------K-P------------.-M--.----.------A..-.-.------.------KT---.---E-----.Q-..R--....--...-.-...............................
C_ET3.KS95050    -------------I--IQ-KKP-N-T-E--------.-V--.----.-------..-.-.------.------RE--N.---K-----.QD..---....--...-.-...............................
C_ET3.KS95068    -V---K---D-V-I---Q-Q-P-----I--------.-M--.----.------A..-.-.-N---.------Q----.---E--R--.Q-..---....--...-.-...............................
C_ET3.KS95077    D-------A----I---Q-KNP-Q-N---G----E.--G-.-----.A------..-.-.-T--.-Y---G-E--E.--H---E--.IR..L--....S-...N.-T.............................
C_ET3.KS95087    ----F--------I---Q-K-P------------.-V--.----.--------.V.-N---.-----------------E-----.X-..---....-S.K...............................
C_ET3.TKS92024   -V-----------I-----T-A-------G-----.-M--.----.-------..-.-.----K.-----NRQT--E.---N-SR--.Q-..---....--...-.-...............................
C_ET3.TKS92055   -MV--------V-I---Q---T---N--------R.----.----.-------..-.-.-N---.-Y---G---S.---K-K---.E-..L-H....--...-.-...............................
C_ET3.TKS92059   -V-K-----D-V-I-----EKP------------.-M--.----.-------..-.-.------.------KM--E.---G-----.Q-..---....--...-.-...............................
C_ET3.TKS92062   -------------I---Q-K-P---N----------.-M--.----.-------..-.-.------.------KA--D.---K--E--.K-..---....--...-.-...............................
C_ET3.TKS92077   -V---------V-I-----Q-P---E----------.-M-V.----.-------..-.-.------.--I---K---D.---K--SE-.Q-..---....--...-.-...............................
C_ET3.TKS92078A  -V---------V-I---Q-K-P-------S-----.-M--.----.-------..-.-.------.-------T--N.---E--ER-.QK..---....--...-.-...............................
C_ET3.TKS92078B  -V---------V-I-----QQPE-----------.-M--.----.------G..-.-.------.-----G-----.---E--R--.QD..---....--...-.-...............................
C_ET3.TKS92083   -V-------D-V-I-----QQP------------.-M--.----.------G..-.-.------.-----G-----.---E--R--.QD..---....-N...-.-...............................
C_ET3.TKS92090   T--------D-V-I---Q-KNP------------.-M--.----.------A..-.-.------.-------T---.---E-----.Q-..---....--...S.-...............................
C_ET3.TKS92092   --------I---------------N----------.-L--.----.-------..-.-.----K.-Y-------KQ.-----SA--.E-..---....--...-.-...............................
C_ET3.TKS92102   -V-K-----D-V-I-----K-P-------G-----.-M--.----.-------..-.-.------.---E---QV---.---E-----.Q-..---....--...S.-...............................
C_ET3.TP95001    -R-----I-----N---QFSDP-N-T----------.-V--.----.-------..-.-.------.----V-RSA---.---Q-VIQ-.KT..-VG....--...-.-...............................
C_ET3.TP95046    -V-K---------I-----K-P------------.-M--.----.-------..-.-.----R.-------TT---.---E--E--.Q-..---....--...-.-...............................
C_ET3.TP95059    VV--------------IQ-K-P-Q-N----------.-V--.----.A-F---G..-.-.------.------GQ----.--ED-K---.K-..---....--...-.-...............................
C_ET3.TP95075    -V---K---D-V-I---Q-K-P-------G-----.-V--.----.-------..-.-.------.-Y----KT-SD.--RD-S---.Q-..---....K-...-.-...............................
C_ET3.TP95091    T------------I---QF--T---N-K--------.-F--.----.------.-.-.GE---.------G----A.-----SR--.G-..---....-R...-.-...............................
C_ET3.TS95001    TV-K-K-------I---Q-KKP-Q-N----------.-M--.----.-------..-.-.------.---------A---.---E-----.Q-..---....--...-.-...............................
C_ET3.TS95002    -------I-----I---Q-----A-N----------.--G-.----.-L----A..-.-.------.----V-G----V.--E--KN--.T-..Y--....-N...S.-K.............................
C_ET3.TS95004    -V---------V-------TKP------------.-M--.----.-------..-.-.------.------KT---.---E-RG--.Q-..R--....--...-.-...............................
C_ET3.TS95007    ---K-----DHF-K-----E-P-K-----S-----.-M--.----.------E..-.-.------.---------H.A--KI----.L-..QS.....--...S.-R.............................
C_ET3.TS95009    -V-----------I-----KKP------------.-M--.----.------G..-.-.------.----V---A-DE.---E--E--.HK..---....-N...-.-...............................
C_ET3.TS95010    --------A--------Q-K-P-K----------.-V--.----.-------..-.-.------.-Y-H-NGTT---.--EE-KG--.RK..--L....--...-.-...............................
C_FR1.FRMP102    V------------I---Q-K-P------------.-M--.----.-------..-.-.------.-----------.---E-----.Q-..---....--...-X...............................
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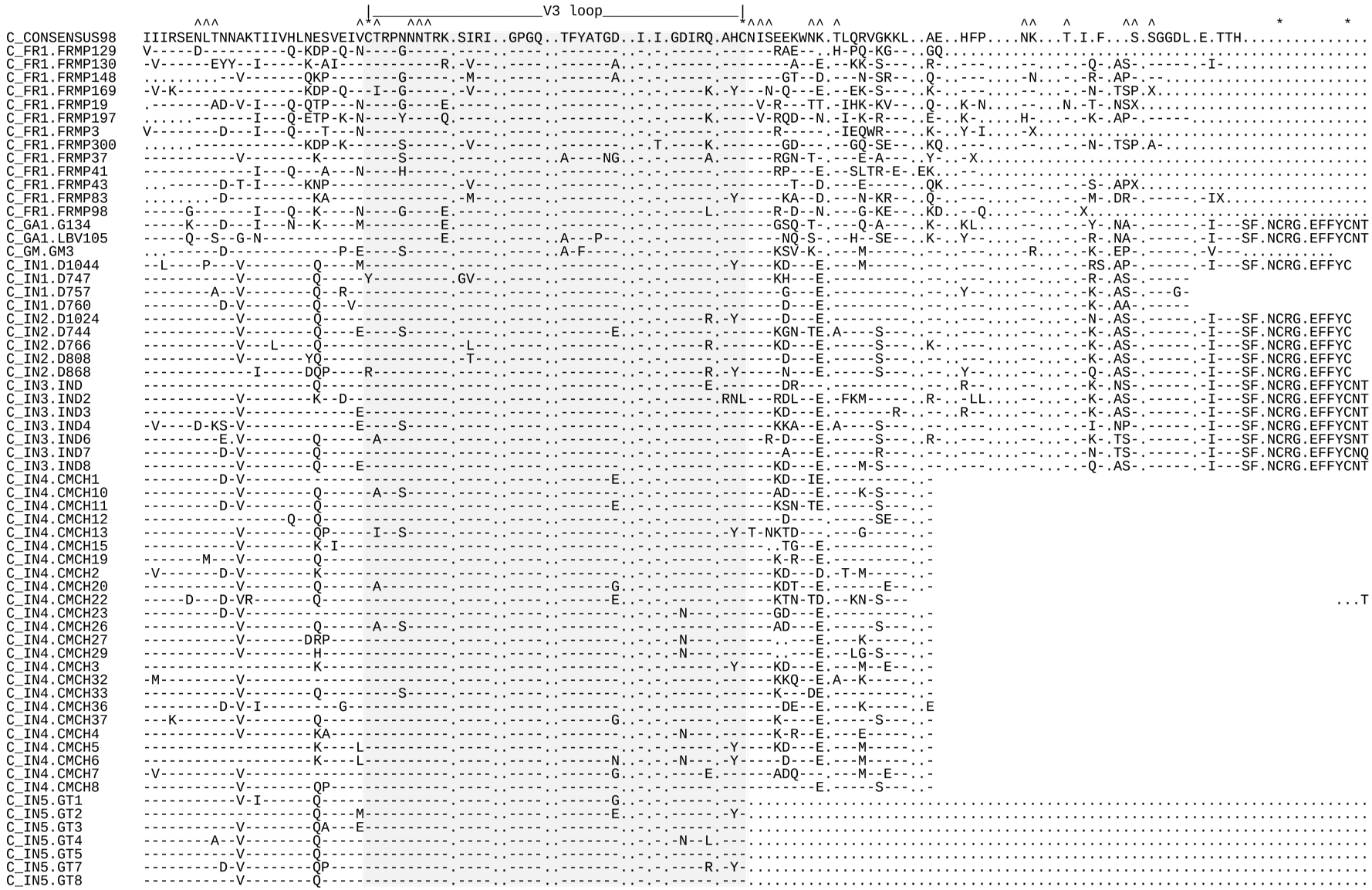
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C_FR1.FRMP300
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C_FR1.FRMP41
C_FR1.FRMP43
C_FR1.FRMP83
C_FR1.FRMP98
C_GA1.G134
C_GA1.LBV105
C_GM.GM3
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C_IN1.D757
C_IN1.D760
C_IN2.D1024
C_IN2.D744
C_IN2.D766
C_IN2.D808
C_IN2.D868
C_IN3.IND
C_IN3.IND2
C_IN3.IND3
C_IN3.IND4
C_IN3.IND6
C_IN3.IND7
C_IN3.IND8
C_IN4.CMCH1
C_IN4.CMCH10
C_IN4.CMCH11
C_IN4.CMCH12
C_IN4.CMCH13
C_IN4.CMCH15
C_IN4.CMCH19
C_IN4.CMCH2
C_IN4.CMCH20
C_IN4.CMCH22
C_IN4.CMCH23
C_IN4.CMCH26
C_IN4.CMCH27
C_IN4.CMCH29
C_IN4.CMCH3
C_IN4.CMCH32
C_IN4.CMCH33
C_IN4.CMCH36
C_IN4.CMCH37
C_IN4.CMCH4
C_IN4.CMCH5
C_IN4.CMCH6
C_IN4.CMCH7
C_IN4.CMCH8
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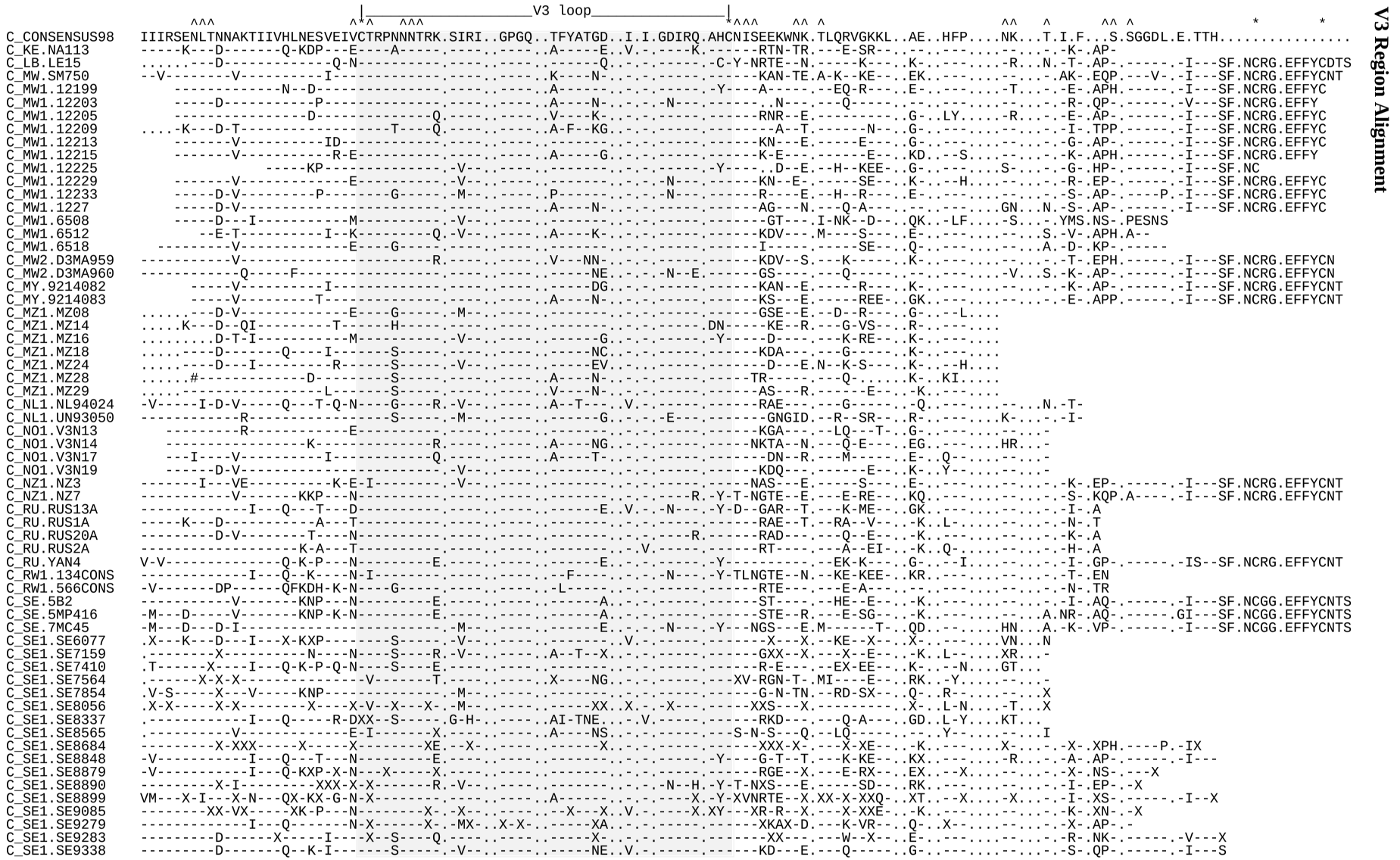
C_IN5.GT8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C_KE.NA113
C_LB.LE15
C_MW.SM750
C_MW1.12199
C_MW1.12203
C_MW1.12205
C_MW1.12209
C_MW1.12213
C_MW1.12215
C_MW1.12225
C_MW1.12229
C_MW1.12233
C_MW1.1227
C_MW1.6508
C_MW1.6512
C_MW1.6518
C_MW2.D3MA959
C_MW2.D3MA960
C_MY.9214082
C_MY.9214083
C_MZ1.MZ08
C_MZ1.MZ14
C_MZ1.MZ16
C_MZ1.MZ18
C_MZ1.MZ24
C_MZ1.MZ28
C_MZ1.MZ29
C_NL1.NL94024
C_NL1.UN93050
C_NO1.V3N13
C_NO1.V3N14
C_NO1.V3N17
C_NO1.V3N19
C_NZ1.NZ3
C_NZ1.NZ7
C_RU.RUS13A
C_RU.RUS1A
C_RU.RUS20A
C_RU.RUS2A
C_RU.YAN4
C_RW1.134CONS
C_RW1.566CONS
C_SE.5B2
C_SE.5MP416
C_SE.7MC45
C_SE1.SE6077
C_SE1.SE7159
C_SE1.SE7410
C_SE1.SE7564
C_SE1.SE7854
C_SE1.SE8056
C_SE1.SE8337
C_SE1.SE8565
C_SE1.SE8684
C_SE1.SE8848
C_SE1.SE8879
C_SE1.SE8890
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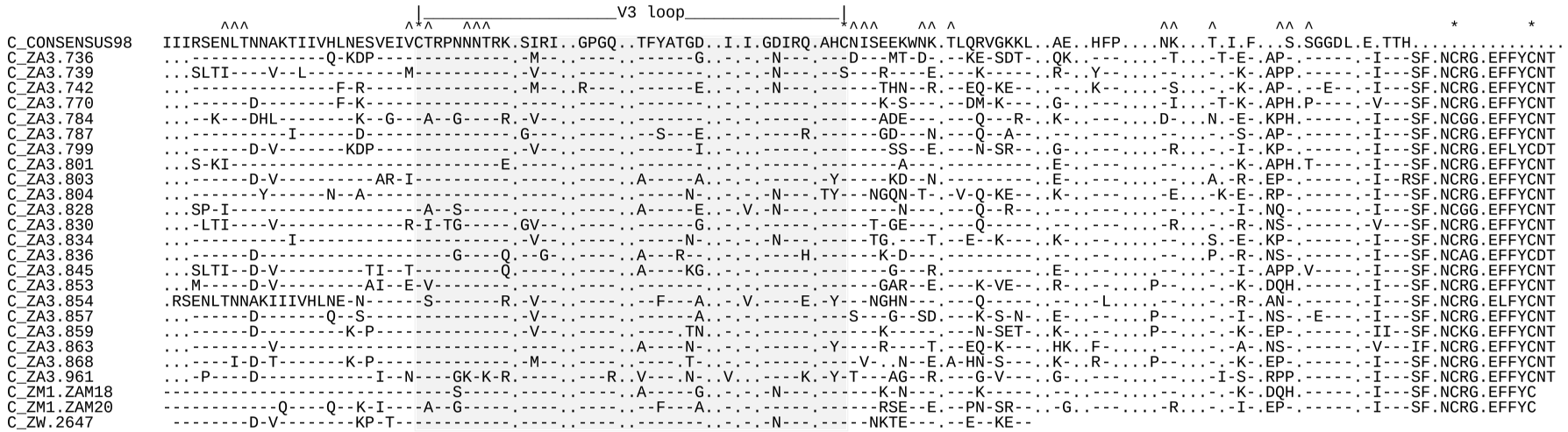
C_SE1.SE9279
C_SE1.SE9283
C_SE1.SE9338

V3 Region Alignment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C_ZA3.742
C_ZA3.770
C_ZA3.784
C_ZA3.787
C_ZA3.799
C_ZA3.801
C_ZA3.803
C_ZA3.804
C_ZA3.828
C_ZA3.830
C_ZA3.834
C_ZA3.836
C_ZA3.845
C_ZA3.853
C_ZA3.854
C_ZA3.857
C_ZA3.859
C_ZA3.863
C_ZA3.868
C_ZA3.961
C_ZM1.ZAM18
C_ZM1.ZAM20
C_ZW.2647

```
                                                        |____________________V3 loop_______________|
                      ^^^                             ^*^    ^^^                                      *^^^    ^^ ^                          ^^   ^     ^^ ^                  *       *
D_CONSENSUS98 IIIRSENLTNNAKIIIVQLNESVTINCTRPYNNTRQ.STHI..GPGQ..ALYTT....I.I.GDIRQ.AHCNISGAEWNK.TLQQVAKKL..GD..LL.....NKT..T.IIF.KPS.SGGDP?EITTHSF.NCGG.EFFYCNT
D_BI.BU009CON ------------------------------K-I-R.G---..-L-R..-Y---.G..-.E.-KKG-.P--K-N--G---.-----I---..R-..-F.....--...-.---.--P.----L.-------.----.--------
D_BR.RJ100    VM---------I-N----F----E------------.N-Q-..-----..TF--SKM..-.-------.-Y-E--EKK---.--R---S--..--..--.....--...-.---.---.-----.-------.----.--------
D_CF.402019   --V------D---T-----K---N-S----N-YK--.G-P-..-L--.------.R..V..-----K.------RK---N.---K------.RE..-F.....--S..K.-N-.Q-H.----L.-V-----.-Q-.------ -
D_CI.CI13     ------------------------------N-----.G---..----.------.G..V..-----K.------KA---.----I-I---.RN..--.....--...-.---.NS-.---G-.--I----.----.------ -
D_CI1.2121    ......-----V-T---------------N-K---.R-P-..-R--.------KG..-.V..N----.------TDQ---.------I---..-E..-Y.....--...-.---.--P.-----.-------.----.------N-
D_CI1.4574    ......---D-V-T----F----P-T-I--N-----.-----..----.--FF--.Q..E..-.-T-K.-Y----RED--T.---R------..--..-Y.....--...-K---.E--.-----.-------.----.------N-
D_CM1.CMR370  .----------I-N----F-DTIN-T-I--G----R.GI-L..A--E..-FX-GGD..-.-------.------R-K--N.-S-E------..-Y..--.....--...-I---.---.-----.-------.--A-.------G-
D_CM1.CMR61D  -M---K--NDDT-N----F---ID-T-V--N----K.-I--..--R-..---A-G..V..-RN--A.-Y---N-TK--N.--R-------..-E..--.....--...-K---.R--.--K--.-------.--K-.------N-
D_CM1.CMR6811 .M---------V-N-GG----P-N-T-L--N----K.-I-M..----.--F--.N..-.-------.-Y-E---.----.---------..SG..--N.....--...-.---.--P.-----.-----T-.----.--S---N-
D_CM1.CMR683  .M---------L-N------K--E-T-V--N----R.-I--..----.------.N..-.-.N--K.-F-T-D-KK--N.----------..-K..V-.....--...-.---.---.-----.-------.----.---S--L-
D_CM1.CMR684  .M-----F---L-N------K--E-T-V--N----R.-I--..-T--.------.N..-.-.N--K.-F-T-N-T.--N.---K------..SI..--.....--...-.---.---.-----.-------.----.------F-
D_GA1.G109    ------D------N------V--S------G-K---.K-P-..-L--.-----S.K..M..-V-R-K.----V-ATD--N.----------..--..--.....--...-N-.-S-.-----.-------.----.--------
D_GA1.G141    ---------D-T-N------D-IV---I--N-----.----..----.--F--.R..V..-------.-Y-E-N-TK--N.------R---..-N..--.....--...-.---.---.-----.-V-----.--R-.--------
D_GH.GH3      -------------T----F------------D-R--.R-P-..-L--..-F---RF..R..-------.------SKK--E.------R---..--..--.....--...-.-V-.---.-----.-------.----.------S-
D_GH1.NJ1     -------------T----F-----------N-----.----..----.------.R..V..-----K.-Y----TEQ---.------V---..-...............................................-
D_GH1.NJ7     ---------D---V---------P------N-----.----..----.------.Q..V..-----K.------KKD-D-.------I---..K................................................-
D_KE.NA116    ------D-------------K----D-I--------.G---..---R..-YF--.E..-.T.------.-Y-K-N-TA---.--E-------..RG..-V.....--...-A---.---                                   -
D_KE1.KEN966  -----------------------------------.--R-..-----.T-F--.K..-.-------.-------------G---.---R------..--..--                                               -
D_KE1.KEN97   -------------T----------P-----------.G---..---R..-Y---.N..-.-------.------R-----.-------R-..--..--                                               -
D_KE1.KEN986  -----------------------P-T----------.G---..---R..-T-F--.K..-.-------.------E-----.---L--R---..-G..--                                               -
D_KE2.B59     -----G---D---V-------------------L-.---M..---R..--F-....TK.-I-K----.------TG---.------T---..R-
D_KE2.G80     -----K-----------F-----------S--KDK..MR-..-----.--F--...NN.-I------.-Y-HVEQNGILY.
D_LB.LE22     ......---D---N-----------T----S----E.-I-M..---R..-F--M...GD.VT----K.-------.N--N.--R-I------..--..--.....-L-...-.---.NS-.----L.-------.----.-----Y-S
D_ML.103      -------------N-----------T-I--------.----..----.------....TK.-I----------KG--R.-------R---..-G..--.....--...-.-L-.QAA.-----.
D_NL.A1       -----Q-ISD-T-T---H---T-Q------N----R.-I-V..-----..-F-A-GD..-.-.-N--K.---D-N-TQ---.--E--KN---..KT..HFP.....--...-Q-.NQ                                  -
D_NL2.AO93021 -------I-H-T-N---H-----V------------.----..----.--F--NR..-.-------.-----S----D--R.---R--T---..-N..--.....-T-...-K-                                      -
D_NL2.UG93071 -V-----------T------K-IE-T-A--S----K.GI--..-----..-YF-A.E..-.T.------.-------TN-SV.A--------..--..--.....--...-K-T-                                    -
D_NL2.UG94015 -M---------------------I------N-----.-I--..----.------.N..-.-------.------EKA---.----------..--..--.....-R-...---                                      -
D_NL2.ZR8911  ---------D-T-N-----KK-IS-K-I--N-----.----..----.------.Q..V..-----K.-Y----KT--DN.-------E---..-K..--N....TRI..-.-K-                                   -
D_NL2.ZR9011  ---------D-T-N------K-IE-E----N-----.--P-..----.------.K..V..-------.-Y-T-NRT--DS.---K------..-N..--.....--...-.---                                   -
D_NL2.ZR9291  -------------T----------E-T-R-------.G---..----.------.E                                                                                         -
D_RU.RUS14A   -------------------------------I--.R-P-..-L--.------.R..R..-E---R.------K-A-K-.--E-------..KV..-F.....-R-...-D-.-                                     -
D_RU.RUS14A   -----------T-N----------L-T-I-----NTRKGIT-..-----..-F--.Q..R.VI------.-Y-K----A---.---R------..-N..--.....--...-N-.................................-
D_SE.3B       -------------V----------------------.----..---R..-Y---....TK.-I----------REG---.----------..-G..-F.....-Q-...-.---.---.-----.-------.----.------S
D_SE.3MP43    -------------V----------S-----------.----..---R..-Y---....TK.-I---G-.------REG---.-------N---..-G..-F.....-Q-...S.--L.---.-----.G------.----.------S
D_SE1.SE6095  -------X-----T-------T--------------K.GV--..-----..--F-E..Q-.V.---------.L-X-Q---.------X----..--..--.....-Q-...-.---.--H.--
D_SE1.SE6184  .------F--------------IP-------K-K--.G---..---R..--F-S...EV.-.R---K.-Y-T-NETK---.---ER--T---..RG..-V.....L-T-..-.
D_SE1.SE6274  .----K---D---N-----X-----------X-RIR.R---..-S-X..-V-X-...X-.X.-NX--.-X-X--XXA-X-.---X--X----..-X..-F.....---.
D_SE1.SE6339  .--------D---T----F--T-------XN-X---.G---..----.--F-L...XV.X.-------.-------EEX--X.---------..--..-F.....---.
D_SE1.SE6488  -------------X-------Q--P-T-V-------T.----..---R..-FF--...X-.-.-X--.------EXL---.---H---X---..--..--.....--...-.---.--P.----L.-----X
D_SE1.SE6687  .-------XD---N---XF-K---------G------.-IR-..----.------...Q-.-.-N----.------RT---N.--X--TT---..EN..-F.....---.
D_SE1.SE7076  .------I-----N---------V---S---E-K-R.-IR-..-I-R..GQAI$...TNK-T------.-Y--VNR-G-I-.---------..-G..--.....---.
D_SE1.SE7386  .------------------------------R.----..----.------...K-.-.-------.-Y-----G---.---------..K-..--.....-L-..A.
D_SE1.SE7565  .-----------------------------------.----..---R..-F---..S-.V.-------.------KV-R-K---.---------..--..-V.....-R-..K.
D_SE1.SE8384  .---------XKL-#---------IP-X-X---XK---.R-P-..---X..--H--...KX.LX---G-.-X-X----G---.-------X---..--..I-.....---.
D_SE1.SE8564  .-------------T----X----X-X-XX-X-XXXX.RSIX.I---..K-F--X.......-T-------.-Y-T-RE-----.---------..-G..-F.....---.
D_SE1.SE8603  .-V------------I----T-K------N----N.-IR-..-----..-F-A-...GA.-T-----.------V-RS---.---------..--..--.....---.
D_SE1.SE8680  -V----------------------------N----K.-V--..-----..-F-A-...GD.VI-------.------E-A---.---------..--..--.....-Q-..-.---.E--.-----.------
D_SE1.SE9048  -------------T-------T-X--------X--X.GVXX..---X..GQXLF...TXQ-V--------.------RTQ---.--X-I-T---..-X..-X....NXT-..-.---.--H.--
D_SE1.SE9340  -----X-I-----V-------T---X------N--K.-VR-..-----..SF-A-...GA.-I-------.-Y----R-----.---KLXT---..RQ..-I.....--...-X-.---.--X--.------
D_SE1.SEU1352 .---------X---N----F-------------G-KI-X.RIX-..-R--.----X...GV.G.------.-Y----XT----.I-K---T---..-N..-F....N---.
D_SN.SE365    -------------T----F----M----------K--.R-P-..-L--..V-H--.R..V.K.-------.------KER---.-----VR---..K-..-F.....--...-.---.E--.-----.--A----.--R-.------ -
D_TZ1.TAN     -------F-------------I-------SRV--.GA--..---R..-Y-A-.N..-.F.------.-R------A---.--ER--N---..R-..--N.....-QP.-.---.--                                  -
D_TZ1.TAN1    --V-------------------S------S-----.--R-..-----..----N.K..-.-.-N---.------V-KIK---.-------N---..RE..--.....--...-N-.--                                  -
D_TZ1.TAN12   -------------T---------Q-T-A--------.--R-..-----..-F-S.K..-.-.-N---.------TR-A---.---------..-G..--.....-Q-..-.-V-.--                                  -
D_TZ1.TAN13   ---------A----N-----------------E-M--.R-P-..-L--..--V-S.R..-.K.-R--P.-Y----ES-HR.---------..--..-F.....--...-L-.--                                  -
D_TZ1.TAN2    -----------------------P------------.G---..---R..-Y---.R..-.L.-N---.---S--VIK---.---------..R-..--.....-I...-K---.--                                  -
D_TZ1.TAN3    --------------------K-------------I-.G---..---R..-Y---.D..-SVI--------.----------E.---------..--..--.....-Q-..-.---.--                                  -
D_TZ1.TAN4    ---------------------------------I-.K-S-..-R--.------.E..T.R.---K-.-F-K---IA---.---------..R-..-F.....--...-.---.--                                  -
D_TZ1.TAN5    -------------N-------------------I--.R-P-..-S--.------.R..R..-------.-Y-E--E-G---.---------..R-..--.....--...-.---.-S                                  -
D_TZ1.TAN6    -----------------------P------------.G---..---R..-Y---.R..-.V.-N---.---S--VIK---.---------..R-..--.....-I...-K---.--                                  -
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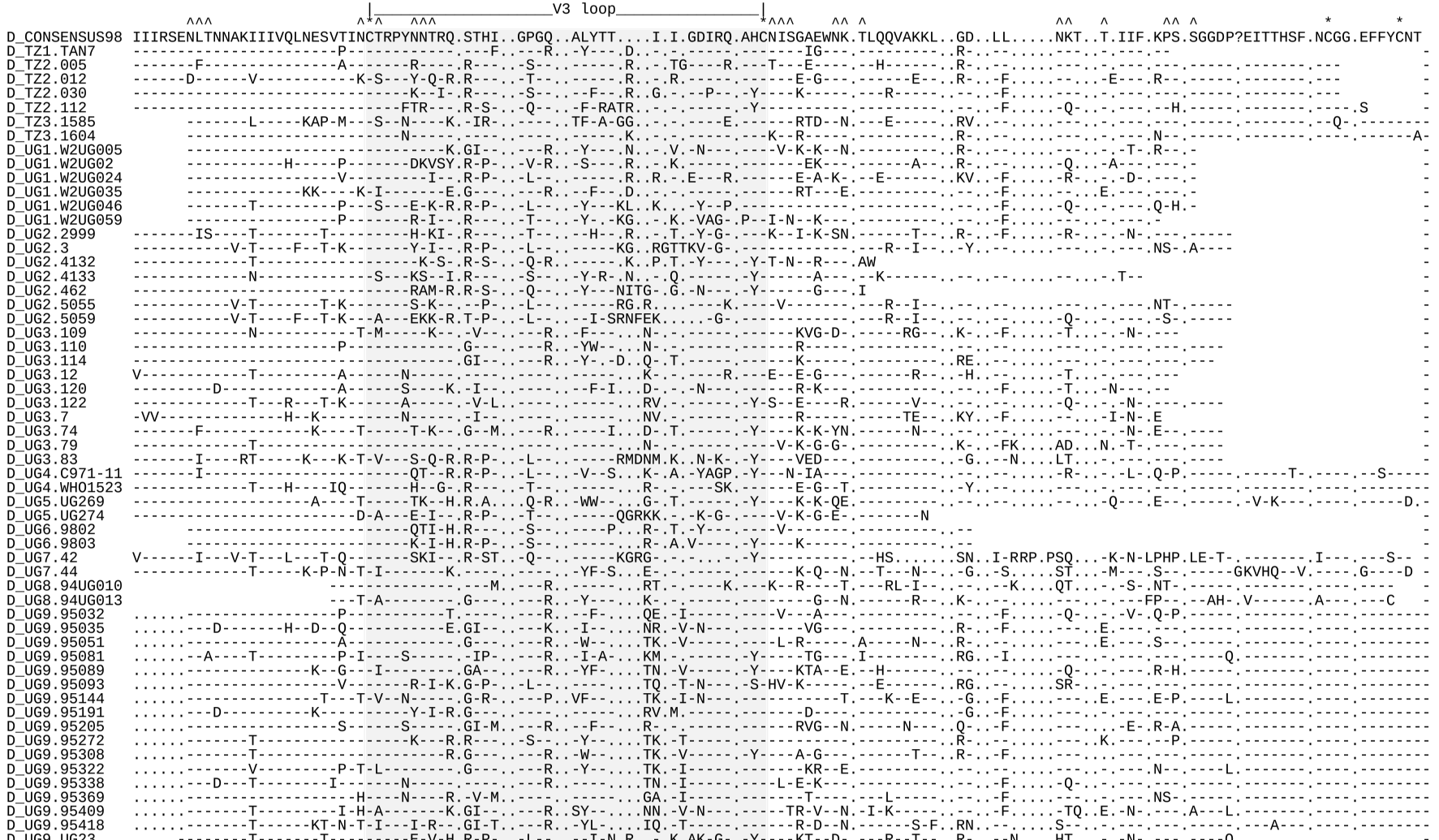
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D_TZ2.030
D_TZ2.112
D_TZ3.1585
D_TZ3.1604
D_UG1.W2UG005
D_UG1.W2UG02
D_UG1.W2UG024
D_UG1.W2UG035
D_UG1.W2UG046
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D_UG2.3
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D_UG2.4133
D_UG2.462
D_UG2.5055
D_UG2.5059
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D_UG3.110
D_UG3.114
D_UG3.12
D_UG3.120
D_UG3.122
D_UG3.7
D_UG3.74
D_UG3.79
D_UG3.83
D_UG4.C971-11
D_UG4.WHO1523
D_UG5.UG269
D_UG5.UG274
D_UG6.9802
D_UG6.9803
D_UG7.42
D_UG7.44
D_UG8.94UG010
D_UG8.94UG013
D_UG9.95032
D_UG9.95035
D_UG9.95051
D_UG9.95081
D_UG9.95089
D_UG9.95093
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D_UG9.95191
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D_UG9.95272
D_UG9.95308
D_UG9.95322
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D_UG9.95369
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D_UG9.95418
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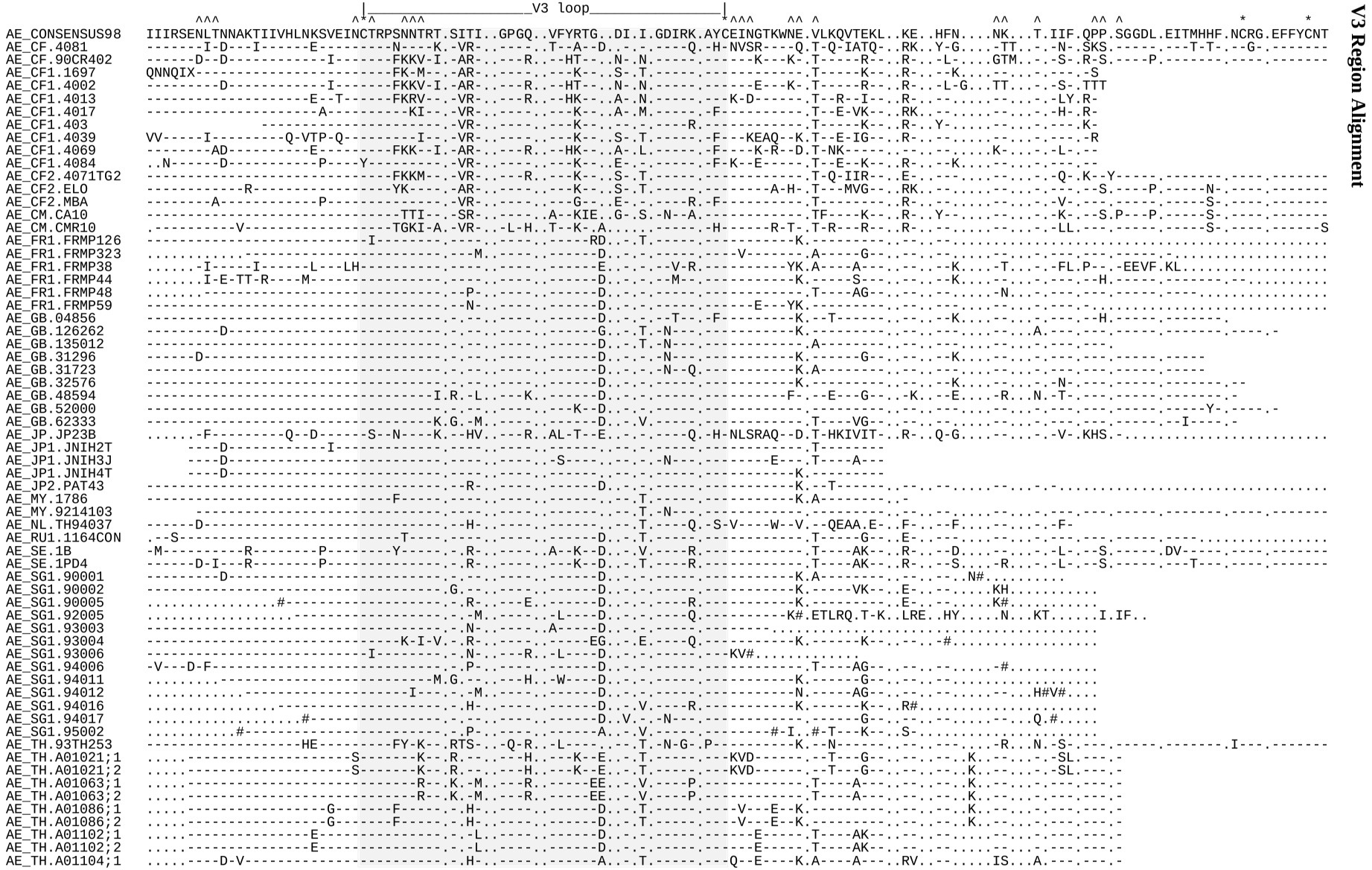
D_ZA.ZA500
D_ZA.ZA501
D_ZA.ZA505

V3 Region Alignment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AE_CF.4081
AE_CF.90CR402
AE_CF1.1697
AE_CF1.4002
AE_CF1.4013
AE_CF1.4017
AE_CF1.403
AE_CF1.4039
AE_CF1.4069
AE_CF1.4084
AE_CF2.4071TG2
AE_CF2.ELO
AE_CF2.MBA
AE_CM.CA10
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AE_JP2.PAT43
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AE_MY.9214103
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AE_SE.1PD4
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AE_SG1.90002
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AE_SG1.92005
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AE_SG1.93006
AE_SG1.94006
AE_SG1.94011
AE_SG1.94012
AE_SG1.94016
AE_SG1.94017
AE_SG1.95002
AE_TH.93TH253
AE_TH.A01021;1
AE_TH.A01021;2
AE_TH.A01063;1
AE_TH.A01063;2
AE_TH.A01086;1
AE_TH.A01086;2
AE_TH.A01102;1
AE_TH.A01102;2
AE_TH.A01104;1

```
                                            |____________________V3 loop________________|
                        ^^^                ^*^   ^^^                                    *^^^    ^^ ^                     ^^   ^      ^^ ^              *       *
AE_CONSENSUS98    IIIRSENLTNNAKTIIVHLNKSVEINCTRPSNNTRT.SITI..GPGQ..VFYRTG..DI.I.GDIRK.AYCEINGTKWNE.VLKQVTEKL..KE..HFN....NK...T.IIF.QPP.SGGDL.EITMHHF.NCRG.EFFYCNT
AE_TH.A01104;2    .....----D-V------------------------.--H-..----..------A.--.T.-----.---Q--E----K.A----A---..RV..---....IS...A.---.---.-
AE_TH.A05244;1    .....-------------------------------.----..----..------E.--.-.----Q.------------.T-E------..--..---....--...-.---.---.-
AE_TH.A05244;2    .....-------------------------------.----..----..------E.--.-.----Q.------------.T-E------..--..---....--...-.---.---.-
AE_TH.A06008;1    .....--------N---------K------------.----..----..------D.--.K.--T--.------E-N---.T-----K--..--..---....--...-.---.---.-
AE_TH.A06008;2    .....--------N---------K------------.----..----..------D.--.K.--T--.------E-N---.T-----K--..--..---....--...-.---.---.-
AE_TH.A06070;1    .....---------------E--K------------.----..----..------D.--.T.-----.-----------K.-----KK--..--..---....--...-.---.---.-
AE_TH.A06070;2    .....---------------E--K------------.----..----..------D.--.T.-----.-----------K.-----KK--..--..---....--...-.---.---.-
AE_TH.A06145;1    .....----------M--------------------.----..----..M-----D.--.-.-----.------------.T----AR--..--..---....--...-.---.---.-
AE_TH.A06145;2    .....----------M--------------------.----..----..M-----D.--.-.-----.------------.T----AR--..--..---....--...-.---.---.-
AE_TH.A06157;1    .....-------------------------------.----..----..------D.--.-.-----.------------.---------..--..---.T..--...-.---.---.-
AE_TH.A06157;2    .....-------------------------------.----..----..------D.--.-.-----.------------.---------..--..---.T..--...-.---.---.-
AE_TH.A12058;1    .....-------------------------------.----..----..----I-D.--.-.-----.------------.A--------..--..---.N..--...-.---.---.-
AE_TH.A12058;2    .....-------------------------------.----..----..----I-D.--.-.-----.------------.A--------..--..---.N..--...-.---.---.-
AE_TH.A12103;1    .....-------------------------------.--R-..----..------D.--.-.-----.----------K-.T----A---..--..---....--...-.---.---.-
AE_TH.A12103;2    .....-------------------------------.-VR-..----..------D.--.-.-----.----------K-.T----A---..--..---....--...-.---.---.-
AE_TH.A12149;1    .....--------------------S-----T----.--R-..----..------D.--.T.-----.------------.A----AG--..--..---....--...-.---.---.-
AE_TH.A12149;2    .....--------------------S-----T----.--R-..----..------D.--.T.-----.------------.A----AG--..--..---....--...-.---.---.-
AE_TH.B04034;1    .....-------------------------F-----.--P-..----..---K--E.--.-.-----.------E-----.-----A---..-V..---.N..--...-.-S-.--S.-
AE_TH.B04034;2    .....-------------------------F-----.-VP-..----..---K--E.--.-.-----.------E-----.-----A---..-V..---.N..--...-.-S-.--S.-
AE_TH.C18         ........X----------------S-----T----.-TP-..----..AW----D.--.T.-----.----V-------.T-R------..--..---....--...-.---.-K-.T-........................
AE_TH.CM240       ------D-----------------------------.----..---R..------..--.-.N----.-----------K.---------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH.E11419;1    .....---------T-----R---------------.----..---R..------D.--.-.----Q.------K-----.T----AG--..--..---....--...-.---.K-S.-
AE_TH.E11419;2    .....---------T-----R---------------.-M--..---R..------D.--.-.----Q.------K-----.T----AG--..--..---....--...-.---.K-S.-
AE_TH.E11429      -------------------H----------------.-M--..---R..------D.--.-.----Q.------E-E--K.-----VG--..--..---....--...-.-T-.---.-----.-------.----.-------
AE_TH.JP23A             ---D----------T----------THK-K.RM-L..---H..---S--..--.T.-----.-----------K.A--------..--..--I....--...-.-V-.---.-
AE_TH.N764                ---------------------K----------.----..----..------..--.-.N----.------------.T----AK--..N-..---....K-...-.---.H--.-----.VV-----.----.-------
AE_TH.T8178           --------------------------------.--S-..----..------..--.-.-----.------------.A-T----N-..--..--H....--...-.-L-.---.-----.---T---.----.-------
AE_TH1.8639                T--------------------------.R---..----..------..--.-.-----.------------.A--------..--..---....--...-.---.---.-----.-L-----.----.-------
AE_TH1.8657            -------------------------------.----..----..I-----..--.-.-----.------------.A--------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH1.8659               ----------------------------.----..----..------..--.-.-----.------------.---------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH1.8663            -------------------------------.----..----..------..--.-.-----.-----------K.---------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH1.867          ----------------------------------.----..----..------..--.-.N----.------------.A----AG--..--..---....--...-.---.H--.-----.VV-----.--S-.-------
AE_TH1.8673           --------------------------------.----..----..------..--.T.N----.------------.A-R------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH1.8683       ------E-----------------------------.--P-..----..------..--.-.N----.------------.T--------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH1.TA1067             ----------------------------.---M..----..------..--.-.----R.-------K---K.A--------..--..--I....--...K.---.---.-----
AE_TH1.TA7792             ---------------------------P.----..----..------..--.-.-----.-----------K.A--------..--..---....--...-.--C.---.----P.-
AE_TH1.TA7794             ----------------------------.----..----..---K--..--.-.N----.------------.A--------..--..---....--...-.---.---.-----.-------.----
AE_TH1.TA8173             ----------------------------.--P-..----..------..--.-.-----.------------.A--------..--..---....--...-.---.---.-----.---T---
AE_TH1.TA8176             ----------------------------.----..----..------..--.-.-----.----V-------.A--------..--..---....--...-.---.---.-----.-------
AE_TH10.92TH001   ------------------------------------.--N-..----..------..--.-.-----.------------.--R------..--..--I....-R...-.---.---.-----.-------.----.-------
AE_TH10.92TH011   -------------I----------------------.----..----..------..--.-.N----.----------Y-.------K--..--..--T....--...-.---.---.-----.---T---.----.-------
AE_TH2.TN235      ------------------------------------.--P-..----..A-----..--.-.-----.------------.--T------..--..---....--...-.---.---.-----.-------.--X-.-------
AE_TH2.TN238      ------------------------------------.----..----..------..--.-.-T---.------S-R---.A-----G--..--..---....--...-.---.---.-----.-------.----.-------
AE_TH2.TN239      ------------------------------------.----..----..------..--.-.N----.------------.A--------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH2.TN24       ------------------------------------.----..----..------..--.-.-----.------------.------GE-..--..---....--...-.---.---.-----.-------.----.-------
AE_TH2.TN240      ------D-----------------------------.----..----..------..--.-.N----.-----------K.---------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH2.TN242      ------------------------------------.----..----..------..--.-.---X-.------R-----.A-----K--..--..---....--...-.-L-.---.-----.-------.----.-------
AE_TH2.TN243      ---------D-------------G----------XP.---X..----..------..--.-.----X.-----------R.---------..--..---....--...-.---.---.-----.-------.----.-------
AE_TH2.TN244      -----------------------V------------.----..----..------..--.-.-----.--------E--K.A--------..--..---....--...P.---.---.-----.-------.----.-------
AE_TH3.W2TH00           ------------------------------.--N-..----..------..--.-.-----.------------.--R------..--..--I....-R...-.---.---.-
AE_TH3.W2TH003          ------------------------------.---V..----..------..--.T.-----.----V-------.T-----KN-..--..---....--...-.---.---.-
AE_TH3.W2TH005          ------------------------------.--P-..----..------..--.-.-----.-----------K.---------..--..--K....--...-.---.---.-
AE_TH3.W2TH006          ------------------------------.----..----..------..--.-.----Q.------E-----.T-----K--..--..---....--...-.---.X--.-
AE_TH3.W2TH007          -----V------------------------.--N-..----..------..--.-.-----.-----------K.---------..--..---....--...-.-M-.---.-
AE_TH3.W2TH009          ------------------------------.----..----..------..--.-.-----.------R-----.A-----K--..E-..---....--...-.---.---.-
AE_TH3.W2TH01           -------I----------------------.----..----..------..--.-.N----.----------Y-.------K--..--..--T....--...-.---.---.-
AE_TH3.W2TH015          ------------------------------.G---..----..------..--.-.-----.-----------K.-----X---..--..---....--...-.---.-
AE_TH3.W2TH018          ------------------------------.----..----..I-----..--.-.-----.------------.A--------..--..--K....--...-.---.-
AE_TH3.W2TH019          -----------------K------------.----..----..------..--.-.-----.-H------E---.A-----K--..--..---....--...-.---.---.-
AE_TH3.W2TH02           ------------------------------.-L--..----..------..--.-.-----.-----------K.A--------..--..---....--...-.---.---.-
AE_TH3.W2TH020          ------------------------------.-L--..----..------..--.-.-----.------------.A--------..--..---....--...-.---.---.-
AE_TH3.W2TH022          ------------------------------.----..----..------..--.-.----R.-----------K.A--------..--..---....--...-.---.---.-
AE_TH3.W2TH023          ------------------------------.--N-..----..------..--.-.-----.------------.---K-----..--..---....--...-.---.---.-
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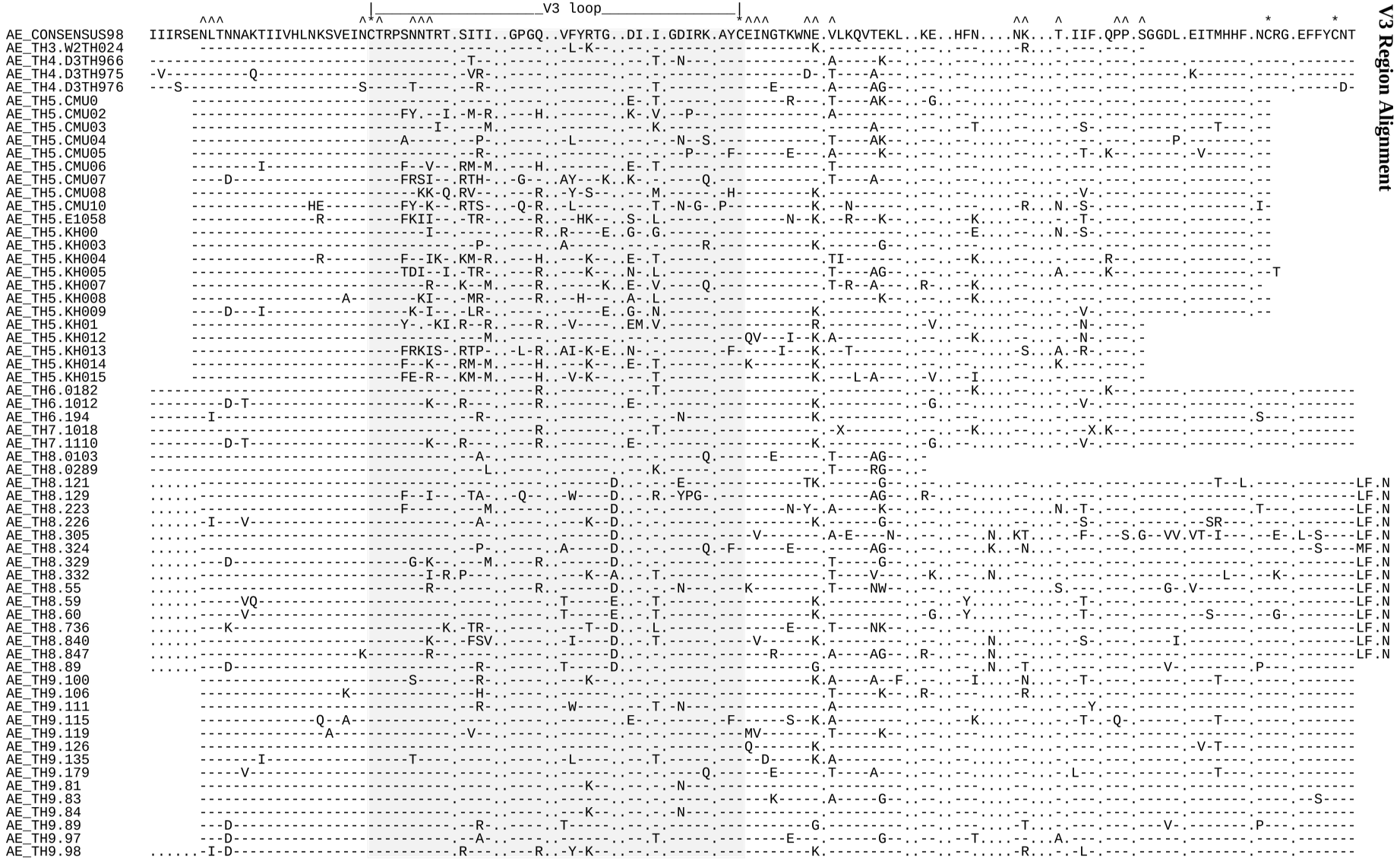
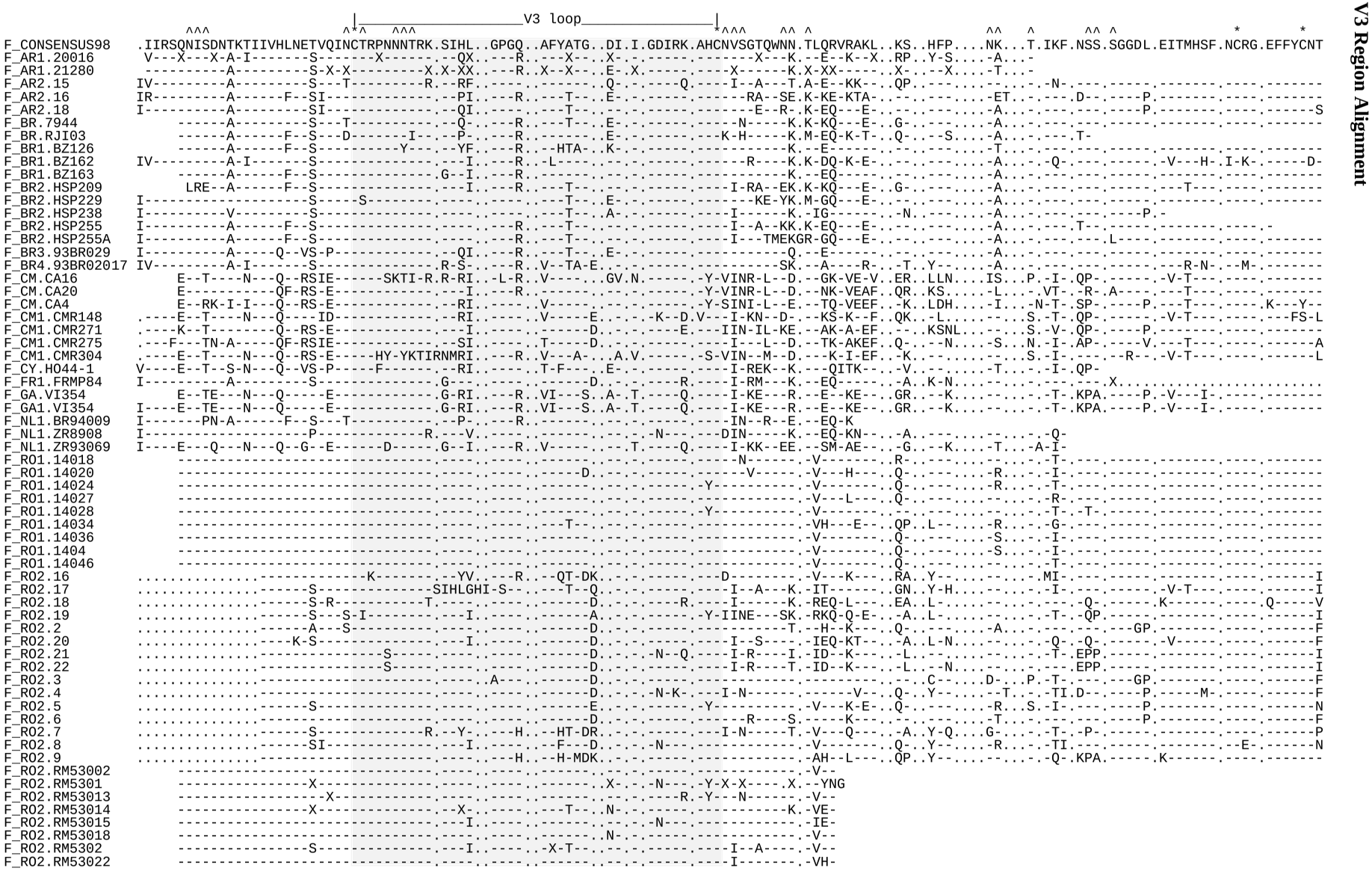
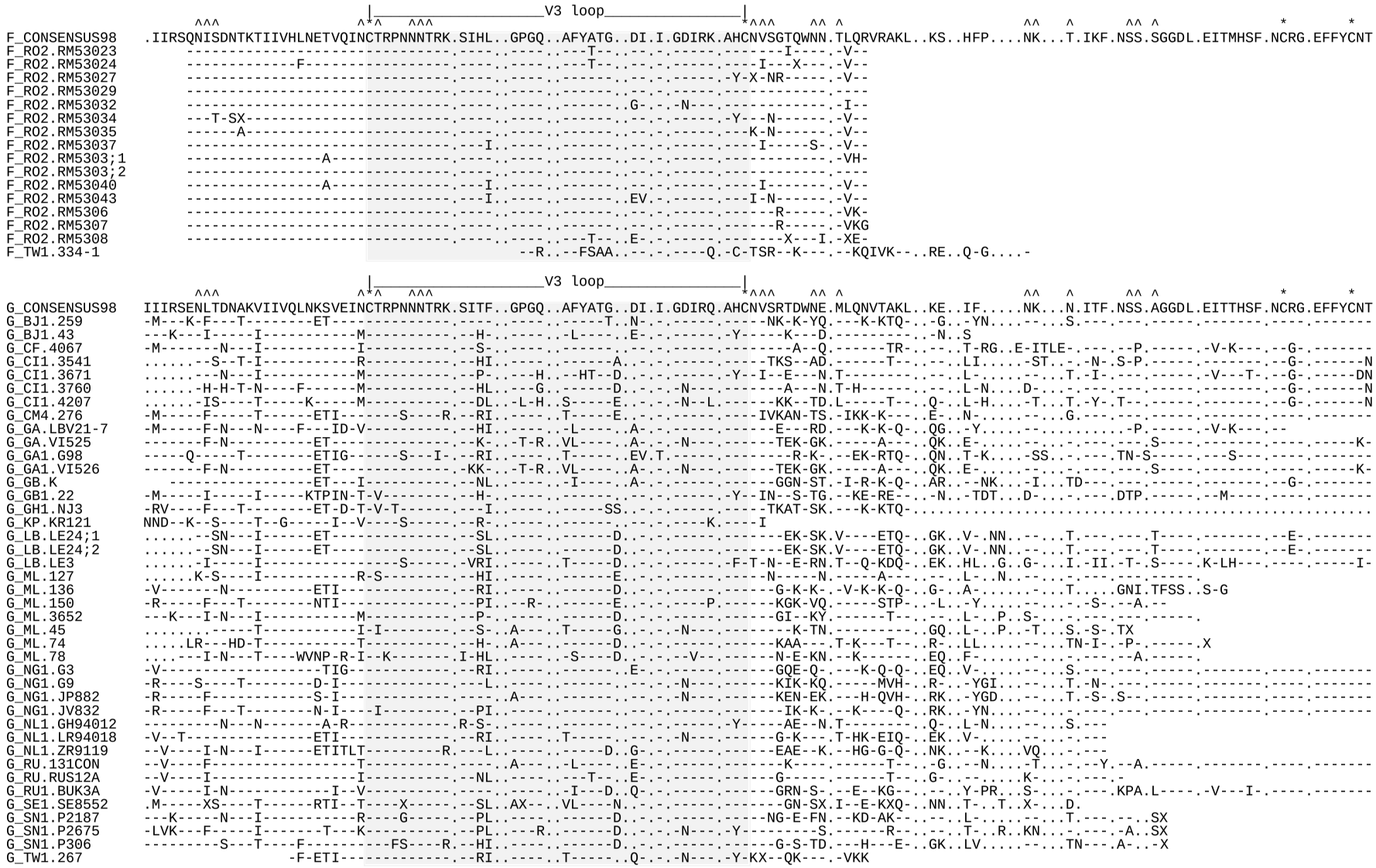
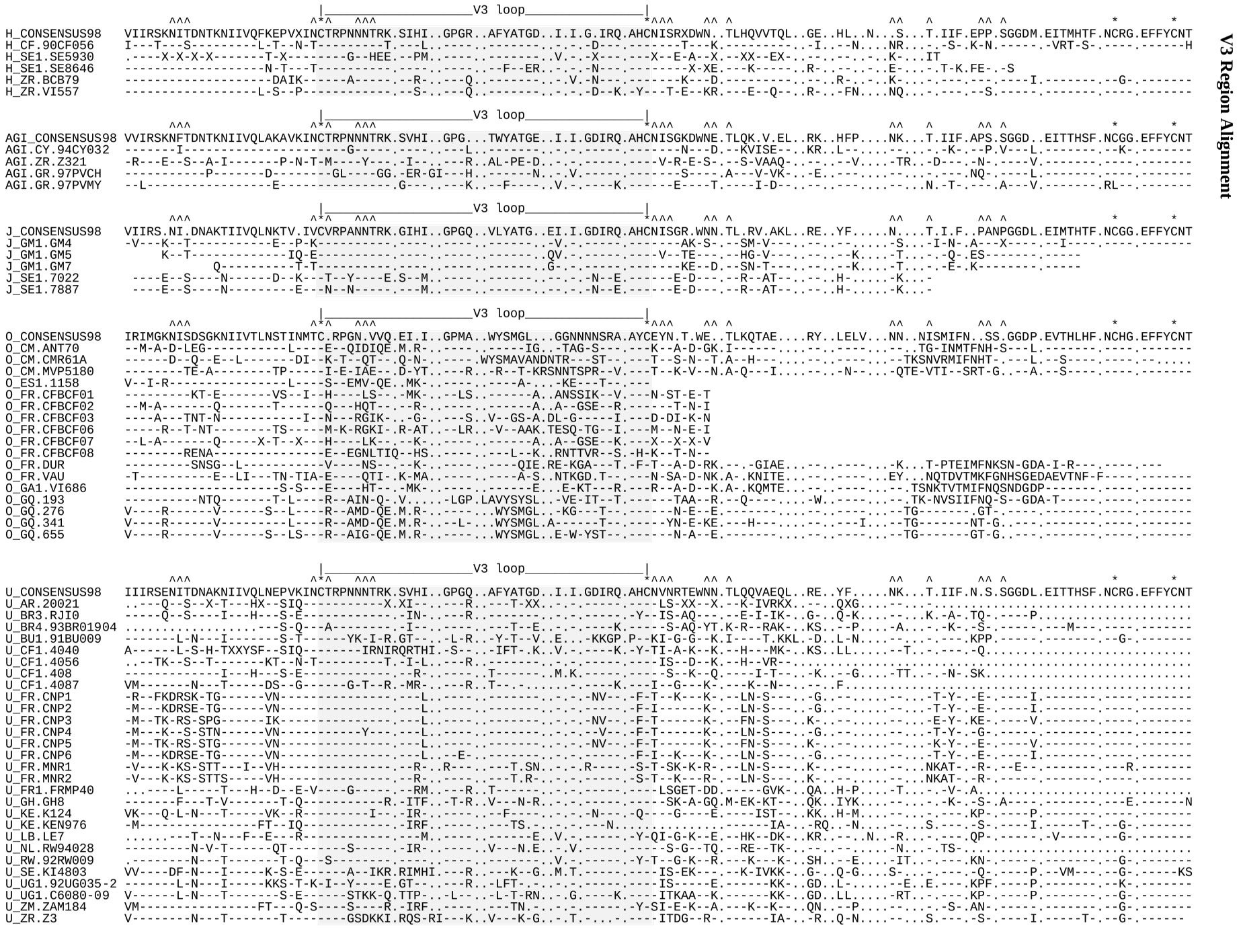

V3 loop
V3 Region Alignment
AE_CONSENSUS98 IIIRSENLTNNAKTIIVHLNKSVEINCTRPSNNTRT.SITI..GPGQ..VFYRTG..DI.I.GDIRK.AYCEINGTKWNE.VLKQVTEKL..KE..HFN....NK...T.IIF.QPP.SGGDL.EITMHHF.NCRG.EFFYCNT
AE_TH3.W2TH024
AE_TH4.D3TH966
AE_TH4.D3TH975
AE_TH4.D3TH976
AE_TH5.CMU0
AE_TH5.CMU02
AE_TH5.CMU03
AE_TH5.CMU04
AE_TH5.CMU05
AE_TH5.CMU06
AE_TH5.CMU07
AE_TH5.CMU08
AE_TH5.CMU10
AE_TH5.E1058
AE_TH5.KH00
AE_TH5.KH003
AE_TH5.KH004
AE_TH5.KH005
AE_TH5.KH007
AE_TH5.KH008
AE_TH5.KH009
AE_TH5.KH01
AE_TH5.KH012
AE_TH5.KH013
AE_TH5.KH014
AE_TH5.KH015
AE_TH6.0182
AE_TH6.1012
AE_TH6.194
AE_TH7.1018
AE_TH7.1110
AE_TH8.0103
AE_TH8.0289
AE_TH8.121
AE_TH8.129
AE_TH8.223
AE_TH8.226
AE_TH8.305
AE_TH8.324
AE_TH8.329
AE_TH8.332
AE_TH8.55
AE_TH8.59
AE_TH8.60
AE_TH8.736
AE_TH8.840
AE_TH8.847
AE_TH8.89
AE_TH9.100
AE_TH9.106
AE_TH9.111
AE_TH9.115
AE_TH9.119
AE_TH9.126
AE_TH9.135
AE_TH9.179
AE_TH9.81
AE_TH9.83
AE_TH9.84
AE_TH9.89
AE_TH9.97
AE_TH9.98

```
                                                    |____________________V3 loop_______________|
       ^^^                       ^*^    ^^^                                                     *^^^     ^^ ^                         ^^   ^       ^^ ^               *        *
AE_CONSENSUS98   IIIRSENLTNNAKTIIVHLNKSVEINCTRPSNNTRT.SITI..GPGQ..VFYRTG..DI.I.GDIRK.AYCEINGTKWNE.VLKQVTEKL..KE..HFN....NK...T.IIF.QPP.SGGDL.EITMHHF.NCRG.EFFYCNT
AE_TW1.286       X.---------------H--------I--------.G-H-..----..------..-.-.-N---.------R----R.A----MK--..RD
AE_TW1.346            L---A----------E---------NK----.-MG-..-Q-I..LL--R-..AV.V.--KIQ.--SN--KA---K.----I----..R-..Q-GK...I
AE_TW1.396        V------------------------------KK-A.-LR-..----..---T-E..G-.N.----R.-----------.----------..D-..--K....--
AE_UK1.11643     -------------------------------I--.-FR-..----..--HK--..S-.T.-----.-----------K.A---A---..--..---....--...-S-.---.---.-----.-------.----.-------
AE_US.POC30506   --------------------E--------------.-VR-..----..------..-.T.-----.------E-----.T---------..--..--K....--...-.---.---.-----.----L--.----.-------
AE_UY.UR2        ------------------------------------.---M..----..------..-.-.-----.------------.A----G---..--..---....--...-.---.---.-----.-------.T---.-------
AE_UY.UR4        --------------------------------I-.----..----..------..-.K.-----.----V-----K.---------..--..---....--...L.---.---.-----.-------.----.-------
AE_UY.UR6        ------------------------------------.--N-..----..------..-.-.-----.------E---TK.---------..--..--K....--...-.---.---.-----.-------.--K-.-------
AE_UY.UR7        ------------------------------------.---M..----..------..-.-.-----.------------.A----G---..--..---....--...-.---.---.-----.-------.S---.-------
AE_VN.10         -------------N----------------------.--P-..----..------D..-.-.-----.-----------Y-.--E---GE-..-K..---....--...-.---.---.-----.--
AE_VN.12         ------------------------------------.G--M..----..------D..-.-.---K-.------------.--E---G--..--..---....--...-.---.---.-----.---T---.S---.-------
AE_VN.15         ---------D--------------S---------K.----..---R..------D..-.-.-----.------------.------R--..E-..---.N..--...-L-.---.-----.---T---.S---.-------
AE_VN.16         ------------------------------------.---M..----..------D..-.-.-----.------------.------G--..--..---....--...-.---.---.-----.---T---.S---.-------
AE_VN.17         ------------------------------------.G---..----..------D..-.-.-----.------E-E-K-.--N--KG--..--..---.N..--...A.-D-.---.----P.G-----.--T-.-------
AE_VN.18         T-----------------------------------.---M..----..------D..-.-.-----.------------.--R---G--..--..---....--...-.-T-.---.-----.---T---.S---.-------
AE_VN.20;1       ------D------A----------------------.G--M..----..------D..-.-.-E---.------------.------G--..--..---....--...-.-T-.---.-----.---T---.S---.-------
AE_VN.20;2       -----------------------------------I.RM-M..---H..------D..-.-.-----.------------.------G--..--..---....--...-.-S-.---.-----.--
AE_VN.21         ----------------Q-------------------.----..----..------D..-.-.-----.------------.---------..--..---.R..--...-.---.---.-----.-------.----.-------
AE_VN.22         ------D-----------------------------.---M..----..I-----D..-.-.-----.------------.--E---G--..--..---....--...-.---.---.-----.---T---.S---.-------
AE_VN.23         ------------------------------------.-M--..----..------D..-.-.-----.------------.-----AG--..--..---.N..--...-.-F-.---.-----.---T---.----.-------
AE_VN.24         ------------------------------------.---M..----..------D..-.-.-----.------------.------G--..--..---....--...-.---.--L.-----.---T---.S---.-------
AE_VN.25         -------------N----------------------.---M..----..------D..-.-.-----.---K--------.------G--..--..---....--...-.---.---.-----.--X
AE_VN.26         ------------------------------------.---M..----..------D..-.-.-----.----------H-.---------..--..---....--...S.---.---.-----.---T---.----.-------
AE_VN.27         ----F-D-----------------------------.----..----..I-----D..-.-.N--R.------E---.---------..--..---.N..--...-.---.---.-----.-------.----.-------
AE_VN.28         ------------------------------------.---M..----..------D..-.-.-----.----------K-.T---AG--..--..Y-....--...-.---.--S.-----.---T---.----.-------
AE_VN.6C1        ------------------------------------.---M..----..------D..-.-.-----.-----R-----.------G--..--..---....--...-.---.---.-----.--
AE_VN.6C2        ------------------------------------.---M..----..------D..-.-.-----.---G--R-----.------G--..--..---....--...-.---.---.-----.--
AE_VN.7          -------------------------------F-----.----..----..-L--P-G..-.-.----R.------------.T-T--G--..--..---.Y..--...-.---.---.-----.--
AE_VN.8C1        ------------------------------------.-L--..----..------D..-.-.----Y.----------R.A-----N-..--..---.N..-M...-.---.---.-----.--
AE_VN.8C2        ------------------------------------.-L--..----..------D..-.-.----Q.----------K.A--------..--..---.N..--...-.---.---.-----.--
AE_VN.9C1        ------------------------S-----------.R--M..---R..------D..-V.-----.------------.---------..--..---.K..--...-.-T-.---.-----.--
AE_VN.9C2        ------------------------S----D------.R--M..---R..------D..-V.-----.----------K.--T--A---..--..---.K..--...-.-N-.---.-----.--
AE_VN1.BX6       ------------------------------------.X--M..----..------..-.-.-----.------------.------G--
AE_VN1.CT5                                ----------.--P-..----..------..-.T.-----.----------K.--------I..--..---....--...-.-T-.TTS..---
AE_VN1.DN3                        ----X---------------.---M..----..------..-.-.-----.------------.-
AE_VN2.VN1       ------------------------------------.--A-..----..------..-.-.-----.----------K.---------..--..---....--...-.-S-.---.----P.--
AE_VN2.VN2       ------------------------------------.-L--..----..------..-.-.-----.----------K.A--------..--..---....--...-.-T-.---.----P.--
AE_VN2.VN3       ------------------------------------.---M..----..------..-.-.-----.------R-E---.--E--AG--..--..---....--...-.-V-.---.----P.--
AE_VN2.VN4       ------------------------------------.---M..----..------..-.-.-----.----------K.---------..--..---....--...-.---.---.----P.--
```


V3 loop



Analyses


V3 loop
H_CONSENSUS98
H_CF.90CF056
H_SE1.SE5930
H_SE1.SE8646
H_ZR.BCB79
H_ZR.VI557
AGI_CONSENSUS98
AGI.CY.94CY032
AGI.ZR.Z321
AGI.GR.97PVCH
AGI.GR.97PVMY
J_CONSENSUS98
J_GM1.GM4
J_GM1.GM5
J_GM1.GM7
J_SE1.7022
J_SE1.7887
O_CONSENSUS98
O_CM.ANT70
O_CM.CMR61A
O_CM.MVP5180
O_ES1.1158
O_FR.CFBCF01
O_FR.CFBCF02
O_FR.CFBCF03
O_FR.CFBCF06
O_FR.CFBCF07
O_FR.CFBCF08
O_FR.DUR
O_FR.VAU
O_GA1.VI686
O_GQ.193
O_GQ.276
O_GQ.341
O_GQ.655
U_CONSENSUS98
U_AR.20021
U_BR3.RJI0
U_BR4.93BR01904
U_BU1.91BU009
U_CF1.4040
U_CF1.4056
U_CF1.408
U_CF1.4087
U_FR.CNP1
U_FR.CNP2
U_FR.CNP3
U_FR.CNP4
U_FR.CNP5
U_FR.CNP6
U_FR.MNR1
U_FR.MNR2
U_FR1.FRMP40
U_GH.GH8
U_KE.K124
U_KE.KEN976
U_LB.LE7
U_NL.RW94028
U_RW.92RW009
U_SE.KI4803
U_UG1.92UG035-2
U_UG1.C6080-09
U_ZM.ZAM184
U_ZR.Z3

A Subtype

At this time there are viral sequences from 417 HIV-1 infected individuals associated with HIV-1 subtype A. The A subtype consensus sequence (A_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position in an alignment of these sequences. All of these sequences have been published and/or have been made available for printing in the database by their authors.

1) **BJ1.ID:** These 18 sequences are from female prostitutes, born in either Ghana or Togo, who live in Benin. 15 are from directly sequenced PCR products, derived via RT-PCR from patient serum RNA. 3 (233, 251 and 253) are from cloned PCR products, also by RT-PCR from serum RNA. Another subtype A sequence (366, U61870) is not included here, because it was nearly identical (254 of 255 bases identical) to the SF170 (M66533) sequence from Rwanda isolated in 1988, and thus it likely represents a lab artifact. [Heyndrickx et al.(1996)]. Accession numbers U61854–U61869, U61871 and U61873. Two subtype G isolates were also found in this study.
2) **BY.BLR10A:** This sequence is from Byelorussia. [Lukashov et al.(1995)]. Accession number L38411.
3) **CA.HWCL1:** This sequence is the first published sequence of subtype A HIV-1 in Canada. The patient had moved from Uganda in 1983, and was diagnosed as HIV+ in 1989. Viral RNA was recovered from archived, stored patient serum by binding viral particles to CD4-coated wells of an ELISA plate. The RT-PCR amplification product was cloned and 10 clones were sequenced. It is not clear whether this sequence is from a single clone, or a consensus of all 10. [Montpetit(1995)]. Accession number U34049.
4) **CF1.ID:** These thirteen sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. The sequences are consensus sequences from cloned PCR products. DNA was isolated from co-cultured PBMCs. [Murphy et al.(1993)] Accession numbers L11457–L11458, L11461–L11463, L11469–L11471, L11474–L11475, L11477–L11479, L11484–L11496, L11498, L11518 and L11523–L11524. Some of them were sequenced again by Schmitt et al. unpublished: U43275, CF1.4023; U43109, CF1.4054; U43139, CF1.11423; U43136, CF1.1286.
5) **CF2.GAN and SAS:** These sequences were kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg, France. They are part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. Accession numbers U43111, U43171, M81063, M81064.
6) **CI1.ID:** These six sequences are from six different AIDS patients suffering from pulmonary tuberculosis at the Pneumology Hospital of Cocody, Abidjan, Ivory Coast. In this study sequences came from coculture (on donor PBMCs) supernatant viral RNA, proviral DNA from each patients' PBMCs after coculture with donor PBMCs, and proviral DNA directly from uncultured PBMCs. PCR or RT-PCR was used to amplify the env V3 region, and 4-7 cloned PCR products were sequenced. A total of 66 sequences from the six patients were published. All 66 were subtype A, and intrapatient sequences were more similar than interpatient sequences [Audoly et al.(1996)]. Accession numbers U59559–U59624.
7) **CI2.CI-ID:** These sequences are from 11 of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-14 and CI-20 were symptomatic, and the others were asymptomatic. CI-14, CI-45 and CI-47 were serologically dually reactive for HIV-1 and HIV-2. The C2V3 region is part of a 900 bp sequence. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3–4 clones were sequenced, and the consensus of those clones is presented here. [Janssens et al.(1994a)]. Accession numbers X72024–X72027, X72030–X72039, X72043–X72056, and X72057–X72065.
8) **CI3.ID:** These 21 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000449, AF000450, AF000452, AF000453, AF000454, AF000455, AF000456, AF000457, AF000459, AF000462, AF000464, AF000465, AF000466, AF000467, AF000470, AF000471, AF000472, AF000473, AF000474, AF000475, AF000493

9) **CM1.CA-ID:** These sequences are 11 of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic (CA7, CA11, CA15, CA17, CA18, and CA21) and symptomatic (CA1, CA2, CA6, CA19 and CA22) individuals. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. [Nkengasong et al.(1994)]. The other six sequences were subtypes B, E, F and H. Accession numbers for the subtype A sequences: X80438, X80440, X80442, X80444–X80447, X80449, X80450, X80453, X80454.
10) **CM2.CMR61:** CMR61 is one of two A group sequences from a 23 year old female commercial sex worker from Cameroon who was found to be triple-infected with subtypes A and D, as well as O group HIV-1 [Takehisa et al.(1997b)]. The other subtype A sequence from the same patient is labelled as CMR709 and is from a separate blood sample. Accession numbers U58148, U58150.
11) **CM3.ID:** These 15 sequences are all from Cameroon. Takehisa et al unpublished 1997. Accession numbers U69992–U69996, U70000, U70002–U70008, U70010 and U70014
12) **CM4.ID:** These 17 subtype A sequences are from 1994-1995 samples from 211 Cameroonian AIDS patients [Takehisa et al.(1998)]. Of the 43 HIV patients sequenced, 17 were subtype A, 1 was subtype B, 2 were subtype C, 1 was subtype G. Accession numbers for the entire set are AF023064–AF023081.
13) **CY.HOcon:** This is a consensus sequence from four individuals who were epidemiologically linked to one another: a father, a mother, their child and a woman who was a heterosexual partner of the father. These samples, like others in this study (see also subtypes B, C, F and I) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. PBMC DNA was PCR amplified and cloned. Individual clones were sequenced. The father (patient HO34) was 36 years old and asymptomatic. He was known to have been seropositive for at least 2 years and had a CD4 count of 410. The mother (patient HO17) was 35, had been infected for at least two years, had a CD4 count of 2 and died in May 1994. The child (patient HO49) was 2 years old, had been infected since birth, and was asymptomatic, with a CD4 count of 1,211. The partner of the father (patient HO42) was 45 years old, had been infected for at least 4 years, was symptomatic with CD4 count of 80, and died in August 1994. Because of the close epidemiological linkage, a consensus of all 5 sequences is presented here. [Kostrikis et al.(1995)]. Accession numbers U28683 (child); U28674, U28719 (father); U28677 (father's partner); U28665 (mother).
14) **ET.TP95001:** This study describes the distribution of HIV-1 subtypes in Ethiopia. HIV-1 RNA was collected from sera (from a majority of asymptomatic individuals) and RT-PRC amplified and sequenced directly. One subtype A and numerous subtype C sequences were found [Abebe et al.(1997)]. Accession number U88756.
15) **FR1.ID:** These 6 sequences are from members of the French military who are believed to have been infected while deployed outside of France (Djibouti, Guyana, and Central African Republic). Other sequences from this study were subtypes B, C, E, F, and unclassified. [Lasky et al.(1997)]. Accession numbers for subtype A were U58800–U58806 and U58778.
16) **FR2.ID:** These 6 subtype A sequences are from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in france were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession numbers Z95442, Z95446, Z95447, Z95448, Z95451 and Z95452.
17) **GA1.ID:** These 6 sequences are from Gabon. Two (G41, G135) are from 1988-1989 samples from patients with AIDS living in Franceville Gabon. VI685 is from a 1992 sample of an AIDS patient from the Libreville General Hospital. VI1076 is from a 1993 sample of an AIDS patient from the Libreville General Hospital. LBV2310 and LBV23 are from 1988 samples from asymptomatic individuals sampled from the general population. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession numbers X90914, LBV23; X90915, G135; X90917, G41; X90918, LBV2310; X90921, VI1076; X90924, VI685. See also subtypes C, D, F, G and O sequences from this same study.
18) **GH.D687:** A single sequence from an individual from Ghana. Virus was cocultured on PBMCs and the env gene was PCR amplified. Provided by Georg-Speyer Haus, Frankfurt, Germany (Dr. Ursula Dietrich). [Dietrich et al.(1993)]. Accession numbers L07652, X68407.

19) **GH2.ID:** These 7 sequences are from Ghana. Subtypes D and an A/G recombinant were also detected in this study [Takehisa et al.(1997a)]. Pol gene sequence is available for GH9 (U67040). Accession numbers for subtype A are U67051–U67054, U75457–U75459.
20) **GH3.ID:** These 13 sequences are from Ghana. Subtypes D and G were also detected in this study [Ishikawa et al.(1996)]. Two additional subtype A sequences are not included here (GH14 U67689 and GH17 U67690) because they were greater than 98% identical to sequences reported by Takehisa et al [Takehisa et al.(1997a)] and may be from the same patients, although labelled differently in the two studies (GH14 here 99% identical to GH15 by Takehisa; GH17 here 98.2% identical to GH16 by Takehisa). Accession numbers for subtype A are U67685–U67700.
21) **IN1.ID:** These two entries are from 1992 dried blood spot samples from Vellore near Madras, in Tamil Nadu state in southern India. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. Samples came from previously identified HIV seropositive homosexual men. Other samples from the same region were all sub (see C_IN4.). [Cassol et al.(1996)]. Accession numbers U53286 and U53291.
22) **IN2.GT6:** This sequence is from India. Seven other sequences from this publication were subtype C (see C_IN5.ID). [Tsuchie et al.(1993)]. Accession number D13425.
23) **KE.K89:** This sequence is named "KENYA" in the GenBank entry, but is identified as K89 in the original manuscript. It is a Kenyan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22943. A gag gene sequence from the same isolate is found with accession number L11774.
24) **KE.KEN-ID:** These 19 sequences were derived from patients who were part of a 1990–1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. [Janssens et al.(1994c)]. K976 (U12992) was listed as subtype unclassified in the paper, but seems to be subtype A in our analysis. Accession numbers for the subtype A sequences in this study: U12987–U13006.
25) **KE1.ID:** These 6 sequences were derived from patients who were part of a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from each patient were sequenced. Two other patients from this study had viral subtypes C and D. [Zachar et al.(1996a)]. Accession numbers U32658, U33763, U33764, U33766, U33767 and U34905.
26) **KE2.ID:** These 4 sequences are part of a set of 13 subtype A sequences are from Kenya. The other 9 subtype A sequences were too short to include here. Another 5 sequences from this set were found to be subtype D. The Q23 sequence is from a female recently infected with HIV-1, from Mombasa, Kenya. Blood was drawn on June 13, 1994 for the env region sequences [Poss et al.(1997)] and in July 1993 for a sequence of the complete genome of Q23 (unpublished 1998). Accession numbers AF004885-AF004891, AF03159-AF03161, AF004892, AF004895, AF004897-AF004899. Out of these 14 (13 A and 5 D), 12 were too short to be included (AF004885-AF004891).
27) **LB1.ID:** These 10 subtype A sequences are from a study of 25 sequences from a study of multiple HIV-1 subtypes in Lebanon [Pieniazek et al.(1998)]. Of the 26 samples, 25 were classified as HIV-1: 10 were subtype B, 10 were subtype A, 1 was subtype C, 1 was subtype D and 3 were recombinants or untyped. The other sample was classified as HIV-2 subtype B. Accession numbers AF025691, AF025693, AF025695, AF025699, AF025700, AF025703, AF025709, AF025710, AF025711 and AF025712 are HIV-1 subtype A.
28) **ML.3665** This subtype A sequence is from a study that looks at the prevelance of different subtypes of HIV-1 and HIV-2 circulating in female commercial workers in Bamako, the capital city of Mali [Peeters et al.(1998)]. A total of 176 CSWs were tested and 81 were HIV infected. Of the 81, 63 were infected with HIV-1, 7 were infected with HIV-2 and 11 were dually infected with HIV-1 and HIV-2. HMA assays indicated that 80 percent of HIV-1 infections were with subtype A virus. Only 9 viruses, with ambiguous HMA results, were sequenced. Out of these 9 sequences one was subtype A, one was subtype D and 7 were subtype G. Accession number Y14364.

29) **NL1.ID:** These 13 sequences are from recent immigrants to The Netherlands from various countries. The first two letters of the ID represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76877, GH902304; L76903, GH9401488; L76883, GH915200; L76913, GH9501283; L76893, GH929927; L76896, ZR9303337; L76870, RW890388; L76875, RW893568; L76905, TZ9401664; L76881, KE913514; L76891, UG928308; L76887, AO924646; L76889, TZ925825
30) **RU1.ID:** These 2 sequences are from Russia. Bobkov et al. 1996 Unpublished. Accession numbers: U33098, IVA6; U33097, GAN1.
31) **RU2.ID:** These two sequences are from patients living in Kaliningrad, Russia, [Leitner et al.(1996b)]. RU21 is a 40 year old male heterosexual, believed to have become infected in the Ivory Coast in 1988. RU24 is a 44 year old heterosexual male, believed to have become infected in Democratic Republic of Congo (formerly Zaire). Sequences were determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. Although RU24 is listed in the publication as unclassified subtype, this sequence clusters in phylogenetic analyses with SAS (U43171) and BJ193 (U61859) which are classified as subtype A. Because of the A-outlier nature of the RU24 env sequence, the authors also sequenced the gag P17 region of this sample, and found that it fell with subtype A (sequence not submitted to the databases). RU21 is a more typical subtype A. Accession numbers U69656 and U69658.
32) **RU3.IID:** These 12 highly related sequences are from a set of 41 sequences from 12 IV drug users in Russia. Uncultured PBMC DNA was PCR amplified and cloned and individual clones sequenced. [Bobkov et al.(1997a)]. Although the sequences are similar enough to each other to suggest direct epidemiological linkage, no such linkage, other than the fact that they are all IV drug users, is indicated. Gag p17-24 and Env V4-V5 were also sequenced. Accession numbers U93611, U93612, U93614, U93616, U93618, U93620, U93622, U93624, U93627, U93629, U93631, U93633, U93635, U93636, U93637, U93638, U93642, U93643, U93645, U93646, U93647, U93648, U93650, U93651, U93655, U93656, U93657, U93658, U93659, U93660, U93661, U93665, U93666, U93668, U93671, U93673, U93675, U93676, U93677, U93678 and U93679. See also the A/B recombinant HIV-1 recently identified in Kaliningrad [Liitsola et al.(1998)].
33) **RW.564C:** This sequence represents 10 identical sequences generated from PCR amplified plasma RNA from one of three infants in a Dutch mother/infant study. Patient pair 564 was from Rwanda. A sample was collected from the infant at 30 months of age. Samples were also collected from the mother at 12 and 30 months after the birth. Mother sequences are not included in this consensus. [Mulder-Kampinga et al.(1993)], [Mulder-Kampinga et al.(1995)], [Lepage et al.(1996)], and [Kampinga et al.(1997)]. The child 564 Env sequence is from the entry with Accession number Z47881. Mother 564 sequences are in entries with Accession numbers Z47882–Z47902. Mother sequences are not included in this alignment. Gag gene sequences from mother/child pairs are also available in entries with accession numbers Z47903–Z47911, Z47912–Z47928, Z47929–Z47935 and Z47936–Z47950. The second mother/child pair was from the Netherlands, see G_NL.127C. The third mother/infant pair in this study was from the Netherlands, see B_NL.114C.
34) **RW.SF1703:** This sequence is from Rwandan isolate sf170, a biologically active clone reported to be macrophage-tropic. [Cheng-Mayer et al.(1988)]. See also U61870, which is not reported to be from SF170, but is greater than 99% identical to it. From this same isolate; 537 bases of the 5' LTR are in M66534, 619 bases of nef are in M81729 and 508 bases of tat and rev are in M66535. For env, the Accession number is M66533.
35) **RW1.W2RW-ID:** These are six of seven sequences from asymptomatic individuals from Rwanda sampled in 1992. The seventh sequence (92RW009) has now been sequenced over the complete genome and found to be A/C recombinant. Thus it has been moved to the U_RW section. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are: [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession numbers U08630–U08640, U08645, U08647–U08665, U08763–U08766, and U08793–U08794. One of these sequences may be mislabelled in the database; U08634 is labelled as patient 016, but is identical to sequences from patient

008. Sequences from samples 92RW020 and 92RW021 were greater than 98% identical to each other, so only 92RW021 is presented here. 92RW20 has been reported to be NSI and use the CCR5 coreceptor [Dittmar et al.(1997)].

36) **RW2-ID:** Nine consensus sequences from Rwanda. Saah, A. Unpublished 1994. Accession numbers U23216–U23373.

37) **RW3.PV:** Bex,F. et al. Unpublished. These five sequences are from Rwandese patients with AIDS. The sequencing was done by the EEC Centralized Facility for HIV genome characterization, Georg-Speyer-Haus, Frankfurt, Germany. The complete envelope gene for PVP1 is available from a clone obtained after short-term co-culture on donor PBMCs. Two other shorter sequences of PVP1 env direct from patient PBMCs are also available. Accession numbers L07082–L07091. L07088 and L07089 were withdrawn from the databases by the authors, who felt they may represent PCR artifacts.

38) **RW4.ID:** These 8 consensus sequences and 2 individual sequences, are from 7 infants and 3 mothers in a study of mother-infant transmission in Rwanda [Kampinga et al.(1997)], [Lepage et al.(1996)], [Mulder-Kampinga et al.(1995)] and [Simonon et al.(1994)]. Mother 566 was apparently infected with both subtype A and subtype C HIV-1, but the env regions from the child clones were all subtype A. See also C_RW1.ID. Accession numbers for child 566 are Z76160–Z76161, Z76167–Z76168, Z76169–Z76176, Z76233–Z76248, Z76262–Z76273, Z76708-Z76716 and Z76717–Z76724; mother 730, Z76353–Z76362; child 564, Z76074–Z76083; mother 226, Z76046; child 538, Z76134–Z76143, Z76373–Z76382, Z76393–Z76412; child 074, Z75958; child 082, Z75998–Z76009, Z76650; child 081, Z75959–Z75968; child 618, Z76198–Z76207; mother 439, Z76048–Z76057, Z76064–Z76068 and Z76070, Z75979-Z75988.

39) **SE.H4:** This sequence is from an infant, born in Sweden to a woman who was believed to have been infected sexually in Uganda [Contag et al.(1997)]. HIV-1 isolation from the mothers was conducted during the three trimesters, a few days after deleivery and 6 months after parturition. The children were born between June 1989 and August 1992 and were followed by virus isolation at birth and at 3, 6, 12 and 18 months of age unless circumstances called for an extra sample. Breast-feeding was denied by all of the women described. See also B_SE5.ID#, C_SE2.ID#, D_SE.H3 and E_SE.H1. Accession numbers U56274–U56283 and U56328.

40) **SE1.ID:** These 24 sequences are from a study of 270 HIV-1 infected individuals living in Sweden [Alaeus et al.(1997)]. 80 of these 270 were thought to have been infected in Africa, prior to moving to Sweden, or infected directly by someone who had just immigrated from Africa. Of these 80, 75 blood samples were available from 33 men and 42 women, from 15 different African countries. The 24 subtype A sequences were from individuals who were thought to have been infected in Tanzania (SE8538 U76147), Uganda (SE6882 U76140, SE7172 U76118, SE7535 U76154, SE8891 U76160, SE8553 U76149, SE8889 U76170, SE7823 U76132, SE9572 U76182, SE7888 U76119 SE7889 U76143, SE7441 U76137, SE9281 U76175, SE7727 U76125, SE8735 U76159 and SE8131 U76121), Somalia (SE7253 U76165), Kenya (SE8566 U76186, SE8132 U76145, SE7531 U76141 and SE8876 U76168), Ethiopia (SE9488 U76180), Ivory Coast (SE7812 U76142), Mauritania (SE9562 U76181) and Mozambique (SE8551 U76151). Two individuals (SE7108 U76131 and SE7019 U76138) were epidemiologically linked to others (SE8566 and SE7531 respectively) and are not included in this alignment.

41) **SG1.ID:** This sequence is from a study done on HIV-1 sequences from Singapore. Other sequences in this set were subtypes B, C and E. Sethoe et al in press 1998.

42) **SN1.ID:** These 10 sequences are from a study done on individuals infected with non-B clade virus who were randomly obtained from a cohort of registered commercial sex workers in Senegal West Africa [Cao et al.(1997)]. PBMC were seperated, cryopreserved and shipped to USA for CTL studies. Of the 14 sequences evaluated 10 were subtype A, three were subtype G and 1 was subtype C. Accession numbers for the set are AF020819–AF020832.

43) **TW1.ID:** These 2 sequences are from Taiwan. Another sequence in the set was subtype A/G recombinant, clustering with subtype G in the Gag p24 region [Lee et al.(1998)]. Patient A1 was a 38 year old male sailor who was found to be seropositive in 1989, and was believed to be infected via heterosexual contact. Patient A3 was a 59 year old woman identified as seropositive in 1995 and also infected heteroseually. Accession numbers AF020600 and AF020602. Gag p24 sequences are found with accession numbers AF020948, AF020950.

44) **TZ2.ID:** These two sequences were from patients at a clinic in Dar es Salaam, Tanzania. The individuals from which the virus was cultured showed clinical signs of AIDS, and the year of viral isolation was

1988. Viral cDNA was PCR amplified from donor PBMC, and one cloned PCR product per donor was sequenced. [Siwka et al.(1994)]. Accession numbers U12408, U12409.

45) **TZ3.ID:** These 4 sequences are from the Mara region of rural northwest Tanzania. [Robbins et al.(1996)]. Subtype D was also found in this study. Accession numbers U61875–U61878.
46) **TZ4.ID:** These 25 sequences are part of a set of 86 sequences from samples collected from symptomatic AIDS patients in December 1995 at Mbeya Referal Hospital in southwest Tanzania. Uncultured PBMC DNA was PCR amplifed and directly sequenced. Serotyping was also done on all samples to test the ability of serology to subtype these A, C, D and recombinant HIV-1 isolates [Hoelscher et al.(1997)].
47) **UA1.ID:** These 17 sequences are from a study of molecular epidemiology of an HIV-1 subtype A subcluster among injection drug users in Southern Ukraine. Recently another IVDU epidemic in Kaliningrad was found to be caused by HIV-1 that is subtype A in gag and subtype B in env [Liitsola et al.(1998)]. The subtype A gag region was closely related to the subtype A gag of HIV-1 from this Ukraine epidemic. Accession numbers AF025580–AF025596.
48) **UG.1033:** This sequence is a consensus sequence of blood and CSF samples taken from a Ugandan patient 1033, CDC class IV-A. [Keys et al.(1993)]. Accession numbers Z23177, Z23182–Z23184, and Z23220–Z23223.
49) **UG.92UG037:** This sequence is from a complete genome PCR amplified from proviral DNA. The patient was a 31 year old asymptomatic female from Entebe, Uganda. [Gao et al.(1996b)]. Accession number U51190. See also U09124, U09127, U15119.
50) **UG.964:** A single sequence used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. The sequence was derived from PCR amplified DNA from peripheral blood leukocytes. The patient was an asymptomatic individual from Uganda. [Pestano et al.(1995)]. Accession number U11599. See also B_US17.ID, C_UG1.45, and D_UG7.ID.
51) **UG.U455:** This sequence is from the 1985 Ugandan isolate U455; the complete genomic sequence is available. [Oram et al.(1990)]. The env ORF in this sequence is interrupted by an in-frame stop codon beyond the COOH end of the V5 region. Accession number M62320.
52) **UG.UG06:** This sequence is from blood collected from the Mulago Teaching Hospital in Kampala, Uganda. Viral RNA was harvested after 10-14 days of coculture with donor PBMCs and reverse-transcribed with AMV-RT. The env V3 region was pCR amplifed and cloned. This sequence is from an individual clone. [Atkin et al.(1993)], [Pestano et al.(1993)]. Accession number M98503.
53) **UG1.W2UG-ID:** Three sequences from asymptomatic individuals from Uganda in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are: [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession numbers U08666–U08669, U08767–U08770, U08788–U08792, U08795 and U09125.
54) **UG2-ID:** These 11 sequences are part of a set of sequences derived from 22 Ugandans who were attending an AIDS clinic, sampled in 1990. Consensus, PCR-clones, peripheral blood DNA. [Albert et al.(1992)]. Accession numbers M98902–M98905, M98908–M98910, M98914–M98917, M98919, M98924–M98928, M98938–M98941, M98946–M98966, and M98976–M98978.
55) **UG4.UG-ID:** Two Ugandan sequences from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22957 and L22951.
56) **UG5.ID:** These 8 sequences are from Gulu, northern Uganda. They are from direct sequence of PCR product amplified from uncultured PBMCs. Blood samples were drawn from 217 pregnant women attending a clinic in Gulu, northern Uganda. Ages ranged from 17 to 37 years. The 29 seropositive women (13.4% of the 217 tested) were all asymptomatic. [Buonaguro et al.(1995)]. Accession numbers U44878–U44880, U44882, U44883 and U44885–U44887. Two subtype D sequences were also found in this study (see D_UG8).
57) **UG6.ID:** These sequences are from Uganda. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Accession numbers AF000496, AF000497, AF000498, AF000499, AF000500, AF000501, AF000502, AF000503,

AF000504, AF000505, AF000506, AF000507, AF000508, AF000509, AF000510, AF000511, AF000512, AF000513, AF000514, AF000515, AF000516

58) **ZA.134:** This sequence is from a study of 72 seropositive women from South Africa [Moodley et al.(1998)]. The mean age was 26 years. Patient 134 was asymptomatic. Data from this study shows the dramatic growth of HIV-1 subtype-C in this population in South Africa. See also C_ZA3.ID and B_ZA.0117. Accession number AF053286.

59) **ZR1.ID:** These ten sequences are part of a set of 14 A and D sequences from women from Democratic Republic of Congo (formerly Zaire); 8 were healthy, 4 showed minor signs of illness, and 2 had AIDS. PCR-direct, peripheral blood DNA. [Potts et al.(1993a)]. Accession numbers L19624–L19626, L19628–L19630, L19632–L19634, and L19636.

60) **ZR2.ID:** These 4 sequences are from Democratic Republic of Congo (formerly Zaire). They are unpublished, by M. Reitz et al. Accession numbers U43097–U43100.

B Subtype

At this time we have included viral sequences from 1289 HIV-1 infected individuals associated with HIV-1 subtype B. The B subtype consensus sequence (B_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position in an alignment of these sequences. Please note that none of the studies which have published sequences of only the V3 loop sequences are included here, as the DNA sequences were deemed too short for phylogenetic analyses. (For example, LaRosa G, et al., *Science* **249**:932–935 (1990) and Fouchier RAM, et al., *J. Virol.* **66**:3183–3187 (1992).)

1) **AR.21281:** This sequence is from direct sequencing of PCR product from uncultured PBMCs, from a 1993 sample from Buenos Aires, Argentina. The patient had AIDS and reported promiscuous heterosexual risk behavior. Two other samples taken from unrelated patients in 1993 were subtypes F and one was found to be a subtype B/F recombinant. [Marquina et al.(1996)]. Accession number U68525.
2) **AR1.ID:** These 11 sequences are from Rosario, Argentina. A total of 24 patients from different risk groups visiting a clinic in Rosario were included in this study. Of the 14 sequences determined, 11 were found to belong to subtype B and 3 were found to belong to subtype F. DNA was extracted from whole blood and PCR amplified. PCR products were directly sequenced. Subtypes of all 24 patients were tested by HMA. [Campodonico et al.(1996)]. Accession numbers U37030, U37031 and U37034–U37042.
3) **AU.979H** This sequence is a subtype B env sequence from Australia [Wang et al.(1998)]. This paper discusses a patient infected with a rare HIV-1 strain with a cysteine at position 13 within the V3 loop and a GHI insertion on the NH2 side of the loop tip. Accession numbers AF052979–AF053001.
4) **AU1.ID:** Put forth as evidence that coinfection by multiple HIV-1 strains can occur in vivo, these three concensus (MRC1,MRC2, and MRC3) come from an Australian homosexual male who had been infected by more than one sexual partner, and harbored three distinct strains of HIV-1 B. The authors also found recombinant sequences, not included here. The sequences were PCR amplified from plasma RNA and PBMC DNA. [Zhu et al.(1995)]. Accession numbers U16372–U16388.
5) **AU2.C18CG:** This sequence is one of a group relating to an Australian blood donor infected with HIV-1 and six Australian recipients, all of whom remain symptom free with normal CD4 counts 10 to 14 years after infection. [Deacon et al.(1995)]. Samples from only the donor, D36 (U37271), and two patients, C18 (U37267, U37270) and C98 (U37268, U37269), appear to have been sequenced. These sequences have deletions in the nef gene and in the region of overlap of nef and the U3 region of LTR. The authors point to the importance of NEF or the U3 region of LTR in determining the pathogenicity of HIV-1 and suggest this strain of HIV-1 as a possible basis for a live attenuated vaccine. The complete genome of the virus from recipient C18 is in the entry with accession number U37270. Other complete genomes from this set are found with accession numbers AF042100–AF042106.
6) **AU3.ID:** In this analysis of transmitting and non-transmitting mothers and the infants to whom the virus was transmitted, the authors claim that differences in variability of the env V3 loop crown octapeptide (HIGPGRAF in this clone) were significantly correlated with vertical transmission. Sequences were determined by PCR directly from uncultured PBMCs and cloned PCR products. Only seven of the sequences are presented here: from infants, and nontransmitting mothers from which at least 250 bp was sequenced. 1089, 1063, 961 and JW are the infants. Accession numbers for transmitting mothers and their infants are: U66627–U66633, U66638–U66645 and U66650–U66653. Accession numbers for nontransmitting or indeterminate mothers are: U66625, U66626, U66634–U66637, U66646–U66649 and U66654–U66660. Database entries for many of these sequences contain ”nnn” in error, the paper shows these positions as deletions, not unknown sequence. Nef sequences from the LW-JW mother-infant pair of long-term survivors were published in [Wang et al.(1997b)], [Wang et al.(1997a)], [Saksena et al.(1997)] with accession numbers U73339–U73369.
7) **BB1.ID:** These 3 sequences are from a study that was done on Barbados patients who tested negative for Leptospira infection, implicating other diseases [Roth98]. After doing a survey, 10 HIV-1 positive patients originally hospitalized during 1990-1994 and whose medical histories suggested HIV-1 illness at the time of Leptospira testing, were found to be HIV-1 infected with symptoms suggesting accute primary infection. Three of the 10 samples were successfully RT-PCR amplified from stored serum RNA. The LL6 PCR product was directly sequenced, the other two were cloned and sequenced. One sequence from each patient is included here. Accession numbers U80239, U80246 and U80247.

8) **BE.SIMI84** One of two cloned env sequences from a patient with AIDS from Belgium. A vaccinia construct that expresses this gene was created to vaccinate the patient's non-infected brother with the goal of immune therapy by adoptive transfer of lymphocytes. [Bex et al.(1994)]. Accession number L07421.
9) **BR.002con** This consensus sequence is from entries with accession numbers L35489–L35493. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. Ranjbar,S. et al. Unpublished (1994).
10) **BR.BZ** This sequence is from an individual in a Brazilian HIV cohort study. PBMC DNA was PCR amplified in two sequential rounds, and six cloned PCR products were sequenced on both strands. A single clone containing an uninterrupted envelope open reading frame was reported. [da Costa et al.(1995)]. Accession number U28336.
11) **BR1.ID:** These 21 sequences represent the B env subtype sequences found among 22 Brazilian outpatients with varying degrees of disease progression. They are consensus sequences from cloned PCR products. PCR was performed on PBMC DNA. [Potts et al.(1993b)]. Accession numbers for 21 of the 56 clones from which consensus sequences were calculated: L19225–L19236, L19240–L19246 and L20963. The other sequence was subtype F (L19237).
12) **BR2.W2BR-ID:** These 13 sequences are from individuals from Brazil. They are consensus sequences from cloned PCR products. Some of the clones were from cell-culture DNA, and some from cell-culture supernatant RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. [De Wolf et al.(1994)], [Osmanov et al.(1994)], [Gao et al.(1994a)]. Accession numbers U08670–U08714, U08771–U08778, U08780–U08782, U08792, U08796, U08797–U08800.
13) **BR3.RJ- or SP-ID:** These 32 sequences came from the Brazilian cities Rio de Janeiro and Sao Paulo. The sequences that are very short, containing V3 loop fragments insufficient for phylogenetic analysis, are not included here (5 of the 26). The full set included 20 viral sequences of the B subtype, an F subtype and a B-F recombinant (see subtypes F and U). The year of isolation for the sequences ranged from 1990–1992 for Rio de Janeiro, and 1992 for Sao Paulo. The only two with CD4+ cells < 200 were RJ636 and RJ27. The CDC clinical class ranged from II-IV. DNA extracted from PBMCs of HIV infected individuals was amplified, and the PCR product was directly sequenced. [Morgado et al.(1994)] [Sabino et al.(1994c)] and [Sabino et al.(1996)]. More recent unpublished sequences from the same isolates are also included here. Accession numbers U00400–U00401, U00403, U00405, U00407–U00414, U00416–U00418, U00421, U00424–U00425, U00427, U08975, U31586, U31587 and U31589–U31591.
14) **BR4.BZ-ID:** These 2 sequences are from seropositive Brazilian patients. Virus was cultured on donor PBMCs and proviral DNA was harvested from positive cultures. PCR was used to generate sequencing templates. [Louwagie et al.(1994)]. Accession numbers L22087 and L22088. The gag gene sequences from these same isolates are also available in L11752 and L11754. See also F_BR2.BZ-ID.
15) **BR5.ID:** These 10 sequences are from entries with accession numbers L19328–L19337. Bandea, C. I. Unpublished (1993).
16) **BR6.ID:** These six sequences are from patients living in cities in Brazil (P3, Sao Paulo; P4, P6 and P7, Bahia; P8, Parana; P9, Rio de Janeiro) and sampled between 1987 and 1989. Sequences were determined from directly sequenced PCR products (except P6 which was a cloned PCR product), after coculture of patient PBMCs with donor PBMCs. [Couto-Fernandez et al.(1994)]. Accession numbers X78512–X78517.
17) **BR7.ID:** This sequence is from the WHO isolate 92BR028 clone 8, from Brazil. It was isolated from a 35 year-old bisexual male from Salvador, Brazil in 1992.
18) **BR8.19b:** This subtype B sequence is from Brazil [Janini et al.(1998)]. This study describes a case of horizontal (heterosexual) and subsequent vertical (mother to infant) transmission of 2 HIV-1 subtypes, B and C [Janini et al.(1998)]. DNA sequence analysis of pol, gag and env genes confirmed the presence of subtypes B and C in 3 family members. Accession numbers for env, gag and pol genes of both subtypes are U83689–U83699. Subtype B env accessions are U83689, U83691 and U83693.
19) **BR9.ID:** These 10 subtype B sequences are from a study of the prevalence of GWG in the V3 loop tip in Brazil [Covas et al.(1998)]. PCR products were first screened for the Proline to Tryptophan variation via RFLP prior to sequencing. Overall prevalence of the GWG sequence as indicated by RFLP was 57%

(43 of 75). The prevalence in females (72%) was higher than that in males (32%) and newborns (40%). Accession numbers U80824–U80833.

20) **CA1.ID:** These 19 sequences are from 19 different Vancouver, Canada homosexuals represented in 36 database entries by N. Michael et al. Accession numbers U52888–U52906, U53103–U53119. Patients A and B (U52888–U52904) were described in [Michael et al.(1997)] as a normal-progressor rapid-progressor pair, with patient A being the rapid progressor. Only patient A sequence (U52889) is presented here, as patient B sequences were closely related. The C patients were local controls, also homosexuals from Vancouver, who are not well described in the publication. Patient A sequences from U52901 and U52902 are greater than 99% identical to JR-CSF over their entire length, and U52904 has some regions of identity to JR-CSF. Another linked pair in this set included patients C108 and C118, of which only C108 is presented here. Patient A died of AIDS-related P. carinii pneumonia on October 6, 1995, almost exactly 10 months after experiencing symptoms of primary HIV infection. Patient A was homozygous for for an HLA-DR1 allele previously found to be assosiated with rapid progression. Patient A never seroconverted for HIV, despite high viral load and the ability to seroconvert for hepatitis B after vaccination in 1990.
21) **CH1.ID:** These 19 sequences came from 24 individuals living in Geneva, Switzerland who were recently infected at the time of blood drawing. Samples were collected between January 1988 and September 1993. Sequences were determined directly from PCR products of uncultured PBMC DNA or serum cDNA. All subjects were asymptomatic, 19 subjects had p24 antigen levels ranging from 5 to 6,357 pg/ml and 5 subjects had no detectable p24 antigen. Two subjects were epidemiologically linked (K11 and K16) so only one of those two is presented here. Two other individuals showed identical DNA sequences over the entire V3 region (K53 and K77) so only one of them is presented here. Three other individuals (K13, K42 and P4) had sequences nearly identical to the LAI (IIIB) laboratory strain of HIV. Although the authors are convinced that these are not contaminants, and that a IIIB-like strain of HIV is circulating in Geneva, they are not included in this alignment. [Antonioli et al.(1995)]. Accession numbers U10957–U10980.
22) **CI.CI-22:** A single B subtype sequence from a set of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-22 was symptomatic. The C2V3 region is part of a 900 bp fragment that was sequenced for each individual. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3 clones were sequenced, and the consensus of those clones is presented here. [Janssens et al.(1994a)]. Accession numbers X72040–X72042.
23) **CM.CA5:** A single B subtype sequence from a set of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals, specifically, patient CA-5 was asymptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. [Nkengasong et al.(1994)]. Accession number X80452.
24) **CM.277** This sequence is from a 1994-1995 study of 211 Cameroonian AIDS patients [Takehisa et al.(1998)]. Of the 43 HIV samples sequenced, 17 were subtype A, 1 was subtype B, 2 were subtype C, 1 was subtype G. Accession number AF023083.
25) **CN.1798:** This sequence is from a dried blood spot collected in 1992 from the spouse of an IV drug user in China. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession number U53316.
26) **CN.RL42:** This sequence is from a complete genome from an asymptomatic IV drug user in China. [Graf et al.(1998)]. Accession number U71182.
27) **CN1.ID:** These 54 sequences are form the Yunnan Province, China. No information is yet available. Unpublished 1995, Y. Shao and H. Wolf. Several of these sequences (U20009, U20012, U20013, U20018, U20023, U20024) are greater than 96% identical to the SF2 strain of HIV-1 (see B_US.SF2). Accession numbers U20001–U20054.
28) **CU.94CU053:** This sequence is from a bisexual male, most probably infected via heterosexual contact in 1992, in Cuba. Virus was isolated in 1994, 2 years after seroconversion, by cocultivation of patient PBMCs with donor PBMCs. This isolate exhibits a rapid/high, syncytium-inducing phenotype. [Gomez et al.(1996)]. Accession number U48855.
29) **CY1.HO:** These sequences are from samples, like others in this study (see also subtypes A, C, F and I), which were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. PBMC DNA was PCR amplified and cloned. Individual clones were sequenced. Patient 04 was a 24 year old man, asymptomatic with a CD4 count of 516, who had lived abroad, and had been seropositive for at least 4 years. Patient

11 was a 29 year old homosexual man, symptomatic with a CD4 count of 277, and seropositive for at least 7 years. Patient 21 was a 38 year old bisexual man, asymptomatic with a CD4 count of 743, who was infected in Greece and seropositive for at least 4 years. Patient 25 was a 34 year old heterosexual man, asymptomatic with a CD4 count of 650, who had lived in the U.S. and was seropositive for at least 6 years. Patient 27 was a 20 year old homosexual man, asymptomatic with a CD4 count of 709, infected in Cyprus and seropositive for at least 2 years. Patient 28 was a 39 year old homosexual woman, asymptomatic with a CD4 count of 430, infected in Cyprus and seropositive for at least 1 year. Patient 29 was a 49 year old heterosexual man, asymptomatic with a CD4 count of 420, infected in Cyprus and seropositive for at least 2 years. Patient 39 was a 37 year old heterosexual man, asymptomatic with a CD4 count of 470, had lived in Greece and was seropositive for at least 5 years. Patient 40 was a 29 year old heterosexual woman, symptomatic with a CD4 count of 92, who had lived in the U.S. and was seropositive for at least 6 years. Patient 43 was a 36 year old homosexual man, symptomatic with a CD4 count of 396, who had lived in the U.K. and Greece and had been seropositive for at least 6 years. Patient 45 was a 32 year old heterosexual man, asymptomatic with a CD4 count of 453, who was infected in Cyprus and seropostitive for at least 1 year. Patient 46 was a 32 year old heterosexual man, whose partner had died of AIDS, asymptomatic with a CD4 count of 107, had lived in the U.K. and was seropositive for at least 4 years. Patient 48 was a 22 year old hemophiliac man, asymptomatic with a CD4 count of 276, who had been seropositive for at least 11 years. Patient 50 was 32 year old homosexual man, whose partner had AIDS, asymptomatic with a CD4 count of 315, who had been seropositive for at least 1 year. Accession numbers U28663, U28666 (04); U28664 (11); U28667–U28671 (21, 25, 27, 28, 29); U28675, U28676 (39, 40); U28678 (43); U28680–U28682 (45, 46, 48); U28684 (50).

30) **CZ.BTSPR:** This sequence is from a 32 year old homosexual man from Prague, Czech Republic. It was included as part of a study of HIV-1 sequences from the neighboring Slovak Republic. DNA from cocultured PBMCs was PCR amplified and the PCR product cloned. Eight clones were sequenced from each patient, although only one sequence is presented in the publication and in the database. It is not stated whether each single sequence is a consensus of the eight clones or a single clone. [Zachar et al.(1996b)]. Accession number U53195.
31) **DE.D31:** This sequence is from isolate D31. [Kreutz et al.(1992)]. It has never been well described, it is only shown as HIV1-D31 in figure 3 of the paper. The complete genome has been sequenced. Accession number U43096.
32) **DE.HAN:** This sequence is from an infectious clone from the German isolate DE.HAN-2. [Sauermann et al.(1990)]. Isolate HAN2 was isolated from a 39 year old homosexual German patient with AIDS related complex in 1986. This patient died from complications of AIDS in 1987. HAN2 was highly cytopathic in T cell line MT-2 it was able to productively infect MT-4, H9 or Jurkat cell lines. Genomic DNA from infected MT-2 cells was used to prepare a lambda phage genomic library. Two full-length clones, HAN2/2 and HAN2/3 were purified. HAN2/3 was used for DNA sequencing. Accession number U43141.
33) **DE.Serocons:** This sequence is a consensus sequence from 7 hemophilia patients who all received the same lot of beta-propiolactone and UV-light inactivated clotting factor in Bonn or Goetingen, Germany, from November 1989 to March 1990. The virus and the patients have been extensively studied over time, since initial seroconversion. The sequences which were combined to create the consensus were from proviral DNA from cultured PBMCs, PCR amplified and cloned. [Kasper et al.(1994)]. Accession numbers S76444 and S76446.
34) **DE1.ID:** These 7 sequences are from a Neurology thesis by I. Weber of Rostock, Germany. They are from blood and CSF specimens from 6 patients. For each of the patients, phylogenetic analysis showed that blood and CSF sequences were more similar to each other than to other database sequences. For one patient, one of the two blood sequences was different enough from another blood and CSF pair to be included here. Accession numbers Z78482, Z78485-Z78493.
35) **DE2.ID:** These 4 sequences are from a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and 6 Scottish intravenous drug users. The sequences were used in a study of HIV-1 vpr, vpu, and env V3 regions and how they vary between risk groups. [Kuiken et al.(1996b)]. Accession numbers Z68529, Z68530, Z68537 and Z68538.

36) **ES.ID:** These 36 sequences are from 41 patients sampled in Madrid, Spain between 1985 and 1991. Proviral DNA was extracted from uncultured patient PBMCs and the C2V3 region was PCR amplified. The PCR products were directly sequenced. Two of the sequences reported in this set (D22-28 and D22-48) were 99.5% identical to the LAI (IIIB) lab strain of HIV-1 and are not included here. 3 other goups of sequences had members that were greater than 98% identical to each other (R1, R2 and R3; THF13-2, THF12-24; S1, S4) and only one of each of them is presented here. [Quinones-Mateu et al.(1996)]. Accession numbers U40533–U40552 and U45286–U45307.

37) **ES.S61:** This sequence is from a 1989 blood sample from a 4 year-old boy from Madrid, Spain with CDC stage P2CD2 disease. Virus was cocultured on PBMCs and MT-2 cells prior to sequencing. The SI/NSI pheonotype of this isolate on MT-2 cells was traced to a single amino acid change in the V3 loop [Sanchez-Palomino et al.(1993)] and [Olivares et al.(1997)]. Accession numbers L04604, L04605, L04606 and L05659.

38) **FR.J91:** This sequence is from one of the JBB clones from the French patient Bru. [Wain-Hobson et al.(1991)] and [Guo et al.(1991)]. Accession numbers X57449–X57459 and X57461.

39) **FR.LAI:** This sequence is from the French isolate LAI (formerly BRU) which is also referred to as IIIB. [Wain-Hobson et al.(1985)]. Also see: [Alizon et al.(1986)], [Lukashov & Goudsmit(1995)] and [Wain-Hobson et al.(1991)]. Accession numbers K02013, L23090–L23103, X01762, L48380–L48399, M64178–M64223, M64406–M64415 and M64768–M64775. Other sequences which are of this type include: PV22, K02083; MFA, M33943 [Stevenson et al.(1990)]; F12, Z11530; BH8, K02011; BH10, M15654; TH4, L31963; MCK1, D86068; PM213, D86069; F12CG, Z11530; LL13, U80242; and HXB, AF033819, K03455, M38432 and M14100. The variation of the IIIB isolate in culture was studied by [Lockey et al.(1996)], Accession numbers U54647, U54649, U54651, U54653, U54655, U54657, U54659, U54665, U54667, U54681, U54683, U54685 and U54689. The variation of IIIB/LAI in 9 years of infection in a chimpanzee has been studied by [Wei & Fultz(1998)], Accession numbers U56866–U56883 and U56888–U56899. The IIIB/LAI isolate of HIV-1 has also been extensively studied in cases such as the infected lab worker. See for example [Reitz et al.(1994)], [Pincus et al.(1994)] U12030–U12055. The tropism of isolates from the lab worker for primary PBMCs and failure to grow in T-cell lines was localized to the V3-loop by Lishan Su et al. [Su et al.(1997)]. Recombinant virus pNL4-3, with envelope from LAI(BRU) and gag-pol from NY5 has also been studied: [Adachi et al.(1986)] Accession number M19921, [Duensing et al.(1995)] Accession number L42371 and [Salminen et al.(1995)] Accession number U26942. Other database entries with IIIB-LAI sequences can be found in the patented sequences section of GenBank, in the cloning vector section, and in the primate section (for example U19867, A00647, A04321 and M18404).

40) **FR1.ID:** These 4 sequences are from Toulouse, France. In this study, 4 mother-infant pairs were followed during pregnancy and after birth. The inter- and intra-patient sequence similarities of this set of 308 sequences has been controversial, because some infant sequences were identical to sequences from other mothers. For purposes of this V3 section, only one sequence from each of the 4 infants is presented here. [Briant et al.(1995)], [Korber et al.(1995)] and [Learn et al.(1996)]. Database entries for all 308 sequences are found with accession numbers U24717-U24999 and U25001-U25025.

41) **FR2.ID:** These 20 sequences are from members of the French military who are for the most part believed to have been infected while deployed outside of France (Chad, Djibouti, Gabon, Guyana, Mayotte and Cameroon). An additional sequence (FRMP040, U58787) was listed as subtype C in the paper, but clustered with subtype B in analysis done at the HIV Database and it has been listed as subtype unclassified until more information is available. Other sequences from this study were subtypes A, C, E, F, and unclassified. [Lasky et al.(1997)]. Accession numbers for subtype B were U58808–U58826 and U58777.

42) **FR3.ID:** These 11 sequences are from individuals from France with primary HIV-1 infection during the peak of viremia. All of these are subtype B sequences. Ataman-Onal et al unpublished (1998). Accession numbers AF041125–AF041135.

43) **FR4.ID:** These 3 subtype B sequences are from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in france were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession numbers Z95455, Z95456 and Z95460

44) **GA.OYI:** This sequence is from the Gabonese isolate OYI (designated elsewhere as isolate 397), isolated from a healthy HIV-1 infected individual. GA.OYI appears to have been the first viral sequence from Africa that phylogenetically clustered with North American viruses. [Huet et al.(1989)]. Accession number M26727.
45) **GB.AIT:** This sequence is from an individual at the time of seroconversion. Proviral DNA was extracted from PBMCs from a patient who was viraemic and had an equivocal HIV-1 antibody status, and the env V3 region was PCR amplified. The PCR products were cloned and the DNA sequence determined for 15 clones. These data showed that the V3 region contained only limited sequence heterogeneity with a major variant (shown here) accounting for 66% of the protein quasispecies present. [Ait-Khaled & Emery(1993)]. Accession number S69598.
46) **GB.CAM1:** This sequence is from the British isolate CAM1. McIntosh A, and Karpas A, Thesis (1991), Cambridge University, England. Accession numbers D10112, D00917.
47) **GB.GB8** This subtype B sequence is from a study in which entire env gene (gp160) of GB8, a British HIV-1 isolate, was cloned, sequenced and aligned with other reference strains [Vella et al.(1995)]. Accession number Y13716.
48) **GB.Man** This sequence was PCR amplified from the 1959 "Manchester sailor" kidney tissue. The sequence of the complete genome is available and clusters with subtype B contemporary HIV-1 sequences. [Zhu & Ho(1995)]. Accession number U23487.
49) **GB.V-ID:** A set of six sequences from a study of hemophiliacs from Scotland who were originally thought to have been infected by the same batch of factor VIII. (ScV12 is a sequence from a hemophiliac from the U.S., included as a control). All are consensus sequences of multiple direct PCR sequences obtained from limiting dilution of PBMCs. The Scottish hemophiliacs were infected in 1984 and the PBMCs were obtained for analysis in 1989. Although the samples were potentially related, they were deemed sufficiently divergent in this region for inclusion in this set. [Simmonds et al.(1990)], and [Balfe et al.(1990)]. Accession numbers M61327–M61346 and M61391–M61407. Database entries with accession numbers M84240–M84317 are more sequences from patient 82, taken over the period from 1984–1991. [Holmes et al.(1992)], [Leigh Brown & Cleland(1996)]. Database entries with accession numbers L13488–L13497 are also from these patients [Zhang et al.(1993)], as are U58393–U58465 [Cleland et al.(1996)], [Ludlam et al.(1985)]. Gag p17 genes from the same population were published in [LeighBrown(1997)].
50) **GB1.CPHL1:** This is a consensus from the British isolate 93–08020, clones 1, 4, 7, 18, 19 and 43. It was referred to as 93–08020 in [Arnold et al.(1995c)] and was isolated from the patient referred to as CPHL1 in [Arnold et al.(1995a)]. CPHL1 is a surgeon and CPHL2 was a patient of his in 1986, approximately 7 years prior to sampling for this study. Because sequences from CPHL1 and CPHL2 are no more similar to each other than to sequences from the general population, transmission cannot be concluded, and both sequences are included in this alignment. Accession numbers U21100 (clone 1) and U23112–U23116 (clones 18, 19, 4, 43 and 7 respectively).
51) **GB2.CPHL2:** This is a consensus from the British isolate 93–17305, clones 3, 11, 18 and 25 [Arnold et al.(1995c)]. It was isolated from the patient referred to as CPHL2 in [Arnold et al.(1995a)]. Accession numbers U23117–U23120 (clones 11, 18, 25 and 3 respectively).
52) **GB3.ID:** The CPHL7 sequence is a sequence from the British isolate 94–24612, clone 13 [Arnold et al.(1995c)]. It was isolated from the patient referred to as CPHL7 in [Arnold et al.(1995a)]. Accession number U23126. U23127 is a second clone from this same isolate. Sequences from three other patients epidemiologically linked to CPHL7 (CPHL6, accession numbers U23130–U23132; CPHL8, U23128–U23129; CPHL9, U23133–U23135) are not included in this alignment. The 4995 sequence is from entries with accession numbers U23136–U23138.
53) **GB4.ID:** These eight sequences are from British isolates from St. Bartholomew's Hospital, London (M23470, M26864, M30156, M37677 and M37658) and Hammersmith Hospital, London (AC, JB and WB). Sequences were determined from cloned PCR products from PCR amplified DNA from either cocultured (M23470 and M26864) or uncultured (M30156, M37677, AC, JB and WB) patient PBMC proviral DNA. [Douglas et al.(1996)]. Complete envelope gp160 sequences were determined for at least one clone from each patient. Ugandan samples also sequenced in this report were subtypes D or D/A recombinant. Accession numbers for London samples were U36859–U36864, U36869, U36870, U36872–U36880 and U36882.

54) **GB5.ID:** These 11 sequences are from Scotland. They are part of a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and six Scottish intravenous drug users, from which regions of vpr, vpu and env were sequenced. The authors found consistent differences in the sequences between the homosexuals and IV drug users. Only 34 of the 47 patients' sequences are reported in the publication. [Kuiken et al.(1996b)]. See also B_NL12 and B_DE2 sets.
55) **GB6.ID:** These 5 subtype B sequences were obtained from a study done on 15 individuals. Eleven of the specimens were from heterosexuals, two were from injecting drug users and one was from a homosexual. Two specimens were from one woman whose risk behavior was not known, and who seemed to be dually infected with subtype B and the AE(CM240) circulating recombinant form. The specimens were collected in England from individuals whose history indicated that they had become infected in Southeast Asia, particularly Thailand [Belda98]. Accession numbers for the sequences are AJ224176-AJ224200.
56) **GM.GM6:** A sequence from Gambia, as yet unpublished. Bobkov et al. 1996 unpublished. Accession number U33101. See also Gambian sequences of subtypes C and J.
57) **HT.RF:** This sequence is from the full-length lambda clone HAT-3, from Haitian isolate RF. RF is from a 28 year old Haitian male who had moved to the United States at age 25, in 1980. He had no history of IV drug use, homosexuality or blood transfusions. In October 1983 he had 20 lb weight loss, giardia with diarrhea, thrush, and diffuse lymphadenopathy. His CD4/CD8 ratio was 0.08. He died in December, 1983. Primary culture from a November 1983 blood sample was co-cultured on HUT-78 cells. [Reitz et al.(1992)] [Starcich et al.(1986)] [Popovic et al.(1984)]. Accession numbers M17451 and M12508.
58) **HT1.D-ID:** These seven sequences are from Haitians, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratories of Dr. Beatrice Hahn at the University of Alabama, and Dr. Marcia Kalish at the Centers for Disease Control, Atlanta, GA. Except for D2HA590, the full gp160 was sequenced from clones derived from expanded culture stocks. D2HA590 is a direct sequence from PCR amplified DNA from expanded culture. The sequence ID numbers are abbreviated, for example D2HA590 can be read as DAIDS sequence (D), isolated in 1992 (2), Haitian (HA), patient 301590 (590). Full length env for some of these have been expressed [Gao et al.(1996a)]. Accession numbers: U08441–U08447, U04900. Both U08441 and U08442 are sequences from patient HT1.D1HA651 and are identical over the region of interest. Accession numbers for additional clones derived from these patients: U04901–U04906.
59) **HT2.H-ID:** These 25 sequences are from Haitians. All sequences were PCR amplified from the infected individuals PBMCs, and this set includes direct sequences of PCR amplification products, consensus sequences of multiple clones of PCR products plus one direct sequence, and single clones of PCR products. Full length env for some of these have been expressed [Gao et al.(1996a)]. These sequences were provided by the Centers for Disease Control, Atlanta, GA USA (Dr. Chin-Yih Ou), and John Hopkins University School of Hygiene and Public Health, Balimore, MD USA (Dr. Neal Halsy), and the Centers for Development and Health, Complexe Medico Sociale de la Cite Soleil, Port-au-Prince, Haiti (Dr. Reginald Boulos). Accession numbers L07145–L07161, L07163–L07165, L07167–L07207, L07209–L07239, L07241–L07246, U08441–U08447.
60) **ID.1701:** This sequence is from a dried blood spot collected in 1992 from a male homosexual patient in Indonesia. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession number U53317.
61) **ID1.ID:** These 7 sequences are from a set of 14 sequences from Indonesia [Porter et al.(1997)]. Accession numbers U68195–U68201. Subtype E was also identified in 7 other samples from Indonesia in this study. PCR products were directly sequenced from either uncultured PBMC DNA or cocultured PBMC DNA.
62) **IN.IND9:** This sequence was from a heterosexually infected patient from New Delhi, India. DNA was isolated from cocultured PBMCs after one week of culture. PCR product was cloned and a single clone was sequenced. [Tripathy et al.(1996)]. Accession number U31364. See also C_IN3.ID.
63) **IN1.ID:** These four sequences were isolated in Hyderabad, Andhra Pradesh, in southern India. The C2V3 region of env was amplified by nested priming from DNA from PBLs from fresh blood samples. Date of sampling and health status of HIV-1 infected individuals is unknown. [Baskar et al.(1994)]. Accession numbers L29091–L29094.
64) **IT.ID:** These two sequences are consensus sequences from 4 clones each. They were obtained from PCR-amplified proviral DNA from Langerhans cells from skin patches from a deceased AIDS victim

in Italy [Sala et al.(1995)]. Small V1-V2 region sequences and V3-loop sequences from the same skin samples were published in [Sala et al.(1994)]. Entries with accession numbers U20670–U20677 were used here. Entries with accession numbers Z34376–Z34458, Z34470–Z34513 and Z34515 were V1-V2 and V3-loop sequences from the same patient.

65) **IT.PD:** This sequence is from the thymus of a 26 year old male with CDC stage III disease. Proviral DNA was PCR amplified from genomic DNA extracted from patient thymocytes, and the PCR product was directly sequenced. A V3 sequence from PBMC proviral DNA was also determined, as were gp41 sequences from both thymus and blood. [Calabro et al.(1995)]. Accession numbers U09254–U09255.
66) **IT.RM1:** This sequence is from a patient from Milan, Italy who was homozygous for the delta-32 deletion in CCR5 [Balotta et al.(1997b)]. Accession number U92491.
67) **IT1.ID:** These 10 sequences are from infants infected in utero. The sequences came from PCR amplified DNA of uncultured PBMCs, PCR amplified DNA of cultured PBMCs, or from RNA from serum collected at or shortly after delivery. [Scarlatti et al.(1993)] and [Halapi et al.(1997)]. Accession numbers L08277–L08286. Sequences from the mothers of these infants are also available in entries with accession numbers L08287–L08372 and more sequences are available with accession numbers AF023344–AF023419.
68) **IT2.ID:** These 3 sequences are from unpublished sequences in entries with accession numbers X92424–X92426.
69) **IT3.ID:** These 12 sequences are consensus sequences from 12 individual patients in a study of long term non-progressors and rapid progressors, from Milan, Italy [Balotta et al.(1997a)]. Accession numbers U95381–U95497.
70) **IT4.ID:** These 10 subtype B sequences are from a set of 450 subtype B sequences from a mother-infant study in which maternal samples were collected within seven days of deleivery [Salvatori et al.(1997)]. Peripheral blood samples from the children were supplied by the Pediatric department of University of Padova. All of children were full term infants born by spontaneous vaginal delivery; none were breast fed. The children were followed clinically and immunologically every month during the first three months of life and then every 2-3 months. One sample from each infant is included here ie. U75185, U75101, U75081 , U75016, U74997, U74922, U74900, U74841, U74819, U74772
71) **JP.ETR:** A Japanese isolate from long-term cell culture with a truncated env gene, due to a point mutation of a CAG codon to a TAG stop codon. [Shimizu et al.(1992)]. Accession numbers D12582, D01205–D01207, D12584 and D12571.
72) **JP.GUNA:** A Japanese 1989 isolate HIVGUN, infectious to T cells, was adapted to grow in fibroblast-like BT cells. A single amino acid change at the tip of the V3 loop was shown to be responsible for the change in tropism, GPGR to GSGR. [Takeuchi et al.(1991)]. Accession number M59192.
73) **JP.JH23A:** This sequence is from a Japanese patient dually infected with HIV-1 subtypes B and E [Xin et al.(1995a)]. Accession number D67089. See also D67090, E_JP.JH23B.
74) **JP.JH32:** This is a sequence from a lambda clone of Japanese isolate JH3, which was isolated in 1986 from a 10 year old Japanese Hemophiliac. [Komiyama et al.(1989)]. Accession number M21138.
75) **JP.JNIH1M:** This sequence is from a Myanmarese (Burmese) individual living in Japan, obtained by direct sequencing of PCR-amplified proviral DNA from peripheral blood mononuclear cells. [Weniger et al.(1994)]. Accession number L32084.
76) **JP.KM03:** This sequence is from a 28 year old hemophilia B patient with CDC stage IV disease and T-cell count of 20, living in Japan. The authors [Hattori et al.(1991)] also sequenced the V3 region from 28 other Japanese individuals, but only the V3-loop amino acid sequence is available from the other patients. Accession number S70936.
77) **JP1.ID:** These 10 sequences are from 12 patients with varying rates of disease progression. Patients 1 and 2, both extremely rapid progressors who died of AIDS within 8 months (patient 1) and 3 years (patient 2) of infection by sexual contact in 1991. These two shared very similar sequences and were suspected to be epidemiologically linked, so only patient 2 sequence is presented here. Patients 8, 9, 15, 19, 47, 63 and 65 were infected between 1983 and 1985 by contaminated blood products. Patients 20 and 28 were infected by sexual contact. Sequences were determined by either RT-PCR from plasma viral RNA or PCR from uncultured PBMC proviral DNA. PCR products were cloned prior to sequencing. Each of these 11 sequences is a single clone, taken as representative of that patient. [Shioda et al.(1997)]. Accession numbers AB002829–AB002974, AB002988–AB003019. Patient 43 was infected with subytpe E.

78) **JP2.ID:** These 4 sequences are from 5 hemophiliacs from Japan. Two of the 5 (AB010410 and AB010412) were very similar to each other so only AB010410 is included here. [Okamoto et al.(1998)]. Accession numbers AB010409–AB010413.
79) **KP.Kr111:** This sequence is from an unpublished database entry with accession number X93580.
80) **LB1.ID:** These 10 subtype B sequences are from a study of 25 sequences from a study of multiple HIV-1 subtypes in Lebanon [Pieniazek et al.(1998)]. Of the 26 samples, 25 were classified as HIV-1: 10 were subtype B, 10 were subtype A, 1 was subtype C, 1 was subtype D and 3 were recombinants or untyped. The other sample was classified as HIV-2 subtype B. Accession numbers AF025692, AF025694, AF025696,AF025698, AF025701, AF025702, AF025704, AF025706, AF025708 and AF025714 are HIV-1 subtype B.
81) **LT.LIT:** These 5 sequences are from Lithuania. [Lukashov et al.(1995)]. Accession numbers: L38417, LIT18A; L38412, LIT11A; L38419, LIT21A; L38416, LIT17A; L38420, LIT17A.
82) **MM1.ID:** These two sequences are from Myanmarese (Burmese) individuals living in Myanmar, obtained by direct sequencing of PCR-amplified proviral DNA from peripheral blood mononuclear cells. [Weniger et al.(1994)]. Patient 02 is a male IV drug user, and 05 is a female prostitute, both were from Mandalay. Accession numbers L32088, L32089.
83) **MM2.ID:** These 5 sequences are from dried blood spots collected in 1992 from a male STD patient (1782), a female prostitute (1739), and 3 IV drug users (1748, 1755 and 1763) in Myanmar. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession numbers U53304–U53308.
84) **MY1.ID:** These 11 sequences are from IV drug using prisoners in a prison in Kuala Lumpur, Malaysia. All 11 of these sequences cluster in phylogenetic analysis with subtype B sequences found in Thailand (sometimes referred to as B' or Thai-B). PCR products amplified from uncultured PBMCs were directly sequenced. [Brown et al.(1996)]. This report also included subtypes C and E in Malaysia. Accession numbers U65538–U65548.
85) **NL.114C** This consensus sequence represents sequences generated from PCR amplified plasma RNA from one of three infants in a Dutch mother/infant study. Samples were collected from the infant at birth, at 6 weeks and at 9 months of age. Samples were also collected from the mother before birth, at birth and after birth. Mother sequences are not included in this consensus. [Mulder-Kampinga et al.(1993)]. [Mulder-Kampinga et al.(1995)]. Infant 114 is from Accession numbers L21111–L21153. Mother 114 sequences are from Accession numbers L21028–L21110. Infant 127 sequences are from Accession numbers Z47817–Z47832. Mother 127 sequences are from Accession numbers Z47833–Z47880. Gag gene sequences from mother/child pairs are also available in the entries with accession numbers Z47903–Z47911; Z47912–Z47928; Z47929–Z47935; Z47936–Z47950. The second mother/child pair was also from the Netherlands, see G_NL.127C. The third mother/infant pair in this study was from Rwanda, see A_RW.564C.
86) **NL.168:** This is a consensus sequence of 3 clones after culturing in PBMC. The isolate was originally from an AIDS patient in Amsterdam. [Wrin et al.(1995)]. Accession numbers U15030–U15032. A V3-loop (105 bp) segment from the original isolate has been previously reported. [Fouchier et al.(1992)]. Accession number L06694. Nuetralization assays were done with other clones of this virus [LaCasse et al.(1998)] accession numbers AF035532–AF035534. LaCasse state that the primary isolate was SI phenotype and used both CCR5 and CXCR4 receptors and that a T-cell line adapted isolate derived from the primary isolate used only CXCR4.
87) **NL.wolfscon:** This is a consensus sequence from 6 patients infected with the same unit of blood in Amsterdam. [et al(1992)]. Accession numbers U04530–U04537.
88) **NL.X1con:** This is a consensus sequence of 10 clones from a recipient in a donor-recipient study. Sequences from donor Y and recipient X2 are also part of this study, but are not included here. [Cornelissen et al.(1995)]. Accession numbers Z47505–Z47514 are from X1. Other new sequences analyzed in this paper include Z47411–Z47540. Sequences M91828–M91838 (donor H and recipient O, referred to as patients A14 and A13, respectively in [Wolfs et al.(1992)] see B_NL1.A13) were also re-analyzed in this study.
89) **NL1.ID:** These nine sequences are part of a study of presumed donor-recipient pairs from an HIV-1 transmission study conducted in the Netherlands. If pairs were extremely close or identical, only the recipient is included here. Recipient samples were from the first sample to be antibody positive, and are numbers

1,3,5,7,9, and 13. These sequences are consensus sequences of multiple clones from PCR amplified serum RNA. [Wolfs et al.(1992)]. Recipient A1 was also studied as patient H1 in [Kuiken et al.(1993)] and so is not included here (see B_NL4.H1). Accession numbers M91819–M91827, M91829, M91831–M91832, M91839, M91857–M91870, M91872, M91874, M91881–M91884, M91891, M91893, 91895–M91908, M91910, M91911–M91926. Number 13, and the donor were also analyzed in [Cornelissen et al.(1995)].

90) **NL2.ID:** These two sequences are part of a Dutch study of mutations occurring over a five year period (starting in 1985) in two patients. Serum RNA was PCR amplified and multiple clones were sequenced. The consensus for each patient is shown. [Wolfs et al.(1991)] and [Zwart et al.(1992)]. Accession numbers M74591–M74684.
91) **NL3.NET-ID:** These six consensus sequences from the Netherlands are samples from AIDS patients, using serum samples to generate PCR clones from viral RNA for sequencing. [Zwart et al.(1993)]. Accession numbers L01282–L01297.
92) **NL4.ID:** These 74 sequences represent a study of early seroconverters from different times with different risk factors for transmission during the AIDS epidemic in the Netherlands. The year the sample was taken is indicated in the last part of the sequence name. The risk group of the individual from whom the virus is derived is indicated in the first letter of the sequence name (I, B and H for IVDUs, hemophiliacs, and homosexuals, respectively). Viral genomic RNA from sera was PCR amplified and amplification product was directly sequenced. [Kuiken et al.(1993)]. Accession numbers Z29219–Z29225, Z29256–Z29258, and Z29262–Z29325, U23670.
93) **NL5.ID:** These 18 consensus sequences are from a study of patients with, and without, AIDS dementia complex (ADC) in the Netherlands. Not all patients were from the Netherlands. Samples were collected between 1986 and 1992. Viral genomic RNA from sera and/or cerebral spinal fluid was reverse transcribed and PCR amplified and clones were sequenced. [Kuiken et al.(1995)] Accession numbers Z37531–Z37534, Z37734–Z37963, Z37970–Z37971
94) **NL6.ID:** 16 is a consensus sequences of four sequences used in a study of HIV-1 envelope-mediated syncytium formation. The consensus represents four clones from one patient, two clones of the consensus are SI and two are NSI. 320 is a single SI clone. The sequences were derived from PCR amplified DNA from provirus cultured in PHA-stimulated PBMCs [Andeweg et al.(1992)]. Accession numbers L08655–L08662. Complete genomes from patient 320 SI and NSI strains are found in entries with accession numbers U34603 and U34604 [Guillon et al.(1995)], tat and other genes from patient 320, some of the same isolates, are found with Accession numbers M64489–M64492 [Groenink et al.(1992)]. Another env sequence from patient 320 is found with accession number AF069524 [Follis et al.(1998)].
95) **NL7.ID:** These two consensus sequences are from sets of sequences (Accession numbers U05797, U13240, U13241, U13243–U13247 for consensus 537 and U13242, U13248–U13252 for 1058) used in a study on the dynamics of HIV sequence changes in vivo and the utility of heteroduplex analysis. Both sequences were derived from PCR amplified PBMC DNA. Consensus 537 represents a set of sequences from a Dutch patient with a relatively stable CD4+ cell count at 62 months post-seroconversion. Consensus 1058 represents sequences from another Dutch patient whose CD4+ cell count at 73 months post-seroconversion was declining faster than 537's. [Delwart et al.(1994)]. See also US10.ID.
96) **NL8.672** This is a sequence from a patient early in infection, before, or around the time of seroconversion. Three other patients studied in this paper (537, 1058 and 594), had previously been reported. See B_NL4.594, B_NL7.1058con and B_NL7.537con. [Shpaer et al.(1994)] and [Delwart et al.(1995)]. Accession numbers U23651–U23663, U23667, U23670. See also US11.ID.
97) **NL9.ID:** These 19 sequences are from a cohort of homosexual men living in Amsterdam who seroconverted between 1985 and 1989. The sequences are from direct sequencing of PCR products after RT-PCR from serum RNA. Samples for h1, h139, h491, h1140 and h1234 were obtained at seroconversion. Samples for h138 and h1136 were obtained 12 months and 29 months after seroconversion respectively. The sequence for h320 was obtained from proviral DNA, 2 months after seroconversion. [Zwart et al.(1994a)] and [Zwart et al.(1994b)]. Accession numbers L25884 and U05786–U05808. More sequences from this same cohort of men were published in [Kuiken et al.(1996b)] and [Kuiken et al.(1996a)] Accession numbers Z67875–Z67876, Z67885–Z67939, Z67941–Z67960, Z68015–Z68089, Z68109–Z68110. Some vpr, vpu and other region sequences are available from some of these patients as well. Some of the database entries for this set appear to be duplicates of sequences reported in other studies.

98) **NL10.ID:** These 13 sequences are from recent immigrants to The Netherlands from various countries. The first two letters of the ID represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76842-L76863, L76878, SR903853; L76897, SR9304737; L76879, SR911515; L76874, UM893272; L76912, UM9403860; L76888, SR925752; L76890, SR926969; L76894, GQ9301341; L76882, MA913670; L76886, SR923572; L76873, BR891413; L76910, UM9403051; L76885, GF921953.
99) **NL11.ID:** These 2 sequences are consensus sequences of 81 clones (patient N) and 105 clones (patient F) from serum, sigmoid tissue and fecal matter from each patient. All sequences from patient N were more similar to other sequences from patient N than to any other sequence in the database. Likewise all sequences from patient F were most similar to other patient F sequences. [van der Hoek et al.(1996)]. Accession numbers Z76463–Z76648.
100) **NL12.ID:** These sequences are part of a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and six Scottish intravenous drug users, from which regions of vpr, vpu and env were sequenced. The authors found consistent differnces in the sequences between the homosexuals and IV drug users. Only 34 of the 47 patients' sequences are reported in the publication. [Kuiken et al.(1996b)]. See also B_GB5 and B_DE2 sets. Some of the patients in this study have been previously studied. For example, entries with accession numbers Z68061 and U05787 are both from the same patient.
101) **NL13.ID:** These two sequences are from an Amsterdam Cohort Study on HIV infection and AIDS in homosexual men [van't Wout et al.(1998)]. ACH0208 and ACH0039 seroconverted during the course of the study and progressed to AIDS within 5 years thereafter. The subjects ACH0208 and ACH0039 had both SI and NSI virus variants. After seroconversion the SI variants were first detected then NSI in both the subjects. AF022285, AF021652 are the ones that are included here. The complete set has accession numbers AF022257–AF022302.
102) **NO1.ID:** These 36 sequences are from Norwegian patients who were part of the Oslo HIV cohort study [Engelstad(1996)]. Uncultured PBMC DNA was PCR amplified in two nested PCR reaction steps. PCR products were directly sequenced. Where two peaks of equal height were observed at a single position, IUPAC ambiguity codes were used. Health, sex, year of sample (1989-1992), and risk group (IVDU, Het, Homo, Hemo) for each patient were noted in a table in the publication. Four subtype C sequences were also part of this set (X92913, X92914, X92917, X92918). Accession numbers for the 36 subtype B sequences are X92902–X92912, X92915, X92919–X92941.
103) **NZ1.ID:** These 8 subtype B sequences are from New Zealand [Dwyer et al.(1998)]. Of the 10 isolates sequenced, 8 were subtype B and 2 were subtype C. Accession numbers AF052622–AF052629. Risk factors were heterosexual (NZ1, NZ6), homosexual (NZ2, NZ8–NZ12) and IVDU (NZ4). NZ1 and NZ6 were from females.
104) **PR1.D-ID:** These four sequences are from Puerto Rico, and were generated as part of the DAIDS variation program in the laboratory of Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. The C2V3 region was directly sequenced from PCR amplification of DNA from viral culture. The sequence ID numbers are abbreviated; for example D2PR732 can be read as DAIDS sequence (D), isolated in 1992 (2), Puerto Rico (PR), patient 301732 (732). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. Accession numbers U04926–U04929.
105) **PY.ID:** Ten sequences from 10 patients living in Asunçion, Paraguay. All 10 were male patients with symptoms of AIDS. Virus was propagated in tissue culture for an unstated length of time prior to harvesting proviral DNA for PCR and sequencing. PCR products were directly sequenced. PY.3614, PY.3615 and PY.12837 were syncytium-inducing and the other 7 were not. The tenth sequence, PY.3614p was PCR amplified directly from patient PBMCs with no culturing. The significant differences between the cultured sequence from this patient (PY.3614c) and the direct sequence, indicates that the virus that grew out in culture was a minority of the virus present in PBMC. The sequence of PY.3614c is not included in this alignment. [Cabello et al.(1995)]. Accession numbers U28949–U28959.
106) **RU1.RUS:** These 2 sequences are from [Lukashov et al.(1995)]. Accession numbers: L38405, RUS3A; L38407, RUS4A.

107) **RU2.ID:** These 15 sequences are from homosexuals living in St. Petersburg, Russia. Malykh et al unpublished (1995). Accession numbers U40283–U40285 and U40319–U40330.

108) **RU3.ID:** These 13 sequences are from Rostov, St. Petersburg, Sochy, Ecaterinberg, Komi Republic, and Nizhny Tagil, Russia. Sequences were determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. Although several of these cases were suspected to have epidemiological linkage (RU9 and RU10 are beleived to have been infected by the same individual, sequences from the index case are not available; RU11, RU13 and RU27 were all thought to share a common index case, although none of them was directly infected by the index case), the sequences do not clearly indicate such epidemiological linkage and all 13 sequences are presented here. [Leitner et al.(1996b)]. Accession numbers U69646–U69652, U69654, U69657, U69660, U69662, U69666 and U69667.

109) **SE.pt11s113:** This sequence is from one (patient 11 sample 113, collected in 1988) of a set of 13 samples from 9 epidemiologically linked individuals. The index case (patient 1) was a Swedish male who is believed to have contracted HIV while visiting Haiti in 1980. Six Swedish females were infected (patients 2,4,5,7,8 and 11) by patient 1. Two males (patients 6 and 10) were then infected by these females, and two HIV-infected children (patients 3 and 9) were born to the women. Sequences from each patient were determined by PCR amplification from uncultured PBMCs and direct sequencing. Heterogeneous sites were indicated with IUPAC codes. Extensive phylogenetic analysis was done to determine which methods accurately reconstructed the true phylogeny. [Leitner et al.(1996a)]. Accession numbers U68496–U68521.

110) **SE1.ID:** Seven sequences that are consensus sequences of blood and CSF samples taken from each patient. The CDC disease stage class for the patients are as follows: II pts 930, 2815; III pt 931; IV-E pt 2951; IV-A pt 1032; and IV-C2 pts 1433, 1866. [Keys et al.(1993)]. Accession numbers Z23178–Z23181, Z23185–Z23189, Z23192–Z23195, Z23200–Z23219, Z23224–Z23227, Z23232–Z23235, and Z23240–Z23255.

111) **SE2.ID:** These five sequences are from patients in Goetebotg, Sweden each of whom had recently seroconverted at the time of sampling in 1985-1990. Sequences from the sexual partners of all five patients who were believed to have transmitted the virus to these recipients were also determined, but are not shown here due to the great similarity to the recipient sequences (94% to 99% identity). Three of the recipients (R1, R3 and R4) were homosexual, and the other two were heterosexual. [Furuta et al.(1994)]. Accession numbers U10929–U10950.

112) **SE3.ID:** These 5 sequences are from a study of the ability of beta-chemokines RANTES, MIP-1alpha and MIP-1beta to inhibit primary isolates with SI and NSI phenotypes. The conclusion was that NSI viruses were inhibited by these beta-chemokines, whereas SI viruses were not. Each viral isolate was cocultured on PHA-stimulated donor PBMCs for 3 days, PBMC DNA was harvested, PCR amplified, and the PCR product directly sequenced. For each of these 5 patients (labelled patients A-E) one SI and one NSI isolate were sequenced, only the NSI sequence is presented here. [Jansson et al.(1996)]. Accession numbers U76078–U76087.

113) **SE4.ID:** These 4 sequences are from a study of 270 HIV-1 infected individuals living in Sweden [Alaeus et al.(1997)]. 80 of these 270 were thought to have been infected in Africa, prior to moving to Sweden, or infected directly by someone who had just immigrated from Africa. Of these 80, 75 bloods samples were available from 33 men and 42 women, from 15 different African countries. The 4 subtype B sequences were from individuals who were thought to have been infected in Kenya (SE8613 U76158), Eritrea (SE8875 U76167), Rwanda (SE7898 U76133) and Mauritania (SE7901 U76144).

114) **SE5.ID:** These 2 subtype B sequences are from a study that includes the analysis of HIV-1 strains in seven cases of mother-to-child transmission in Sweden [Contag et al.(1997)]. HIV-1 isolation from the mothers was conducted during the three trimesters, a few days after deleivery and 6 months after parturition. The children were born between June 1989 and August 1992 and were followed by virus isolation at birth and at 3, 6, 12 and 18 months of age unless circumstances called for an extra sample. Breast-feeding was denied by all of the women described. See also A_SE.H4B, C_SE2.ID#, D_SE.H3 and E_SE.H1. Accession Numbers U56263-U56335.

115) **SG1.ID:** These 26 sequences are from Singapore. Other sequences in this set were subtypes A, C and E. Sethoe et al in press 1998.

116) **SK1.ID:** These nine sequences are from homosexual men living in the inner city of Bratislava, in the Slovak Republic. Patients 11, 12, 15 and 23 were classified as CDC stage A1 and were not taking any

medication. Patients 18 and 20 were CDC stage B2 and were taking AZT. Patients 9 and 28 were CDC stage C3 and were taking AZT. No information is available for patient 22. Two other patients (10 and 51) were included in this study, but their sequences are not shown here because after their sequences proved to be similar to sequences from patients 9 and 28, respectively, epidemiological investigation indicated that they (9 and 10; 28 and 51) had been sexual partners. DNA from cocultured PBMCs was PCR amplified and the PCR product cloned. Eight clones were sequenced from each patient, although only one sequence is presented in the publication and in the databases. It is not stated whether the single sequence is a consensus of the eight clones or a single clone.[Zachar et al.(1996b)]. Accession numbers U53192–U53194, U53196–U53203.

117) **TH.93TH067:** This sequence is from Thailand. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. [Penny et al.(1996)]. Accession numbers U39258 and U39259.

118) **TH.T8174:** This sequence comes from a study of the genetic heterogeneity and epidemiological distribution of HIV1 in Thailand. The host was an intravainous drug user and the sequence was obtained from PCR amplified PBMC DNA. [Ou et al.(1993)]. Accession numbers L19238 and L07446 are from the same patient. See also E_TH.T8178.

119) **TH1.ID:** These ten sequences are from individuals from Thailand. PCR-direct, peripheral blood PBMC DNA. [Ou et al.(1992b)] and [Ou et al.(1993)]. (Published erratum appears in Lancet **342**:250 (1993).) Accession numbers L07442, L07449–L07456 and L07460.

120) **TH2.ID:** The TB132 sequence is from a set of isolates from HIV seropositive individuals from Thailand. PCR, PBMC co-culture, DNA. Full env sequence is available. [McCutchan et al.(1992)]. Please note: the TB132 locus name in the database corresponds to the McCutchan et al. "BK132" isolate. Accession number L03697. The CM237 sequence is from PBMC proviral DNA. [Mascola et al.(1994)]. Accession number L14570. See also B_US14

121) **TH3.W2TH-ID:** 2 sequences from Thailand from asymptomatic individuals. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April 1994 supplement to the *Human Retroviruses and AIDS 1993* database. [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession numbers U08715–U08719, U08801–U08802, and U08783–U08784.

122) **TH4.ID:** These twelve sequences are B subtype sequences from Thailand. Ten were genetically most similar to HIV-1 found in the Americas and Europe; these sequences were derived from people infected prior to 1988 (diagnosed in 1986 or 1987). The other two (N762 and N763) were designated B' and were isolated from people with more recent infections, 1988 and 1992. The sequences were obtained from PCR amplified PBMC DNA. The naming of the sequences submitted to the databases does not correspond with the naming of the sequences in the paper. [Kalish et al.(1994)]. Accession numbers for the entire set of thirteen sequences studied in this publication: U15576–U15588.

123) **TH5.ID:** These three sequences are B subtype sequences from Thailand. Two individuals believed to be dually infected with subtypes B and E were analyzed. It is not clear from the paper or the database entries, which sequences came from individual 1 and which from 2. [Artenstein et al.(1995)]. Accession numbers U21471, U21473, U21475. See also E_TH6.ID.

124) **TH6.ID:** These 4 entries are from 1992 dried blood spot samples from Thailand. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. Samples came from 3 previously identified HIV seropositive IV drug users (58, 11, 15) and a homosexual (86). Other samples from the same region were all subtype E (see E_TH8.). [Cassol et al.(1996)]. Accession numbers U53310, U53311, U53314 and U53315.

125) **TH7.ID:** These 70 sequences are from IV drug users in Bangkok, Thailand, who were undergoing methadone treatment at 14 treatment clinics. Blood samples were collected between January and April, 1994. Uncultured PBMC DNA from each patient was PCR amplified, and the PCR product was directly sequenced (except for patient 108, in which PCR product was cloned and 2 clones were sequenced, one shown here). Of the 84 patients sampled, 69 were Thai B, one (091) was typical subtype B, and 14 were

subtype E. [Kalish et al.(1995)]. Accession numbers U22543–U22547, U22549–U22552, U22554–U22556, U22558–U22560, U22562–U22566, U22568–U22574, U22576–U22603, U22605–U22608, U22610, U22613–U22616, U22618–U22623 and U22626. See also E_TH9.

126) **TH8.ID:** These 12 subtype B sequences are out of the 95 sequences reported in a paper out of which only 26 were submitted to the databases with accession numbers U85085-U85060 [Subbarao et al.(1998)]. The samples of these sequences were collected from 215 asymptomatic HIV-1 individuals from June 1994 through January 1995 at 9 regional medical centres in northern, central and southern Thailand. Out of the 215 participants 65 were injecting drug users and 150 reported sexual risk behaviors out of which 51 were female sex workers, 41 attended antenatal clinics, 9 had STD's, 41 men with heterosexual behavior and 8 were men who had sex with men. Out of the 215 specimens subtyped 175 were subtype-E, 37 were subtype-B' and 2 were typical subtype-B. See also subtype E for the same study.

127) **TH9.ID:** These 8 subtype B sequences are from a study that was performed to evaluate the sensitivity and specificity of PEIA and HMA for determination of subtypes B and E and to determine proportion of these subtypes in Bangkok over time [Wasi et al.(1995)]. The paper and its related references give no significant information about the patients used in this study. This paper gives a brief account of only 3 of 9 patients: specimens 087 and 088 are both from 32 year old females who were infected in 1988 and specimen 091 is a 40 year old male who was infected in 1988. Accession numbers U22614, U22615, U22616, U22618, U22619, U22620, U22621 and U22622.

128) **TT.QZ4589:** This sequence is from Trinidad. W. Blattner et al. Unpublished 1995. Accession number U32396.

129) **TW1.ID:** These 16 sequences are from healthy HIV-1 carriers or AIDS patients from Taiwan [Chang et al.(1997)]. Three subtype B sequences in this set were greater than 97% identical to the HXB2/LAI lab strain (see B_FR.LAI) of HIV-1, and are not included here (TW83, U73049; TW271, U73059; and TW335, U73061). The manuscript reports that 123 of 143 sequences from Taiwan were subtype B, but only 27 of the 143 sequences were submitted to the sequence databases. Other subtypes found in Taiwan in this study were E (17 cases), C (1 case), F (1 case) and G (1 case). Accession numbers for B subtype are U73045–U73054, U73056, U73057, U73059, U73061 and U73063–U73069.

130) **US.ACP1:** This virus was cultured from a seronegative man with Kaposi's sarcoma. (See: [Ho et al.(1989)]). ACP1 was the sequenced after one passage in PBMCs. Accession number M80660. The sequence AC-H9 (M80661) was also derived from this patient. [Ashkenazi et al.(1991)].

131) **US.AD39:** This sequence is one recipient sequence from a set of 36 clones from a homosexual donor-recipeient pair. Other donor-recipient pairs were studied by quantitative homoduplex tracking assay (QHTA) but only this pair was sequenced. [Zhu et al.(1996)]. Accession numbers U50780-U50815.

132) **US.ADA:** This sequence is from the monocytropic U.S. isolate ADA. [Westervelt et al.(1991)]. The complete genome of a derivative of this isolate has been reported to have been sequenced in [Theodore et al.(1996)]. The complete genome is from a macrophage tropic HIV-AD8 isolate, derived from HIV-AD87, which was in turn derived from HIV-ADA. Accession numbers M60472, AF004394.

133) **US.ALA1:** This sequence is from an infectious clone of the 1985 U.S. isolate AL-1, taken from a patient with AIDS. Buckler-White, A. et al., Unpublished (1988). Accession number M38430.

134) **US.BAL1:** This sequence is from the macrophage tropic U.S. isolate BAL, harvested from lung alveolar tissue. Reitz M, et al., Unpublished (1990). Accession numbers M68893, M68894. The entry with accession number M63929 is 98% identical to this sequence and is also derived from the BAL isolate [Hwang et al.(1991)]. The BAL1 sequence has all four characteristics of the "Dutch IDU" sequences of subtype B described by [Lukashov et al.(1998)].

135) **US.BCSG3:** This is a fragment of a full genomic sequence from the provirus SG3, cloned as a single proviral unit. This clone replicates more efficiently in chimpanzeee than in human lymphocytes, and is extremely cytopathic and cyncytium inducing (SI) in immortalized human T-cell lines. [Ghosh et al.(1993)]. Accession number L02317.

136) **US.BRVA:** This sequence is from U.S. isolate BRVA, which was taken from the brain tissue of a AIDS patient with neurological disorders. [Anand et al.(1989)]. Accession number M21098.

137) **US.BWB:** This consensus sequence is from sequences derived from PCR amplified PBMC DNA from brain tissue. [Monken et al.(1995)]. Accession numbers L17088–L17126.

138) **US.CDC42:** This sequence is from an infectious clone of the U.S. isolate CDC-451 [Desai et al.(1986)]. It was isolated in 1984 from a 16 year old hemophelia A patient, who died of AIDS in June, 1984.

The viral isolate was propagated on H9 cells prior to cloning into Lambda phage and M13 phage for sequencing. Accession number M13137.

139) **US.DH12:** The DH12 isolate has been extensively characterized [Shibata et al.(1995)], [Cho et al.(1998)]. It is dual-tropic, using CCR3, CCR5 and CXCR4 coreceptors. Chimeric molecular clones with the macrophage-tropic AD8 isolate have been made, showing that either V1-V2 or V3 regions of env from DH12 can confer the ability to use CXCR4 onto AD8. The DH12 isolate was passaged in human and chimpazee PBMCs prior to cloning. A complete genome sequence is available. GenBank accession numbers AF069139 and AF069140.

140) **US.Diaz:** This sequence is one of a set of 223 closely related sequences. All 223 sequences came from 3 patients with a common source of HIV, a blood donor and two recipients of this donor's blood [Zhang et al.(1997)]. Accession numbers for all 223 sequences are U29433–U29437, U29956–U30145, and U43035–U43054. Gag sequences from 12 clones are also available in entries U31573–U31584.

141) **US.FASH:** This sequence is also known as 91US005.11 from the WHO Global program on AIDS. It is from a 17 year old female with primary symptomatic infection (PSI) from Birmingham, Alabama, USA. The risk factor for this individual was reported as heterosexual contact. The sequence indicates that this clone is subtype B. Blood was drawn in 1991. Although this clone has a 34 bp deletion followed by a premature stop codon in the envelope gene, relative to other subtype B sequences, the env protein was strongly positive in a CAT complementation assay. The patient from which this clone was isolated experienced rapid CD4 decline. In addition to the 17 amino acid truncation of the gp41 peptide, the env gene has a mutation at amino acid position 721 (bases 2157-2159) replacing tyrosine with cysteine (Y721C). This mutation has been shown in SIV to increase cell surface concentrations envelope glycoprotein (LaBranche,C.C. et al, J. Virol. 69: 5217- 5227 1995). The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic [Gao et al.(1996a)]. Accession number U27434.

142) **US.HOBR:** This sequence is also known as 91US006.10 from the WHO Global program on AIDS. It is from a 28 year old male with primary symptomatic infection (PSI) from Birmingham, Alabama, USA. The risk factor for this individual was reported as homosexual contact. The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic [Gao et al.(1996a)]. Accession number U27443.

143) **US.JFL:** This sequence is from a non-infectious clone from the monocytropic U.S. isolate JFL. [McNearney et al.(1990)]. Accession number M31451. Other sequences from HIV-1 isolates epidemiologically linked to this isolate can be found in database entries with accession numbers L06256–L06273. [McNearney et al.(1993)].

144) **US.JM:** This sequence, along with B_US.WM, came from viral isolates after short term culture in PBMCs, PCR amplification, and cloning of PCR products. Both are from asymptomatic, seropositive individuals. [Ashkenazi et al.(1991)]. Accession number M80662, M80661.

145) **US.JRCSF:** This sequence is from an infectious clone of the 1986 U.S. isolate JRCSF, derived from from the CSF of a patient who died with Kaposi's sarcoma and severe AIDS encephalopathy. The infectious clone JRFL was isolated from the brain of the same patient. JRFL does not replicate in Jurkat, U937 or HUT78 cells. JRFL does replicate in mononuclear phagocytes, and the macrophage-tropic region of the virus was determined by domain swapping with NL4-3 to reside in a 157 amino acid region of gp120 including the V3 loop. [O'Brien et al.(1990)]. Accession numbers U63632, M38429, U45960. Also see: [Pang et al.(1990)], [Pang et al.(1991)], [Koyanagi et al.(1987)], [Klasse et al.(1996)].

146) **US.MN:** This sequence is from U.S. isolate MN, taken from a 6 year old male pediatric AIDS patient from the Newark, New Jersey area in 1984. His mother was an IV drug user who died of pneumonia in 1982. His father was also HIV seropositive. A complete genome of isolate MN is found in M17449. Other sequences from this patient from the 1984 blood sample and from a 1987 sample taken shortly before death (U72495) are available also. [Reitz et al.(1992)] [Gurgo et al.(1988)]. Accession number M17449. See also L48364–L48379 [Lukashov & Goudsmit(1995)]. Another complete genome of isolate MN is found with accession number AF075719.

147) **US.NY5CG:** This sequence is from the 1984 U.S. isolate NY5. [Willey et al.(1986)]. Accession number M38431. See also GenBank accession number K03346. A recombinant between NY5 and LAI has also been extensively studied, see B_FR.LAI entry.

148) **US.P896:** This sequence represents a molecular clone from an primary isolate derived from a Jamaican man who immigrated to Philadelphia 15 years earlier. At the time of viral isolation, he had no antiviral therapy, but was an AIDS patient with $<$ 10 CD4 cells per mm3. The infectious molecular clone from which this sequence was derived is both macrophage-tropic and extremely cytopathic in lymphocytes. [Collman et al.(1992)] and [Kim et al.(1995)]. Accession numbers M96155, U39362.

149) **US.RJS:** This is a consensus of six biologically characterized clones from patient RJS, isolate 4. The HIV-1 infected individual had been infected for five years at the time of isolation in 1985. Patient RJS was a 31 year old homosexual male from Claifornia, who reported having sexual encounters with at least 1000 partners while HIV-infected, from 1980 to 1985 [Hahn et al.(1986)]. Virus was isolated via coculture on donor PBMCs prior to cloning and sequencing. Complete env sequence is available. [Daniels et al.(1991)] and [Fisher et al.(1988)]. Accession numbers M37491 and M37573–M37577.

150) **US.SB(A-C):** These three sequences are from 1988 U.S. isolates taken from a woman, her daughter and her sexual partner. The three viruses are epidemiologically linked, however the amino acids sequences appeared sufficiently divergent in this region to merit the inclusion of all three samples. Sequences were directly sequenced from PCR amplification products after the virus was briefly cultured. [Burger et al.(1991)]. GenBank accession numbers M77228–M77230.

151) **US.SC:** This sequence is from the 1984 U.S. isolate SC, from an AIDS patient. [Gurgo et al.(1988)]. Accession number M17450.

152) **US.SF128:** This clone was isolated from the spinal cord tissue of a patient with dementia, after coculture with PBMCs. It is macrophage tropic, infecting macrophages but not T-cells [Liu et al.(1990)]. Accession numbers M95292 and M38673. The ability to infect macrophages versus HUT 78 cells was mapped to the region between a StuI site in env and a XhoI site in nef, by replacing this region in SF2 with the same region from SF128.

153) **US.SF162:** This sequence is from an infectious clone from the U.S. isolate SF162, cultured from the cerebrospinal fluid of a patient with toxoplasmosis. [Cheng-Mayer et al.(1990)]. Accession numbers M38428, M65024.

154) **US.SF2:** This sequence is from an infectious clone from the U.S. isolate ARV-2. ARV-2/SF2 was isolated from a patient with oral candidiasis after co-culture with mitogen-stimulated PBMCs in 1984 [Levy et al.(1984)]. [Sanchez-Pescador et al.(1985)]. Accession numbers K02007 and I07977. HIVSF13 (Accession number L07422) is a more infectious virus taken from the same patient five months later, when he had developed Kaposi's sarcoma and Pneumocystis carinii pneumonia [Cheng-Mayer et al.(1991)]. SF2 and SF13 are 98% identical to one another. The variation of SF2 in 9 years of infection in a chimpanzee has been studied by [Fultz(1997)], accession numbers U56884–U56887. This chimpanzee, infected by both SF2 and LAV-1b strains of HIV-1 was studied and developed AIDS [Novembre et al.(1997)], [Davis et al.(1998)] and [Wei & Fultz(1998)] accession numbers AF006015–AF006032, AF027771–AF027785, AF049494 and AF049495.

155) **US.SF33:** This sequence is from an infectious clone from the 1984 U.S. isolate SF33. [York-Higgins et al.(1990)]. Accession number M38427.

156) **US.TN-ID:** These eight sequences are from asymptomatic individuals identified after donating blood in Memphis, Tennessee, USA. [Slobod et al.(1994)]. Accession numbers U09140–U09175.

157) **US.twinABcon:** This sequence is a consensus of a set of 27 env sequences from a pair of heterozygotic perinatally HIV-1 infected twins who were observed during their first 2 years of life. Twin A remained asymptomatic through her first 2 years while twin B developed AIDS at six months and died at 22 months of age. Patient PBMCs were cocultured with donor PBMCs, prior to DNA extraction and PCR amplification. Approximately 500 copies of HIV proviral DNA per PCR reaction were used. PCR products were cloned prior to sequencing. Viral phenotypes from both infants, and all time points were also assessed. All were found to be non-syncytium inducing, but they differed in their ability to infect primary macrophages. Overall, it seems that the production of neutralizing antibodies by the healthy twin was the most important clinical factor. [Hutto et al.(1996)]. GenBank accession numbers U47562-U47588 for the envelope sequences and U47589-U47613 for tat sequences from the same blood samples.

158) **US.UNC116:** This subtype B sequence is from a patient UNC116 who was born in 1969 with severe Haemophilia A and received over 50000 U of non-heat treated factor VIII concentrates between 1978–1984 [Michael et al.(1998)]. The parents of the subject were CCR5-/- and CCR5+/-. The samples were obtained from patient UNC116 between 1985 and 1992 were of SI genotype based on presence of

positively charged amino acids in the V3 loop region. UNC116 is the first demonstration of exclusive and persistent CXCR4 usage in an HIV-1 infected individual. Accession number AF034385.

159) **US.WEAU:** This sequence was kindly provided prior to publication by Sajal K. Ghosh. It is from a cultured isolate from a patient described as "patient 1" in [Clark et al.(1991)] and as WEAU 0575 in [Piatak et al.(1993)]. The sequence is from a fully infectious complete, cloned genome. It has a high tropism for T-cells and is syncytium-inducing. Accession number U21135.

160) **US.WM:** This sequence, along with B_US.JM, came from viral isolates after short term culture in PBMCs, PCR amplification, and cloning of PCR products. Both are from asymptomatic, seropositive individuals. [Ashkenazi et al.(1991)]. Accession number M80663.

161) **US.WMJ22:** This sequence is from the isolate WMJ22, isolated from a 4 year old female with AIDS, born in Florida to a woman of Haitian descent living in the U.S. Virus was cocultured on an immortalized T-cell line. [Hahn et al.(1986)] and [Starcich et al.(1986)]. Accession numbers M12507, K03457.

162) **US.WR27:** This sequence is from a complete genome. It represents first complete PCR-derived sequence of a U.S. clinical isolate of genotype B expanded only in primary PBMC. This provirus harbors a uniquely truncated V3 loop. WR27 was a patient with clinical progression to WR stage 5 when blood was drawn for viral isolation in 1988. This sequence is a from a PCR clone from a primary isolate that was expanded in PBMC. The virus isolate had an SI phenotype. [Salminen et al.(1995)]. Accession number U26546.

163) **US.YU:** This is a consensus sequence of eight lambda phage clones and 12 PCR amplified clones derived from the uncultured brain tissue of a patient with AIDS dementia complex. A macrophage tropic clone (YU-2) is almost identical to the consensus sequence of YU in this region, with only a single amino acid change (K to N) 10 amino acids from the carboxy-terminal end of the sequence. [Li et al.(1991)]. Complete genomic sequences are available for two of the HIV1YU clones, along with biological characterizations of four of the HIV1YU clones: [Li et al.(1992)]. The GenBank accession numbers for the YU-10 and YU-2 complete genomes are M93259 and M93258, respectively. Accession numbers for the other clones are M89972–M89984.

164) **US1.HC-ID:** These are forty 1990–1991 U.S. samples, from the study of the dentist who was thought to have been the source of HIV-1 infection of six of his patients. Only the dentist's viral sequence and the Florida control sequences are shown here; the six epidemiologically and genetically linked patients are excluded from this alignment because their viral sequences were very similar to the dentist's. All sequences were PCR amplified from patient PBMCs. Most are direct sequences from the amplification products, although some are consensus sequences of multiple clones of PCR products and one direct sequence. [Ou et al.(1992a)]. Accession numbers for the 75 sequences in this set: M90847–M90853, M90881–M90886, M90894–M90900, M90907–M90912, M90914–M90956, M90958–M90964, M92100–M92133, L22590–L22606 and U06872-U06919. See also [Korber & Myers(1992)], [Crandall(1995)], [Smith & Waterman(1992)], [DeBry et al.(1993)], [Palca(1992b)], [Palca(1992a)], [Abele & DeBry(1992)], [Hillis & Huelsenbeck(1994)], [Ciesielski et al.(1991)] and [Ciesielski et al.(1994)]. In a related study [Delwart et al.(1995)] heteroduplex mobility tracking assays were used to re-analyze samples from this set, again supporting the dental to patient transmission hypothesis.

165) **US2.D-ID:** These 15 sequences are from the USA, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratory of Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. The C2V3 region was directly sequenced from PCR amplification products of DNA from viral culture. The sequence ID numbers are abbreviated, for example D2US711 can be read as DAIDS sequence (D), isolated in 1992 (2), United States (US), patient 301711 (711). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. Full length envelope genes from some of these clones have been expressed, [Gao et al.(1996a)]. Accession numbers U04907–U04915, U04918 and U04921–U04925.

166) **US3.D-ID:** These four sequences are from the US, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. gp160 sequences of clones from expanded culture stocks are available. The sequence ID numbers are abbreviated, for example D2US711 can be read as DAIDS sequence (D), isolated in 1992 (2), United States (US), patient 301711 (711). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. Accession numbers U08448–U08449 and U08451–U08452. Accession numbers for additional clones from these patients: U04916–U04917 and U04919–U04920,

167) **US4.ZhuPt-ID:** Sequences from five primary seroconverters. Consensus, PCR-clones, peripheral blood PBMC DNA. Although sequences were also available from two of the donors, only sequences from five recipients are shown here. [Zhu et al.(1993)]. Accession numbers L21224–L21328, L21331-L21348, L21372–L21373, L21376–L21377, L21380–L21381, L21384–L21389, L21393–L21394, L21397–L21398, L21400–L21401, L21404, L21405, L21408, L21410–L21411, L21414, L21417–L21418, L21421, L21426–L21427, L21430–L21432, L21434–L21437, L21440–L21442, L21445, L21447, L21449–L21450, L21453–L21454, L21457, L21459, L21462–L21463, L21468, L21472-L21515, L21519–L21520, L21522–L21523, L21525–L21526, L21528–L21533, L21535–L21536, L21538–L21539, L21541, L21543, L21545–L21546, L21548, L21550–L21551, L21553–L21554, L21556, L21558–L21559, L21561–L21569, L21571–L21578, L21580, L21582, L21584, L21586, L21588 and L21590.

168) **US5.pt-ID:** A consensus of PCR-clones, peripheral blood DNA. These two sequences were part of a study of blood sequences compared to brain sequences from six individuals. [Korber et al.(1994)]. Accession numbers U05360–U05568.

169) **US6.-ID:** Each sequence is a consensus sequence of several cloned PCR products from PBMC proviral DNA from an individual infant. These sequences were part of a study of mother-infant transmission. Infant blood samples were taken from 1 week (infant 7) to 34 months (infant 4) post-partum. Dates of sample collection were: Infant 1, 10/25/91; Infants 2–4, 10/31/91; Infant 5, 2/6/92; Infant 6, 8/30/93; Infant 7 5/13/93. Maternal sequences were also reported as part of this set, but are not used in building these consensus sequences. [Ahmad et al.(1995)]. Accession numbers U16390–U16652.

170) **US7.-ID:** Each sequence is a consensus sequence of several cloned PCR products from PBMC proviral DNA from an individual patient. These sequences were part of a study of early samples (1984-1986) from the San Francisco region. One of the samples (552-3) was HIV negative but was determined to be contaminated with blood from another (565-3) so the six samples from 552-3 and 565-3 are made into one consensus here (565). Another sample (552-5) from patient 552 was not contaminated, and it is presented as B_US11.552, because a larger region was reported in that publication. [Sabino et al.(1994b)] Accession numbers L20371–L20380. More V3 and tat sequences from these individuals are discussed in [Sabino et al.(1994a)]. Accession numbers U00243–U00399 and U01513–U01529.

171) **US8.-ID:** These sequences were from a study of three recipients of contaminated blood. Recipient 1 (R1) and recipient 2 (R2) each received blood from different donors. A third recipient, not presented here, received blood from both donors. All three recipients were neonates. R1 received erythrocytes from donor 1 on 19 October, 1984 at the age of 3.5 weeks. For R1 the sequence of one of the two clones (2E) is presented here. R2 received erythrocytes from donor 2 on 24 September, 1984 at the age of 2 months. For R2 a consensus of 6 clones is presented here. Blood samples for this study were drawn in March 1986. R1 had slow weight gain, and R2 had lymphadenopathy at time of sample collection. [Diaz et al.(1995)]. Accession numbers U11188 = R1–2E, U11189 not used; U11203, U11196, U11199, U11192–U11194 = R2 six clones. The tat and envelope V4-V5 regions of clones from these same individuals are also available in U11173–U11178, U11180, U11205–U11209.

172) **US9.-ID:** These are four consensus sequences for samples taken over a range of time from four different subjects. Blood samples for S1 were drawn in Nov ’85, Jul ’87, Jan ’88 and May ’89. Blood samples for S2 were drawn in May ’85, Apr ’87 and Oct ’87. Blood samples for S3 were drawn in Jun ’87 and Dec ’87. Blood samples for S4 were drawn in Jan ’85, Jan ’89 and Jun ’89. S2, S3 and S4 had decreasing CD4 counts during the study period. S1 had fluctuating CD4 counts. [McNearney et al.(1992)]. GenBank accession numbers L03430–L03453 and L23575–L23588 = S1; L03454–L03477 and L23618–L23633 = S2; L03478–L03490 and L23589–L23600 = S3; L03491–L03515 and L23601–L23617 = S4.

173) **US10.ID:** These three consensus sequences are from sets of sequences used in a study on the dynamics of HIV sequence changes in vivo and the utility of heteroduplex analysis. All sequences were derived from PCR amplified PBMC DNA. The MA145 consensus represents sequences (GenBank accession numbers U00821, U00822, U00831–U00839) taken from an asymptomatic male from Massachusetts over a period of 4.5 years starting April 1989. Patient MA, from the US, was infected in 1984 or 1985, and had been experiencing neurological disorders prior to 1989 [Kusumi et al.(1992)]. The SFBI and SFPE consensuses represent sequences (Accession numbers U13373–U13380 and U13381–U13388 respectively) taken from two patients with AIDS from San Francisco. [Delwart et al.(1994)]. Other sequences from patient MA can be found in database entries with accession numbers U00804–U00822,

U00831– U00850, U00873–U00888, M79342–M79354 and M90025–M90046. Other SFBI sequences can be found in U13240–U13252. See also NL7.ID.

174) **US11.ID:** These four consensus and seven individual sequences came from patients early in infection, before, or around the time of seroconversion. Sequences for 306, 419, 349, and 074 are consensus sequences. [Shpaer et al.(1994)] and [Delwart et al.(1995)]. Accession numbers U23664–U23666, U23668, U23669, U23671–U23708, L20381. See also B_NL8.ID.

175) **US12.ID:** These six sequenses were used in an investigation into the transmission of HIV-1 from one child (CHA), who had received zidovudine, to another child (CHB), who harbored a zidovudine-resistant strain. The presence of the zidovudine-resistant strain in child A and B, and the lack of such a strain in child 2's mother was used to show that child B was infected by child A and not by child B's mother. LC sequences are from children used as local controls. All sequences were derived from PCR amplified PBMC DNA. [Fitzgibbon et al.(1993)]. Accession numbers L12751–L12756, L19695, L19697, S66942. L12756 is listed as "isolate 100" in the databases, but seems to be the "group B consensus sequence" used for phylogenetic analysis.

176) **US13.ID:** These three consensus sequences are from three IV drug users in Florida. Proviral DNA sequences were obtained from blood, cerebrospinal fluid and dorsal root ganglia from each of the three individuals. Sequences for V1-V5 of env, were PCR amplified, cloned and sequenced. [Shapshak et al.(1995)]. [Xin et al.(1995b)]. The sequence for patient 149 is a consensus of all 24 clones in Accession numbers U16094–U16117. The sequence for 141 is a consensus of database entries labelled as being from patient 141 with the exception of: R5D, R6D, R7D, R2D and R4D, which were similar to IIIB strains of HIV-1; and R1R, R3R, R7R, R8R and R9R, which were similar to samples from patient 144. The sequence for 144 is a consensus of database entries labelled as being from patient 144 with the exception of: R3R, R6R, R9R, R12R, R13R and L1D, which were similar to IIIB strains of HIV-1; and C3D, C4D, C7D, C8D and C10D, which were similar to samples from patient 141. While infection of each individual with multiple strains of HIV (including one very similar to the IIIB lab strain) is a possible explanation of these findings, we are only including one consensus sequence from each patient for this alignment. The authors are currently (1996) resequencing new samples from these patients. Accession numbers for patients 141 and 144 are U16032–U16093, U25191–U25261.

177) **US14.ID:** These four sequences are from DNA from PBMC. [Mascola et al.(1994)]. Accession numbers L14573–L14576. See also B_TH2, E_TH2.

178) **US15.ID:** These six consensus sequences are from a study of infants. Blood samples were collected from six infants over time. [Strunnikova et al.(1995)]. Accession numbers U22682–U22810, U22834 and U22835.

179) **US16.ID:** These two consensus sequences were used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. Both sets of sequences were from PCR amplified DNA from peripheral blood leukocytes. Patient ARTC1 was an asymptomatic individual from New York and ARTC3 was an AIDS patient from New York. [Pestano et al.(1995)]. Accession numbers U11586–U11594. See also A_UG1.964, C_UG1.45, and D_UG7.ID.

180) **US17.ID:** CB7 is one sequence from a set of 12 clones from two different samples (six clones each) from the same patient, collected in 1988 and 1990, plus two more clones as yet unpublished. The patient seroconverted in 1985. The patient did not receive any antiviral therapy until 1992. The patients CD4 count was 1035 in 1988 and 807 in 1990. The patient's PBMS were cocultured with donor PBMC for an unspecified length of time before cultured DNA was isolated and PCR amplified. Individual clones of PCR product were then sequenced. [Wang et al.(1995)]. Accession numbers U16324–U16335 and U19706–U19711. The other 8 sequences are individual clones from 8 different patients, all from the same clinic in Boston, MA. Individual CB7 was again included in this study, [Wang et al.(1996a)] [Wang et al.(1996b)]. Accession numbers U60152–U60162 and U27658–U27669.

181) **US18.ID:** These 22 sequence are from a study of a HIV-1 infected dentist and many of his HIV-1 infected patients. In this case, no evidence was found for dentist to patient, patient to dentist, or patient to patient transmission. [Jaffe et al.(1994)]. Accession numbers U11454–U11490. Unfortunately the dentist sequences were not submitted to the databases.

182) **US19.ID:** These two sequences are from a comparison of a mother who transmitted HIV to her infant and a mother who did not. One of the sequences (nontransmitter-283 accession number U07839) was 99.4% identical to the LAI strain of HIV-1 and is not included here. Sequences from the transmitter and

nontransmitter were highly similar with the exception of sequence nontransmitter-217 (U07836). Thus a consensus of the similar sequences is included here as VA1-consensus, and the nontransmitter-217 outlier is presented separately as VA2. [Ayyavoo et al.(1996)]. Accession numbers U07833–U07841 and U07891–U07917.

183) **US20.ID:** These three sequences are from a study of mother-infant transmission. Only child consensus sequences are used here, but mother and child clonal sequences are reported in [Roth et al.(1996)]. Proviral DNA was PCR amplified from uncultured patient PBMCs. Cloned PCR products were sequenced. Child 1 was 27 months old, child 2 was 5 months old and child 3 was 21 months old when blood was drawn for sequencing. Sequences, including those from the mothers, are in database entries with accession numbers U47745–U47807.

184) **US21.ID:** These six sequences are from six different patients, all men from the Chicago, Illinois, USA MACS cohort. In the study, P1 & P2 were rapid progressors, P3 & P4 normal progressors, and P5 & P6 non-progressors. Their estimated years of seroconversion are as follows: P1, 1985; P2, 1985; P3, 1986; P4, 1986; P5, 1985; and P6, 1984. A total of 292 sequences of the C2-V5 region of envelope were completed. In the database entries the sample numbers are of the form Px.y-z, where x stands for the patient number, y is the number of months after the estimated date of seroconversion, and z is the clone number. Each of the six sequences presented here is a consensus of all clones from that patient. [Wolynsky et al.(1996)]. Accession numbers U35895–U36185.

185) **US22.ID:** These 12 sequences are from a study of variability of tat and env genes. Lorenzo et al (1996) Unpublished. Accession numbers U57104–U57216. Tat sequences from these clones are also available (U57217–U57304).

186) **US23.ID:** These 3 sequences are from a study of variability of vif and env genes. [Sova et al.(1995)]. Uncultured or short-term cultured PBMC proviral DNA was PCR amplified, and several clones from each PCR reaction were sequenced. Only one clone sequence from each patient is presented here. Accession numbers U50615–U50628. Vif sequences from these patients are also available (U41055, U41056, U41179–U41182 and U42229–U42282).

187) **US24.ID:** These 5 sequences are from unpublished database entries by Schwartz et al. Accession numbers U49518–U49640, U51311–U51326 and U45860–U45876.

188) **US25.RM:** This sequence is from a blood recipient M who recieved a red blood cell pack from donor W in October 1984. Blood was sampled from recipient M for this sequence in Janurary 1986, 15 months after the transmission event. Sequences from donor W (collected in January 1987, 27 months after transmission) and another recipient (O, collected in November 1986, 20 months after an RBC pack tranfusion in March 1985) are also available [Delwart et al.(1995)]. Accession numbers U22826–U22828.

189) **US26.ID:** These two sequences are from: A) a slow progressor, patient A, a 26 year old caucasian male who lost an average of 31 CD4+ cells/ml per year during the first 3 years of infection, and remains healthy; and B) a rapid progressor, patient B, a 38 year-old caucasian male who lost an average of 175 cells/ml per year during the first 3 years of infection. Both patients were infected from the same source but patient B picked up two divergent subtype B forms (one shared with patient A, and one unique to patient B). In the database entries, patient B is labelled as “14” and patient A as “13”. [Liu et al.(1997)]. Sequences were determined by PCR from uncultured PBMC DNA and RT-PCR from plasma viral RNA. PCR products were cloned prior to sequencing. One representative clone from patient A was picked for the “13A” sequence presented here, and one of the divergent B sequences was picked for the “14B” sequence presented here. Accession numbers U56146–U56235, U79034–U79113.

190) **US27.ID:** These 5 sequences are from infants infected perinatally and followed over time after birth as part of the Los Angeles Perinatal Transmission Study [Ganeshan et al.(1997)]. DNA sequences were determined from cloned PCR products from uncultured patient PBMCs.

191) **US28.ID:** These 13 sequences are from studies of long-term survivors. Patient 3799 was transfused with HIV-1 infected blood in October, 1982 at the age of 30, and has remained asymptomatic, with very low viral load and fairly stable CD4 counts for over 13 years. The donor, as well as two other recipients of his blood, have all died from complications of AIDS. The husband of 3799, as well as two children born and breastfed after the 1982 transfusion, are all HIV-negative. [Michael et al.(1995)] and [Schwartz et al.(1997)]. The other patients showed varying rates of disease progession. During the study, only 101867 (sequence not available) died of AIDS. Sequences were PCR amplified directly from patient PBMC without coculture, cloned and sequenced. Only one clone from each patient is presented here.

Accession numbers U60670–U60733. Entries with accession numbers U24443–U24487 are also from patient 3799, but not V3 region.

192) **US29.ME1:** This sequence is from a 40 year old patient in the Pittsbugh AIDS Clinical Trials Unit. [Chen et al.(1997)] descibes a new method, called "progressive amplification" for obtainining full-length infectious molecular clones of HIV. In this study, two clones were generated and the env gp120 completely sequenced. One (ME1) was from the patient when asymptomatic, and both the viral isolate (367), and the molecular clone (ME1) grew on macrophages but not T-cells (Macrophage tropic) and did not show cytopathic effect on either MT-2 or PBMCs (NSI). The other (ME46) was from an isolate (828) taken from the same patient 20 months later, when the patient had AIDS. This isolate and the clone derived from it were able to grow on both mactophages and T-cells. It induced cytopathic effect in MT-2 cells and PBMCs (SI). Accession numbers U66221, U66222. The paper also reports on sequences from "patient P" in figure 5b, but those sequences are not available.

193) **US30.ID:** These 10 sequences are from rapid and slow progressors who were studied in 1990-1994. The subjects were all asymptomatic and taking AZT (zidovudine) at the beginning of the study. Patients A, C, E, G and I were classified as slow progressors, while patients B, D, F, H and J were classified as rapid progressors. Two sequences appear to be mislabelled: U69410 labelled patient G clusters with patient E, and U69380 labelled as patient E clusters with patient G. Eight of the ten patient F, 1993 sequences are suspiciously similar (greater than 98% identical) to the HXB2R lab strain of LAI/IIIB. Each sequence is a single clone from one patient, although several clones from each patient at two time points are available [McDonald et al.(1997)]. Accession numbers U69282–U69481.

194) **US31.ID:** This study demonstrates the influence of three monoclonal antibodies IgG1b12, 2G12, and 2F5 to the HIV-1 envelope glycoprotein, and a tetrameric CD4-IgG molecule (Cd4-IgG2), for the ability to neutralize primary HIV-1 isolates from the genetic clades A through F and from group O. Each of the reagents broadly and potently neutralized B clade isolates [Trkola et al.(1996)]. Accession numbers are U79721, U79720, U79719.

195) **US32.ID:** These 29 subtype B sequences are from Hawaii. Patients ranged in age from 27-48. Most of them are Caucasians. Risk goups included heterosexuals and IDU's. Accession numbers AF016547–AF016579.

196) **US33.ID:** These 2 sequences are from patients (11258 and 11428) from USA who were sampled many times, with several clones sequenced at each time point Markham et al, unpublished 1999. Accession numbers AF016779 and AF016823 were used here. All 65 sequences were taken from these two patients so only 2 are included here. The complete set had accession numbers AF016760–AF016825.

197) **US34.ID:** These 4 subtype B sequences are from the USA. Unpublished by deOliveira et al.

198) **US35.ID:** These 16 sequences are from San Franscisco Men's Health Study participants who seroconverted while under observation. All patients had an envelope with subtype B. Eight percent of these individuals reported homosexual/bisexual contact, 20% were exclusively heterosexual not necessarily at risk [McCutchan et al.(1998)]. Accession numbers AF025749–AF025764.

199) **US36.SC14:** This subtype B sequence is from a recent seroconverter (SC14) from the San Franscisco Men's Health Study participants. McCutchan et al. unpublished (1998). Two sequences from this individual were hypermutated, and two were more normal. Accession numbers U90932–U90935.

200) **US37.ID:** This subtype B sequence is from a study in which peripheral blood mononuclear cells were isolated by density gradient centrifugation from 2 HIV-1 seropositive volunteers who were participating in a study of cell mediated immune responses to HIV infection [Ray et al.(1998)]. Initially neither of them had developed symptomatic HIV-1 infection, subject AA developed Herpes zoster ophthalmicus and died during the study period, subject BB(U78831) remained asymptomatic. Sequences from subject AA are not inclueded here because they were too short, the complete gp120 of subject BB was available. Accession number L78831 for BB and L78832 for AA.

201) **US38.ID:** These 2 subtype B sequences are from a study that describes a case of simultaneous transfusion of 2 HIV-1 infected units of blood into one individual [Diaz et al.(1996)]. The patient was a 54-year male with oatcell carcinoma of the lung, being treated with prednisone at the time of index transfusion. He was transfused in November 1984 with a pool of platelet concentrates, two of which were subsequently determined to have been from HIV-1 seropositive donors. Accession numbers for D1 are U43988, U43993 and U43994. Accession numbers for D2 are U43997, U44003–U44007 and U44010. The study also

includes a set of tat sequences with accession numbers U43986-U43992, U43995, U43996, U43998, U43999, U44000, U44001, U44002, U44008, U44009, U44011-U44023.

202) **US39.ID:** These 49 subtype B sequences are from vaccine clinical trials [Connor et al.(1998)]. Nine are from vaccinees who received a gp120 vaccine derived from MN. Eight are from vaccinees who received a gp120 vaccine derived from SF2. Two are from vaccinees who received placebo. The rest are from local controls who were not vaccinated. These were volunteers involved in clinical trials of MN and SF2 gp120 vaccines who became HIV-infected after vaccination. Accession numbers for the entire set are U84792–U84887.

203) **US40.ID:** These 20 subtype B sequences are the result of study done from 1992-1994 in which a few newly infected HIV-1 patients who resided in South Bronx New York were studied [Irwin et al.(1997)]. Out of these sequences 2 were subtype A and 20 were subtype B. Accession numbers U90181–U90200.

204) **US41.ID:** These 5 sequences are from a study that included 106 sequences with accession numbers U96502-U96608. Only one clone from each patient is included here. One gag sequence with accession number Z97081, is also presented in this study [Delwart et al.(1998)]. Semen and blood specimens were obtained from patients at Stanford University Medical Center. Patient JO and PE were infected for unknown length of time and each had clinical AIDS at the time of sampling. The PE sample patient died within one year of sampling while patient JO was asymptomatic on combination retroviral therapy 6 years after sampling and had a few kaposi's sarcoma lesions. Patients 613, 064 and MA were all asymptomatic and were infected for 11yrs, 5yrs and 6yrs respectively prior to sampling. Accession numbers U96502, U96523, U96546, U96571 and U96579.

205) **UY1.ID:** These 9 sequences are from 22-37 year old patients with CDC stage IV disease (except 726 at stage III). All are from Montevideo Uruguay. Four were homosexuals (270 352, 093 and 672), two were IV drug users (406 and 726), and the other 3 were heterosexuals (1699, 1193 and 376) [D. et al.(1996)]. Accession numbers U66414–U66422.

206) **VE.ID:** These 8 sequences are from 8 individuals in Venezuela. Patient PBMCs were cocultured with donor PBMCs. Proviral DNA was harvested PCR-amplified. PCR products were directly sequenced. Nearly complete env gp120 sequences were determined, as well as pol gene sequences. [Quinones-Mateu et al.(1995)]. Accession numbers U16764–U16778, even numbers are env, odd numbers are pol.

207) **VN1.HCM9:** This sequence is from South Vietnam. [Menu et al.(1996)]. The sequence is from Ho Chi Minh city, from a woman infected by her HIV seropositive sexual partner who was thought to have been infected while traveling in Europe. Three other sequences in this study were found to be subtype E. Accession number U29209.

208) **ZA.0117:** This sequence is from a study of 72 seropositive women from South Africa [Moodley et al.(1998)]. The mean age was 26 years. Patient 0117 was asymptomatic. Data from this study shows the dramatic growth of HIV-1 subtype-C in this population in South Africa. See also C_ZA3.ID# and A_ZA.134. Accession number AF053279.

209) **ZA1.ID:** These 7 sequences are from 7 individuals in South Africa. ZA504 was from a 33 year old white male homosexual with AIDS and the virus was syncytium-inducing (SI). ZA508 was from a 32 year old white male bisexual with ARC and the virus was NSI. ZA509 was from a 30 year old white male homosexual with AIDS and the virus was SI. ZA524 was from a 49 year old white male bisexual with AIDS and the virus was NSI. ZA510 was from a 29 year old white male heterosexual with ARC and the virus was SI. ZA512 was from a 26 year old white male homosexual with ARC and the virus was SI. ZA513 was from a 3 year old black male blood transfusion recipient with AIDS and the virus was SI. All samples were collected at the Tygerberg Hospital in the Western Cape region of South Africa between 1984 and 1992. DNA was harvested from cocultured PBMCs and the env gene was PCR amplified and cloned into pBSKS+ for sequencing. Each sequence is from a single cloned PCR product. [Engelbrecht et al.(1995)]. Accession numbers L48063–L48066, L48069, L48071 and L48073. Database entries U33770 and U33774–U33779 are shorter env gene fragments from these same clones.

C Subtype

At this time there are viral sequences from 339 HIV-1 infected individuals associated with HIV-1 subtype C. The C subtype consensus sequence (C_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

1) **BR.91c:** This subtype C sequence is from Brazil. This study describes a case of horizontal (heterosexual) and subsequent vertical (mother to infant) transmission of 2 HIV-1 subtypes, B and C [Janini et al.(1998)]. DNA sequence analysis of pol. gag and env genes confirmed the presence o subtypes B and C in 3 family members. Accession numbers for env, gag and pol genes of both subtypes are U83689–U83699. Subtype C env accessions are U83690, U83692 and U83694.
2) **BR.W2BR025:** This sequence is part of a gp160 sequence from an asymptomatic individual from Brazil, sampled in 1992. A clone was derived from an expanded viral culture, expressed and sequenced. This sequence was provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences from this patient can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are: [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession number U15121. This sequence is from a 23 year old male hemophilia patient from Porto Alegre, Brazil. He had seroconverted more than 1.2 months prior to the date this blood sample was collected in 1992. He was asymptomatic, and had not taken any anti-retroviral therapy prior to sampling. The HIV isolate exhibited an NSI phenotype, when assayed by the WHO [Gao et al.(1996a)]. 92BR025 is similar to another WHO sample; 91BR015. Accession number U52953. Entries with accession numbers U08720, U08785, U09126, U09132 and U09133 are also from W2BR025.
3) **BR1.HSP203** Although this sequence is listed as unpublished in the database, it seems to be an extension of work published in [Morgado et al.(1994)], [Sabino et al.(1994c)] and [Sabino et al.(1996)]. It is from San Paulo, Brazil. Accession number U31585.
4) **BR2.91BR015:** This sequence is from Brazil. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. 91BR015 is similar to another WHO sample; 92BR025. [Penny et al.(1996)]. Accession numbers U39234 and U39238.
5) **BI1.ID:** These eight sequences are from Burundi. They are part of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. 91BU009 groups with subtype D in a neighbor- joining tree of the V3 region and is presented as an undetermined subtype in the section of the compendium. [Penny et al.(1996)]. Accession numbers U39252 and U39233, 91BU001; U39248 and U39237, 91BU002; U39239 and U39242, 91BU003; U39241 and U39243, 91BU004; U39240 and U39257, 91BU005; U39244 and U39246, 91BU006; U39245, U39247 and U39249, 91BU007; U39250 and U39251, 91BU008; U39253 and U39254, 91BU009 is subtype CD recombinant.
6) **BY1.ID:** These 3 sequences are from Byelorussia. [Lukashov et al.(1995)]. Accession numbers: L38410, BLR9A; L38409, BLR8A; L38408, BLR5A.
7) **CM11.ID:** These 2 sequences are from 1994-1995 samples from 211 Cameroonian AIDS patients [Takehisa et al.(1998)]. Of the 43 HIV isolates sequenced, 17 were subtype A, 1 was subtype B, 2 were subtype C and 1 was subtype G. Accession numbers AF023082, AF023084.
8) **CY.HO021:** This is a sequence from a 51 year old woman whose husband had died of AIDS. She was born and lived in Zambia, before moving to Cyprus. She was asymptomatic, with a CD4 count of 200, and she had been seropositive for at least 6 years. This sample, like others in this study (see also subtypes A, B, F and I) was collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. DNA was extracted from patient PBMCs and PCR amplified. After a second round of PCR, products were cloned and sequenced. Two clones from patient 02 were sequenced. [Kostrikis et al.(1995)]. Accession numbers U28321 and U28661.
9) **DJ1.DJ-ID:** These two sequences from Djibouti were from a a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral

isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22940 and L23065.

10) **ET2.ID:** These nine sequences of Ethiopian isolates were part of a cohort considered to be heterosexually infected. PBMC DNA was PCR amplified and directly sequenced. [Salminen et al.(1996)]. For patient 2220, who had slim disease and AIDS, almost full length HIV-1 genome was PCR amplified from PBMC DNA and cloned. Proviral DNA from others in the cohort was PCR amplified and directly sequenced. Other regions of the genome are available for these isolates as well. [Salminen et al.(1996)]. Accession numbers U45481–U45502 (V3 region), U15060–U15066 and U45503–U45504 (LTR NF-kB/NRE regions), M64001–M64009 (gag p7 region), M64015–M64018 (env gp41 region) and U46016 (C2220 complete genome).
11) **ET3.ID:** These 93 sequences are from a study that describes the distribution of HIV-1 subtypes in Ethiopia. HIV-1 RNA was collected from sera (from a majority of asymptomatic individuals) and a 284bp fragment covering the V3 region was amplifed by RT-PCR and directly sequenced. All sequences were subtype C except for one subtype A [Abebe et al.(1997)]. Accession numbers U88727–U88755, U88757–U88821.
12) **FR1.ID:** These 14 sequences are from members of the French military who are believed to have been infected while deployed outside of France (Djibouti). An additional sequence (FRMP040, U58787) was listed as subtype C in the paper, but clustered with subtype B in analysis done at the HIV Database and it has been listed as subtype unclassified until more information is available. Other sequences from this study were subtypes A, B, E, and F. [Lasky et al.(1997)]. Accession numbers for subtype C were U58785, U58786, U58788–U58799.
13) **FR2.ID:** This subtype C sequence is from a study that was done to assess the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in France were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession number Z95464.
14) **GA1.ID:** These 2 sequences are from Gabon. G134 is from a 1988 or 1989 sample from a patient with AIDS living in Franceville, Gabon. LBV105 is from a 1988 sample from an asymptomatic individual sampled from the general population of Libreville. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession numbers X90912, G134; X90913, LBV105. See also subtypes A, D, F, G and O sequences from this same study.
15) **GB1.00513:** This sequence is from the British isolate 93–00513. [Arnold et al.(1995c)]. Accession number U21099.
16) **IN1.D-ID:** These four sequences are from samples from high risk patients in India, PCR clones, DNA, PBMC culture. [Dietrich et al.(1993)]. Accession numbers L07651 and L07653–L07655; X65638–X65640 and X68406.
17) **IN2.D-ID:** These five sequences are from samples from high risk patients in India, primarily stage I. They were nested PCR amplified from DNA obtained from uncultured PBMC from patients serologically defined as HIV-1/HIV-2 mixed infections. [Grez et al.(1994)]. Accession numbers U07098 and U07100–U07103.
18) **IN3.ID:** These 8 sequences sequence were isolated from Pune and New Delhi, India. All 8 sequences were from heterosexually infected patients from New Delhi, or Pune, India. DNA was isolated from cocultured PBMCs after one week of culture. PCR product was cloned and a single clone was sequenced. [Tripathy et al.(1996)]. Accession numbers U29179, U29694–U29698, U31362 and U31363. See also B_IN.IND9.
19) **IN4.ID:** These 24 sequences are from 1992 dried blood spot samples from Vellore near Madras, in Tamil Nadu state in southern India. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. Samples came from previously identified HIV seropositive STD patients (1, 3, 5, 6, 7, 11, 12, 13, 19, 20, 23, 29, 33), spouses of infected men (2, 4, 10, 16, 22, 26, 27), female prostitutes (36, 37) or bisexual men (8, 32). Two homosexual men from the same region had subtype A HIV-1 (see A_IN1.9 and 14). [Cassol et al.(1996)]. Accession numbers U53278–U53285, U53287–U53290, U53292–U53303.
20) **IN5.ID:** These 7 sequences are from India. Another sequence from this publication was subtype A (see A_IN2). [Tsuchie et al.(1993)]. Accession numbers D13420–D13424, D13426, D13427.

21) **KE.NA113:** This sequence was derived from a patient who was part of a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from the patient were sequenced. Seven other patients from this study had viral subtypes A and D. [Zachar et al.(1996a)]. Accession number U33762.
22) **LB.LE15:** This subtype C sequence is from a study of 25 sequences from a study of multiple HIV-1 subtypes in Lebanon [Pieniazek et al.(1998)]. Of the 26 samples, 25 were classified as HIV-1: 10 were subtype B, 10 were subtype A, 1 was subtype C, 1 was subtype D and 3 were recombinant or untyped. The other sample was classified as HIV-2 subtype B. Accession number AF025697 is HIV-1 subtype C.
23) **MW.SM750:** This sequence is from cloned PCR amplified cocultured PBMC DNA. SM750 was a black male sampled in the gold mines in Malawi in 1989. [Becker et al.(1995)]. Accession number U06719.
24) **MW1.ID:** These 13 sequences are from pregnant women with risk factors from Malawi. PCR-direct, peripheral blood DNA. [Orloff et al.(1993)]. Accession numbers L07427–L07441, L15721–L15735.
25) **MW2.D-ID:** These two sequences are from individuals from Malawi, generated as part of the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. The C2V3 was excised from full gp160 sequences, derived from clones from expanded culture stocks. The sequence ID numbers are abbreviated, for example D3MA959 can be read as DAIDS sequence (D), isolated in 1993 (3), Malawi (MA), patient 301959 (959). Accession numbers U08453–U08454.
26) **MY.ID:** These 2 sequences are from IV drug using prisoners in a prison in Kuala Lumpur, Malaysia. PCR products amplified from uncultured PBMCs were directly sequenced. Both of these prisoners had received medical treatment in India which included blood transfusion and organ transplants, and it is likely that they were infected in India. [Brown et al.(1996)]. This report also included subtypes B and E in Malaysia. Accession numbers U65549–U65550.
27) **MZ1.ID:** These 7 subtype C sequences are from a study of seven heterosexual patients residing in Maputo, Mozambique [Engelbrecht et al.(1998)]. Blood was obtained in June 1996. Envelope V3 region was directly PCR amplified from uncultured PBMCs. The 300 bp PCR product was directly sequenced. Accession numbers AF045628–AF045634.
28) **NL1.ID:** These 2 sequences are from a Dutch woman whose partner was a recent immigrant to The Netherlands from Democratic Republic of Congo (formerly Zaire), and from a recent immigrant to The Netherlands from either Zambia or Democratic Republic of Congo (formerly Zaire). The first two letters of the ID represent the two letter country code for the previous residence of the patient (UN = unknown). The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. The sequence from the Dutch/Democratic Republic of Congo (formerly Zaire) patient is not unequivocably a sub sequence, it may be subtype A or unclassifiable. [Lukashov et al.(1996)]. Accession numbers L76908, NL9402418; L76898, UN9305091.
29) **NO1.ID:** These 4 sequences are from Norwegian patients who were part of the Oslo HIV cohort study [Engelstad(1996)]. Uncultured PBMC DNA was PCR amplified in two nested PCR reaction steps. PCR products were directly sequenced. Where two peaks of equal height were observed at a single position, IUPAC ambiguity codes were used. Health, sex, year of sample (1989-1992), and risk group (IVDU, Het, Homo, Hemo) for each patient were noted in a table in the publication. The four subtype C sequences were all from heterosexuals who had sex with persons from Zambia (3) or South Africa (1). Thirty-six subtype B sequences were also part of this set (see B_NO1.ID:). Accession numbers X92913, X92914, X92917 and X92918.
30) **NZ1.ID:** These 2 subtype C sequences are from New Zealand. Out the ten strains sequenced, 8 were subtype B and 2 were subtype C [Dwyer et al.(1998)]. Accession numbers AF052630, AF052631. Both NZ3 and NZ7 were females infected heterosexually by partners who had previously lived in Africa.
31) **RU.ID:** These 4 sequences are from Russia. [Lukashov et al.(1995)]. Accession numbers: L38418, RUS20A; L38404, RUS2A; L38406, RUS1A; L38414, RUS13A.
32) **RU1.YAN4:** This sequence is from Russia. Bobkov et al. 1996 Unpublished. Accession number U33109.
33) **RW1.ID:** These two sequences are consensus sequences of many clones from mothers infected in Rwanda. Mulder-Kampinga et al., Unpublished (1996) and [Kampinga et al.(1997)]. Mother 566 was apparently dually infected with HIV-1 subtypes A and C. See also A_RW4.ID. Accession numbers for mother 566

are Z76183, Z76188–Z76197, Z76218-Z76231, Z76284–Z76293, Z76295–Z76299, Z76301, Z76303–Z76311, Z76322–Z76342 and Z76725–Z76732; for mother 134, Z76039–Z76042 and Z76044.

34) **SE1.ID:** These 16 sequences are from a study of 270 HIV-1 infected individuals living in Sweden [Alaeus et al.(1997)]. 80 of these 270 were thought to have been infected in Africa, prior to moving to Sweden, or infected directly by someone who had just immigrated from Africa. Of these 80, 75 bloods samples were available from 33 men and 42 women, from 15 different African countries. The 16 subtype C sequences were from individuals who were thought to have been infected in Ethiopia (SE9279 U76174, SE8899 U76161 and SE7854 U76122), Eritrea (SE7410 U76128 and SE8848 U76166), Somalia (SE8879 U76169), Tanzania (SE8684 U76157, SE9085 U76173 and SE7564 U76184), Uganda (SE7159 U76117), Botswana (SE9283 U76176), Zambia (SE8056 U76120), Zimbabwe (SE8565 U76148, SE8337 U76114, SE9337 U76178 and SE9338 U76179), Kenya (SE8890 U76171) and Mozambique (SE6077 U76123). SE8337 and SE9337 are not included in this alignment because they are from the sex partners of SE8565 and SE9338 respectively, and aver very similar to those sequences.
35) **SE2.ID:** These 2 subtype C sequences are from a study that includes the analysis of HIV-1 strains in seven cases of mother-to-child transmission in Sweden [Contag et al.(1997)]. HIV-1 isolation from the mothers was conducted during the three trimesters, a few days after deleivery and 6 months after parturition. The children were born between June 1989 and August 1992 and were followed by virus isolation at birth and at 3, 6, 12 and 18 months of age unless circumstances called for an extra sample. Breast-feeding was denied by all of the women described. See also A_SE.H4, B_SE5.ID#, D_SE.H3 and E_SE.H1. Accession Numbers U56263-U56335.
36) **SG1.ID:** These 3 sequences are from Singapore. Other sequences in this set were subtypes A, B and E. Sethoe et al in press 1998.
37) **SN.SE364:** A Senegalese sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22944.
38) **SN.P1581:** This sequence is from a study done on individuals infected with non-B clade virus who were randomly obtained from a cohort of registered commercial sex workers in Senegal, West Africa. PBMC were seperated, cryopreserved and shipped to USA for CTL studies [Cao et al.(1997)]. Of the 14 sequences evaluated 10 were subtype A, three were subtype G and 1 was subtype C. Accession number AF020821.
39) **SO.1574:** This sequence is a consensus sequence of blood and CSF samples taken from the Somalian patient 1574, CDC classification II. [Keys et al.(1993)]. Accession numbers Z23188, Z23190–Z23191, and Z23228–Z23231.
40) **SO.SM145:** A Somalian sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22946.
41) **TW.252** This sequence is one of a set of sequences from Taiwan. Other sequences in the set were subtypes B, E, F or G. [Chang et al.(1997)]. Accession number U73055.
42) **TZ1.1588:** This sequence is from the Mara region of rural
43) **TZ2.ID:** These 47 sequences are part of a set of 86 sequences from samples collected from symptomatic AIDS patients in December 1995 at Mbeya Referal Hospital in southwest Tanzania. Uncultured PBMC DNA was PCR amplifed and directly sequenced. Serotyping was also done on all samples to test the ability of serology to subtype these A, C, D and recombinant HIV-1 isolates [Hoelscher et al.(1997)].
44) **UG.45:** A single sequence used in a study of the impact of sequence variation on the distrinution and seroreactivity of linear antigenic epitopes. The sequence was derived from PCR amplified DNA from peripheral blood leukocytes. The patient was an asymptomatic individual from Uganda. [Pestano et al.(1995)]. Accession number U11597. See also A_UG1.964, B_US17.ID, and D_UG7.ID.
45) **UG.UG268:** A Ugandan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22948.

46) **UG1.ID:** These 3 sequences are from Uganda. Blood specimens from 1100 patients were collected in 5 districts of Uganda, out of these 739 were selected for further subtyping in env or pol regions. Subtype A and D specific probes were used to type the C2V3 region. Subsequent sequence analysis of 19 randomly selected specimens revealed subtypes D(n=16), C(n=3). Accession numbers AF016329, AF016330 and AF016331.
47) **ZA.NOF:** This sequence is from a South African individual who was part of a study of HIV-1 strains in India. This sequence was found to be closer to the Indian sequences, than are other isolates from Africa. PCR amplified DNA from PBMC cultures were sequenced. [Dietrich et al.(1993)] and [Becker et al.(1995)]. Accession numbers L07426 and U06716. See also C_IN3.ID, B_IN.IND9.
48) **ZA1.ID:** These 2 sequences are from 2 individuals in South Africa. ZA514 was from a 59 year old mixed-race male heterosexual with AIDS and the virus was NSI. ZA517 was from a 33 year old mixed-race male heterosexual with ARC and the virus was NSI. The samples were collected at the Tygerberg Hospital in the Western Cape region of South Africa between 1984 and 1992. DNA was harvested from cocultured PBMCs and the env gene was PCR amplified and cloned into pBSKS+ for sequencing. Each sequence is from a single cloned PCR product. [Engelbrecht et al.(1995)]. Accession numbers L48067–L48068. Database entries U33781 and U33782 are shorter env gene fragments from these same clones. See also B_ZA and D_ZA sequences from this same study.
49) **ZA2.ID:** These 3 sequences are from clones from PCR amplified cocultured PBMC DNA. Dlu was a black male sampled at the Tygerberg Hospital in Cape Town, South Africa in 1990. Gom was a black male sampled at the Tygerberg Hospital in Cape Town, South Africa in 1990. BooyD was a mixed-race female mother sampled at the Tygerberg Hospital in Cape Town, South Africa in 1990. A short sequence from a seropositive child of BooyD is presented in entry U07015. [Becker et al.(1995)]. Accession numbers U07237, U06717 and U06718.
50) **ZA3.ID:** These 44 subtype C sequences are from a study of gold miners from Westonaria, a district situated 50km from Johannesberg (South Africa) [Bredell et al.(1998)]. The men were 18-65 years of age and employed as migrant workers living in single-sex hostels on the mines. Serostatus at the time of employment, date of seroconversion and geographical place of infection are unknown. Samples 95ZA853BWA and 96ZA119BWA were from same patient taken 2 months apart. 19 of 43 individuals were from South Africa, 13 were from Lesotho, 5 were from Botswana and 3 each were from Swaziland and Mozambique.
51) **ZA4.ID:** These 21 subtype C sequences are from a study of 72 HIV-1 seropositive women from the KwaZulu-Natal region of South Africa [Moodley et al.(1998)]. The mean age of the women was 26 years. All but one of the women were asymptomatic with a mean CD4 count of 459 cells/ml. One patient (KZN149) had a CD4 count of 75 cells/ml and had AIDS. Data from this study shows the dramatic growth of HIV-1 subtype C in this population in South Africa. See also A_ZA.134 and B_ZA.0117. Accession numbers AF053277-AF053299.
52) **ZM1.ZAM-ID:** Two sequences from Zambia, from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22954 and L22956.
53) **ZW.2647:** This sequence is a consensus sequence taken from blood and CSF samples taken from Zimbabwe patient 2647, CDC classification II. [Keys et al.(1993)]. Accession numbers Z23196–Z23199 and Z23236–Z23239.

D Subtype

At this time there are viral sequences from 133 HIV-1 infected individuals associated with HIV-1 subtype D. The D subtype consensus sequence (D_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

1) **BI.BU009con:** This is a consensus sequence from 8 clones from a 36 year old female with CDC stage IV AIDS and pulmonary tuberculosis, from Bujumbura, Burundi. PBMCs from the patient were cocultured with donor PBMCs for 2 weeks, at which time large syncytia formed and the culture became antigen positive. The env region was then PCR amplified by nested PCR and cloned. [Ranjbar et al.(1995)] and [Ranjbar(1995)]. Accession numbers L35452–L35459.
2) **BR.RJ100** This subtype D sequence was from a male of unreported age and unknown risk group from Rio de Janeiro, Brazil. He is thought to have been recently infected at the time of sampling for this sequence in September 1996, because he was a blood donor in early 1995. The patient's CD4 count was 96 cell/ml in Septembe, 1996 and 290 cells/ml in January 1997, after antiretroviral therapy had been initiated [Morgado et al.(1998)]. Accession number AF000238. In this study of 131 HIV-infected individuals, 106 were classified as subtype B by HMA and 20 were classified as subtype F. Only this one sample was sutbype D, and it was the only one sequenced.
3) **CF.4020:** This sequence was the only D subtype from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. It is a consensus from cloned PCR products, derived from cultrued proviral DNA. [Murphy et al.(1993)]. A full gp120 sequence from this isolate was kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg, France. It is a part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system [Richalet-Secordel et al.(1994)]. The year of isolation and health status of individuals from which the viruses were isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. Sequences of clones from sample 4093 (Accession numbers L11517, L11517) which was taken from the same patient as 4020 one year later, are closely related and are not included here. Accession numbers L11472–L11473, U43138.
4) **CI.CI-13:** A single D subtype sequence from a set of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-13 was symptomatic, and serologically dually reactive for HIV-1 and HIV-2. The C2V3 region is part of a 900 bp fragment that was sequenced for each individual. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3–4 clones were sequenced, and the consensus of those clones is presented here. [Janssens et al.(1994a)]. Accession numbers X72028–X72029.
5) **CI1.ID:** These 2 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000469, AF000451.
6) **CM.CMR61D:** CMR61 is one of two D group sequences from a 23 year old female commercial sex worker from Cameroon who was found to be triple-infected with subtypes A and D, as well as O group HIV-1 [Takehisa et al.(1997b)]. The other sequence from the same patient is labelled as CMR709 and is from a separate blood sample. Accession numbers U58149, U58151, U58155.
7) **CM2.ID:** These four sequences are all from Cameroon [Takehisa et al.(1998)]. Accession numbers U70013, U70012, U70011
8) **FR1.ID:** These 9 subtype D sequences are from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in france were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession numbers Z95450, Z95466, Z95467, Z95468, Z95469, Z95470, Z95471, Z95472 and Z95473.
9) **GA1.ID:** These 2 sequences are from 1988 or 1989 samples from patients with AIDS living in Franceville Gabon. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced, [Delaporte et al.(1996)]. Accession numbers X90919, G109; X90920 G141. See also subtypes A, C, F, G and O sequences from this same study.

10) **GB1.CPHL4:** This sequence is a consensus from the British isolate 93–43424, clones 2, 6 and 35. It was referred to as 93–43424 in [Arnold et al.(1995c)] and as CPHL4 in [Arnold et al.(1995a)]. Accession numbers U21098 (clone 35) and U23121–U23122 (clones 2 and 6 respectively). CPHL4 is a female who is believed to have contracted the virus from CPHL5 through heterosexual contact, over 8 years prior to the date samples were collected for this analysis. Sequences from CPHL5 (U23123–U23125) are not included in this alignment due to this epidemiological relationship.
11) **GH.GH3:** This sequence is from Ghana. Subtypes A and an A/G recombinant were also detected in this study [Takehisa et al.(1997a)]. Accession number U67049.
12) **GH1.ID:** These 2 sequences are from Ghana. Subtypes A and G were also detected in this study [Ishikawa et al.(1996)]. Accession numbers for subtype D are U67682 and U67684.
13) **KE.NA116:** This sequence was derived from a patient who was part of a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from the patient were sequenced. Seven other patients from this study had viral subtypes A and C. [Zachar et al.(1996a)]. Accession number U33765.
14) **KE1.KEN-ID:** These three patients were part of a 1990–1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. [Janssens et al.(1994c)]. Accession numbers for subtype D sequences in this publication: U12984–U12986.
15) **KE2.ID:** These 2 sequences are part of a set of 5 subtype D sequences from Kenya. The other 3 subtype D sequences were too short to include here. Another 13 sequences from this set were found to be subtype A [Poss et al.(1997)]. Accession numbers AF004885-AF004891, AF03159-AF03161, AF004892, AF004895, AF004897-AF004899. Out of these 18 (13 A and 5 D), 12 were too short to be included (AF004885-AF004891).
16) **LB.ID:** This subtype D sequence is from a study of 25 sequences from a study of multiple HIV-1 subtypes in Lebanon [Pieniazek et al.(1998)]. Of the 26 samples, 25 were classified as HIV-1: 10 were subtype B, 10 were subtype A, 1 was subtype C, 1 was subtype D and 3 were recombinant or untyped. The other sample was classified as HIV-2 subtype B. Accession number AF025705 is HIV-1 subtype D.
17) **ML.103** This subtype D sequence is from a study that looks at the prevelance of different subtypes of HIV-1 and HIV-2 circulating in female commercial workers in Bamako, the capital city of Mali [Peeters et al.(1998)]. A total of 176 CSWs were tested and 81 were HIV infected. Of the 81, 63 were infected with HIV-1, 7 were infected with HIV-2 and 11 were dually infected with HIV-1 and HIV-2. HMA assays indicated that 80 percent of HIV-1 infections were with subtype A virus. Only 9 viruses, with ambiguous HMA results, were sequenced. Out of these 9 sequences one was subtype A, one was subtype D and 7 were subtype G. Accession number Y14362.
18) **NL.A11:** This sequence is from a Dutch study of presumed HIV-1 donor-recipient pairs. This sequence is from a recipient at the time of seroconversion; the donor was a Democratic Repulic of Congo (formerly Zaire) woman living in the Netherlands (patient A12 accession numbers M91840–M91848). The sequences from both donor and recipient were extremely similar, so only the recipient (patient A11) is shown here. This sequence is a consensus sequences of multiple clones from PCR amplified serum RNA. [Wolfs et al.(1992)]. Accession numbers M91849–M91856.
19) **NL2.ID:** These 7 sequences are from recent immigrants to The Netherlands from various countries. The first two letters of the ID represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76900, UG9307184; L76907, ZR9402261; L76892, ZR929193; L76904, UG9401525; L76895, AO9302187; L76872, ZR891183; L76876, ZR901100.
20) **RU.RUS14A** This sequence is from [Lukashov et al.(1995)]. Accession number L38415.
21) **SE.H3B** This subtype D sequence is from a study that includes the analysis of HIV-1 strains in seven cases of mother-to-child transmission in Sweden [Contag et al.(1997)]. HIV-1 isolation from the mothers was conducted during the three trimesters, a few days after deleivery and 6 months after parturition. The children were born between June 1989 and August 1992 and were followed by virus isolation at birth and at 3, 6, 12 and 18 months of age unless circumstances called for an extra sample. Breast-feeding

was denied by all of the women described. See also A_SE.H4, B_SE5.ID#, C_SE2.ID# and E_SE.H1. Accession numbers U56263–U56335.

22) **SE1.ID:** These 16 sequences are from a study of 270 HIV-1 infected individuals living in Sweden [Alaeus et al.(1997)]. 80 of these 270 were thought to have been infected in Africa, prior to moving to Sweden, or infected directly by someone who had just immigrated from Africa. Of these 80, 75 bloods samples were available from 33 men and 42 women, from 15 different African countries. The 17 subtype D sequences were from individuals who were thought to have been infected in Democratic Republic of Congo (formerly Zaire) (SE6687 U76135 and SEu1352 U76116), Uganda (SE8681 U76156, SE8680 U76155, SE6274 U76130, SE6488 U76164, SE7565 U76124, SE7386 U76127, SE6184 U76139, SE6958 U76136, SE6339 U76129, SE8384 U76146, SE7076 U76134 and SE8603 U76153), Eritrea (SE8420 U76115 and SE8564 U76150), Kenya (SE9048 U76172 and SE9340 U76177) and Gambia (SE6095 U76163). SE6958 and SE8681 are not presented here because they are from the sex partners of SE6184 and SE8680 respectively. Accession numbers for the entire set of all subtypes are U76114-U76186 and L41176-L41179.
23) **SN.SE365:** A Senegalese sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22945.
24) **TZ1.TAN-ID:** These ten sequences are from a set of 14 Tanzanian samples from symptomatic individuals, using serum samples taken in 1988 to generate PCR clones from viral RNA for sequencing. [Zwart et al.(1993)]. Accession numbers L01298–L01339.
25) **TZ2.ID:** These eight sequences were from patients at a clinic in Dar es Salaam, Tanzania. The individuals from which the virus was cultured showed clinical signs of AIDS, and the year of viral isolation was 1988. Viral cDNA was PCR amplified from donor PBMC, and one cloned PCR product per donor was sequenced. [Siwka et al.(1994)]. Accession numbers U12406, U12407, U12410–U12415.
26) **TZ3.ID:** These 4 sequences are from the Mara region of rural northwest Tanzania. [Robbins et al.(1996)]. Subtype A was also found in this study. Accession numbers U61875 and U61879–U61881.
27) **TZ4.ID:** These 13 sequences are part of a set of 86 sequences from samples collected from symptomatic AIDS patients in December 1995 at Mbeya Referal Hospital in southwest Tanzania. Uncultured PBMC DNA was PCR amplifed and directly sequenced. Serotyping was also done on all samples to test the ability of serology to subtype these A, C, D and recombinant HIV-1 isolates [Hoelscher et al.(1997)].
28) **UG.U44342:** This sequence is from a Ugandan. Consensus of PCR-clones, peripheral blood DNA. Intact env sequences are available from this sample. [Bruce et al.(1993)]. Accession numbers M98408–M98416 and duplicate entries with accession numbers Z19524–Z19531, Z19533.
29) **UG.UG23:** This sequence is from blood collected from the Mulago Teaching Hospital in Kampala, Uganda. Viral RNA was harvested after 10-14 days of coculture with donor PBMCs and reverse-transcribed with AMV-RT. The env V3 region was PCR amplifed and cloned. This sequence is from an individual clone. [Atkin et al.(1993)], [Pestano et al.(1993)]. Accession number M98504.
30) **UG1.W2UG-ID:** Twelve sequences from asymptomatic individuals from Uganda in 1992. Each sequence is a consensus from cloned PCR products derived from cell-cultured proviral DNA or culture supernatant RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994c)]. Accession numbers U08721–U08741, U08786–U08787, U08803–U08809, U08821–U08824, U27399, U43386. A sequence not reported to be related to these Ugandan isolates is suspected to represent lab contamination of PCR reactions with one of these isolates: U58827 (FRMP153) is 99% identical to 92UG046.
31) **UG2.ID:** These twelve sequences are from 1986–1987 Ugandan samples. Each sequence is a consensus from cloned PCR products derived from uncultured proviral DNA harvested directly from patient PBMCs. [Oram et al.(1991)]. No database entries exist for these sequences.
32) **UG3.ID:** These 11 sequences are part of a set of sequences derived from 22 Ugandans who were attending an AIDS clinic. Blood samples were obtained in 1990. Each sequence is a consensus from cloned PCR products derived from uncultured proviral DNA harvested directly from patient

PBMCs. [Albert et al.(1992)]. Accession numbers L00614–L00618, L00733–L00737, M98894–M98899, M98901, M98906–M98907, M98911–M98913, M98918, M98920–M98923, M98929–M98937, M98942–M98945 and M98967–M98975.

33) **UG4.ID:** One to 4 clones of each these Ugandan isolates were sequenced, but only one clone is shown here. [Douglas et al.(1996)]. Other Ugandan isolates sequenced in this study were subtype D/A recombinant. London subtype B clones were also reported. Complete envelope gp160 sequences were reported for all isolates. Accession numbers U36867, U36868, U36871, U36884–U36887.
34) **UG5.UG-ID:** Three Ugandan sequences from a set of HIV-1 viral isolates from Africa. Health status of the individuals from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22947 and L22949–L22950.
35) **UG6.ID:** Three Ugandan sequences from a set of HIV-1 viral isolates from Africa. All three individuals from which the virus was cultured had AIDS, and the year of viral isolation was 1987. Viruses were cultured with HUT-78 cells for an unspecified length of time. The V3 region of env (gp160) was amplified, cloned and sequenced. [von Brunn et al.(1995)]. Accession numbers U15005, U15006 and U15007.
36) **UG7.ID:** These sequences were used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. Both sets of sequences were from PCR amplified DNA from peripheral blood leukocytes. All patients were asyptomatic individuals reporting for regular blood drawing at the Nakasero blood transfusion service, Kampala, Uganda. [Pestano et al.(1995)]. Accession numbers U11595, U11596, and U11598. See also A_UG1.964, C_UG1.45, and D_UG7.ID.
37) **UG8.:** These 2 sequences are from Gulu, northern Uganda. They are from direct sequence of PCR product amplified from uncultured PBMCs. Blood samples were drawn from 217 pregnant women attending the clinic in Gulu, northern Uganda. Ages ranged from 17 to 37 years. The 29 seropositive women (13.4%) were all asymptomatic. [Buonaguro et al.(1995)]. Database accession numbers U44881 and U44884. Eight subtype A sequences were also found in this study (see A_UG5).
38) **UG9.ID:** These 16 sequences are from Uganda. Blood specimens from 1100 patients were collected in 5 districts of Uganda, out of these 739 were selected for further subtyping in env or pol regions. Subtype A and D specific probes were used to type the C2V3 region. Subsequent sequence analysis of 19 randomly selected specimens revealed subtypes D(n=16), C(n=3). Accession numbers AF016332–AF016347.
39) **US.AMK:** This sequence comes from a student living in Alabama, who moved from Democratic Republic of Congo (formerly Zaire) to the US in 1988. Virus was isolated from the patients PBMCs; this isolate was PCR amplified, and amplification products from both gag (U08192) and env were subcloned and sequenced. His CD4 count was < 5 cells/mm3, and he was symptomatic at the time of viral isolation. [Gao et al.(1994c)] and [Gao et al.(1996a)]. AMK is also known as 93ZR001. Accession numbers U08193, U27419.
40) **ZA.ID:** These 5 sequences are from 5 individuals in South Africa. ZA500 was from a 41 year old white male homosexual with ARC and the virus was non-syncytium-inducing (NSI). ZA501 was from a 24 year old white male bisexual with AIDS and the virus was SI. ZA505 was from a 36 year old white male homosexual with AIDS and the virus was SI. ZA506 was from a 33 year old white male homosexual with AIDS and the virus was SI. ZA507 was from a 37 year old white male homosexual with AIDS and the virus was SI. All samples were collected at the Tygerberg Hospital in the Western Cape region of South Africa between 1984 and 1992. DNA was harvested from cocultured PBMCs and the env gene was PCR amplified and cloned into pBSKS+ for sequencing. Each sequence is from a single cloned PCR product. [Engelbrecht et al.(1995)]. Accession numbers L47608, L48061, L48062, L48070 and L48072. Database entries U33769, U33771–U33773 and U33780 are shorter env gene fragments from these same clones. See also B_ZA and C_ZA1 sequences from this same publication.
41) **ZR.ELI:** This sequence is from the Democratic Republic of Congo (formerly Zaire) isolate ELI. [Alizon et al.(1986)] and [Goodenow et al.(1989)]. The complete genomic sequence and an infectious clone are available. In the 1995 Compendium (pages III-45 and III-47), ELI was listed as an unlikely D/A mosaic, with only gp41 being weakly A-like. Accession numbers M27949, K03454 and X04414.
42) **ZR.JY1:** This sequence is from Democratic Republic of Congo (formerly Zaire) isolate Z-84, clone JY1. [Yourno et al.(1988)]. Accession number J03653.

43) **ZR.MAD:** This sequence is from an asymptomatic Democratic Republic of Congo (formerly Zaire) woman who was seropositive for HIV-1 by several French-approved HIV tests and and by HIV-1 western blot. The viral sequences obtained for the env V3 region and gp41 show that this isolate belongs to M-group subtype D. [Cohen et al.(1995)]. Accession number X83216. A region of gp41 is also sequenced, see X83215.
44) **ZR.MAL:** This sequence is from a non-infectious clone of the Democratic Republic of Congo (formerly Zaire) isolate MAL. [Alizon et al.(1986)]. The complete genomic sequence and an infectious clone from the isolate MAL are available. MAL is known to be recombinant between subtypes A, D and I. Accession numbers K03456 and X04415.
45) **ZR.NDK:** This sequence is from an infectious clone of the Democratic Republic of Congo (formerly Zaire) isolate NDK. The molecular clone is highly cytopathic in vitro. [Spire et al.(1989)]. The complete genomic sequence is available. Accession number M27323.
46) **ZR.Z2Z6:** This sequence is from an infectious clone of Democratic Republic of Congo (formerly Zaire) isolate Z2. Theodore T, and Buckler-White A, unpublished. The complete genomic sequence is available. Accession number M22639. See also [Srinivasan et al.(1987)]. The database entry with accession numbers K03458 and M16322, which is from the same isolate.
47) **ZR1.ID:** These four sequences are part of a set of 14 A and D sequences from women from Democratic Republic of Congo (formerly Zaire). 8 were healthy, 4 showed minor signs of illness, and 2 had AIDS. Sequences were determined by directly sequencing PCR products derived from uncultured proviral DNA harvested directly from patient PBMCs. [Potts et al.(1993a)]. Accession numbers L19623, L19627, L19631 and L19635.

E Subtype (AE)

At this time there are viral sequences from 227 HIV-1 infected individuals associated with HIV-1 subtype E. The E subtype consensus sequence (E_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors. The E subtype is called "Circulating Recombinant Form" (AE) in other sections of this database, because all E subtype env sequences are found in a mosaic form with A subtype similarities in the rest of the genome.

1) **CF.90CF402** 90CF402, previously named CAR-E 4002 or 90CR402, was obtained from a man from Bangui, Central African Republic, who had lymphadenopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. The virus was first adapted to growth in chimpanzee cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. [Gao et al.(1996b)]. The complete genome is found with Accession number U51188.
2) **CF1.ID:** These eight sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. Consensus, PCR-clones, cell culture, DNA. [Murphy et al.(1993)]. Accession numbers L11459–L11460, L11463–L11468, L11476, L11480–L11481, L11504–L11505, L11511–L11513, L11519–L11521 and U43137. Another sequence from patient 4039 is found with accession number U43112.
3) **CF2.ID:** These three sequences were kindly provided prior to publication by Dr. M.P. Kieny of Transgene, Strasbourg Cedex, France. They are part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C. Mathiot and B. You (Pasteur Inst., Bangui), grown by F. Barre-Sinoussi and A. Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D. Schmitt and M.P. Kieny. Database accession numbers U43110, U43170 and U43173.
4) **CM.CA10:** A single E subtype sequence from a set of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals, specifically, CA10 was symptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. [Nkengasong et al.(1994)]. Accession number X80439.
5) **CM.CMR10:** This sequence is from Cameroon. Takehisa et al unpublished-1997. Accession number U69991
6) **FR1.ID:** These six sequences are from members of the French military who are believed to have been infected while deployed in Cambodia between 1992 and 1995. Other sequences from this study were subtypes A, B, C, F, and unclassified. [Lasky et al.(1997)]. Accession numbers for subtype E were U58779–U58784.
7) **FR2.ID:** This subtype E sequence is from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in france were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession number Z95454.
8) **GB1.11643:** This sequence is from the British isolate 94–11643. The sequence was determined from PCR-amplified lymphocyte DNA. The gag gene from this isolate was subtype A, as is the gag gene from all subtype E virus studied to date. The patient is thought to have contracted the virus in Thailand, but currently lives in the United Kingdom. [Arnold et al.(1995c)]. Accession number U21109.
9) **GB2.ID:** These 10 subtype E sequences were obtained from a study done on 15 individuals. Eleven of the specimens were from heterosexuals, two were from injecting drug users and one was from a homosexual. Two specimens were from one woman whose risk behavior was not known, and who seemed to be dually infected with subtype B and the AE(CM240) circulating recombinant form. The specimens were collected in England from individuals whose history indicated that they had become infected in Southeast Asia, particularly Thailand [Belda98]. Accession numbers for the sequences are AJ224176-AJ224200.
10) **ID1.ID:** These 7 sequences are from a set of 14 sequences from Indonesia [Porter et al.(1997)]. Accession numbers U68189–U68194. Subtype B was also identified in 7 other samples from Indonesia in this study. PCR products were directly sequenced from either uncultured PBMC DNA or cocultured PBMC DNA.

11) **JP.JH23B:** This sequence is from a Japanese patient dually infected with HIV-1 subtypes B and E [Xin et al.(1995a)]. Accession number D67090. See also D67089, B_JP.JH23A.
12) **JP1.ID:** These three sequences are from one Japanese and two Thai individuals living in Japan, obtained by direct sequencing of PCR-amplified proviral DNA from peripheral blood mononuclear cells. [Weniger et al.(1994)]. NIH3J is from a male Japanese national. NIH2T and NIH4T are from Thai female prostitutes, living in Japan. Accession numbers L32085–L32087.
13) **JP2.Pat43:** This sequence is from a study of rapid versus slow progressors in Japan. Patient 43 was a rapid progressor infected through sexual contact in 1992 after testing negative in 1991, [Shioda et al.(1997)]. Other sequences in this study were subtype B. Accession numbers AB002975–AB002987.
14) **MM.1786:** This sequence is from a dried blood spot collected in 1992 from a Female STD patient in Myanmar. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession number U53309.
15) **MY.9214103:** This sequence is from a Thailand infant who was adopted by Malaysians, and now lives in Malaysia. PCR products amplified from uncultured PBMCs were directly sequenced. [Brown et al.(1996)]. This report also included subtypes B and C in Malaysia. Accession number U65551.
16) **NL.TH94037:** This sequence is from a recent immigrant to The Netherlands from Thailand. The blood sample was collected in 1994. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR product was directly sequenced. [Lukashov et al.(1996)]. Accession number L76911.
17) **RU1.1164con:** This is a consensus of 3 clones from a single patient RU1164 from Russia. [Bobkov et al.(1997b)]. The patient was a 21 year old asymptomatic commercial sex worker who first tested HIV positive in April, 1996. Blood was collected for this sequence in May, 1996. She reported having travelled to Singapore in 1994-1996 and having multiple sexual clients there. DNA from uncultured PBMCs was PCR amplified, cloned and sequenced. Patient RU1164 lives in Khabarovsk kray in the far eastern part of the Russian Federation. This is the first report of subtype E in Russia. Accession numbers U93607, U93608, U93609.
18) **SE.H1** This subtype E sequence is from a study that includes the analysis of HIV-1 strains in seven cases of mother-to-child transmission in Sweden [Contag et al.(1997)]. HIV-1 isolation from the mothers was conducted during the three trimesters, a few days after deleivery and 6 months after parturition. The children were born between June 1989 and August 1992 and were followed by virus isolation at birth and at 3, 6, 12 and 18 months of age unless circumstances called for an extra sample. Breast-feeding was denied by all of the women described. See also A_SE.H4, B_SE5.ID#, C_SE2.ID# and D_SE.H3. Accession Numbers U56263-U56335.
19) **SG1.ID:** These 13 sequences are from Singapore. Other sequences in this set were subtypes A, B and C. Sethoe et al in press 1998.
20) **TH.93TH253:** This sequence is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93th253 was isolated in 1993 and expanded in human PBMCs, then expanded in H9 cells, and followed by lambda cloning and sequencing. The complete genome has been sequenced. [Gao et al.(1996b)]. Accession number U51189.
21) **THC18:** This sequence is derived from an HIV-1 infected mother enrolled in Bangkok in a perinatal transmission study. Her plasma was screened for gp120 binding antibody, CD4/gp120-binding inhibition, to subtype B (MN/H9), and Thai E (SL7/SupT1) using native gp120 antigens and neutralizing antibody to subtype B and Thai E isolates. In these assays, THC18 plasma showed a pattern of antibody reactivity similar to other E sera. The genetic subtype of this HIV-1 isolate was identified by HMA. [Louisirirotchanakul et al.(1997)]. Accession number U96782.
22) **TH.CM240:** This sequence is from a 21 year old asymptomatic man from northern Thailand. The route of infection is believed to be heterosexual transmission. The blood sample was collected in 1990. The patient's PBMCs were cocultured with stimulated donor PBMCs and proviral DNA was harvested for PCR amplification and sequening of a cloned full-length genome PCR product. [Carr et al.(1996)]. The complete genome is found in the databases with accession number U54771.
23) **TH.N764:** This sequence is from a survey of IV drug using prisoners in Thailand. 12 of 13 sequences from Thai prisoners were of subtype B; N764, from patient (THP13) represents the only subtype E

sequence identified in this set, from a prisoner infected in 1989. The sequences were obtained from PCR amplified PBMC DNA. [Kalish et al.(1994)]. Accession number U15588.

24) **TH.T8178:** This sequence comes from a study of the genetic heterogeneity and epidemiological distribution of HIV1 in Thailand. The host was a female prostitute and the sequence was obtained from PCR amplified PBMC DNA. [Ou et al.(1993)]. Accession number L19239. See also B_TH.T8174.
25) **TH1.ID:** These twelve sequences are from a set of 23 individuals from Thailand. PCR-direct, peripheral blood PBMC DNA. Referred to as Thai subtype A in [Ou et al.(1992b)] and [Ou et al.(1993)]. (Published erratum appears in *Lancet* **342**:250 (1993).) Accession numbers L07443–L07445, L07447, L07448, L07450 L07457, L07458–L07464.
26) **TH2.ID:** Six of these eight sequences are from 16 isolates from HIV seropositive individuals from Thailand. Sequences were from PCR products derived from co-cultured PBMC DNA. The full length envelope gene sequences are available. [McCutchan et al.(1992)]. Please note: the "TN-ID" locus names in the database correspond to the McCutchan et al.'s "CM-ID" isolates. Accession numbers L03697–L03701 and L03703–L03704. The other two (TH238, TN240) are also from Thailand, DNA from PBMC. [Mascola et al.(1994)]. Accession numbers L14571, L14572.
27) **TH3.W2TH-ID:** Fifteen sequences from asymptomatic individuals from Thailand in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; and [Gao et al.(1994a)]. Accession numbers U08810–U08811, U08825–U08836 and U08742–U08761. The entry with accession number U09131 is also TH_W2TH022.
28) **TH4.D-ID:** These three sequences are part of a set of sequences generated for the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. They are clones from expanded culture stocks, and are excised from full gp160 sequences. The sequence ID numbers are abbreviated, for example D3TH966 can be read as DAIDS sequence (D), isolated in 1993 (3), Thai (TH), patient 301966 (966). [Gao et al.(1996a)]. Accession numbers U08456–U08458.
29) **TH5.ID:** These seventeen consensus and five individual sequences are from twenty two patients with AIDS involved in a study of genotypic and phenotypic characteristics of Thai HIV-1. Blood samples were collected between July and December 1993. All sequences were derived from PCR amplified PBMC DNA, after patient PBMCs were cocultured with virus-free donor PBMCs. CMU01, CMU03, CMU04, CMU05, CMU07, and CMU10 are NSI, the rest are SI, as determined by syncytium formation in the cocultured cells. CM = Chang Mai University Hospital. KH = Kavila Army Hospital. All subjects were males and reported past contact with commercial female sex workers, but no history of drug injection, blood transfusion or homosexual contact. [Yu et al.(1995)]. Accession numbers U25550–U25626. Longer sequences from samples KH003, KH005, KH008, CMU02, CMU08 and CMU010 were determined in 1996 [McCutchan et al.(1996a)]. Accession numbers U48264–U48269.
30) **TH6.ID:** These three sequences are E subtype sequences from Thailand. Two individuals believed to be dually infected with subtypes B and E were analyzed. It is not clear from the paper or the database entries which sequences came from individual 1 and which from 2. [Artenstein et al.(1995)]. Accession numbers U21472, U21474, U21476. See also B_TH5.ID.
31) **TH7.ID:** These two sequences are from samples collected in 1993 in Thailand. Patients 1018 and 1110 were asymptomatic. [McCutchan et al.(1996a)]. Accession numbers U48273–U48274.
32) **TH8.ID:** These two sequences were from dried blood spots collected in 1992 from a heterosexual (0289) and an IV drug user (0103). DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession numbers U53312 and U53313.
33) **TH9.ID:** These 14 sequences are from 84 IV drug users in Bangkok, Thailand, who were undergoing methadone treatment at 14 treatment clinics. Blood samples were collected between January and April, 1994. Uncultured PBMC DNA from each patient was PCR amplified, and the PCR product was directly sequenced. Of the 84 patients sampled, 69 were Thai B, one (091) was typical subtype B, and 14 were subtype E. [Kalish et al.(1995)]. Accession numbers U22542, U22548, U22553, U22557, U22561, U22567, U22575, U22604, U22609, U22611, U22612, U22617, U22624 and U22625. See also B_TH7.
34) **TH10.ID:** These sequences are from Thailand. They are part of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two clones from

each isolate were sequenced. [Penny et al.(1996)]. Accession numbers U39256 and U39260, 92TH002; U39255 and U39261, 92TH011.

35) **TH11.ID:** These 16 sequences are from northern Thailand. HIV-1 env DNA was PCR amplified from uncultured patient PBMC DNA and PCR products were cloned prior to sequencing. 2 of the patients each had 3 complete env gene clones sequenced: E11429 and A10121 accession numbers AF015916-AF015921. The others only had the V3 region sequenced. All isolates in this study were subtype E. Patients E11429 and A10121 were both sampled very close to seroconversion. A10121 was a female commercial sex worker who tested HIV antibody negative in April 1993, HIV positive in July 1993, and blood was drawn for these sequences in January, 1994. E11429 was a male military conscript who tested HIV antibody negative in May 1993, seropositive in November 1993, and blood was drawn for these sequences in January, 1994 [Yu et al.(1997)]. Accession numbers for the V3-region set are AF015612–AF015626.
36) **TH12.ID:** These 14 subtype E sequences are from a set of 95 sequences reported, of which only 26 were submitted to the databases with accession numbers U85085-U85060 [Subbarao et al.(1998)]. The samples of these sequences were collected from 215 asymptomatic HIV-1 individuals from June 1994 through January 1995 at 9 regional medical centres in northern, central and southern Thailand. Out of the 215 participants, 65 were injecting drug users and 150 reported sexual risk behaviors out of which 51 were female sex workers, 41 attended antenatal clinics, 9 had STD's, 41 men with heterosexual behavior and 8 were men who had sex with men. Out of the 215 specimens subtyped, 175 were subtype-E, 37 were subtype-B' and 2 were typical subtype-B. See also subtype B for the same study.
37) **TW1.ID:** These 3 sequences are from healthy HIV-1 carriers or AIDS patients from Taiwan [Chang et al.(1997)]. Other subtypes found in Taiwan in this study were B, C, F and G. Accession numbers U73060, U73062 and U73070.
38) **US.POC30506:** This sequence is from a U.S. serviceman who aquired an HIV-1 infection while deployed in Thailand. He was asymptomatic when the sample for this sequence was collected in 1993. [McCutchan et al.(1996a)]. Accession number U48272.
39) **UY.ID:** These four sequences are from Uruguayan servicemen who aquired HIV-1 infections while deployed as United Nations peacekeepers in Cambodia in 1993. All four were asymptomatic when samples were collected for these sequences in 1993. [McCutchan et al.(1996b)]. Accession numbers U48275–U48278.
40) **VN1.ID:** These 3 sequences are from South Vietnam. [Menu et al.(1996)]. The sequences were from IV drug users in Ho Chi Minh city and Dong Nai, and a female prostitute in Can Tho. A fourth sequence, from Ho Chi Minh city, was found to be subtype B. Accession numbers U29206-U29208.
41) **VN2.ID:** These 4 sequences are from South Viet Nam. VN1 and VN2 were from healthy 17 and 25 year old female prostitutes from Can Tho and An Giang. VN3 and VN 4 were from male IV drug users. VN3 was 43, had pruritus and splenomegaly, and was from Nha Trang. VN4 was 31, healthy and was also from Nha Trang. [Nerurkar et al.(1996)]. Accession numbers U45239, U45240, U48719 and U48720.
42) **VN3.ID:** These 19 subtype E sequences are from Vietnam. The blood samples for this study were collected in April/May and August/September 1995 from 8 HIV-1 seropositive CSW in Ho Chi Minh city, Can Tho and An Giang provinces and from 16 IDU in Ho Chi Minh city, Hanoi, Nha Trang and An Giang province. Results showed that CSW and IDU in Vietnam were genetically most similar to Subtype E strains from Cambodia.[Nerurkar et al.(1997)]. Accession numbers U90068-U90090.

NOTE:

1) While the sequences in this subtype were distinct over this region of env from the other four env subtypes, in the gag gene it is not possible to make a distinction between this subtype and subtype A. What this means is that the isolates for which both gag and env are sequenced which cluster together as the "A" subtype in gag, are very distinctive in env and are broken down into two subtypes. env "A" and env "E". This holds true for the E subtypes sequences that originated in Thailand, as well as the E subtype isolate from the Central African Republic for which gag sequence was obtained. [McCutchan et al.(1992)]; [Louwagie et al.(1993)]; and [Murphy et al.(1993)]. Complete genomes of subtype A and subtype E viruses became available in late 1996 [Gao et al.(1996b)], accession numbers U51188–U51190.

2) The relative lack of diversity in the Thai sequences in this subtype relative to the other subtypes is likely to be a consequence of the short time span of the HIV-1 subtype E epidemic in Thailand. [McCutchan et al.(1992)], and [Ou et al.(1992b)].

F Subtype

At this time there are viral sequences from 80 HIV-1 infected individuals associated with HIV-1 subtype F. The F subtype consensus sequence (F_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published.

1) **AR1.ID:** These two sequences are from direct sequencing of PCR products from uncultured PBMCs, from 1993 samples from Buenos Aires, Argentina. Patient 21280 had AIDS and reported IV drug abuse. Patient 20016 was asymptomatic and HIV risk behavior was unknown. Two other samples taken from unrelated patients in 1993 were subtypes B or B/F recombinant. [Marquina et al.(1996)]. Accession numbers U68522 and U68524.
2) **AR2.ID:** These 3 sequences are from Rosario, Argentina. A total of 24 patients from different risk groups visiting a clinic in Rosario were included in this study. Of the 14 sequences determined, 11 were found to belong to subtype B and 3 were found to belong to subtype F. DNA was extracted from whole blood and PCR amplified. PCR products were directly sequenced. Subtypes of all 24 patients were also tested by HMA. [Campodonico et al.(1996)]. Accession numbers U37032, U37033 and U37043.
3) **BR.7944:** This sequence represents a single env F subtype sequence found among 22 Brazilian outpatients with varying degrees of disease progression. It was identified by Potts et al. as the single sequence which did not cluster with North American sequences in phylogenetic analysis. Consensus, PCR clones, peripheral blood PBMC DNA. [Potts et al.(1993b)]. Accession number L19237.
4) **BR.RJI03:** An F subtype sequence from Rio de Janeiro, Brazil. 26 additional B and a B-F recombinant were also observed in this set. Year of isolation for RJI03 was 1993, from a woman of CDC clinical stage II. [Morgado et al.(1994)]. DNA was amplified directly from PBMCs of an HIV infected woman with CDC stage II disease, and the PCR product was directly sequenced. Accession number U00422. See also [Sabino et al.(1994c)] Accession number U08974.
5) **BR1.BZ-ID:** Three sequences from Brazil of the F subtype. Full length env (gp160) was amplified from proviral DNA of cultured PBMCs, cloned and sequenced. [Louwagie et al.(1994)]. Accession numbers L22082, L22084 and L22085. The gag gene of these same isolates is found in L22083, L22086 and L11751. Although shown in figure 2B of the paper as clustering with subtype F in the gag region, BZ126 (L22083) seems to be a subtype A outlier with a strong similarity to subtype C at the 3' end, and is 99% identical to A/C recombinant ZAM184. See also B_BR4.BZ-ID.
6) **BR2.HSP:** These 5 sequences are from Sao Paulo Brazil. They seem to be an extension of work published in [Morgado et al.(1994)] and [Sabino et al.(1994c)]. They are proviral DNA sequences from cloned PCR products, from unclultured PBMCs [Sabino et al.(1996)]. Accession numbers U31588, U31592–U31595.
7) **BR4.93BR02017:** This sequence is part of a set of sequences generated through the WHO Global Programme on AIDS. The virus was derived from a 52 year old asymptomatic male, from Rio de Janeiro, Brazil, whose route of infection is thought to be due to bisexual contact. The blood sample was taken in 1993. The env sequence clusters with HIV-1 subtype F sequences. The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic [Gao et al.(1996a)]. Accession number U27401.
8) **CM.CA-ID:** These sequences are 3 of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals; specifically patients CA16 and CA20 were asymptomatic and patient CA4 was symptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. The F subtype designation of these sequences is tentative. Although the F subtype sequences from Cameroon and Brazil consistently form a clade in phylogenetic analyses, the branch lengths between isolates from the two countries are typical of inter-subtype distances, and sequences from the two countries each form their own distinct clade within the F subtype (HIV database and Wouter Janssens, personal communication). [Nkengasong et al.(1994)]. Accession numbers for the subtype F sequences are X80443, X80448 and X80451.
9) **CM1.ID:** These four sequences are all from Cameroon. Takehisa et al unpublished-1997. Accession numbers U70001, U69999, U69998, U69997
10) **CY.HO44-1:** This is a single sequence from two individuals who were heterosexual partners of one another. Patient 16 was a 29 year old bisexual male who was born and lived in Democratic Republic of

Congo (formerly Zaire), before moving to Cyprus. He was symptomatic with a CD4 count of 60 and had been seropositive for at least 6 years. Patient 44 was a 32 year old heterosexual female. She was asymptomatic with a CD4 count of 1,136. These samples, like others in this study (see also subtypes A, B, C, and I) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. DNA was extracted from patient PBMCs and PCR amplified. After a second round of PCR, products were cloned and sequenced. One clone from patient 16 and one from patient 44 were sequenced. [Kostrikis et al.(1995)]. Because of the close epidemiological linkage, only the clone from patient 44 is presented here. Accession numbers U28662 (16) and U28679 (44).

11) **FR2.ID:** This subtype F sequence is from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in france were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession number Z95465.
12) **FR1.ID:** This sequence is from a member of the French military who is believed to have been infected while deployed in the Central African Republic in 1992. Other sequences from this study were subtypes A, B, C, E and unclassified. [Lasky et al.(1997)]. Accession number U58807.
13) **GA1.VI354:** This sequence is from a 1989 sample from a patient with AIDS living in Libreville, Gabon. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession number X90923. See also subtypes A, C, D, G and O sequences from this same study.
14) **NL1.ID:** These 3 sequences are from recent immigrants to The Netherlands from Brazil and Democratic Republic of Congo (formerly Zaire). The first two letters of the ID represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76899, ZR9306911; L76871, ZR890819; L76901, BR9400960.
15) **RO1.ID:** These nine sequences are from isolates from Romanian children, in different clinical stages. All isolates showed cytopathic properties in peripheral blood mononuclear cells. DNA sequences are direct sequences of PCR products amplified from co-cultured PBMCs. The patients are also known as RM(A-J). [Dumitrescu et al.(1994)]. Accession numbers L19571–L19579.
16) **RO2.ID:** These fifteen sequences are from isolates from Romanian children, infected nosocomially, and adults, infected through heterosexual transmission or transfusion. DNA sequences are direct sequences of PCR products amplified from co-cultured PBMCs. [Apetrei et al.(1997)]. Accession numbers Z83284–Z83303.
17) **RO3.RM-ID:** These 24 sequences are from isolates from orphaned Romanian children, ranging in age from 2.5 to 6 years, admitted to a clinic in Tirgu Mures, Romania. All children were referred to this clinic with serious infections and are believed to have been infected horizontally in different orphanages. Virus was isolated after coculture with donor PBMCs. Proviral DNA from cocultured PBMCs was PCR amplified and the PCR products were directly sequenced. [Holm-Hansen et al.(1995)]. Accession numbers X77964–X77987.
18) **RU1.ID:** These 3 sequences are from St. Petersburg and Armavir, Russia. Sequences were determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. [Leitner et al.(1996b)]. RU26 is believed to have been infected by RU20, so only the RU26 sequence is shown here. RU20 was infected by a woman, whose husband was infected by HIV-1 while living in Congo. RU22, RU23 and RU29 were all heterosexually infected by the same HIV-1 infected man, thus only RU22 is presented here. RU30 is believed to have been infected in 1993 while traveling in the Congo. Accession numbers U69655, U69657, U69659, U69661, U69663 and U69664.
19) **TW.3341:** This sequence is one of a set of sequences from Taiwan. Other sequences in the set were subtypes B, C, E or G. [Chang et al.(1997)]. Accession number U67765.

G Subtype

At this time there are viral sequences from 41 HIV-1 infected individuals associated with HIV-1 subtype G. The G subtype consensus sequence (G_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

1) **BJ1.ID:** These 2 sequences are from female prostitutes, born in either Ghana or Togo, who live in Benin. 43 is from directly sequenced PCR product, derived via RT-PCR from patient serum RNA. 259 is from cloned PCR product, also by RT-PCR from serum RNA. [Heyndrickx et al.(1996)]. Accession numbers U61872 and U61874. Subtype A sequences were also determined in this study.
2) **CF.4067:** This sequence was associated with the C subtype in first analysis of the C2V3 region ([Murphy et al.(1993)]), but when a full gp120 sequence became available from this isolate, and phylogenetic analysis was performed including some of the new subtype G sequences, it was more closely associated with G. The full length sequence was kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg Cedex, France. It is part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. Accession numbers L11499 and L11500, U43169.
3) **CF1.15166:** A single sequence from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. It is a consensus from PCR clones from cultured proviral DNA. [Murphy et al.(1993)]. Accession number L11525. Other sequences from this study were subtypes A, D, E and unclassified. This sequence was originally listed as subtype C in the publication, as was the 4067 isolate.
4) **CI1.ID:** These 4 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000458, AF000460, AF000463, AF000468.
5) **CM.276** This sequence is from a 1994-1995 study of 211 Cameroonian AIDS patients [Takehisa et al.(1998)]. Of the 43 HIV isolates sequenced, 17 were subtype A, 1 was subtype B, 2 were subtype C and 1 was subtype G. Accesion number AF023072.
6) **FR1.ID:** These 7 subtype G sequences are from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in france were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession numbers Z95449, Z95453, Z95457, Z95458, Z95459, Z95461 and Z95463.
7) **GA.LBV217:** A sequence from Gabon from a set of HIV-1 viral isolates from Africa. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a full length env sequence. [Janssens et al.(1994b)]. Accession number U09664.
8) **GA.VI525:** A sequence from Gabon from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1994)] and [Janssens et al.(1994b)]. Accession numbers L22953 and U09665. The same isolate was classified as subtype H in gag, [Louwagie et al.(1993)], Accession number L11792.
9) **GA1.ID:** These 2 sequences are from Gabon. G98 is from a 1988 or 1989 sample from a patient with AIDS living in Franceville, Gabon who moved there from Niger. VI526 is from a 1990 sample from an AIDS patient at the Libreville General Hospital. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession numbers X90916, G98; X90922, VI526. See also subtypes A, C, D, F and O sequences from this same study.
10) **GB1.22:** This sequence is a consensus of three clones from an infected infant in a mother-infant transmission study. The sequences were obtained via PCR from cell lysates, with sequencing of cloned PCR

products. The infant was 3 months old at the time of blood drawing, and had pneumonia. [Arnold et al.(1995b)]. Accession numbers U26304–U26306. Envelope sequences for the mother are found in database entries U26301–U26302, and gag sequences for mother and infant are in U26303 and U26307.

11) **GH3.ID:** This sequence is from Ghana. Subtypes A and D were also detected in this study [Ishikawa et al.(1996)]. Another report from Ghana [Takehisa et al.(1997a)] showed that a Ghana env subtype G isolate was A/G recombinant, with pol gene related to subtype A. Although this sequence appears to be phylogenetically related to that one, we have no pol sequence for this isolate, and thus no solid evidence of it being A/G recombinant. Accession numbers for subtype G is U67683.
12) **KP.Kr121** This sequence is from an unpublished database entry with accession number X93469.
13) **ML1.ID:** These 7 subtype G sequences are from a study that looks at the prevelance of different subtypes of HIV-1 and HIV-2 circulating in female commercial workers in Bamako, the capital city of Mali [Peeters et al.(1998)]. A total of 176 CSWs were tested and 81 were HIV infected. Of the 81, 63 were infected with HIV-1, 7 were infected with HIV-2 and 11 were dually infected with HIV-1 and HIV-2. HMA assays indicated that 80 percent of HIV-1 infections were with subtype A virus. Only 9 viruses, with ambiguous HMA results, were sequenced. Out of these 9 sequences one was subtype A, one was subtype D and 7 were subtype G. Accession numbers Y14356, Y14357, Y14358, Y14359, Y14360, Y14361 and Y14363
14) **NG1.ID:** These four sequences are G subtype sequences from Nigeria [Abimiku et al.(1994)]. JP882 and JV832 were derived from AIDS patients, and G3 and G9 from healthy women. G9 was cultured on the T cell line CEM-SS, and the other three isolates were cocultured with uninfected donor PBMCs. DNA from viral cultures was PCR amplified, cloned and sequenced. Accession numbers U13208–U13209, U13211 and U13213. Complete genomes for JV1083 (aka JV832, 92NG083) and G3 (aka 93NG003) are available in database entries U88826 and U88825, respectively.
15) **NL.127C** This consensus sequence represents sequences generated from PCR amplified plasma RNA from one of three infants in a Dutch mother/infant study. A sample was collected from the infant at 1.5 months of age. Samples were also collected from the mother before birth, at birth and after birth. Mother sequences are not included in this consensus. [Mulder-Kampinga et al.(1993)]. [Mulder-Kampinga et al.(1995)]. Infant 127 sequences are from Accession numbers Z47817–Z47832. Mother 127 sequences are from Accession numbers Z47833–Z47880. Gag gene sequences from mother/child pairs are also available in entries with accession numbers Z47903–Z47911; Z47912–Z47928; Z47929–Z47935; Z47936–Z47950. The second mother/child pair was also from the Netherlands, see B_NL.114C. The third mother/infant pair in this study was from Rwanda, see A_RW.564C.
16) **NL1.ID:** These 4 sequences are from recent immigrants to The Netherlands from Brazil and Democratic Republic of Congo (formerly Zaire). The first two letters of the ID represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76880, ZR911976; L76906, LR9401885; L76884, UM9210113; L76902, GH9401230.
17) **RU1.ID:** RU16 is from Volgograd, Russia. The sequence was determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. [Leitner et al.(1996b)]. RU16 is a 21 year old female who was infected nosocomially. The nosocomial outbreak in southern Russia began with an index case, an infant born in Elista, to a HIV-1 infected mother whose husband is believed to have been infected in the Congo. Over a period of several months in 1988-1989, over 250 patients, mostly children, were infected perenterally with contaminated needles in several hospitals [Bobkov et al.(1994a)], [Lukashov et al.(1995)], [Bobkov et al.(1997c)]. This sequence clusters with the other Russian subtype G sequences, which were also part of this nosocomial outbreak. Accession number U69653. Other sequences from this Russian outbreak can be found with accession numbers L38413, U08355–U08368, U30312, U30313, U27445, U51295. Several of these are from the WHO isolate 92RU131 (U27445), from a 3.5 year old female from Rostov-on-Don, isolated in 1992, which has been classified as G/A recombinant [Gao et al.(1996a)]. The CF.4067 sequence is more closely related to these Russian G sequences, than are some other G sequences from Russia, such as BUK3a from Uzbekistan. Other sequences, with only 105 bp of V3 loop data are available in entries with accession numbers U10701-U10859, these include a mother who is thought to have been infected by her infant during breast feeding [Bobkov et al.(1994b)].
18) **SE1.ID:** This sequence is from a study of 270 HIV-1 infected individuals living in Sweden [Alaeus et al.(1997)]. 80 of these 270 were thought to have been infected in Africa, prior to moving to Sweden,

or infected directly by someone who had just immigrated from Africa. Of these 80, 75 bloods samples were available from 33 men and 42 women, from 15 different African countries. The subtype G sequence was from an individual (SE8552 U76152) who was thought to have been infected in Uganda. Accession numbers for the entire set of all subtypes are U76114-U76186 and L41176-L41179.

19) **SN1.ID:** These 3 sequences are from a study done on individuals infected with non-B clade virus who were randomly obtained from a cohort of registered commercial sex workers in Senegal, West Africa [Cao et al.(1997)]. PBMC were seperated, cryopreserved and shipped to USA for CTL studies. Of the 14 sequences evaluated 10 were subtype A, three were subtype G and 1 was subtype C. Accession numbers AF020826, AF020830 and AF020831.
20) **TW.267:** This sequence is from directly sequenced PCR product from uncultured PBMCs from Taiwan. [Chang et al.(1997)]. Most of the Taiwanese sequences determined in this study were subtype B, but subtypes C, E and F were also found. Database accession number U73058.
21) **UG.JW3:** This single sequence of subtype G HIV-1 is from a female patient with stage IV disease and CD4 count of 20, from Uganda. The patient had recently migrated to the United Kingdom from Uganda, but contracted the HIV in Uganda. The sequence is referred to as JW3 in [Kaleebu et al.(1995)] but was previously referred to as K1, by the HIV database. It has been given the name 92UG975.10 by the World Health Organization. Accession numbers U22010, U27426.
22) **UZ1.BUK3a:** This sequence is from a 39 year old male caucasian heterosexual who lived in Uzbekistan [Bobkov et al.(1996a)]. The patient tested HIV-1 seropositive in June 1991, blood was collected for this sequence in November, 1992. He reported living in Mozambique in 1984-1985 where he was admitted to the hospital several times, but reported having no sexual relations during this time. His wife in Uzbekistan was HIV-1 seropositive in 1991 and died of AIDS in 1995. He reported having sexual relations with a woman in Uzbekistan in 1986-1987 shortly after returning from Mozambique, and this woman and her husband were both found to be HIV-1 seropositive in 1991. Patient BUK died of AIDS in November, 1993. Proviral DNA from uncultured PBMCs was PCR amplied in nested double reactions. The PCR product was cloned into pUC18 plasmid prior to sequencing. Accession numbers U33095, U33096.

H Subtype

At this time there are viral sequences from 5 HIV-1 infected individuals associated with HIV-1 subtype H. The H subtype consensus sequence (H_CONSENSUS_98) generated from these 5 sequences was based on the most common amino acid found in each position of an alignment. Both of these sequences have been published and/or have been made available for printing in the database by their authors. Eight sequences that are too short for classification are closer to H than to other subtypes. The locus names (ID's) and sources of the sequences are:

1) **CF.90CF056:** This sequence is from a 1990 blood sample from the Central African Republic. It was originally published as an unclassified subtype, [Murphy et al.(1993)], with accession number L11497. It was later classified as subtype H, [Janssens et al.(1994b)]. The complete genome was sequenced in 1997, Feng Gao unpublished 1997, and appears to be subtype H thoughout the genome, accession number AF005496. L11497 contains an 8 base-pair, frameshifting insertion, relative to AF005496, near the 3' end of its sequence, which is a third copy of an 9 bp direct repeat.
2) **CM.CA13:** A sequence from Cameroon from a set of HIV-1 viral isolates from Africa used to define the prototype G and H env sequences. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a 900 base pair sequence. [Janssens et al.(1994b)] and [Nkengasong et al.(1994)]. The H subtype association is not always clearly apparent using some sets of background sequences for comparison, and neighbor joining trees (HIV database, Wouter Janssens, personal communication), although parsimony trees confirmed the original association documented in [Janssens et al.(1994b)]. Accession numbers X80441 and U09667.
3) **RU1.MLY10:** This sequence is from Russia [Bobkov et al.(1996c)]. Patient MLY was a recipient of a 1987 blood transfusion from patient SLH. Patient SLH had a history of sexual contact with an HIV-1 seropositive student from Democratic Republic of Congo (formerly Zaire). Patient MLY gave birth to a child by caesarian section (soon after which she received the transfusion), and the child was later determined to be HIV infected, presumably via transmission during a 3-month period of breast feeding. Accession numbers: U33104 U33105, MLY; U33106 U33107 U33108, SHL.
4) **SE1.ID:** These 2 sequences are from a study of 270 HIV-1 infected individuals living in Sweden [Alaeus et al.(1997)]. 80 of these 270 were thought to have been infected in Africa, prior to moving to Sweden, or infected directly by someone who had just immigrated from Africa. Of these 80, 75 bloods samples were available from 33 men and 42 women, from 15 different African countries. The 2 subtype D sequences were from individuals who were thought to have been infected in Democratic Republic of Congo (formerly Zaire) (SE5930 U76126) and Uganda (SE8646 U76162). Accession numbers for the entire set of all subtypes are U76114-U76186 and L41176-L41179.
5) **ZR.VI557:** A sequence from Democratic Republic of Congo (formerly Zaire) from a set of HIV-1 viral isolates from Africa used to define the prototype G and H env sequences. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a 900 base pair sequence. [Janssens et al.(1994b)]. Accession number U09666.

Circulating Recombinant form AGI

At this time there are viral sequences from 4 HIV-1 infected individuals associated with HIV-1 Circulating Recombinant form AGI. The AGI consensus sequence reflects the sequencing of two clones from one individual and one clone from each of the others. Three of these sequences have been published.

1) **CY.HOcon:** This is a consensus sequence from two individuals who were heterosexual partners of one another, and former IV drug users. They had lived for several years in Athens, Greece as well as in Cyprus. These samples, like others in this study (see also subtypes A, B, C, and F) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. Patient HO31 was a 24 year old asymptomatic female known to have been HIV seropositive for at least 5 years. Patient HO32 was a 35 year old asymptomatic male, also seropositive for at least 5 years. DNA was extracted from patient PBMCs and PCR amplified. After a second round of PCR, products were cloned and sequenced. Two clones from HO32 and one from HO31 were sequenced. [Kostrikis et al.(1995)]. Accession numbers U28672, U28673 and U28685. A complete genome from HO32 is available with accession number AF049337.
2) **GR1.ID:** These two sequences are from complete genomes of viruses isolated from individuals living in Greece Nasioulas et al in press 1999. PVCH was previously described as GR11 [Nasioulas et al.(1998)]. Accession numbers have not yet (01/05/99) been assigned for the complete genomes. Accession number AF049292 is GR11. The complete genomes are included in the 1998 Compendium complete genome alignment.

J Subtype

At this time there are viral sequences from 5 HIV-1 infected individuals associated with HIV-1 subtype J. The J subtype consensus sequence (J_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published or made available to the database for printing.

1) **GM1.GM:** Three sequences from Gambia, as yet unpublished, which cluster with the two Swedish sequences by Leitner in the V3 loop region. Accession numbers U33099, U33100, U33102. Bobkov et al. 1996 unpublished. GM4 (U33099 U43105) has been published in [Bobkov et al.(1996b)] as a G/?/C recombinant in the env V1-V5 region, with the ? region covering the V3 loop. See also Gambian sequences of subtypes B and C.
2) **SE1.SE:** Two sequences from Sweden, both from patients who were recent immigrants from Democratic Republic of Congo (formerly Zaire) [Leitner et al.(1995)]. Sample 7022 was collected in December 1993 from an asymptomatic female with a CD4 count of 184. Her first known seropositive sample is from May 1990, but epidemiological investigation indicated that she was infected in Democratic Republic of Congo (formerly Zaire) between 1981 and 1986. Sample 7887 was collected in October 1994 from an asymptomatic male who had tested seronegative in Sweden in January 1993, and who had a seropositive sample in August 1994. His CD4 count was normal at 567. Both patients were heterosexual and a thorough epidemiological investigation revealed no contact or shared contacts between the two. The two sequences were 95% identical to each other over 255 bases of env and 98% identical to each other over 460 bases of gag. Accession numbers L41176 and L41177. Gag gene sequences from these same individuals are in L41178 and L41179 and complete genomes are available with accession numbers AF082394 and AF082395 which will be published by Alaeus et al. 1999 in press.

N Group

At this time there are viral sequences from just one HIV-1 infected individual associated with HIV-1 group N that have been published and/or have been made available for printing in the database by their authors. The N group consensus sequence (N_CONSENSUS_98) generated from this sequences was based on this sequence. This sequence represents a set of sequences that are extremely divergent relative to other HIV-1's. The subtypes A-H have been grouped together under the heading "M" for main group. "O" group sequences are as different from one another as are sequences from different "M" subtypes, and the N group sequence is nearly equidistant from M, O and SIV-CPZ sequences.

1) **CM.YBF30:** This sequence is from 40 year old woman with AIDS living in Cameroon [Simon et al.(1998)]. The authors report that several other patients were infected with HIV-1 that was distantly related to HIV-1 groups M and O, and they found pol gene sequences in two of these individuals which clustered with the N group, seperate from the M and O groups. The complete genome is available with accession number AJ006022.

O Group

At this time there are viral sequences from 17 HIV-1 infected individuals associated with HIV-1 group O that have been published and/or have been made available for printing in the database by their authors. The O group consensus sequence (O_CONSENSUS_98) generated from these sequences was based on the most common amino acid found in each position of the alignment; when there was no consensus in a position an "X" was used. These sequences represent a set of sequences that are extremely divergent relative to other HIV-1's. The subtypes A-H have been grouped together under the heading "M" for main. "O" sequences are as different from one another as are sequences from different "M" subtypes.

1) **CM.CA9:** This sequence is from an individual living in Cameroon. [Janssens et al.(1994d)]. No database entry is yet available. The pol gene from this isolate has Accession number X78476.
2) **CM.ANT70:** The complete viral genome has been sequenced from this viral isolate derived from a symptomatic Cameroonian, CDC stage III. [R. et al.(1990)] and [Vanden Haesevelde et al.(1994)]. Accession number M31171. LTR and partial env sequences were also presented in L20587 and L23119.
3) **CM.MVP5180:** The complete viral genome has been sequenced from an isolate derived from a Cameroonian woman, sampled in 1991; the donor died of AIDS in 1992. The viral isolate MVP-5180 was grown in several human T-cell lines and the monocytic U937 line. [Gurtler et al.(1994)]. Accession number L20571. MVP-5180 was shown to be syncytia inducing (SI) on SupT1 cells [Vallejo et al.(1998)].
4) **CM.CMR61:** This sequence is one of two O group sequences from a 23 year old female commercial sex worker from Cameroon who was found to be triple-infected with subtypes A and D, as well as O group HIV-1 [Takehisa et al.(1997b)]. Accession numbers U58152, U58153.
5) **ES.1158:** This sequence was from a 35 year old man from Spain. Two blood samples from this same man were collected in April and September 1995. The V3 region was PCR amplified from uncultured PBMCs, cloned into pGEM-5ZF and an indiviudal clone sequenced. The April sequence is shown here. The sequence from the September blood sample (681, Accession number U62617) is also available. Accession number U62618. The topism of this isolate, and more sequences from this isolate and a related one, were studied by [Vallejo et al.(1998)] with accession numbers AF009608–AF009611. ES1158 and ES1159 were able to infect SupT1 cells but did not induce syncytia.
6) **FR.CF:** These seven consensus sequences are from Cameroonian patients living in France. [Loussert-Ajaka et al.(1995)]. PBMC proviral DNA was PCR amplified and 3-6 clones from each patient were sequenced. The consensus of the 3-6 clones is presented. Accession numbers U24562–U24568. Gag gene sequences for these patients are also available with Accession numbers U24706–U24712.
7) **FR.DUR:** This sequence is as yet unpublished, by J.H.M. Cohen et al. Accession number X84327.
8) **FR.VAU:** This sequence was derived from an isolate from a French woman who died of AIDS in 1992. DNA was extracted from VAU infected PBMCs, PCR amplified, cloned, and gp160 env was sequenced. The viral isolate was highly cytopathic. [Charneau et al.(1994)]. Accession number X80020.
9) **GA1.VI686:** This sequence is from a 1992 sample from a Gabonese woman with AIDS, taken at the Libreville General Hospital in Gabon. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Janssens et al.(1994d)], [Delaporte

et al.(1996)]. Accession number X96526. The pol gene from this isolate has Accession number X78477. See also subtypes A, C, D, F and G sequences from this same study.

10) **GQ1.ID:** These 4 subtype O seuences are from a study in Equitorial Guinea that was selected as a likely region to identify HIV-1 group O infections because it borders Cameroon and includes an island just off the coast of cameroon [Hunt et al.(1997)]. Four sera were suspected to contain HIV-1 group O related viruses because of their unusual serological reactivity in selected commercial assays and western blots. PHYLIP analysis of the complete env sequences clearly indicated that they clustered with group O sequences and were closest in lineage to HIV-ANT70. Four samples were selected out of which 655Ha was from a sexually transmitted disease clinic, 341Ha was from a pregnant woman, 193Ha was from a tuberculosis patient and 267Ha was from a patient whose diagnosis was unknown.
11) **US.MD1:** This sequence is from a woman living in the USA who had emigrated from Africa [Vallejo et al.(1998)]. No other patient information was available. MD1 was not able to grow on SupT1 cells and thus did not induce syncytia. Accession numbers AF009612–AF009613.

Uncertain Classification

At this time there are viral sequences from 19 HIV-1 infected individuals that are not clearly associated with any of the HIV-1 genetic subtypes A through J. They either appeared distinct from the subtypes A-J in phylogenetic analysis, or else the subtype association was unclear, with different associations in different analyses. For some of the shorter gene fragments, subtype associations might have been established if more sequence information was available or if a different set of sequences was included in the background set used to define subtype associations. Some of these sequences may be representatives of subtypes as divergent as A-J, but only a single limited sample is yet available. Still others may represent recombinant genomes.

1) **AR.20021:** This B/F recombinant sequence is from direct sequencing of PCR product from uncultured PBMCs, from a 1993 sample from Buenos Aires, Argentina. The patient was asymptomatic and HIV risk behavior was unknown. Three other samples taken from unrelated patients in 1993 were subtypes F (2) or B (1). [Marquina et al.(1996)]. Accession number U68523.
2) **BI1.91BU009:** This C/D sequence is from Burundi. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. 91BU009 groups with subtype D in a neighbor- joining tree of the V3 region and with subtype C in other regions. [Penny et al.(1996)]. Accession numbers U39253 and U39254.
3) **BR4.93BR01904** This sequence is part of the WHO Global Programme on AIDS. The virus was derived from a twenty-year old asymptomatic male patient in Rio de Janeiro, Brazil, who presumably contracted the virus through bisexual contact. Blood sample was taken in 1993 [Gao et al.(1996a)]. This sequence appears to be a recombinant of subtypes B and F. Accession numbers U27404, U27408 and U27444. All three confirm the subtype F/B recombination in env.
4) **BR.93BR029:** This sequence is another B/F recombinant from Brazil. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. [Penny et al.(1996)]. Another env sequence from this same patient was determined by a second group. [Gao et al.(1996a)]. Accession numbers U27413, U39235, U39236 and AF005495 (complete genome). LTR sequence from this isolate is in the entry with accession number U51291.
5) **BR.RJI03** This sequence is B-F recombinant in the V3 region. DNA was amplified directly from PBMCs of an HIV infected woman with CDC stage II/A disease in August, 1992, and the PCR product was directly sequenced [Morgado et al.(1994)]. More V3 region sequences from this individual (RJ549 from April 1992) and her sexual partner (RJ548 from April 1992) were also sequenced [Sabino et al.(1994c)]. Accession numbers U00420, U08953–U08955, U08956–U08960, U08962–U08964, U10019–U10029, U08972, U08973 and U08965–U08971.
6) **CF1.ID:** These four sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. Consensus, PCR-clones, cell culture, DNA. [Murphy et al.(1993)]. Accession numbers L11482–L11483 (4040) is most likely subtype D, L11497 (4056) is most likely subtype H and Janssens et al. classified 4056 as an H subtype sequence [Janssens et al.(1994b)]., L11508–L11510 (4081) is most likely a recombinant, and L11514–L11515 (4087) is most likely subtype A. D. Schmitt provided an unpublished sequence of CF.4081, U43174.
7) **ET.ID:** This Ethiopian sequence is from a complete genome presented in three segements in the database (U92049–U92051). It has been found by the authors to be an A/C recombinant [Sherefa et al.(1998)]. Accession number U92049.
8) **DJ.DJ-ID:** These three sequences from Djibouti were from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was 1991. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Later, complete genomes were PCR amplified and cloned [Carr et al.(1998)] and determined to be AG recombinant with breakpoints similar or identical to thoise found in IbNG. DJ258 is NSI and uses the CCR5 coreceptor [Trkola et al.(1998)]. Accession numbers L22939, L22941, L23064 (env); AF063223, AF063224 (complete genomes).

9) **FR.BCB69:** This subtype A/C sequence is from a study that was done to access the reliability of heteroduplex mobility. 199 samples from patients originating from 26 countries and living in France were selected. 37 strains belonging to different subtypes were sequenced and results were found to be in concordance to HMA results [Loussert-Ajaka et al.(1998)]. Accession number Z95445.
10) **FR.BCB79** This study presents an env sequence of subtype AGH recombinant virus isolated from a woman living in Paris who moved there from the Democratic Republic of Congo (formerly Zaire). This isolate was identified as an H subtype by a heteroduplex mobility assay on V3-V5 region. The sequence of gag was an A/G recombinant (accession Y13196). Accession number Y13197.
11) **FR1.ID:** This sequence is from a member of the French military who is believed to have been infected while deployed in Djibouti in 1991. It was classified as subtype C in [Lasky et al.(1997)]. However, it has a GPGR V3 loop tip, and clusters with subtype B in phylogenetic analysis done for this section of the HIV Database Compendium. All other subtype C as of November 1997 have GPGQ at the tip of the V3 loop. Other sequences from this study were subtypes A, B, C, E, and F. [Lasky et al.(1997)]. Accession number U58787.
12) **FR.CNP1:** This sequence is from a set of 8 sequences from a report that provides molecular evidence for transmission of HIV from an HIV-infected surgeon to one of his patients [Blanchard et al.(1998)]. The orthopedic surgeon was working in a suburb of Paris, France. He probably became infected in 1983 but was not tested for HIV infection until 1994. During those 11 years he had performed 3,004 surgeries, but only one woman, born in 1925, became HIV seropositive after surgery. The sequences from both surgeon and patient are apparently recombinants between subtypes A and F. Accession numbers U85912–U85919.
13) **GA.VI191:** This sequence from Gabon was from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22952. It was identified as a G/A recombinant sequence based on Gag gene sequence in the entry with accession number L11783.
14) **GH.GH8:** This A/G recombinant sequence is from Ghana. Subtypes A and D were also detected in this study [Takehisa et al.(1997a)]. Accession number U67039.
15) **KE.K124:** A Kenyan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. This isolate is not clearly associated with D subtype; however, Louwagie and colleagues found that it associated with the D subtype in env, and the A subtype in gag. Using parsimony analysis, we found that it was difficult to determine a clear association, and this observation was confirmed by Wouter Janssens (personal communication). Accession number L22942.
16) **KE.KEN976** This is a single unclassified sequence from a set of patients who were part of a 1990–1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. [Janssens et al.(1994a)]. Accession number U12992. Although unclassified by the authors, it seems to be subtype A by our analysis.
17) **LB1.ID:** These 3 sequences are from a study of 25 sequences from a study of multiple HIV-1 subtypes in Lebanon [Pieniazek et al.(1998)]. Of the 26 samples, 25 were classified as HIV-1: 10 were subtype B, 10 were subtype A, 1 was subtype C, 1 was subtype D and 3 were recombinant or unclassified. The other sample was classified as HIV-2 subtype B. Accession numbers AF025707, AF025713 and AF025715 are HIV-1 subtypes AG, untyped and AD respectively.
18) **NG.IBNG:** An envelope gp120 sequence from Nigeria was kindly provided by Dr. Tom Howard from the University of Southern California (USC) [Howard et al.(1994)] and the complete genome has now been sequenced [Howard & Rasheed(1996)]. Originally classified as subtype A, it has more recently been shown to be a mosaic between subtypes A and G. Accession numbers U48628 and L39106. It is the prototype of a circulating recombinant form, as many AG recombinants with identical recombination breakpoints which cluster with this sequence in phylogenetic analysis have now been found in many regions of Africa.
19) **NL.RW94028:** This sequence is from a recent immigrant to The Netherlands from Rwanda. The blood sample was collected in 1994. Viral RNA was prepared from patient serum and RT-PCR was used to

amplify the V3 region of the env gene. The PCR product was directly sequenced. [Lukashov et al.(1996)]. Database accession number L76909.

20) **RW.92RW009:** This sequence is from a complete genome of a 1992 isolate from Rwanda. The env region clusters with subtype A, but overall the genome is A/C recombinant or mosaic, [Gao et al.(1994a)], [Gao et al.(1994b)], [De Wolf et al.(1994)]. Accession numbers U08793, U16220, U16221, U16222, U88823, U13441. A Gag gene is available with accession number U86545.
21) **SE.KI4803:** This sequence is from patient number 24 described in [Asjo et al.(1986)] and [Fredriksson et al.(1991)]. Several molecular clones from this patient have been extensively characterized in [Tan et al.(1993)]. Complete env gp120 sequences for 8 clones were determined in [McKeating et al.(1996)] and one of the 8 sequences (clone 13) is presented here. Accession numbers for 7 if the 8 clones (clone 32 was not submitted to the databases) are U57788–U57794. A complete genome from isolate KI4803 has reportedly been sequenced, but not yet submitted to the databases (Fenyo,EM personal communication). The patient had AIDS at the time of viral isolation in 1985. The virus exhibited rapid/high phenotype [Asjo et al.(1986)] and when gp120 from this isolate was swapped into the HXB2 genome, the ability of the chimeras to grow in various cell lines correlated with the gp120 [McKeating et al.(1996)]. Although the amino acid sequences translated from these sequence entries are clearly subtype B, the DNA sequences do not cluster with any of the HIV-1 M-group subtypes. The codon useage of these sequences is similar to the codons used for optimal high-level expression in E.coli, and it is possible that these sequences were reverse-translated from amino acid sequences. The authors have been contacted, but have not responded.
22) **TW.A2** This sequence is from Taiwan. The two other sequences in this set were subtype A. this sequence was found to be A/G recombinant, clustering with subtype G in the Gag p24 region but with subtype A in env [Lee et al.(1998)]. Patient A2 was a 56 year old female first found to be seropositive in 1991, infected via heterosexual transmission. Accession number AF02060. Gag p24 sequence is found with accession number AF020949.
23) **TZ1.MB6729:** This sequence is part of a set of 86 sequences from samples collected from symptomatic AIDS patients in December 1995 at Mbeya Referal Hospital in southwest Tanzania. Uncultured PBMC DNA was PCR amplifed and directly sequenced. Serotyping was also done on all samples to test the ability of serology to subtype these A, C, D and recombinant HIV-1 isolates [Hoelscher et al.(1997)].
24) **UG1.ID:** Two clones from each of these two D/A recombinant Ugandan isolates were sequenced, but only the sequences of 92UG035 clone 21 and C6080 clone 09 are shown here. [Douglas et al.(1996)]. The publication shows C6080 as subtype A, but analyses done at Los Alamos indicate that it is a D/A recombinant, like 92UG035. Other Ugandan isoaltes sequenced in this study were subtype D. London subtype B clones were also reported. Complete envelope gp160 sequences were reported for all isolates. Accession numbers U36865, U36866, U36881 and U36883.
25) **US.ID:** These 2 subtype A/G sequences are the result of study done from 1992-1994 in which a few newly infected HIV-1 patients who resided in South Bronx New York were studied. Out of these sequences 2 were subtype A and rest 20 were subtype B. This is the first report of a subtype A infection in an American born US resident who had not travelled outside US (patient 866). Patient 912 was born in Africa. Although classified as subtype A in [Irwin et al.(1997)], the sequences cluster with the IBNG sequence which has been shown to be a circulating recombinant form, with subtype A and subtype G regions. Accession numbers U90201, U90202.
26) **ZM.ZAM184:** This Zambian sequence is an outlier, though in some phylogenetic analysis it appears most closely associated with the A subtype. In particular it is closely associated with A_CF.SAS U43171 (100/100 replicates in parsimony analysis of gp120). Health status of the individual from which the virus was cultured was a woman from Lusaka, Zambia who participated in a clinical research study. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)], [Salminen et al.(1997)]. The Salminen paper is based on full-length gag and env genes recoverd directly from peripheral blood mononuclear cells or from primary virus cultures, using serial blood samples from a Zambian woman and a sample from her spouse. DNA sequencing and phylogenetic analysis established that two different A/C recombinant forms of HIV-1 predominated at two time points in the woman. A related but distinct recombinant HIV-1 was recovered from her spouse. Intersubtype recombination apparently played a central role in the evolution of HIV-1 in this couple and may contribute substantially to the rapid emergence of HIV-1 variants whenever mixed-subtype HIV-1 infections occur. Accession number L22955. A complete genome from this isolate is now

available with accession number U86780 and other clones from this patient and her spouse, from blood samples taken in 1989 and 1990, are found with accession numbers U86768-U86781. Recently, another AC recombinant genome from France has been reported to have the same recombination breakpoints and clusters with this sequence in phylogenetic analysis [Loussert-Ajaka et al.(1998)] accession number Z95445.

27) **ZR.Z3:** This sequence is from the 1983 Democratic Republic of Congo (formerly Zaire) isolate Z-3 (non-infectious, possibly due to frame-shift). [Willey et al.(1986)]. Accession number K03347.
28) **ZR.Z321:** This sequence is from the 1976 Democratic Republic of Congo (formerly Zaire) isolate Z321. [Srinivasan et al.(1989)]. Accession number M15896. Earlier listed as subtype A, it was subsequently shown to be recombinant between subtypes A and G [Choi et al.(1997)]. Accession numbers M15896, U76035, U50207, U50208.

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